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(54) Staphylococcus aureus polynucleotides and sequences

(57) The present invention provides polynucleotide sequences of the genome of *Staphylococcus aureus*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

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Description

The present invention relates to the field of molecular biology. In particular, it relates to, among other things, nucleotide sequences of *Staphylococcus aureus,* contigs, ORFs, fragments, probes, primers and related polynucleotides thereof, peptides and polypeptides encoded by the sequences, and uses of the polynucleotides and sequences thereof, such as in fermentation, polypeptide production, assays and pharmaceutical development, among others.

The genus *Staphylococcus* includes at least 20 distinct species. (For a review see Novick, R. P., The *Staphylococcus* as a Molecular Genetic System, Chapter 1, pgs. 1-37 in MOLECULAR BIOLOGY OF THE *STAPHYLOCOCCI,* R. Novick, Ed., VCH Publishers, New York (1990)). Species differ from one another by 80% or more, by hybridization kinetics, whereas strains within a species are at least 90% identical by the same measure.

The species *Staphylococcus aureus,* a gram-positive, facultatively aerobic, clump-forming cocci, is among the most important etiological agents of bacterial infection in humans, as discussed briefly below.

Human Health and *S. Aureus*

Staphylococcus aureus is a ubiquitous pathogen. (See, for instance, Mims *et al.,* MEDICAL MICROBIOLOGY, Mosby-Year Book Europe Limited, London, UK (1993)). It is an etiological agent of a variety of conditions, ranging in severity from mild to fatal. A few of the more common conditions caused by *S. aureus* infection are burns, cellulitis, eyelid infections, food poisoning, joint infections, neonatal conjunctivitis,osteomyelitis, skin infections, surgical wound infection, scalded skin syndrome and toxic shock syndrome, some of which are described further below.

Burns

Burn wounds generally are sterile initially. However, they generally compromise physical and immune barriers to infection, cause loss of fluid and electrolytes and result in local or general physiological dysfunction. After cooling, contact with viable bacteria results in mixed colonization at the injury site. Infection may be restricted to the non-viable debris on the burn surface ("eschar"), it may progress into full skin infection and invade viable tissue below the eschar and it may reach below the skin, enter the lymphatic and blood circulation and develop into septicaemia. *S. aureus* is among the most important pathogens typically found in burn wound infections. It can destroy granulation tissue and produce severe septicaemia.

Cellulitis

Cellulitis, an acute infection of the skin that expands from a typically superficial origin to spread below the cutaneous layer, most commonly is caused by *S. aureus* in conjunction with *S. pyrogenes.* Cellulitis can lead to systemic infection. In fact, cellulitis can be one aspect of synergistic bacterial gangrene. This condition typically is caused by a mixture of *S. aureus* and microaerophilic *streptococci.* It causes necrosis and treatment is limited to excision of the necrotic tissue. The condition often is fatal.

Eyelid infections

S. aureus is the cause of styes and of sticky eye" in neonates, among other eye infections. Typically such infections are limited to the surface of the eye, and may occasionally penetrate the surface with more severe consequences.

Food poisoning

Some strains of *S. aureus* produce one or more of five serologically distinct, heat and acid stable enterotoxins that are not destroyed by digestive process of the stomach and small intestine (enterotoxins A-E). Ingestion of the toxin, in sufficient quantities, typically results in severe vomiting, but not diarrhoea. The effect does not require viable bacteria. Although the toxins are known, their mechanism of action is not understood.

Joint infections

S. aureus infects bone joints causing diseases such osteomyelitis.

Osteomyelitis

S. aureus is the most common causative agent of haematogenous osteomyelitis. The disease tends to occur in

children and adolescents more than adults and it is associated with non-penetrating injuries to bones. Infection typically occurs in the long end of growing bone, hence its occurrence in physically immature populations. Most often, infection is localized in the vicinity of sprouting capillary loops adjacent to epiphysial growth plates in the end of long, growing bones.

Skin infections

S. aureus is the most common pathogen of such minor skin infections as abscesses and boils. Such infections often are resolved by normal host response mechanisms, but they also can develop into severe internal infections. Recurrent infections of the nasal passages plague nasal carriers of *S. aureus*.

Surgical Wound Infections

Surgical wounds often penetrate far into the body. Infection of such wound thus poses a grave risk to the patient. S. aureus is the most important causative agent of infections in surgical wounds. *S. aureus* is unusually adept at invading surgical wounds; sutured wounds can be infected by far fewer *S. aureus* cells then are necessary to cause infection in normal skin. Invasion of surgical wound can lead to severe *S. aureus* septicaemia. Invasion of the blood stream by *S. aureus* can lead to seeding and infection of internal organs, particularly heart valves and bone, causing systemic diseases, such as endocarditis and osteomyelitis.

Scalded Skin Syndrome

S. aureus is responsible for "scalded skin syndrome" (also called toxic epidermal necrosis, Ritter's disease and Lyell's disease). This diseases occurs in older children, typically in outbreaks caused by flowering of *S. aureus* strains produce exfoliation(also called scalded skin syndrome toxin). Although the bacteria initially may infect only a minor lesion, the toxin destroys intercellular connections, spreads epidermal layers and allows the infection to penetrate the outer layer of the skin, producing the desquamation that typifies the diseases. Shedding of the outer layer of skin generally reveals normal skin below, but fluid lost in the process can produce severe injury in young children if it is not treated properly.

Toxic Shock Syndrome

Toxic shock syndrome is caused by strains of *S. aureus* that produce the so-called toxic shock syndrome toxin. The disease can be caused by *S. aureus* infection at any site, but it is too often erroneously viewed exclusively as a disease solely of women who use tampons. The disease involves toxaemia and septicaemia, and can be fatal.

Nocosomial Infections

In the 1984 National Nocosomial Infection Surveillance Study ("NNIS") *S. aureus* was the most prevalent agent of surgical wound infections in many hospital services, including medicine, surgery, obstetrics, pediatrics and newborns.

Resistance to drugs of S. aureus strains

Prior to the introduction of penicillin the prognosis for patients seriously infected with *S. aureus* was unfavorable. Following the introduction of penicillin in the early 1940s even the worst *S. aureus* infections generally could be treated successfully. The emergence of penicillin-resistant strains of *S. aureus* did not take long, however. Most strains of *S. aureus* encountered in hospital infections today do not respond to penicillin; although, fortunately, this is not the case for *S. aureus* encountered in community infections.

It is well known now that penicillin-resistant strains of *S. aureus* produce a lactamase which converts penicillin to pencillinoic acid, and thereby destroys antibiotic activity. Furthermore, the lactamase gene often is propagated episomally, typically on a plasmid, and often is only one of several genes on an episomal element that, together, confer multidrug resistance.

Methicillins, introduced in the 1960s, largely overcame the problem of penicillin resistance in *S. aureus*. These compounds conserve the portions of penicillin responsible for antibiotic activity and modify or alter other portions that make penicillin a good substrate for inactivating lactamases. However, methicillin resistance has emerged in *S. aureus,* along with resistance to many other antibiotics effective against this organism, including aminoglycosides, tetracycline, chloramphenicol, macrolides and lincosamides. In fact, methicillin-resistant strains of *S. aureus* generally are multiply drug resistant.

The molecular genetics of most types of drug resistance in *S. aureus* has been elucidated (See Lyon *et al., Microbiology Reviews* 51: 88-134 (1987)). Generally, resistance is mediated by plasmids, as noted above regarding penicillin resistanc ; how ver, several stable forms of drug resistance have been observed that apparently involve integration of a resistance element into the *S. aureus* genome itself.

Thus far each new antibiotic gives rise to resistance strains, stains emerge that are resistance to multiple drugs and increasingly persistent forms of resistance begin to emerge. Drug resistance of *S. aureus* infections already poses significant treatment difficulties, which are likely to get much worse unless new therapeutic agents are developed.

Molecular Genetics *of Staphylococcus Aureus*

Despite its importance in, among other things, human disease, relatively little is known about the genome of this organism.

Most genetic studies of *S. aureus* have been carried out using the the strain NCTC8325, which contains prophages psi11 psi12 and psi13, and the UV-cured derivative of this strain, 8325-4 (also referred to as RN450), which is free of the prophages.

These studies revealed that the *S. aureus* genome, like that of other *staphylococci,* consists of one circular, covalently closed, double-stranded DNA and a collection of so-called variable accessory genetic elements, such as prophages, plasmids, transposons and the like.

Physical characterization of the genome has not been carried out in any detail. Pattee *et al.* published a low resolution and incomplete genetic and physical map of the chromosome of *S. aureus* strain NCTC 8325. (Pattee *et al.* Genetic and Physical Mapping of Chromosome of *Staphylococcus aureus* NCTC 8325, Chapter 11, pgs. 163-169 in. MOLECULAR BIOLOGY OF THE *STAPHYLOCOCCI,* R.P. Novick, Ed., VCH Publishers, New York, (1990) The genetic map largely was produced by mapping insertions of Tn551 and Tn4001, which, respectively, confer erythromycin and gentamicin resistance, and by analysis of SmaI-digested DNA by Pulsed Field Gel Electrophoresis ("PFGE").

The map was of low resolution; even estimating the physical size of the genome was difficult, according to the investigators. The size of the largest SmaI chromosome fragment, for instance, was too large for accurate sizing by PFGE. To estimate its size, additional restriction sites had to be introduced into the chromosome using a transposon containing a SmaI recognition sequence.

In sum, most physical characteristics and almost all of the genes of *Staphylococcus aureus* are unknown. Among the few genes that have been identified, most have not been physically mapped or characterized in detail. Only a very few genes of this organism have been sequenced. (See, for instance Thornsberry, J. , *Antimicrobial Chemotherapy* 21 Suppl C: 9-16 (1988), current versions of GENBANK and other nucleic acid databases, and references that relate to the genome of *S. aureus* such as those set out elsewhere herein.)

It is clear that the etiology of diseases mediated or exacerbated by *S. aureus* infection involves the programmed expression of *S. aureus* genes, and that characterizing the genes and their patterns of expression would add dramatically to our understanding of the organism and its host interactions. Knowledge of *S. aureus* genes and genomic organization would dramatically improve understanding of disease etiology and lead to improved and new ways of preventing, ameliorating, arresting and reversing diseases. Moreover, characterized genes and genomic fragments of *S. aureus* would provide reagents for, among other things, detecting, characterizing and controlling *S. aureus* infections. There is a need therefore to characterize the genome of *S. aureus* and for polynucleotides and sequences of this organism.

The present invention is based on the sequencing of fragments of the *Staphylococcus aureus* genome. The primary nucleotide sequences which were generated are provided in SEQ ID NOS: 1-5,191.

The present invention provides the nucleotide sequence of several thousand contigs of the *Staphylococcus aureus* genome, which are listed in tables below and set out in the Sequence Listing submitted herewith, and representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan. In one embodiment, the present invention is provided as contiguous strings of primary sequence information corresponding to the nucleotide sequences depicted in SEQ ID NOS:1-5,191.

The present invention further provides nucleotide sequences which are at least 95%, preferably 99% and most preferably 99.9%, identical to the nucleotide sequences of SEQ ID NOS:1-5,191.

The nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence which is at least 95%, preferably 99% and most preferably 99.9%, identical to the nucleotide sequence of SEQ ID NOS:1-5,191 may be provided in a variety of mediums to facilitate its use. In one application of this embodiment, the sequences of the present invention are recorded on computer readable media. Such media includes, but is not limited to:magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

The present invention further provides systems, particularly computer-based systems which contain the sequence

information herein described stored in a data storage means. Such systems are designed to identify commercially important fragments of the *Staphylococcus aureus* genome.

Another embodiment of the present invention is directed to fragments, preferably isolated fragments, of the *Staphylococcus aureus* genome having particular structural or functional attributes. Such fragments of the *Staphylococcus aureus* genome of the present invention include, but are not limited to, fragments which encode peptides, hereinafter referred to as open reading frames or ORFs," fragments which modulate the expression of an operably linked ORF, hereinafter referred to as expression modulating fragments or EMFs," and fragments which can be used to diagnose the presence of *Staphylococcus aureus* in a sample, hereinafter referred to as diagnostic fragments or "DFs."

Each of the ORFs in fragments of the *Staphylococcus aureus* genome disclosed in Tables 1-3, and the EMFs found 5' to the ORFs, can be used in numerous ways as polynucleotide reagents. For instance, the sequences can be used as diagnostic probes or amplification primers for detecting or determining the presence of a specific microbe in a sample, to selectively control gene expression in a host and in the production of polypeptides, such as polypeptides encoded by ORFs of the present invention, particular those polypeptides that have a pharmacological activity.

The present invention further includes recombinant constructs comprising one or more fragments of the *Staphylococcus aureus* genome of the present invention. The recombinant constructs of the present invention comprise vectors, such as a plasmid or viral vector, into which a fragment of the *Staphylococcus aureus* has been inserted.

The present invention further provides host cells containing any of the isolated fragments of the *Staphylococcus aureus* genome of the present invention. The host cells can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic cell, such as a yeast cell, or a procaryotic cell such as a bacterial cell.

The present invention is further directed to polypeptides and proteins, preferably isolated polypeptides and proteins, encoded by ORFs of the present invention. A variety of methods, well known to those of skill in the art, routinely may be utilized to obtain any of the polypeptides and proteins of the present invention. For instance, polypeptides and proteins of the present invention having relatively short, simple amino acid sequences readily can be synthesized using commercially available automated peptide synthesizers. Polypeptides and proteins of the present invention also may be purified from bacterial cells which naturally produce the protein. Yet another alternative is to purify polypeptide and proteins of the present invention can from cells which have been altered to express them.

The invention further provides polypeptides, preferably isolated polypeptides, comprising *Staphylococcus aureus* epitopes and vaccine compositions comprising such polypeptides. Also provided are methods for vacciniating an individual against *Staphylococcus aureus* infection.

The invention further provides methods of obtaining homologs of the fragments of the *Staphylococcus aureus* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. Specifically, by using the nucleotide and amino acid sequences disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

The invention further provides antibodies which selectively bind polypeptides and proteins of the present invention. Such antibodies include both monoclonal and polyclonal antibodies.

The invention further provides hybridomas which produce the above-described antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

The present invention further provides methods of identifying test samples derived from cells which express one of the ORFs of the present invention, or a homolog thereof. Such methods comprise incubating a test sample with one or more of the antibodies of the present invention, or one or more of the Dfs or antigens of the present invention, under conditions which allow a skilled artisan to determine if the sample contains the ORF or product produced therefrom.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the above-described assays.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the antibodies, antigens, or one of the DFs of the present invention; and (b) one or more other containers comprising one or more of the following:wash reagents, reagents capable of detecting presence of bound antibodies, antigens or hybridized DFs.

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents capable of binding to a polypeptide or protein encoded by one of the ORFs of the present invention. Specifically, such agents include, as further described below, antibodies, peptides, carbohydrates, pharmaceutical agents and the like. Such methods comprise steps of: (a)contacting an agent with an isolated protein encoded by one of the ORFs of the present invention; and (b)determining whether the agent binds to said protein.

The present genomic sequences of *Staphylococcus aureus* will be of great value to all laboratories working with this organism and for a variety of commercial purposes. Many fragments of the *Staphylococcus aureus* genome will be immediately identified by similarity searches against GenBank or protein databases and will be of immediate value to *Staphylococcus aureus* researchers and for immediate commercial value for the production of proteins or to control gene expression.

The methodology and technology for elucidating extensive genomic sequences of bacterial and other genomes

has and will greatly enhance the ability to analyze and understand chromosomal organization. In particular, sequenced contigs and genom s will provide the models for developing tools for the analysis of chromosome structure and function, including the ability to identify genes within large segments of genomic DNA, the structure, position, and spacing of regulatory elements, the identification of genes with potential industrial applications, and the ability to do comparative genomic and molecular phylogeny.

FIGURE 1 is a block diagram of a computer system (102) that can be used to implement computer-based systems of present invention.

FIGURE 2 is a schematic diagram depicting the data flow and computer programs used to collect, assemble, edit and annotate the contigs of the *Staphylococcus aureus* genome of the present invention. Both Macintosh and Unix platforms are used to handle the AB 373 and 377 sequence data files, largely as described in Kerlavage *et al., Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences,* 585, IEEE Computer Society Press, Washington D.C. (1993). Factura (AB) is a Macintosh program designed for automatic vector sequence removal and end-trimming of sequence files. The program Loadis runs on a Macintosh platform and parses the feature data extracted from the sequence files by Factura to the Unix based *Staphylococcus aureus* relational database. Assembly of contigs (and whole genome sequences) is accomplished by retrieving a specific set of sequence files and their associated features using extrseq, a Unix utility for retrieving sequences from an SQL database. The resulting sequence file is processed by seq_filter to trim portions of the sequences with more than 2% ambiguous nucleotides. The sequence files were assembled using TIGR Assembler, an assembly engine designed at The Institute for Genomic Research (TIGR") for rapid and accurate assembly of thousands of sequence fragments. The collection of contigs generated by the assembly step is loaded into the database with the lassie program. Identification of open reading frames (ORFs) is accomplished by processing contigs with zorf. The ORFs are searched against *S. aureus* sequences from Genbank and against all protein sequences using the BLASTN and BLASTP programs, described in Altschul *et al., J. Mol. Biol.* 215: 403-410 (1990)). Results of the ORF determination and similarity searching steps were loaded into the database. As described below, some results of the determination and the searches are set out in Tables 1-3..

The present invention is based on the sequencing of fragments of the *Staphylococcus aureus* genome and analysis of the sequences. The primary nucleotide sequences generated by sequencing the fragments are provided in SEQ ID NOS:1-5,191. (As used herein, the "primary sequence" refers to the nucleotide sequence represented by the IUPAC nomenclature system.)

In addition to the aforementioned *Staphylococcus aureus* polynucleotide and polynucleotide sequences, the present invention provides the nucleotide sequences of SEQ ID NOS:1-5,191, or representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan.

As used herein, a "representative fragment of the nucleotide sequence depicted in SEQ ID NOS:1-5,191" refers to any portion of the SEQ ID NOS:1-5,191 which is not presently represented within a publicly available database. Preferred representative fragments of the present invention are *Staphylococcus aureus* open reading frames (ORFs"), expression modulating fragment (EMFs") and fragments which can be used to diagnose the presence of *Staphylococcus aureus* in sample ("DFs"). A non-limiting identification of preferred representative fragments is provided in Tables 1-3.

As discussed in detail below, the information provided in SEQ ID NOS:1-5,191 and in Tables 1-3 together with routine cloning, synthesis, sequencing and assay methods will enable those skilled in the art to clone and sequence all "representative fragments" of interest, including open reading frames encoding a large variety of *Staphylococcus aureus* proteins.

While the presently disclosed sequences of SEQ ID NOS:1-5,191 are highly accurate, sequencing techniques are not perfect and, in relatively rare instances, further investigation of a fragment or sequence of the invention may reveal a nucleotide sequence error present in a nucleotide sequence disclosed in SEQ ID NOS:1-5,191. However, once the present invention is made available (*i.e.,* once the information in SEQ ID NOS:1-5,191 and Tables 1-3 has been made available), resolving a rare sequencing error in SEQ ID NOS:1-5,191 will be well within the skill of the art. The present disclosure makes available sufficient sequence information to allow any of the described contigs or portions thereof to be obtained readily by straightforward application of routine techniques. Further sequencing of such polynucleotide may proceed in like manner using manual and automated sequencing methods which are employed ubiquitous in the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler can be used as an aid during visual inspection of nucleotide sequences. By employing such routine techniques potential errors readily may be identified and the correct sequence then may be ascertained by targeting further sequencing effort, also of a routine nature, to the region containing the potential error.

Even if all of the very rare sequencing errors in SEQ ID NOS:1-5,191 were corrected, the resulting nucleotide sequences would still be at least 95% identical, nearly all would be at least 99% identical, and the great majority would be at least 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-5,191.

As discussed elsewhere hererin, polynucleotides of the present invention readily may be obtained by routine application of well known and standard procedures for cloning and sequencing DNA. Detailed methods for obtaining

libraries and for sequencing are provided below, for instance. A wide variety of *Staphylococcus aureus* strains that can be used to prepare *S aureus* genomic DNA for cloning and for obtaining polynucleotides of the present invention are available to the public from recognized depository institutions, such as the American Type Culture Collection (ATCC").

The nucleotide sequences of the genomes from different strains of *Staphylococcus aureus* differ somewhat. However, the nucleotide sequences of the genomes of all *Staphylococcus aureus* strains will be at least 95% identical, in corresponding part, to the nucleotide sequences provided in SEQ ID NOS:1-5,191. Nearly all will be at least 99% identical and the great majority will be 99.9% identical.

Thus, the present invention further provides nucleotide sequences which are at least 95%, preferably 99% and most preferably 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-5,191, in a form which can be readily used, analyzed and interpreted by the skilled artisan.

Methods for determining whether a nucleotide sequence is at least 95%, at least 99% or at least 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-5,191 are routine and readily available to the skilled artisan. For example, the well known fasta algorithm described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85: 2444 (1988) can be used to generate the percent identity of nucleotide sequences. The BLASTN program also can be used to generate an identity score of polynucleotides compared to one another.

COMPUTER RELATED EMBODIMENTS

The nucleotide sequences provided in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide sequence of SEQ ID NOS:1-5,191 may be "provided" in a variety of mediums to facilitate use thereof. As used herein, Òprovided" refers to a manufacture, other than an isolated nucleic acid molecule, which contains a nucleotide sequence of the present invention; *i.e.,* a nucleotide sequence provided in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide of SEQ ID NOS:1-5,191. Such a manufacture provides a large portion of the *Staphylococcus aureus* genome and parts thereof (*e.g.,* a *Staphylococcus aureus* open reading frame (ORF)) in a form which allows a skilled artisan to examine the manufacture using means not directly applicable to examining the *Staphylococcus aureus* genome or a subset thereof as it exists in nature or in purified form.

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD- ROM; electrical storage media such as RAM and ROM; and hybrids of these categories, such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. Likewise, it will be clear to those of skill how additional computer readable media that may be developed also can be used to create analogous manufactures having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently know methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially- available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data-processor structuring formats (*e.g.,* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. Thus, by providing in computer readable form the nucleotide sequences of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a sequence of SEQ ID NOS:1-5,191 the present invention enables the skilled artisan routinely to access the provided sequence information for a wide variety of purposes.

The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.,* J. Mol. Biol. 215:403410 (1990)) and BLAZE (Brutlag *et al.,* Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system was used to identify open reading frames (ORFs) within the *Staphylococcus aureus* genome which contain homology to ORFs or proteins from both *Staphylococcus aureus* and from other organisms. Among the ORFs discussed

herein are protein encoding fragments of the *Staphylococcus aureus* genome useful in producing commercially important proteins, such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify, among other things, commercially important fragments of the *Staphylococcus aureus* genome.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means.

As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer- based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the present genomic sequences which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *Staphylococcus aureus* genomic sequences possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *Staphylococcus aureus* genome. In the present examples, implementing software which implement the BLAST and BLAZE algorithms, described in Altschul *et al., J. Mol. Biol.* 215: 403-410 (1990), was used to identify open reading frames within the *Staphylococcus aureus* genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention. Of course, suitable proprietary systems that may be known to those of skill also may be employed in this regard.

Figure 1 provides a block diagram of a computer system illustrative of embodiments of this aspect of present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device 114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, *etc.* A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, *etc.*) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114, once it is inserted into the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. During execution, software for

accessing and processing the genomic sequence (such as search tools, comparing tools, *etc.*) reside in main memory 108, in accordance with the requirements and operating parameters of the operating system, the hardware system and the software program or programs.

BIOCHEMICAL EMBODIMENTS

Other embodiments of the present invention are directed to fragments of the *Staphylococcus aureus* genome, preferably to isolated fragments. The fragments of the *Staphylococcus aureus* genome of the present invention include, but are not limited to fragments which encode peptides, hereinafter open reading frames (ORFs), fragments which modulate the expression of an operably linked ORF, hereinafter expression modulating fragments (EMFs) and fragments which can be used to diagnose the presence of *Staphylococcus aureus* in a sample, hereinafter diagnostic fragments (DFs).

As used herein, an "isolated nucleic acid molecule" or an "isolated fragment of the *Staphylococcus aureus* genome" refers to a nucleic acid molecule possessing a specific nucleotide sequence which has been subjected to purification means to reduce, from the composition, the number of compounds which are normally associated with the composition. Particularly, the term refers to the nucleic acid molecules having the sequences set out in SEQ ID NOS:1-5,191, to representative fragments thereof as described above, to polynucleotides at least 95%, preferably at least 99% and especially preferably at least 99.9% identical in sequence thereto, also as set out above.

A variety of purification means can be used to generated the isolated fragments of the present invention. These include, but are not limited to methods which separate constituents of a solution based on charge, solubility, or size.

In one embodiment, *Staphylococcus aureus* DNA can be mechanically sheared to produce fragments of 15-20 kb in length. These fragments can then be used to generate an *Staphylococcus aureus* library by inserting them into lambda clones as described in the Examples below. Primers flanking, for example, an ORF, such as those enumerated in Tables 1-3 can then be generated using nucleotide sequence information provided in SEQ ID NOS: 1-5,191. Well known and routine techniques of PCR cloning then can be used to isolate the ORF from the lambda DNA library of Staphylococcus aureus genomic DNA. Thus, given the availability of SEQ ID NOS:1-5,191, the information in Tables 1, 2 and 3, and the information that may be obtained readily by analysis of the sequences of SEQ ID NOS:1-5,191 using methods set out above, those of skill will be enabled by the present disclosure to isolate any ORF-containing or other nucleic acid fragment of the present invention.

The isolated nucleic acid molecules of the present invention include, but are not limited to single stranded and double stranded DNA, and single stranded RNA.

As used herein, an "open reading frame," ORF, means a series of triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

Tables 1, 2 and 3 list ORFs in the *Staphylococcus aureus* genomic contigs of the present invention that were identified as putative coding regions by the GeneMark software using organism-specific second-order Markov probability transition matrices. It will be appreciated that other criteria can be used, in accordance with well known analytical methods, such as those discussed herein, to generate more inclusive, more restrictive or more selective lists.

Table 1 sets out ORFs in the *Staphylococcus aureus* contigs of the present invention that are at least 80 amino acids long and over a continuous region of at least 50 bases which are 95% or more identical (by BLAST analysis) to an *S. aureus* nucleotide sequence available through Genbank in November 1996.

Table 2 sets out ORFs in the *Staphylococcus aureus* contigs of the present invention that are not in Table 1 and match, with a BLASTP probability score of 0.01 or less, a polypeptide sequence available through Genbank by September 1996.

Table 3 sets out ORFs in the *Staphylococcus aureus* contigs of the present invention that do not match significantly, by BLASTP analysis, a polypeptide sequence available through Genbank by September 1996.

In each table, the first and second columns identify the ORF by, respectively, contig number and ORF number within the contig; the third column indicates the reading frame, taking the first 5' nucleotide of the contig as the start of the +1 frame; the fourth column indicates the first nucleotide of the ORF, counting from the 5' end of the contig strand; and the fifth column indicates the length of each ORF in nucleotides.

In Tables 1 and 2, column six, lists the Reference" for the closest matching sequence available through Genbank. These reference numbers are the databases entry numbers commonly used by those of skill in the art, who will be familiar with their denominators. Descriptions of the numenclature are available from the National Center for Biotechnology Information. Column seven in Tables 1 and 2 provides the gene name" of the matching sequence; column eight provides the BLAST identity" score from the comparison of the ORF and the homologous gene; and column nine indicates the length in nucleotides of the highest scoring segment pair" identified by the BLAST identity analysis.

In Table 3, the last column, column six, indicates the length of each ORF in amino acid residues.

The concepts of percent identity and percent similarity of two polypeptide sequences is well understood in the art. For example, two polypeptides 10 amino acids in length which differ at three amino acid positions (*e.g.*, at positions

1, 3 and 5) are said to have a percent identity of 70%. However, th same two polypeptides would be deemed to have a percent similarity of 80% if, for example at position 5, the amino acids moieties, although not identical, were "similar" (*i.e.*, possessed similar biochemical characteristics). Many programs for analysis of nucleotide or amino acid sequence similarity, such as fasta and BLAST specifically list per cent identity of a matching region as an output parameter. Thus, for instance, Tables 1 and 2 herein enumerate the per cent identity" of the highest scoring segment pair" in each ORF and its listed relative. Further details concerning the algorithms and criteria used for homology searches are provided below and are described in the pertinent literature highlighted by the citations provided below.

It will be appreciated that other criteria can be used to generate more inclusive and more exclusive listings of the types set out in the tables. As those of skill will appreciate, narrow and broad searches both are useful. Thus, a skilled artisan can readily identify ORFs in contigs of the *Staphylococcus aureus* genome other than those listed in Tables 1-3, such as ORFs which are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

As used herein, an "expression modulating fragment," EMF, means a series of nucleotide molecules which modulates the expression of an operably linked ORF or EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments which induce the expression or an operably linked ORF in response to a specific regulatory factor or physiological event.

EMF sequences can be identified within the contigs of the *Staphylococcus aureus* genome by their proximity to the ORFs provided in Tables 1-3. An intergenic segment, or a fragment of the intergenic segment, from about 10 to 200 nucleotides in length, taken from any one of the ORFs of Tables 1-3 will modulate the expression of an operably linked ORF in a fashion similar to that found with the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to fragments of the *Staphylococcus aureus* genome which are between two ORF(s) herein described. EMFs also can be identified using known EMFs as a target sequence or target motif in the computer-based systems of the present invention. Further, the two methods can be combined and used together.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site linked to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, a EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below.

A sequence which is suspected as being an EMF is cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed host in examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

As used herein, a "diagnostic fragment," DF, means a series of nucleotide molecules which selectively hybridize to *Staphylococcus aureus* sequences. DFs can be readily identified by identifying unique sequences within contigs of the *Staphylococcus aureus* genome, such as by using well-known computer analysis software, and by generating and testing probes or amplification primers consisting of the DF sequence in an appropriate diagnostic format which determines amplification or hybridization selectivity.

The sequences falling within the scope of the present invention are not limited to the specific sequences herein described, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequences provided in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably 99% and most preferably 99.9% identical to SEQ ID NOS:1-5,191, with a sequence from another isolate of the same species.

Furthermore, to accomodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the nucleic acid sequences mentioned above. In other words, in the coding region of an ORF, substitution of one codon for another which encodes the same amino acid is expressly contemplated.

Any specific sequence disclosed herein can be readily screened for errors by resequencing a particular fragment, such as an ORF, in both directions (*i.e.*, sequence both strands). Alternatively, error screening can be performed by sequencing corresponding polynucleotides of *Staphylococcus aureus* origin isolated by using part or all of the fragments in question as a probe or primer.

Each of the ORFs of the *Staphylococcus aureus* genome disclosed in Tables 1, 2 and 3, and the EMFs found 5' to the ORFs, can be used as polynucleotide reagents in numerous ways. For example, the sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of a specific microbe in a sample, particular *Staphylococcus aureus*. Especially preferred in this regard are ORF such as those of Table 3, which do not match previously characterized sequences from other organisms and thus are most likely to be highly selective for *Staphylococcus aureus*. Also particularly preferred are ORFs that can be used to distinguish between strains of *Sta-*

phylococcus aureus, particularly those that distinguish medically important strain, such as drug-resistant strains.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Triple helix- formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Information from the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription, for triple-helix formation, or to the mRNA itself, for antisense inhibition. Both techniques have been demonstrated to be effective in model systems, and the requisite techniques are well known and involve routine procedures. Triple helix techniques are discussed in, for example, Lee *et al., Nucl. Acids Res.* 6: 3073 (1979); Cooney *et al., Science* 241: 456 (1988); and Dervan *et al., Science* 251: 1360 (1991). Antisense techniques in general are discussed in, for instance, Okano, *J. Neurochem.* 56: 560 (1991) and OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION, CRC Press, Boca Raton, FL (1988)).

The present invention further provides recombinant constructs comprising one or more fragments of the *Staphylococcus aureus* genomic fragments and contigs of the present invention. Certain preferred recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a fragment of the *Staphylococcus aureus* genome has been inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. For vectors comprising the EMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF operably linked to the EMF.

Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Useful bacterial vectors include phagescript, PsiX174, pBluescript SK and KS (+ and -), pNH8a, pNH16a, pNH18a, pNH46a (available from Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (available from Pharmacia). Useful eukaryotic vectors include pWLneo, pSV2cat, pOG44, pXT1, pSG (available from Stratagene) pSVK3, pBPV, pMSG, pSVL (available from Pharmacia).

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein- I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

The present invention further provides host cells containing any one of the isolated fragments of the *Staphylococcus aureus* genomic fragments and contigs of the present invention, wherein the fragment has been introduced into the host cell using known methods. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or a procaryotic cell, such as a bacterial cell.

A polynucleotide of the present invention, such as a recombinant construct comprising an ORF of the present invention, may be introduced into the host by a variety of well established techniques that are standard in the art, such as calcium phosphate transfection, DEAE, dextran mediated transfection and electroporation, which are described in, for instance, Davis, L. *et al.,* BASIC METHODS IN MOLECULAR BIOLOGY (1986).

A host cell containing one of the fragments of the *Staphylococcus aureus* genomic fragments and contigs of the present invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.,* an ORF) by nucleotide sequence but, due to the degeneracy of the Genetic Code, encode an identical polypeptide sequence.

Preferred nucleic acid fragments of the present invention are the ORFs depicted in Tables 2 and 3 which encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. This is particularly useful in producing small peptides and fragments of larger polypeptides. Such short fragments as may be obtained most readily by synthesis are useful, for example, in generating antibodies against the native polypeptide, as discussed further below.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily employ well-known methods for isolating polpeptides and proteins to isolate and purify polypeptides or proteins of the present invention produced naturally by a bacterial strain, or by other methods. Methods for isolation and purification that can be employed in this regard include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immu-

no-affinity chromatography.

The polypeptides and proteins of the present invention also can be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be alt red to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. Those skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, CV-1 cell, COS cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level.

"Recombinant," as used herein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial"defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g., E. coli,* will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern different from that expressed in mammalian cells.

"Nucleotide sequence" refers to a heteropolymer of deoxyribonucleotides. Generally, DNA segments encoding the polypeptides and proteins provided by this invention are assembled from fragments of the *Staphylococcus aureus* genome and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon.

"Recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. The expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic regulatory elements necessary for gene expression in the host, including elements required to initiate and maintain transcription at a level sufficient for suitable expression of the desired polypeptide, including, for example, promoters and, where necessary, an enhancers and a polyadenylation signal; (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate signals to initiate translation at the beginning of the desired coding region and terminate translation at its end. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an N-terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

"Recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extra chromosomally. The cells can be prokaryotic or eukaryotic. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described in Sambrook *et al.,* MOLECULAR CLONING:A LABORATORY MANUAL, 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference in its entirety.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), alpha-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, when desirable, provide amplification within the host.

Suitable prokaryotic hosts for transformation include strains of *Staphylococcus aureus, E. coli, B. subtilis, Salmonella typhimurium* and various species within the genera *Pseudomonas, Streptomyces,* and *Staphylococcus.* Others

may, also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (available form Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (available from Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter, where it is inducible, is derepressed or induced by appropriate means (*e.g.,* temperature shift or chemical induction) and cells are cultured for an additional period to provide for expression of the induced gene product. Thereafter cells are typically harvested, generally by centrifugation, disrupted to release expressed protein, generally by physical or chemical means, and the resulting crude extract is retained for further purification.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described in Gluzman, *Cell* 23: 175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines.

Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Recombinant polypeptides and proteins produced in bacterial culture is usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

An additional aspect of the invention includes Staphylococcus aureus polypeptides which are useful as immunodiagnostic antigens and/or immunoprotective vaccines, collectively "immunologically useful polypeptides". Such immunologically useful polypeptides may be selected from the ORFs disclosed herein based on techniques well known in the art and described elsewhere herein. The inventors have used the following criteria to select several immunologically useful polypeptides:

As is known in the art, an amino terminal type I signal sequence directs a nascent protein across the plasma and outer membranes to the exterior of the bacterial cell. Such outermembrane polypeptides are expected to be immunologically useful. According to Izard, J. W. et al., Mol. Microbiol. 13, 765-773; (1994), polypeptides containing type I signal sequences contain the following physical attributes: The length of the type I signal sequence is approximately 15 to 25 primarily hydrophobic amino acid residues with a net positive charge in the extreme amino terminus; the central region of the signal sequence must adopt an alpha-helical conformation in a hydrophobic environment; and the region surrounding the actual site of cleavage is ideally six residues long, with small side-chain amino acids in the -1 and -3 positions.

Also known in the art is the type IV signal sequence which is an example of the several types of functional signal sequences which exist in addition to the type I signal sequence detailed above. Although functionally related, the type IV signal sequence possesses a unique set of biochemical and physical attributes (Strom, M. S. and Lory, S., J. Bacteriol. 174, 7345-7351; 1992)). These are typically six to eight amino acids with a net basic charge followed by an additional sixteen to thirty primarily hydrophobic residues. The cleavage site of a type IV signal sequence is typically after the initial six to eight amino acids at the extreme amino terminus. In addition, all type IV signal sequences contain a phenylalanine residue at the +1 site relative to the cleavage site.

Studies of the cleavage sites of twenty-six bacterial lipoprotein precursors has allowed the definition of a consensus amino acid sequence for lipoprotein cleavage. Nearly three-fourths of the bacterial lipoprotein precursors examined contained the sequence L-(A,S)-(G,A)-C at positions -3 to +1, relative to the point of cleavage (Hayashi, S. and Wu, H. C. Lipoproteins in bacteria. J Bioenerg. Biomembr. 22, 451-471; 1990).

It well known that most anchored proteins found on the surface of gram-positive bacteria possess a highly conserved carboxy terminal sequence. More than fifty such proteins from organisms such as *S. pyogenes, S. mutans, E. faecalis, S. pneumoniae,* and others, have been identified based on their extracellular location and carboxy terminal amino acid sequence (Fischetti, V. A. Gram-positive commensal bacteria deliver antigens to elicit mucosal and systemic immunity. ASM News 62, 405410; 1996). The conserved region is comprised of six charged amino acids at the extreme carboxy terminus coupled to 15-20 hydrophobic amino acids presumed to function as a transmembrane domain. Immediately adjacent to the transmembrane domain is a six amino acid sequence conserved in nearly all proteins ex-

amined. The amino acid sequence of this region is L-P-X-T-G-X, where X is any amino acid.

Amino acid sequenc similarities to proteins of known function by BLAST enables the assignment of putative functions to novel amino acid sequences and allows for the selection of proteins thought to function outside the cell wall. Such proteins are w ll known in the art and include "lipoprotein", "periplasmic", or "antigen".

An algorithm for s lecting antigenic and immunogenic *Staphylococcus aureus* polypeptides including the foregoing criteria was developed by the present inventors. Use of the algorithm by the inventors to select immunologically useful *Staphylococcus aureus* polypeptides resulted in the selection of several ORFs which are predicted to be outermembrane-associated proteins. These proteins are identified in Table 4, below, and shown in the Sequence Listing as SEQ ID NOS:5,192 to 5,255. Thus the amino acid sequence of each of several antigenic *Staphylococcus aureus* polypeptides listed in Table 4 can be determined, for example, by locating the amino acid sequence of the ORF in the Sequence Listing. Likewise the polynucleotide sequence encoding each ORF can be found by locating the corresponding polynucleotide SEQ ID in Tables 1, 2, or 3, and finding the corresponding nucleotide sequence in the sequence listing.

As will be appreciated by those of ordinary skill in the art, although a polypeptide representing an entire ORF may be the closest approximation to a protein found *in vivo,* it is not always technically practical to express a complete ORF *in vitro.* It may be very challenging to express and purify a highly hydrophobic protein by common laboratory methods. As a result, the immunologically useful polypeptides described herein as SEQ ID NOS:5,192-5,255 may have been modified slightly to simplify the production of recombinant protein, and are the preferred embodiments. In general, nucleotide sequences which encode highly hydrophobic domains, such as those found at the amino terminal signal sequence, are excluded for enhanced *in vitro* expression of the polypeptides. Furthermore, any highly hydrophobic amino acid sequences occurring at the carboxy terminus are also excluded. Such truncated polypeptides include for example the mature forms of the polypeptides expected to exist in nature.

Those of ordinary skill in the art can identify soluble portions the polypeptide identified in Table 4, and in the case of truncated polypeptides sequences shown as SEQ ID NOS:5,192-5,255, may obtain the complete predicted amino acid sequence of each polypeptide by translating the corresponding polynucleotides sequences of the corresponding ORF listed in Tables 1,2 and 3 and found in the sequence listing.

Accordingly, polypeptides comprising the complete amino acid of an immunologically useful polypeptide selected from the group of polypeptides encoded by the ORFs identified in Table 4, or an amino acid sequence at least 95% identical thereto, preferably at least 97% identical thereto, and most preferably at least 99% identical thereto form an embodiment of the invention; in addition polypeptides comprising an amino acid sequence selected from the group of amino acid sequences shown in the sequence listing as SEQ ID NOS:5,191-5,255, or an amino acid sequence at least 95% identical thereto, preferably at least 97% identical thereto and most preferably at least 99% identical thereto, form an embodiment of the invention. Polynucleotides encoding the foregoing polypeptides also form part of the present invention.

In another aspect, the invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention, particularly those epitope-bearing portions (antigenic regions) identified in Table 4. The epitope-bearing portion is an immunogenic or antigenic epitope of a polypeptide of the invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein is the immunogen. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983).

As to the selection of peptides or polypeptides bearing an antigenic epitope (i.e., that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, for instance, Sutcliffe, J. G., Shinnick, T. M., Green, N. and Learner, R. A. (1983) "Antibodies that react with predetermined sites on proteins", Science, 219:660-666. Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (i.e., immunogenic epitopes) nor to the amino or carboxyl terminals. Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide of the invention. See, for instance, Wilson et al., Cell 37:767-778 (1984) at 777.

Antigenic epitope-bearing peptides and polypeptides of the invention preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 15 to about 30 amino acids contained within the amino acid sequence of a polypeptide of the invention. Non-limiting examples of antigenic polypeptides or peptides that can be used to generate S. aureus specific antibodies include: a polypeptide comprising peptides shown in Table 4 below. These polypeptide fragments have been determined to bear antigenic epitopes of indicated S. aureus proteins by the analysis of the Jameson-Wolf antigenic index, a representative sample of which is shown in Figure 3.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means. See, e.g., Houghten, R. A. (1985) General method for the rapid solid-phase synthesis of large numbers of peptides:

specificity of antigen-antibody interaction at the level of individual amino acids. Proc. Natl. Acad. Sci. USA 82: 5131-5135; this "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten et al. (1986). Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985).

Immunogenic epitope-bearing peptides of the invention, i.e., those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. See, for instance, Geysen et al., supra. Further still, U.S. Patent No. 5,194,392 to Geysen (1990) describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (i.e., a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092 to Geysen (1989) describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. et al. (1996) on Peralkylated Oligopeptide Mixtures discloses linear C1-C7-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods.

Table 4 lists immunologically useful polypeptides identified by an algorithm which locates novel *Staphylococcus aureus* outermembrane proteins, as is described above. Also listed are epitopes or "antigenic regions" of each of the identified polypeptides. The antigenic regions, or epitopes, are delineated by two numbers x-y, where x is the number of the first amino acid in the open reading frame included within the epitope and y is the number of the last amino acid in the open reading frame included within the epitope. For example, the first epitope in ORF 168-6 is comprised of amino acids 36 to 45 of SEQ ID NO:5,192, as is described in Table 4. The inventors have identified several epitopes for each of the antigenic polypeptides identified in Table 4. Accordingly, forming part of the present invention are polypeptides comprising an amino acid sequence of one or more antigenic regions identified in Table 4. The invention further provides polynucleotides encoding such polypeptides.

The present invention further includes isolated polypeptides, proteins and nucleic acid molecules which are substantially equivalent to those herein described. As used herein, substantially equivalent can refer both to nucleic acid and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between reference and subject sequences. For purposes of the present invention, sequences having equivalent biological activity, and equivalent expression characteristics are considered substantially equivalent. For purposes of determining equivalence, truncation of the mature sequence should be disregarded.

The invention further provides methods of obtaining homologs from other strains of *Staphylococcus aureus,* of the fragments of the *Staphylococcus aureus* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. As used herein, a sequence or protein of *Staphylococcus aureus* is defined as a homolog of a fragment of the *Staphylococcus aureus* fragments or contigs or a protein encoded by one of the ORFs of the present invention, if it shares significant homology to one of the fragments of the *Staphylococcus aureus* genome of the present invention or a protein encoded by one of the ORFs of the present invention. Specifically, by using the sequence disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

As used herein, two nucleic acid molecules or proteins are said to "share significant homology" if the two contain regions which prossess greater than 85% sequence (amino acid or nucleic acid) homology. Preferred homologs in this regard are those with more than 90% homology. Especially preferred are those with 93% or more homology. Among especially preferred homologs those with 95% or more homology are particularly preferred. Very particularly preferred among these are those with 97% and even more particularly preferred among those are homologs with 99% or more homology. The most preferred homologs among these are those with 99.9% homology or more. It will be understood that, among measures of homology, identity is particularly preferred in this regard.

Region specific primers or probes derived from the nucleotide sequence provided in SEQ ID NOS:1-5,191 or from a nucleotide sequence at least 95%, particularly at least 99%, especially at least 99.5% identical to a sequence of SEQ ID NOS:1-5,191 can be used to prime DNA synthesis and PCR amplification, as well as to identify colonies containing cloned DNA encoding a homolog. Methods suitable to this aspect of the present invention are well known and have been described in great detail in many publications such as, for example, Innis *et al.,* PCR PROTOCOLS, Academic Press, San Diego, CA (1990)).

When using primers derived from SEQ ID NOS:1-5,191 or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS:1-5,191, one skilled in the art will recognize that by employing high stringency conditions (*e.g.,* annealing at 50-60°C in 6X SSPC and 50% formamide, and washing at 50- 65°C in 0.5X SSPC) only sequences which are greater than 75% homologous to the primer will be amplified. By employing lower stringency

conditions (*e.g.,* hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequenc s which are greater than 40-50% homologous to the primer will also be amplified.

When using DNA probes derived from SEQ ID NOS:1-5,191, or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS:1-5,191, for colony/plaque hybridization, one skilled in the art will recognize that by employing high stringency conditions (*e.g.,* hybridizing at 50- 65°C in 5X SSPC and 50% formamide, and washing at 50- 65°C in 0.5X SSPC), sequences having regions which are greater than 90% homologous to the probe can be obtained, and that by employing lower stringency conditions (*e.g.,* hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences having regions which are greater than 35-45% homologous to the probe will be obtained.

Any organism can be used as the source for homologs of the present invention so long as the organism naturally expresses such a protein or contains genes encoding the same. The most preferred organism for isolating homologs are bacterias which are closely related to *Staphylococcus aureus.*

ILLUSTRATIVE USES OF COMPOSITIONS OF THE INVENTION

Each ORF provided in Tables 1 and 2 is identified with a function by homology to a known gene or polypeptide. As a result, one skilled in the art can use the polypeptides of the present invention for commercial, therapeutic and industrial purposes consistent with the type of putative identification of the polypeptide. Such identifications permit one skilled in the art to use the *Staphylococcus aureus* ORFs in a manner similar to the known type of sequences for which the identification is made; for example, to ferment a particular sugar source or to produce a particular metabolite. A variety of reviews illustrative of this aspect of the invention are available, including the following reviews on the industrial use of enzymes, for example, BIOCHEMICAL ENGINEERING AND BIOTECHNOLOGY HANDBOOK, 2nd Ed., Macmillan Publications, Ltd. NY (1991) and BIOCATALYSTS IN ORGANIC SYNTHESES, Tramper *et al.,* Eds., Elsevier Science Publishers, Amsterdam, The Netherlands (1985). A variety of exemplary uses that illustrate this and similar aspects of the present invention are discussed below.

1. Biosynthetic Enzymes

Open reading frames encoding proteins involved in mediating the catalytic reactions involved in intermediary and macromolecular metabolism, the biosynthesis of small molecules, cellular processes and other functions includes enzymes involved in the degradation of the intermediary products of metabolism, enzymes involved in central intermediary metabolism, enzymes involved in respiration, both aerobic and anaerobic, enzymes involved in fermentation, enzymes involved in ATP proton motor force conversion, enzymes involved in broad regulatory function, enzymes involved in amino acid synthesis, enzymes involved in nucleotide synthesis, enzymes involved in cofactor and vitamin synthesis, can be used for industrial biosynthesis.

The various metabolic pathways present in *Staphylococcus aureus* can be identified based on absolute nutritional requirements as well as by examining the various enzymes identified in Table 1-3 and SEQ ID NOS:1-5,191.

Of particular interest are polypeptides involved in the degradation of intermediary metabolites as well as non-macromolecular metabolism. Such enzymes include amylases, glucose oxidases, and catalase.

Proteolytic enzymes are another class of commercially important enzymes. Proteolytic enzymes find use in a number of industrial processes including the processing of flax and other vegetable fibers, in the extraction, clarification and depectinization of fruit juices, in the extraction of vegetables' oil and in the maceration of fruits and vegetables to give unicellular fruits. A detailed review of the proteolytic enzymes used in the food industry is provided in Rombouts *et al., Symbiosis* 21: 79 (1986) and Voragen *et al.* in BIOCATALYSTS IN AGRICULTURAL BIOTECHNOLOGY, Whitaker *et al.,* Eds., *American Chemical Society Symposium Series* 389: 93 (1989) .

The metabolism of sugars is an important aspect of the primary metabolism of *Staphylococcus aureus.* Enzymes involved in the degradation of sugars, such as, particularly, glucose, galactose, fructose and xylose, can be used in industrial fermentation. Some of the important sugar transforming enzymes, from a commercial viewpoint, include sugar isomerases such as glucose isomerase. Other metabolic enzymes have found commercial use such as glucose oxidases which produces ketogulonic acid (KGA). KGA is an intermediate in the commercial production of ascorbic acid using the Reichstein's procedure, as described in Krueger *et al., Biotechnology* 6(A), Rhine *et al.,* Eds., Verlag Press, Weinheim, Germany (1984).

Glucose oxidase (GOD) is commercially available and has been used in purified form as well as in an immobilized form for the deoxygenation of beer. See, for instance, Hartmeir *et al., Biotechnology Letters* 1: 21 (1979). The most important application of GOD is the industrial scale fermentation of gluconic acid. Market for gluconic acids which are used in the detergent, textile, leather, photographic, pharmaceutical, food, feed and concrete industry, as described, for example, in Bigelis *et al.,* beginning on page 357 in GENE MANIPULATIONS AND FUNGI; Benett *et al.,* Eds., Academic Press, New York (1985). In addition to industrial applications, GOD has found applications in medicine for

quantitative determination of glucose in body fluids recently in biotechnology for analyzing syrups from starch and cellulose hydrosylates. This application is described in Owusu *et al., Biochem. et Biophysica. Acta.* 872: 83 (1986), for instance.

The main sweetener used in the world today is sugar which comes from sugar beets and sugar cane. In the field of industrial enzymes, the glucose isomerase process shows the largest expansion in the market today. Initially, soluble enzymes were used and later immobilized enzymes were developed (Krueger *et al.,* Biotechnology, The Textbook of Industrial Microbiology, Sinauer Associated Incorporated, Sunderland, Massachusetts (1990)). Today, the use of glucose- produced high fructose syrups is by far the largest industrial business using immobilized enzymes. A review of the industrial use of these enzymes is provided by Jorgensen, Starch 40:307 (1988).

Proteinases, such as alkaline serine proteinases, are used as detergent additives and thus represent one of the largest volumes of microbial enzymes used in the industrial sector. Because of their industrial importance, there is a large body of published and unpublished information regarding the use of these enzymes in industrial processes. (See Faultman *et al.,* Acid Proteases Structure Function and Biology, Tang, J., ed., Plenum Press, New York (1977) and Godfrey *et al.,* Industrial Enzymes, MacMillan Publishers, Surrey, UK (1983) and Hepner *et al.,* Report Industrial Enzymes by 1990, Hel Hepner & Associates, London (1986)).

Another class of commercially usable proteins of the present invention are the microbial lipases, described by, for instance, Macrae *et al.,* Philosophical Transactions of the Chiral Society of London 310:227 (1985) and Poserke, Journal of the American Oil Chemist Society 61:1758 (1984). A major use of lipases is in the fat and oil industry for the production of neutral glycerides using lipase catalyzed inter-esterification of readily available triglycerides. Application of lipases include the use as a detergent additive to facilitate the removal of fats from fabrics in the course of the washing procedures.

The use of enzymes, and in particular microbial enzymes, as catalyst for key steps in the synthesis of complex organic molecules is gaining popularity at a great rate. One area of great interest is the preparation of chiral intermediates. Preparation of chiral intermediates is of interest to a wide range of synthetic chemists particularly those scientists involved with the preparation of new pharmaceuticals, agrochemicals, fragrances and flavors. (See Davies *et al.,* Recent Advances in the Generation of Chiral Intermediates Using Enzymes, CRC Press, Boca Raton, Florida (1990)). The following reactions catalyzed by enzymes are of interest to organic chemists:hydrolysis of carboxylic acid esters, phosphate esters, amides and nitriles, esterification reactions, trans-esterification reactions, synthesis of amides, reduction of alkanones and oxoalkanates, oxidation of alcohols to carbonyl compounds, oxidation of sulfides to sulfoxides, and carbon bond forming reactions such as the aldol reaction.

When considering the use of an enzyme encoded by one of the ORFs of the present invention for biotransformation and organic synthesis it is sometimes necessary to consider the respective advantages and disadvantages of using a microorganism as opposed to an isolated enzyme. Pros and cons of using a whole cell system on the one hand or an isolated partially purified enzyme on the other hand, has been described in detail by Bud *et al.,* Chemistry in Britain (1987), p. 127.

Amino transferases, enzymes involved in the biosynthesis and metabolism of amino acids, are useful in the catalytic production of amino acids. The advantages of using microbial based enzyme systems is that the amino transferase enzymes catalyze the stereo- selective synthesis of only L-amino acids and generally possess uniformly high catalytic rates. A description of the use of amino transferases for amino acid production is provided by Roselle-David, *Methods of Enzymology* 136:479 (1987).

Another category of useful proteins encoded by the ORFs of the present invention include enzymes involved in nucleic acid synthesis, repair, and recombination. A variety of commercially important enzymes have previously been isolated from members of *Staphylococcus aureus.* These include Sau3A and Sau96I.

2. Generation of Antibodies

As described here, the proteins of the present invention, as well as homologs thereof, can be used in a variety procedures and methods known in the art which are currently applied to other proteins. The proteins of the present invention can further be used to generate an antibody which selectively binds the protein. Such antibodies can be either monoclonal or polyclonal antibodies, as well fragments of these antibodies, and humanized forms.

The invention further provides antibodies which selectively bind to one of the proteins of the present invention and hybridomas which produce these antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A. M., MONOCLONAL ANTIBODY TECHNOLOGY: LABORATORY TECHNIQUES IN BIOCHEMISTRY AND MOLECULAR BIOLOGY, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth *et al., J. Immunol. Methods* 35: 1-21 (1980), Kohler and Milstein, *Nature* 256: 495-497 (1975)), the trioma technique, the human B- cell hybridoma technique (Kozbor *et al., Immunology Today*

4: 72 (1983), pgs. 77-96 of Cole *et al.*, in MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc. (1985)).

Any animal (mouse, rabbit, *etc.*) which is known to produce antibodies can be immunized with the pseudogene polypeptid . Methods for immunization are well known in the art. Such methods include subcutaneous or interperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection.

The protein which is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to coupling the antigen with a heterologous protein (such as globulin or galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells.

Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al., Exp. Cell Res.* 175: 109-124 (1988)).

Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known in the art (Campbell, A. M., Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)).

Techniques described for the production of single chain antibodies (U. S. Patent 4,946,778) can be adapted to produce single chain antibodies to proteins of the present invention.

For polyclonal antibodies, antibody containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures.

The present invention further provides the above- described antibodies in detectably labelled form. Antibodies can be detectably labelled through the use of radioisotopes, affinity labels (such as biotin, avidin, *etc.*), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, *etc.*) fluorescent labels (such as FITC or rhodamine, *etc.*), paramagnetic atoms, *etc.* Procedures for accomplishing such labelling are well-known in the art, for example see Sternberger *et al.*, J. Histochem. Cytochem. 18:315 (1970); Bayer, E. A. *et al.*, Meth. Enzym. 62:308 (1979); Engval, E. *et al.*, Immunol. 109:129 (1972); Goding, J. W. J. Immunol. Meth. 13:215 (1976)).

The labeled antibodies of the present invention can be used for *in vitro, in vivo,* and in situ assays to identify cells or tissues in which a fragment of the *Staphylococcus aureus* genome is expressed.

The present invention further provides the above-described antibodies immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir, D. M. *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby, W. D. *et al.*, Meth. Enzym. 34 Academic Press, N. Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro, in vivo,* and in situ assays as well as for immunoaffinity purification of the proteins of the present invention.

3. Diagnostic Assays and Kits

The present invention further provides methods to identify the expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using one of the DFs,antigens or antibodies of the present invention.

In detail, such methods comprise incubating a test sample with one or more of the antibodies, or one or more of the DFs, or one or more antigens of the present invention and assaying for binding of the DFs, antigens or antibodies to components within the test sample.

Conditions for incubating a DF, antigen or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the DF or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the Dfs, antigens or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G. R. *et al.*, Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry; PCT publication WO95/32291, and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985), all of which are hereby incorporated herein by reference.

The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based

on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises:(a) a first container comprising one of the Dfs, antigens or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following:wash reagents, reagents capable of detecting presence of a bound DF, antigen or antibody.

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, *etc.*), and containers which contain the reagents used to detect the bound antibody, antigen or DF.

Types of detection reagents include labelled nucleic acid probes, labelled secondary antibodies, or in the alternative, if the primary antibody is labelled, the enzymatic, or antibody binding reagents which are capable of reacting with the labelled antibody. One skilled in the art will readily recognize that the disclosed Dfs, antigens and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4. Screening Assay for Binding Agents

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents which bind to a protein encoded by one of the ORFs of the present invention or to one of the fragments and the *Staphylococcus aureus* fragment and contigs herein described.

In general, such methods comprise steps of:

(a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention, or an isolated fragment of the Staphylococcus aureus genome; and

(b) determining whether the agent binds to said protein or said fragment.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention.

Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides, for example see Hurby *et al.*, Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W. H. Freeman, NY (1992), pp. 289-307, and Kaspczak *et al.*, Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control.

One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, Nucl. Acids Res. 6:3073 (1979); Cooney *et al.*, Science 241:456 (1988); and Dervan *et al.*, Science 251: 1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated

to be effectiv in model systems. Information contained in the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides, and other DNA binding agents.

5. Pharmac utical C mpositions and Vaccines

The present invention further provides pharmaceutical agents which can be used to modulate the growth or pathogenicity of *Staphylococcus aureus,* or another related organism, *in vivo* or *in vitro.* As used herein, a "pharmaceutical agent" is defined as a composition of matter which can be formulated using known techniques to provide a pharmaceutical compositions. As used herein, the "pharmaceutical agents of the present invention" refers the pharmaceutical agents which are derived from the proteins encoded by the ORFs of the present invention or are agents which are identified using the herein described assays.

As used herein, a pharmaceutical agent is said to "modulate the growth or pathogenicity of *Staphylococcus aureus* or a related organism, *in vivo* or *in vitro,*" when the agent reduces the rate of growth, rate of division, or viability of the organism in question. The pharmaceutical agents of the present invention can modulate the growth or pathogenicity of an organism in many fashions, although an understanding of the underlying mechanism of action is not needed to practice the use of the pharmaceutical agents of the present invention. Some agents will modulate the growth or pathogenicity by binding to an important protein thus blocking the biological activity of the protein, while other agents may bind to a component of the outer surface of the organism blocking attachment or rendering the organism more prone to act the bodies nature immune system. Alternatively, the agent may comprise a protein encoded by one of the ORFs of the present invention and serve as a vaccine. The development and use of vaccines derived from membrane associated polypeptides are well known in the art. The inventors have identified particularly preferred immunogenic Staphylococcus aureus polypeptides for use as vaccines. Such immunogenic polypeptides are described above and summarized in Table 4, below.

As used herein, a "related organism" is a broad term which refers to any organism whose growth or pathogenicity can be modulated by one of the pharmaceutical agents of the present invention. In general, such an organism will contain a homolog of the protein which is the target of the pharmaceutical agent or the protein used as a vaccine. As such, related organisms do not need to be bacterial but may be fungal or viral pathogens.

The pharmaceutical agents and compositions of the present invention may be administered in a convenient manner, such as by the oral, topical, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes. The pharmaceutical compositions are administered in an amount which is effective for treating and/or prophylaxis of the specific indication. In general, they are administered in an amount of at least about 1 mg/kg body weight and in most cases they will be administered in an amount not in excess of about 1 g/kg body weight per day. In most cases, the dosage is from about 0.1 mg/kg to about 10 g/kg body weight daily, taking into account the routes of administration, symptoms, *etc.*

The agents of the present invention can be used in native form or can be modified to form a chemical derivative. As used herein, a molecule is said to be a "chemical derivative" of another molecule when it contains additional chemical moieties not normally a part of the molecule. Such moieties may improve the molecule's solubility, absorption, biological half life, *etc.* The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, *etc.* Moieties capable of mediating such effects are disclosed in, among other sources, REMINGTON'S PHARMACEUTICAL SCIENCES (1980) cited elsewhere herein.

For example, such moieties may change an immunological character of the functional derivative, such as affinity for a given antibody. Such changes in immunomodulation activity are measured by the appropriate assay, such as a competitive type immunoassay. Modifications of such protein properties as redox or thermal stability, biological half-life, hydrophobicity, susceptibility to proteolytic degradation or the tendency to aggregate with carriers or into multimers also may be effected in this way and can be assayed by methods well known to the skilled artisan.

The therapeutic effects of the agents of the present invention may be obtained by providing the agent to a patient by any suitable means (*e.g.,* inhalation, intravenously, intramuscularly, subcutaneously, enterally, or parenterally). It is preferred to administer the agent of the present invention so as to achieve an effective concentration within the blood or tissue in which the growth of the organism is to be controlled. To achieve an effective blood concentration, the preferred method is to administer the agent by injection. The administration may be by continuous infusion, or by single or multiple injections.

In providing a patient with one of the agents of the present invention, the dosage of the administered agent will vary depending upon such factors as the patient's age, weight, height, sex, general medical condition, previous medical history, *etc.* In general, it is desirable to provide the recipient with a dosage of agent which is in the range of from about 1 pg/kg to 10 mg/kg (body weight of patient), although a lower or higher dosage may be administered. The therapeutically effective dose can be lowered by using combinations of the agents of the present invention or another agent.

As used herein, two or more compounds or agents are said to be administered "in combination" with each other when either (1) the physiological effects of each compound, or (2) the serum concentrations of each compound can

be measured at the same time. The composition of the present invention can be administered concurrently with, prior to, or following the administration of the other agent.

The agents of the present invention are intended to be provided to recipient subjects in an amount sufficient to decrease the rate of growth (as defined above) of the target organism.

The administration of the agent(s) of the invention may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the agent(s) are provided in advance of any symptoms indicative of the organisms growth. The prophylactic administration of the agent(s) serves to prevent, attenuate, or decrease the rate of onset of any subsequent infection. When provided therapeutically, the agent(s) are provided at (or shortly after) the onset of an indication of infection. The therapeutic administration of the compound(s) serves to attenuate the pathological symptoms of the infection and to increase the rate of recovery.

The agents of the present invention are administered to a subject, such as a mammal, or a patient, in a pharmaceutically acceptable form and in a therapeutically effective concentration. A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient patient. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

The agents of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in admixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, *e.g.*, human serum albumin, are described, for example, in REMINGTON'S PHARMACEUTICAL SCIENCES, 16th Ed., Osol, A., Ed., Mack Publishing, Easton PA (1980). In order to form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of one or more of the agents of the present invention, together with a suitable amount of carrier vehicle.

Additional pharmaceutical methods may be employed to control the duration of action. Control release preparations may be achieved through the use of polymers to complex or absorb one or more of the agents of the present invention. The controlled delivery may be effectuated by a variety of well known techniques, including formulation with macromolecules such as, for example, polyesters, polyamino acids, polyvinyl, pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine, sulfate, adjusting the concentration of the macromolecules and the agent in the formulation, and by appropriate use of methods of incorporation, which can be manipulated to effectuate a desired time course of release. Another possible method to control the duration of action by controlled release preparations is to incorporate agents of the present invention into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization with, for example, hydroxymethylcellulose or gelatine-microcapsules and poly(methylmethacylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions. Such techniques are disclosed in REMINGTON'S PHARMACEUTICAL SCIENCES (1980).

The invention further provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

In addition, the agents of the present invention may be employed in conjunction with other therapeutic compounds.

6. Shot-Gun Approach to Megabase DNA Sequencing

The present invention further demonstrates that a large sequence can be sequenced using a random shotgun approach. This procedure, described in detail in the examples that follow, has eliminated the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols.

Certain aspects of the present invention are described in greater detail in the examples that follow. The examples are provided by way of illustration. Other aspects and embodiments of the present invention are contemplated by the inventors, as will be clear to those of skill in the art from reading the present disclosure.

ILLUSTRATIVE EXAMPLES

LIBRARIES AND SEQUENCING

1. Sh tgun Sequencing Probability Analysis

The overall strategy for a shotgun approach to whole genome sequencing follows from the Lander and Waterman (Landerman and Waterman, Genomics 2: 231 (1988)) application of the equation for the Poisson distribution. According to this treatment, the probability, P_0, that any given base in a sequence of size L, in nucleotides, is not sequenced after a certain amount, n, in nucleotides, of random sequence has been determined can be calculated by the equation $P_0 = e^{-m}$, where m is L/n, the fold coverage." For instance, for a genome of 2.8 Mb, m=1 when 2.8 Mb of sequence has been randomly generated (1X coverage). At that point, $P_0 = e^{-1} = 0.37$. The probability that any given base has not been sequenced is the same as the probability that any region of the whole sequence L has not been determined and, therefore, is equivilent to the fraction of the whole sequence that has yet to be determined. Thus, at one-fold coverage, approximately 37% of a polynucleotide of size L, in nucleotides has not been sequenced. When 14 Mb of sequence has been generated, coverage is 5X for a .2.8 Mb and the unsequenced fraction drops to .0067 or 0.67%. 5X coverage of a 2.8 Mb sequence can be attained by sequencing approximately 17,000 random clones from both insert ends with an average sequence read length of 410 bp.

Similarly, the total gap length, G, is determined by the equation $G = Le^{-m}$, and the average gap size, g, follows the quation, g = L/n. Thus, 5X coverage leaves about 240 gaps averaging about 82 bp in size in a sequence of a polynucleotide 2.8 Mb long.

The treatment above is essentially that of Lander and Waterman, *Genomics* 2: 231 (1988).

2. Random Library Construction

In order to approximate the random model described above during actual sequencing, a nearly ideal library of cloned genomic fragments is required. The following library construction procedure was developed to achieve this end.

Staphylococcus aureus DNA was prepared by phenol extraction. A mixture containing 600 ug DNA in 3.3 ml of 300 mM sodium acetate, 10 mM Tris-HCl, 1 mM Na-EDTA, 30% glycerol was sonicated for 1 min. at 0°C in a Branson Model 450 Sonicator at the lowest energy setting using a 3 mm probe. The sonicated DNA was ethanol precipitated and redissolved in 500 ul TE buffer.

To create blunt-ends, a 100 ul aliquot of the resuspended DNA was digested with 5 units of BAL31 nuclease (New England BioLabs) for 10 min at 30°C in 200 ul BAL31 buffer . The digested DNA was phenol-extracted, ethanol-precipitated, redissolved in 100 ul TE buffer, and then size-fractionated by electrophoresis through a 1.0% low melting temperature agarose gel. The section containing DNA fragments 1.6-2.0 kb in size was excised from the gel, and the LGT agarose was melted and the resulting solution was extracted with phenol to separate the agarose from the DNA. DNA was ethanol precipitated and redissolved in 20 ul of TE buffer for ligation to vector.

A two-step ligation procedure was used to produce a plasmid library with 97% inserts, of which >99% were single inserts. The first ligation mixture (50 ul) contained 2 ug of DNA fragments, 2 ug pUC18 DNA (Pharmacia) cut with SmaI and dephosphorylated with bacterial alkaline phosphatase, and 10 units of T4 ligase (GIBCO/BRL) and was incubated at 14°C for 4 hr. The ligation mixture then was phenol extracted and ethanol precipitated, and the precipitated DNA was dissolved in 20 ul TE buffer and electrophoresed on a 1.0% low melting agarose gel. Discrete bands in a ladder were visualized by ethidium bromide-staining and UV illumination and identified by size as insert (i), vector (v), v+i, v+2i, v+3i, *etc.* The portion of the gel containing v+i DNA was excised and the v+i DNA was recovered and resuspended into 20 ul TE. The v+i DNA then was blunt-ended by T4 polymerase treatment for 5 min. at 37° C in a reaction mixture (50 ul) containing the v+i linears, 500 uM each of the 4 dNTPs, and 9 units of T4 polymerase (New England BioLabs), under recommended buffer conditions. After phenol extraction and ethanol precipitation the repaired v+i linears were dissolved in 20 ul TE. The final ligation to produce circles was carried out in a 50 ul reaction containing 5 ul of v+i linears and 5 units of T4 ligase at 14°C overnight. After 10 min. at 70°C the following day, the reaction mixture was stored at -20°C.

This two-stage procedure resulted in a molecularly random collection of single-insert plasmid recombinants with minimal contamination from double-insert chimeras (<1%) or free vector (<3%).

Since deviation from randomness can arise from propagation the DNA in the host, *E.coli* host cells deficient in all recombination and restriction functions (A. Greener, Strategies 3 (1):5 (1990)) were used to prevent rearrangements, deletions, and loss of clones by restriction. Furthermore, transformed cells were plated directly on antibiotic diffusion plates to avoid the usual broth recovery phase which allows multiplication and selection of the most rapidly growing cells.

Plating was carried out as follows. A 100 ul aliquot of Epicurian Coli SURE II Supercompetent Cells (Stratagene 200152) was thawed on ice and transferred to a chilled Falcon 2059 tube on ice. A 1.7 ul aliquot of 1.42 M beta-

mercaptoethanol was added to the aliquot of cells to a final concentration of 25 mM. Cells were incubated on ice for 10 min. A 1 ul aliquot of the final ligation was added to the cells and incubated on ice for 30 min. The cells were heat pulsed for 30 sec. at 42° C and placed back on ice for 2 min. The outgrowth period in liquid culture was eliminated from this protocol in order to minimize the preferential growth of any given transformed cell. Instead the transformation mixture was plated directly on a nutrient rich SOB plate containing a 5 ml bottom layer of SOB agar (5% SOB agar: 20 g tryptone, 5 g yeast extract, 0.5 g NaCl, 1.5% Difco Agar per liter of media). The 5 ml bottom layer is supplemented with 0.4 ml of 50 mg/ml ampicillin per 100 ml SOB agar. The 15 ml top layer of SOB agar is supplemented with 1 ml X-Gal (2%), 1 ml $MgCl_2$ (1 M), and 1 ml $MgSO_4$/100 ml SOB agar. The 15 ml top layer was poured just prior to plating. Our titer was approximately 100 colonies/10 ul aliquot of transformation.

All colonies were picked for template preparation regardless of size. Thus, only clones lost due to "poison" DNA or deleterious gene products would be deleted from the library, resulting in a slight increase in gap number over that expected.

3. Random DNA Sequencing

High quality double stranded DNA plasmid templates were prepared using an alkaline lysis method developed in collaboration with 5Prime → 3Prime Inc. (Boulder, CO). Plasmid preparation was performed in a 96-well format for all stages of DNA preparation from bacterial growth through final DNA purification. Average template concentration was determined by running 25% of the samples on an agarose gel. DNA concentrations were not adjusted.

Templates were also prepared from a *Staphylococcus aureus* lambda genomic library. An unamplified library was constructed in Lambda DASH II vector (Stratagene). *Staphylococcus aureus* DNA (> 100 kb) was partially digested in a reaction mixture (200 ul) containing 50 ug DNA, 1X Sau3AI buffer, 20 units Sau3AI for 6 min. at 23 C. The digested DNA was phenol-extracted and centrifuges over a 10- 40% sucroce gradient. Fractions containing genomic DNA of 15-25 kb were recovered by precipitation . One ul of fragments was used with 1 ul of DASHII vector (Stratagene) in the recommended ligation reaction. One ul of the ligation mixture was used per packaging reaction following the recommended protocol with the Gigapack II XL Packaging Extract Phage were plated directly without amplification from the packaging mixture (after dilution with 500 ul of recommended SM buffer and chloroform treatment). Yield was about $2.5x10^9$ pfu/ul.

An amplified library was prepared from the primary packaging mixture according to the manufactureer's protocol. The amplified library is stored frozen in 7% dimethylsulfoxide. The phage titer is approximately $1x10^9$ pfu/ml.

Mini-liquid lysates (0.1ul) are prepared from randomly selected plaques and template is prepared by long range PCR. Samples are PCR amplified using modified T3 and T7 primers, and Elongase Supermix (LTI).

Sequencing reactions are carried out on plasmid templates using a combination of two workstations (BIOMEK 1000 and Hamilton Microlab 2200) and the Perkin-Elmer 9600 thermocycler with Applied Biosystems PRISM Ready Reaction Dye Primer Cycle Sequencing Kits for the M13 forward (M13-21) and the M13 reverse (M13RP1) primers. Dye terminator sequencing reactions are carried out on the lambda templates on a Perkin-Elmer 9600 Thermocycler using the Applied Biosystems Ready Reaction Dye Terminator Cycle Sequencing kits. Modified T7 and T3 primers are used to sequence the ends of the inserts from the Lambda DASH II library. Sequencing reactions are on a combination of AB 373 DNA Sequencers and ABI 377 DNA sequencers. All of the dye terminator sequencing reactions are analyzed using the 2X 9 hour module on the AB 377. Dye primer reactions are analyzed on a combination of ABI 373 and ABI 377 DNA sequencers. The overall sequencing success rate very approximately is about 85% for M13-21 and M13RP1 sequences and 65% for dye-terminator reactions. The average usable read length is 485 bp for M13-21 sequences, 445bp for M13RP1 sequences, and 375 bp for dye-terminator reactions.

4. Protocol for Automated Cycle Sequencing

The sequencing was carried out using Hamilton Microstation 2200, Perkin Elmer 9600 thermocyclers, ABI 373 and ABI 377 Automated DNA Sequencers. The Hamilton combines pre-aliquoted templates and reaction mixes consisting of deoxy- and dideoxynucleotides, the thermostable Taq DNA polymerase, fluorescently-labelled sequencing primers, and reaction buffer. Reaction mixes and templates were combined in the wells of a 96-well thermocycling plate and transferred to the Perkin Elmer 9600 thermocycler. Thirty consecutive cycles of linear amplification (i.e.., one primer synthesis) steps were performed including denaturation, annealing of primer and template, and extension; i.e., DNA synthesis. A heated lid with rubber gaskets on the thermocycling plate prevents evaporation without the need for an oil overlay.

Two sequencing protocols were used: one for dye-labelled primers and a second for dye-labelled dideoxy chain terminators. The shotgun sequencing involves use of four dye-labelled sequencing primers, one for each of the four terminator nucleotide. Each dye-primer was labelled with a different fluorescent dye, permitting the four individual reactions to be combined into one lane of the 373 or 377 DNA Sequencer for electrophoresis, detection, and base-

calling. ABI currently supplies premixed reaction mixes in bulk packages containing all the necessary non-template reagents for sequencing. Sequencing can be done with both plasmid and PCR-generated templates with both dye-primers and dye- terminators with approximately equal fidelity, although plasmid templates generally give longer usable sequences.

Thirty-two reactions were loaded per ABI 373 Sequencer each day and 96 samples can be loaded on an ABI 377 per day. Electrophoresis was run overnight (ABI 373) or for 2 1/2 hours (ABI 377) following the manufacturer's protocols. Following electrophoresis and fluorescence detection, the ABI 373 or ABI 377 performs automatic lane tracking and base-calling. The lane-tracking was confirmed visually. Each sequence electropherogram (or fluorescence lane trace) was inspected visually and assessed for quality. Trailing sequences of low quality were removed and the sequence itself was loaded via software to a Sybase database (archived daily to 8mm tape). Leading vector polylinker sequence was removed automatically by a software program. Average edited lengths of sequences from the standard ABI 373 or ABI 377 were around 400 bp and depend mostly on the quality of the template used for the sequencing reaction.

INFORMATICS

1. Data Management

A number of information management systems for a large-scale sequencing lab have been developed. (For review see, for instance, Kerlavage *et al., Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences,* IEEE Computer Society Press, Washington D. C., 585 (1993)) The system used to collect and assemble the sequence data was developed using the Sybase relational database management system and was designed to automate data flow whereever possible and to reduce user error. The database stores and correlates all information collected during the entire operation from template preparation to final analysis of the genome. Because the raw output of the ABI 373 Sequencers was based on a Macintosh platform and the data management system chosen was based on a Unix platform, it was necessary to design and implement a variety of multi- user, client-server applications which allow the raw data as well as analysis results to flow seamlessly into the database with a minimum of user effort.

2. Assembly

An assembly engine (TIGR Assembler) developed for the rapid and accurate assembly of thousands of sequence fragments was enployed to generate contigs. The TIGR assembler simultaneously clusters and assembles fragments of the genome. In order to obtain the speed necessary to assemble more than 10^4 fragments, the algorithm builds a hash table of 12 bp oligonucleotide subsequences to generate a list of potential sequence fragment overlaps. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Beginning with a single seed sequence fragment, TIGR Assembler extends the current contig by attempting to add the best matching fragment based on oligonucleotide content. The contig and candidate fragment are aligned using a modified version of the Smith-Waterman algorithm which provides for optimal gapped alignments (Waterman, M. S., *Methods in Enzymology* 164: 765 (1988)). The contig is extended by the fragment only if strict criteria for the quality of the match are met. The match criteria include the minimum length of overlap, the maximum length of an unmatched end, and the minimum percentage match. These criteria are automatically lowered by the algorithm in regions of minimal coverage and raised in regions with a possible repetitive element. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Fragments representing the boundaries of repetitive elements and potentially chimeric fragments are often rejected based on partial mismatches at the ends of alignments and excluded from the current contig. TIGR Assembler is designed to take advantage of clone size information coupled with sequencing from both ends of each template. It enforces the constraint that sequence fragments from two ends of the same template point toward one another in the contig and are located within a certain ranged of base pairs (definable for each clone based on the known clone size range for a given library).

3. Identifying Genes

The predicted coding regions of the *Staphylococcus aureus* genome were initially defined with the program zorf, which finds ORFs of a minimum length. The predicted coding region sequences were used in searches against a database of all *Staphylococcus aureus* nucleotide sequences from GenBank (release 92.0), using the BLASTN search method to identify overlaps of 50 or more nucleotides with at least a 95% identity. Those ORFs with nucleotide sequence matches are shown in Table 1. The ORFs without such matches were translated to protein sequences and and compared to a non-redundant database of known proteins generated by combining the Swiss-prot, PIR and GenPept databases. ORFs of at least 80 amino acids that matched a database protein with BLASTP probability less than or equal to 0.01 are shown in Table 2. The table also lists assigned functions based on the closest match in the databases.

ORFs of at least 120 amino acids that did not match protein or nucleotide sequences in the databases at these levels are shown in Table 3.

ILLUSTRATIVE APPLICATIONS

1. Production of an Antibody to a *Staphylococcus aureus* Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells using any one of the methods known in the art. The protein can also be produced in a recombinant prokaryotic expression system, such as *E. coli*, or can by chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows.

2. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., Nature 256:495 (1975) or modifications of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., Meth. Enzymol. 70:419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. *et al.* Basic Methods in Molecular Biology Elsevier, New York. Section 21-2 (1989).

3. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than other and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigenadministered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al.*, J. Clin. Endocrinol. Metab. 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. *et al.*, Chap. 19 in:Handbook of Experimental Immunology, Wier, D., ed, Blackwell (1973). Plateau concentration of antibody is usually in the range of 0. 1 to 0. 2 mg/ml of serum (about 12M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in:Manual of Clinical Immunology, second edition, Rose and Friedman, eds., Amer. Soc. For Microbiology, Washington, D. C. (1980)

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi- quantitatively or qualitatively to identify the presence of antigen in a biological sample. In addition, they are useful in various animal models of Staphylococcal disease known to those of skill in the art as a means of evaluating the protein used to make the antibody as a potential vaccine target or as a means of evaluating the antibody as a potential immunothereapeutic reagent.

3. Preparation of PCR Primers and Amplification of DNA

Various fragments of the *Staphylococcus aureus* genome, such as those of Tables 1-3 and SEQ ID NOS:1-5,191 can be used, in accordance with the present invention, to prepare PCR primers for a variety of uses. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approxi-

mately the same. The PCR primers and amplified DNA of this Example find use in the Examples that follow.

4. Gene expr ssion from DNA Sequ nc s Corresponding t ORFs

A fragment of the *Staphylococcus aureus* genome provided in Tables 1-3 is introduced into an expression vector using conventional technology. Techniques to transfer cloned sequences into expression vectors that direct protein translation in mammalian, yeast, insect or bacterial expression systems are well known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism, as explained by Hatfield *et al.*, U. S. Patent No. 5,082,767, incorporated herein by this reference.

The following is provided as one exemplary method to generate polypeptide(s) from cloned ORFs of the *Staphylococcus aureus* genome fragment. Bacterial ORFs generally lack a poly A addition signal. The addition signal sequence can be added to the construct by, for example, splicing out the poly A addition sequence from pSG5 (Stratagene) using BglI and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene) for use in eukaryotic expression systems. pXT1 contains the LTRs and a portion of the gag gene of Moloney Murine Leukemia Virus. The positions of theLTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The *Staphylococcus aureus* DNA is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the *Staphylococcus aureus* DNA and containing restriction endonuclease sequences for PstI incorporated into the 5' primer and BglII at the 5' end of the corresponding *Staphylococcus aureus* DNA 3' primer, taking care to ensure that the *Staphylococcus aureus* DNA is positioned such that its followed with the poly A addition sequence. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with BglII, purified and ligated to pXT1, now containing a poly A addition sequence and digested BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 ug/ml G418 (Sigma, St. Louis, Missouri). The protein is preferably released into the supernatant. However if the protein has membrane binding domains, the protein may additionally be retained within the cell or expression may be restricted to the cell surface. Since it may be necessary to purify and locate the transfected product, synthetic 15-mer peptides synthesized from the predicted *Staphylococcus aureus* DNA sequence are injected into mice to generate antibody to the polypeptide encoded by the *Staphylococcus aureus* DNA.

Alternativly and if antibody production is not possible, the *Staphylococcus aureus* DNA sequence is additionally incorporated into eukaryotic expression vectors and expressed as, for example, a globin fusion. Antibody to the globin moiety then is used to purify the chimeric protein. Corresponding protease cleavage sites are engineered between the globin moiety and the polypeptide encoded by the *Staphylococcus aureus* DNA so that the latter may be freed from the formed by simple protease digestion. One useful expression vector for generating globin chimerics is pSG5 (Stratagene). This vector encodes a rabbit globin. Intron II of the rabbit globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques are well known to those skilled in the art of molecular biology. Standard methods are published in methods texts such as Davis *et al.*, cited elsewhere herein, and many of the methods are available from the technical assistance representatives from Stratagene, Life Technologies, Inc., or Promega. Polypeptides of the invention also may be produced using *in vitro* translation systems such as *in vitro* ExpressTM Translation Kit (Stratagene).

While the present invention has been described in some detail for purposes of clarity and understanding, one skilled in the art will appreciate that various changes in form and detail can be made without departing from the true scope of the invention.

All patents, patent applications and publications referred to above are hereby incorporated by reference.

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
1	1	1419	757	emb|X17301|SAHD	S.aureus DNA for hld gene and for part of agr gene	100	663	663
1	2	3273	2452	emb|X52543|SAAG	S.aureus agrA, agrB and hld genes	99	809	822
1	5	6418	5651	dbj|D14711|STAH	Staphylococcus aureus HSP10 and HSP60 genes	98	223	768
5	1	807	439	emb|X72700|SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidins	81	216	369
5	4	5031	3571	emb|X72700|SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidins	95	424	1461
10	1	86	904	gb|L25288|	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	98	715	819
16	5	5302	6246	gb|U35773|	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds	94	251	945
16	6	6249	7091	gb|U35773|	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds	99	843	843
16	7	7084	7584	gb|U35773|	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds	99	342	501
20	1	995	549	gb|L19300|	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	100	443	447
20	2	1011	841	gb|L19300|	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	91	137	171
20	3	2010	1798	gb|L19300|	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	100	110	213
20	4	5300	3825	gb|M16714|	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	100	948	1476
20	5	4788	4282	gb|M16714|	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	100	309	507
26	1	2	145	gb|U41072|	Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds	100	126	144
26	2	84	557	gb|U41072|	Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds	99	430	474
26	3	763	3531	emb|X74219|SAIL	S.aureus gene for isoleucyl-tRNA synthetase	99	2769	2769
29	3	1261	4392	gb|U66665|	Staphylococcus aureus DNA fragment with class II promoter activity	100	117	3132
31	14	14977	13463	emb|X73889|SAP1	S.aureus genes P1 and P2	99	1351	1515
31	15	14241	13855	emb|X73889|SAP1	S.aureus genes P1 and P2	98	258	387
38	17	14284	13112	gb|M12715|	S.aureus geh gene encoding lipase (glycerol ester hydrolase)	100	372	1173
38	19	13434	15518	gb|M12715|	S.aureus geh gene encoding lipase (glycerol ester hydrolase)	100	2085	2085

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
46	3	519	1727	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8D, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	1209	1209
46	3	1720	2295	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	576	576
46	4	2259	3182	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	97	924	924
46	5	3173	4498	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	1283	1326
46	6	4536	5720	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	1185	1185
46	7	6455	6120	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	99	278	336
48	1	2	955	gb|L25893|	Staphylococcus aureus recA gene, complete cds	99	954	954
50	3	4465	2924	emb|X85029|SAAH	S.aureus AhpC gene	100	88	1542
50	4	4108	3515	emb|X85029|SAAH	S.aureus AhpC gene	98	540	594
54	3	5074	3392	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	100	1668	1683
54	4	4865	4122	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	99	720	744
54	5	5056	4562	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	100	463	495
54	6	11386	8300	gb|J04151|	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	100	3087	3087
58	3	1743	2819	emb|X87104|SADN	S.aureus mdr, pbp4 and tagD genes (SG511-55 isolate)	89	68	1077
58	4	2858	3280	emb|X91786|SAPB	S.aureus abcA, pbp4, and tagD genes	99	423	423
58	5	6005	4701	emb|X91786|SAPB	S.aureus abcA, pbp4, and tagD genes	99	1305	1305
58	6	5677	5378	gb|U29478|	Staphylococcus aureus ABC transporter-like protein AbcA (abcA) gene, partial cds	100	300	300
58	7	5086	6840,	emb|X91786|SAPB	S.aureus abcA, pbp4, and tagD genes	99	1755	1755
72	1	888	445	gb|121854|	S.aureus agr gene encoding an accessory gene regulator protein, complete cds	100	444	444
72	2	2457	1453	emb|X52543|SAAG	S.aureus agrA, agrB and hld genes	99	673	1005

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
82	1	357	3917	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	2396	3561
82	2	4027	7677	emb|X89233|SARP	S.aureus DNA for rpoC gene	99	3171	3651
82	3	7745	8068	gb|U20869|	Staphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, ribosomal protein S7 (rpsG) and ORF 1 genes, partial cds	100	320	324
82	4	8103	8579	gb|U20869|	Staphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, ribosomal protein S7 (rpsG) and ORF 1 genes, partial cds	100	477	477
82	5	8618	8821	gb|U20869|	Staphylococcus aureus ribosomal protein S12 (rpsL) gene, complete cds, ribosomal protein S7 (rpsG) and ORF 1 genes, partial cds	100	154	204
84	1	18	191	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	164	174
84	2	189	893	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	94	705	705
84	3	887	1660	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	99	774	774
84	4	1584	3503	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	98	1920	1920
84	5	3394	4521	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	97	1128	1128
84	6	4519	5643	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	97	1125	1125
96	2	1245	3896	emb|Z18852|SACF	S.aureus gene for clumping factor	83	660	2652
97	2	625	882	gb|U41072|	Staphylococcus aureus isoleucyl-tRNA synthetase (ileS) gene, partial cds	97	68	258
111	1	3	452	gb|L41499|	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	100	450	450
111	2	526	1041	gb|L41499|	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	99	516	516
117	2	1278	1958	gb|M83994|	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	100	61	681

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name ( )	percent ident	HSP nt length	ORF nt length
118	4	3787	4254	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP10; ORF35, complete cds	99	467	468
130	4	2597	3640	emb|X13290|SATN	Staphylococcus aureus multi-resistance plasmid pSK1 DNA containing transposon Tn4003	78	956	1044
130	5	3813	4265	emb|Z16422|SADI	S.aureus dfrB gene for dihydrofolate reductase	98	416	453
130	6	4309	5172	emb|Z16422|SADI	S.aureus dfrB gene for dihydrofolate reductase	98	607	864
136	4	5296	6207	emb|X71437|SAGY	S.aureus genes gyrB, gyrA and recF (partial)	97	838	912
136	5	11680	8987	dbj|D10489|STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	100	2694	2694
136	6	12686	10940	dbj|D10489|STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	99	1947	1947
136	7	12592	11765	gb|S77055|	recF cluster: dnaA-replisome assembly protein...gyrB=DNA gyrase beta subunit (Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt)	99	822	828
143	3	4171	2867	gb|U36379|	Staphylococcus aureus S-adenosylmethionine synthetase gene, complete cds	99	1305	1305
143	4	3100	4281	gb|L42943|	Staphylococcus aureus (clone KIN50) phosphoenolpyruvate carboxykinase (pckA) gene, complete cds	100	1170	1182
143	5	4254	4718	gb|U51133|	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pckA) gene, complete cds	100	449	465
143	9	6977	7261	gb|U51132|	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menE), and o-succinylbenzoic acid synthetase (menC) genes, complete cds	100	75	285
143	10	9464	8361	gb|U51132|	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menE), and o-succinylbenzoic acid synthetase (menC) genes, complete cds	100	1104	1104
143	11	11232	9748	gb|U51132|	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menE), and o-succinylbenzoic acid synthetase (menC) genes, complete cds	100	1485	1485
143	12	10739	10320	gb|U51132|	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menE), and o-succinylbenzoic acid synthetase (menC) genes, complete cds	100	332	420
152	5	2454	3437	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	99	305	984
152	6	3513	4820	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	98	1308	1308
152	7	4818	6230	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	99	1413	1413
153	1	387	1526	gb|S77055|	recF cluster: dnaA-replisome assembly protein...gyrB=DNA gyrase beta subunit (Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt)	99	1140	1140
153	2	1877	2152	gb|S77055|	recF cluster: dnaA-replisome assembly protein...gyrB=DNA gyrase beta subunit (Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt)	100	276	276

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
153	3	2143	2289	gb|S77055|	recF cluster: dnaA=replisome assembly protein...gyrB=DNA gyrase beta subunit (Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt)	99	113	147
154	10	10792	9314	gb|U06451|	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	91	154	1479
154	11	9935	9615	gb|U06451|	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	99	229	321
154	12	9943	10167	gb|U06451|	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	94	123	225
154	13	10089	11501	gb|U06451|	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	99	1326	1413
159	2	2195	1212	dbj|D28879|STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	100	71	984
161	3	2596	2270	gb|M83994|	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	92	203	327
162	1	1406	705	gb|U21221|	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	100	702	702
163	4	1263	1772	gb|U19770|	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	96	127	510
164	7	4774	9117	dbj|D86727|D867	Staphylococcus aureus DNA for DNA polymerase III, complete cds	99	3470	4344
168	7	7448	6447	gb|U21636|	Staphylococcus aureus cmp-binding-factor 1 (cbf1) and ORF X genes, complete cds	100	1002	1002
168	8	9538	7961	gb|U21636|	Staphylococcus aureus cmp-binding-factor 1 (cbf1) and ORF X genes, complete cds	99	1158	1578
173	6	9240	7801	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	100	1440	1440
173	7	11252	9522	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	99	1731	1731
173	8	8285	8704	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	100	420	420
173	9	10168	9839	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	100	330	330
173	10	11815	10829	emb|X14827|SALA	Staphylococcus aureus lacC and lacD genes	100	987	987
173	11	12721	11774	emb|X14827|SALA	Staphylococcus aureus lacC and lacD genes	100	948	948
173	12	12838	12305	gb|M64724|	S.aureus tagatose 6-phosphate isomerase gene, complete cds	100	534	534
173	13	13243	12773	gb|M32103|	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	100	471	471
173	14	14633	13866	gb|M32103|	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	100	768	768

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
178	1	2	655	|gb|U52961|	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	115	654
178	2	2201	1482	|gb|U52961|	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	720	720
178	3	2361	1909	|gb|U52961|	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	453	453
178	4	1551	1853	|gb|U52961|	Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB (lrgB) genes, complete cds	100	303	303
178	5	3541	2777	|gb|L42945|	Staphylococcus aureus lytS and lytR genes, complete cds	99	765	765
178	6	3294	3025	|gb|L42945|	Staphylococcus aureus lytS and lytR genes, complete cds	99	270	270
181	1	1114	590	|gb|M61177|	S.aureus sigma factor (plaC) gene, complete cds	99	499	525
182	1	3	341	|emb|X61307|SASP	Staphylococcus aureus spa gene for protein A	98	277	339
182	2	690	2312	|gb|J01786|	S.aureus spa gene coding for protein A, complete cds	97	1332	1623
182	3	5861	4251	|emb|X61307|SASP	Staphylococcus aureus spa gene for protein A	99	119	1611
185	1	3	824	|gb|U31979|	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroquinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	90	132	822
191	3	841	2760	|emb|X17679|SACO	Staphylococcus aureus coa gene for coagulase	99	1920	1920
191	4	2967	3143	|emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	99	177	177
191	5	5768	4566	|emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	99	250	1203
196	1	1741	872	|gb|L36472|	Staphylococcus aureus lysyl-tRNA sythetase gene, complete cds, transfer RNA (tRNA) genes, 5S ribosomal RNA (5S rRNA) gene, 16S ribosomal RNA (16S rRNA) gene, 23S ribosomal RNA (23S rRNA) gene	99	870	870
198	3	1688	2011	|emb|X93205|SAPT	S.aureus ptsH and ptsI genes	99	324	324
198	4	2005	2310	|emb|X93205|SAPT	S.aureus ptsH and ptsI genes	97	304	306
202	1	163	1305	|emb|X97985|SA12	S.aureus orfs 1,2,3 & 4	99	1143	1143
202	2	1303	2175	|emb|X73889|SAP1	S.aureus genes P1 and P2	94	444	873
210	1	3114	1558	|dbj|D17366|STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	99	1552	1557
210	2	2939	2232	|gb|L41499|	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	99	684	708
214	11	7429	7770	|dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	96	157	342

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
216	3	398	1318	emb|X72700|SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidins	88	265	921
219	2	1810	1071	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	100	60	738
219	3	2979	2035	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	99	945	945
219	4	4359	3196	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	99	1164	1164
219	5	7044	5876	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	98	1869	1869
219	6	6557	5883	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	99	675	675
219	7	6801	6334	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	98	468	468
221	8	10816	10034	gb|L19298|	Staphylococcus aures phosphatidylinositol-specific phospholipase C (plc) gene, complete cds	91	67	783
223	1	2855	1506	gb|U73374|	Staphylococcus aureus type 8 capsulo genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	99	102	1350
234	1	2	1357	emb|X97985|SA12	S.aureus orfs 1,2,3 & 4	100	176	1356
234	2	1694	2485	emb|X97985|SA12	S.aureus orfs 1,2,3 & 4	100	792	792
234	3	2648	3148	emb|X97985|SA12	S.aureus orfs 1,2,3 & 4	99	501	501
234	4	3120	4604	emb|X97985|SA12	S.aureus orfs 1,2,3 & 4	99	1305	1485
236	6	3826	5322	gb|U48826|	Staphylococcus aureus elastin binding protein (ebpS) gene, complete cds	96	648	1497
248	1	2	403	emb|X62288|SAPE	S.aureus DNA for penicillin-binding protein 2	100	103	402
248	2	388	852	gb|L25426|	Staphylococcus aureus penicillin-binding protein 2 (pbp2) gene, complete cds	99	465	465
253	2	1539	1093	gb|U46541|	Staphylococcus aureus sarA gene, complete cds	96	447	447
254	2	150	1835	gb|U57060|	Staphylococcus aureus scdA gene, complete cds	94	142	1686
254	3	1973	2728	gb|U57060|	Staphylococcus aureus scdA gene, complete cds	99	756	756
260	1	2	1900	gb|M90693|	Staphylococcus aureus glycerol ester hydrolase (lip) gene, complete cds	99	1213	1899
265	1	1	942	dbj|D21131|STAS	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	99	941	942

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
265	2	688	476	dbj|D21131|STAS	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	99	213	213
265	3	2418	1765	dbj|D21131|STAS	Staphylococcus aureus gene for a participant in homogeneous expression of high-level methicillin resistance, complete cds	98	69	654
266	1	2	1018	dbj|D14711|STAH	Staphylococcus aureus HSP10 and HSP60 genes	98	743	1017
282	1	1	525	gb|S72488|	hemB=porphobilinogen synthase (Staphylococcus aureus, SA1959, Genomic, 1087 nt)	100	110	525
282	2	516	1502	gb|S72488|	hemB=porphobilinogen synthase (Staphylococcus aureus, SA1959, Genomic, 1087 nt)	100	952	987
284	1	3	170	gb|M63176|	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	98	84	168
284	2	282	1034	gb|M63176|	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	100	712	753
284	3	1028	2026	gb|M63176|	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	99	979	999
284	4	1990	2202	gb|M63176|	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	98	187	213
289	3	1536	1991	gb|M32470|	S.aureus Sau3AI-restriction-enzyme and Sau3AI-modification-enzyme genes, complete cds	99	338	456
303	1	2	868	gb|L01055|	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	99	867	867
303	2	1409	2383	gb|L01055|	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	100	975	975
303	3	2367	3161	gb|L01055|	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	99	793	795
305	1	2707	1355	dbj|D17366|STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	99	1343	1353
311	1	2628	1315	gb|L42945|	Staphylococcus aureus lytS and lytR genes, complete cds	98	1314	1314
312	6	7019	7870	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	74	351	852
323	1	1998	1003	gb|U31175|	Staphylococcus aureus D-specific D-2-hydroxyacid dehydrogenase (ddh) gene, complete cds	98	996	996
326	1	1	237	emb|Y00356|SASP	Staphylococcus aureus V8 serine protease gene	100	108	237
338	1	687	388	emb|X64389|SALE	S.aureus leuF-PB3 gene for F component of leucocidin R	98	259	300
338	2	1828	1088	emb|X64389|SALE	S.aureus leuF-PB3 gene for F component of leucocidin R	97	137	741

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
342	2	579	1754	gb|U06462|	Staphylococcus aureus SA4 FtsZ (ftsZ) gene, complete cds	100	1176	1176
344	2	517	1248	emb|V01281|SANU	S.aureus mRNA for nuclease	98	732	732
349	1	457	230	gb|M20393|	S.aureus bacteriophage phi-11 attachment site (attB)	96	172	228
353	1	1016	516	gb|MM3994|	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	100	187	501
353	2	1582	1046	gb|M83994|	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	99	537	537
356	1	3	674	gb|U20503|	Staphylococcus aureus MHC class II analog gene, complete cds	75	671	672
361	1	1	903	gb|L19298|	Staphylococcus aures phosphatidylinositol-specific phospholipase C (plc) gene, complete cds	98	747	903
361	2	1103	1507	gb|L19298|	Staphylococcus aures phosphatidylinositol-specific phospholipase C (plc) gene, complete cds	97	68	405
373	1	3	1148	emb|X62288|SAPE	S.aureus DNA for penicillin-binding protein 2	99	1146	1146
389	3	1904	1248	emb|X62282|SATS	S.aureus target site DNA for IS431 insertion	97	349	657
400	1	1	540	emb|X61716|SAHL	S.aureus hlb gene encoding sphingomyelinase	99	389	540
400	2	1693	1187	emb|X13404|SAHL	Staphylococcus aureus hlb gene for beta-hemolysin	99	178	507
408	1	1810	1049	gb|S76213|	asp23=alkaline shock protein 23 (methicillin resistant) [Staphylococcus aureus, 912, Genomic, 1360 nt]	99	163	762
418	1	2	217	gb|L41499|	Staphylococcus aureus ORF1, partial cds, ORF2, ORF3, autolysin (atl) genes, complete cds	100	216	216
418	2	854	639	dbj|D17366|STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	100	188	216
421	2	1262	2509	gb|L43098|	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	99	1248	1248
422	1	2	325	gb|K02985|	S.aureus (strain RN450) transposon Tn554 insertion site	96	200	324
427	1	865	434	dbj|D28879|STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	100	432	432
427	2	1829	1122	dbj|D28879|STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	100	151	708
435	1	2	808	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	100	556	807
435	2	832	999	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	100	134	168
436	1	1341	685	emb|X17688|SAFE	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	97	657	657

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match Acession	match gene name	percent ident	HSP nt length	ORF nt length
436	2	2403	1657	emb|X17688|SAFE	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	100	294	747
442	1	347	1300	emb|X72700|SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidins	84	204	954
445	2	1906	2178	gb|L01055|	Staphylococcus aureus gamma-hemolysin components A, B and C (hlgA, hlgB, hglC) genes, complete cds	98	187	273
447	1	167	1078	gb|U19770|	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	100	514	912
447	2	1176	1784	gb|U19770|	Staphylococcus aureus pyrrolidone carboxyl peptidase (pcp) gene, complete cds	96	597	609
454	3	7309	4319	emb|Z18852|SACF	S.aureus gene for clumping factor	75	653	2991
472	4	7896	5479	gb|L25288|	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	99	2418	2418
472	5	8120	6792	gb|L25288|	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	99	1328	1329
475	2	566	889	emb|X52543|SAAG	S.aureus agrA, agrB and hld genes	100	76	324
481	4	1922	1560	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	250	363
481	5	1244	1534	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	224	291
487	2	1388	1188	gb|M83994|	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	98	72	201
489	1	2737	1370	gb|U21221|	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	99	1368	1368
503	2	1135	653	gb|M83994|	Staphylococcus aureus prolipoprotein signal peptidase (lsp) gene, complete cds	100	108	483
511	3	1613	2242	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	84	323	630
511	4	3122	2700	gb|S76213|	asp23=alkaline shock protein 23 (methicillin resistant) [Staphylococcus aureus, 912, Genomic, 1360 nt]	96	423	423
520	2	758	1297	emb|X72014|SAFI	S.aureus fib gene for fibrinogen-binding protein	99	540	540
520	3	1436	1801	eml|X72013|SAFI	S.aureus fib gene for fibrinogen-binding protein	99	221	366
526	1	2150	1092	dbj|D17366|STAA	Staphylococcus aureus atl gene for autolysin, complete cds and other ORFs	99	641	1059

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
528	2	58	963	gb|L19300|	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	99	260	906
528	3	1098	2870	gb|L19300|	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	99	866	1773
530	1	3	434	gb|U31979|	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroquinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	99	432	432
530	2	1211	2395	gb|U31979|	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroquinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	91	1185	1185
530	3	2409	2801	gb|U31979|	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroquinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	88	181	393
530	4	2690	3484	gb|L05004|	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	100	75	795
530	5	3482	4792	gb|L05004|	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	99	905	1311
530	6	4790	5380	gb|L05004|	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	100	196	591
539	1	3	338	emb|X76490|SAGL	S.aureus (bb270) glnA and glnR genes	99	336	336
539	2	336	527	emb|X76490|SAGL	S.aureus (bb270) glnA and glnR genes	100	189	192
554	1	727	365	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	100	54	363
554	2	2175	1252	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	99	918	924
554	3	1574	1374	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	96	122	201
584	2	1019	705	gb|U21221|	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	99	306	315
587	3	1475	4288	emb|Z18852|SACP	S.aureus gene for clumping factor	98	2588	2814
598	1	3881	1953	dbj|D28879|STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	99	1873	1929

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
605	1	2	745	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	98	338	744
609	1	1628	816	emb|X76490|SAGL	S.aureus (bb270) glnA and glnR genes	100	495	813
614	1	1280	642	gb|M32103|	Staphylococcus aureus lac repressor (lacR) gene, complete cds and lacA repressor (lacA), partial cds	99	639	639
626	1	2508	1255	gb|M63176|	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	100	225,	1254
626	2	3315	2284	gb|M63176|	Staphylococcus aureus helicase required for T181 replication (pcrA) gene, complete cds	99	838	1032
629	1	1999	1001	emb|X17688|SAFE	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	99	990	999
629	2	1407	1195	emb|X17688|SAFE	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	98	194	213
631	2	5126	3228	emb|Z18852|SACF	S.aureus gene for clumping factor	82	489	1899
632	1	3	551	emb|Z30588|SAST	S.aureus (RN4220) genes for potential ABC transporter and potential membrane spanning protein	99	549	549
632	2	529	1323	emb|Z30588|SAST	S.aureus (RN4220) genes for potential ABC transporter and potential membrane spanning protein	99	795	795
651	1	1909	1070	gb|L19300|	Staphylococcus aureus DNA sequence encoding three ORFs, complete cds; prophage phi-11 sequence homology, 5' flank	99	478	840
657	2	1800	1105	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	84	456	696
662	1	908	456	emb|X13404|SAHL	Staphylococcus aureus hlb gene for beta-hemolysin	100	369	453
662	2	230	475	emb|X13404|SAHL	Staphylococcus aureus hlb gene for beta-hemolysin	100	246	246
662	3	746	1399	emb|X13404|SAHL	Staphylococcus aureus hlb gene for beta-hemolysin	99	653	654
682	1	956	480	gb|M63177|	S.aureus sigma factor (plaC) gene, complete cds	100	136	477
685	1	1182	592	gb|U65000|	Staphylococcus aureus type-I signal peptidase SpsA (spsA) gene, and type-I signal peptidase SpsB (spsB) gene, complete cds	98	534	591
685	2	1716	1153	gb|U65000|	Staphylococcus aureus type-I signal peptidase SpsA (spsA) gene, and type-I signal peptidase SpsB (spsB) gene, complete cds	96	564	564
697	1	3	527	gb|M63177|	S.aureus sigma factor (plaC) gene, complete cds	100	195	525
697	2	485	784	gb|M63177|	S.aureus sigma factor (plaC) gene, complete cds	97	280	300

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
710	1	15	503	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dit operon ditA, ditB, ditC and ditD genes,complete cds	99	217	489
733	1	26	205	gb|M80252|	Staphylococcus aureus norA1199 gene (which mediates active efflux of fluoroquinolones), complete cds	97	140	180
741	1	1736	1197	dbj|D83951|STAL	Staphylococcus aureus DNA for LukM component, LukF-PV like component, complete cds	81	522	540
752	1	1	636	emb|Y00356|SASP	Staphylococcus aureus V8 serine protease gene	99	618	636
752	2	508	956	emb|Y00356|SASP	Staphylococcus aureus V8 serine protease gene	99	340	369
756	1	1108	709	emb|X01645|SATO	Staphylococcus aureus (Wood 46) gene for alpha-toxin	98	567	600
777	1	1582	950	emb|Z49245|SA42	S.aureus partial sod gene for superoxide dismutase	99	429	633
780	1	1111	557	gb|U20503|	Staphylococcus aureus MHC class II analog gene, complete cds	86	550	555
784	1	73	687	gb|U63529|	Staphylococcus aureus novel antigen gene, complete cds	99	568	615
797	1	182	544	dbj|D14711|STAH	Staphylococcus aureus HSP10 and HSP60 genes	98	363	363
798	1	532	302	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	95	196	231
823	1	3	467	gb|S77055|	rocF cluster: dnaA-replisome assembly protein...gyrB=DNA gyrase beta subunit [Staphylococcus aureus, YB886, Genomic, 5 genes, 3573 nt]	99	156	465
848	1	348	175	gb|L25288|	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	99	174	174
848	2	476	318	gb|L25288|	Staphylococcus aureus gyrase-like protein alpha and beta subunit (grlA and grlB) genes, complete cds	100	131	159
866	1	792	397	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	395	396
883	1	1	285	dbj|D90119|STAN	S. aureus norA gene	99	131	285
884	1	606	334	emb|X52543|SAAG	S.aureus agrA, agrB and hld genes	98	265	273
884	2	716	522	emb|X52543|SAAG	S.aureus agrA, agrB and hld genes	100	195	195
912	2	517	681	emb|Z30588|SAST	S.aureus (RN4220) genes for potential ABC transportor and potential membrane spanning protein	99	163	165
917	1	2	265	gb|M64724|	S.aureus tagatose 6-phosphate isomerase gene, complete cds	99	247	264
917	2	238	396	gb|M64724|	S.aureus tagatose 6-phosphate isomerase gene, complete cds	95	147	159
918	1	2426	1215	emb|X93205|SAPT	S.aureus ptsH and ptsI genes	99	1212	1212

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
967	1	1	411	dbj|D90119|STAN	S. aureus norA gene	97	395	411
991	1	672	337	emb|X52543|SAAG	S.aureus agrA, agrB and hld genes	99	336	336
1000	1	1117	845	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	78	190	273
1001	1	498	265	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	99	234	234
1010	1	1	285	gb|U21221|	Staphylococcus aureus hyaluronate lyase (hysA) gene, complete cds	99	224	285
1046	1	656	330	emb|X72700|SAPV	S.aureus genes for S and F components of Panton-Valentine leucocidins	85	205	327
1060	1	480	286	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	99	180	195
1073	1	1176	589	gb|K02985|	S.aureus (strain RN450) transposon Tn554 insertion site	100	131	588
1079	1	3	230	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	99	228	228
1079	2	218	484	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	100	267	267
1079	3	460	645	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	100	186	186
1092	1	289	146	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	98	124	144
1143	1	1	243	gb|M41177|	S.aureus sigma factor (plaC) gene, complete cds	99	243	243
1157	1	2	136	emb|Z48003|SADN	S.aureus gene for DNA polymerase III	97	127	135
1189	1	720	361	gb|S74031|	norA=NorA (ISP794) [Staphylococcus aureus, NCTC 8325, Insertion, 1820 nt]	99	360	360
1190	1	2	283	gb|M21854|	S.aureus agr gene encoding an accessory gene regulator protein, complete cds	100	282	282
1190	2	1127	888	emb|X52543|SAAG	S.aureus agrA, agrB and hld genes	100	240	240
1225	1	2	163	emb|X17679|SACO	Staphylococcus aureus coa gene for coagulase	97	124	162
1243	1	2	529	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	99	495	528
1244	1	1	210	/gi|S74031|	norA=NorA (ISP794) [Staphylococcus aureus, NCTC 8325, Insertion, 1820 nt]	100	210	210
1301	1	41	472	emb|X76490|SAGL	S.aureus (tb270) glnA and glnR genes	99	299	432

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
1315	1	18	326	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	98	277	309
1519	1	2	175	dbj|D28879|STAP	Staphylococcus aureus gene for penicillin-binding protein 1, complete cds	98	139	174
1663	1	1346	675	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	98	672	672
1797	1	684	324	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	99	321	321
1857	1	1	192	gb|M90536|	Staphylococcus aureus alpha-hemolysin gene, 3' end	98	192	192
1923	1	2	181	emb|X17688|SAFE	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	100	180	180
1957	1	2	346	gb|U60589|	Staphylococcus aureus novel antigen gene, complete cds	99	345	345
1988	1	1	402	dbj|D86240|D862	Staphylococcus aureus gene for unkown function and dlt operon dltA, dltB, dltC and dltD genes,complete cds	100	402	402
2100	1	414	208	gb|M63177|	S.aureus sigma factor (plaC) gene, complete cds	99	207	207
2199	1	1	402	gb|U66664|	Staphylococcus aureus DNA fragment with class II promoter activity	99	131	402
2537	1	308	156	emb|X17688|SAFE	S.aureus factor essential for expression of methicillin resistance (femA) gene, complete cds, and trpA gene, 3' end	99	153	153
2891	1	2	400	gb|L25426|	Staphylococcus aureus penicillin-binding protein 2 (pbp2) gene, complete cds	99	399	399
2950	1	778	398	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	100	358	381
2971	1	3	398	gb|U51132|	Staphylococcus aureus o-succinylbenzoic acid CoA ligase (menE), and o-succinylbenzoic acid synthetase (menC) genes, complete cds	97	272	396
2978	1	618	328	gb|U31979|	Staphylococcus aureus chorismate synthase (aroC) and nucleoside diphosphate kinase (ndk) genes, complete cds, dehydroquinate synthase (aroB) and geranylgeranyl pyrophosphate synthetase homolog (gerCC) genes, partial cds	98	250	291
2985	1	832	464	emb|X17679|SACO	Staphylococcus aureus coa gene for coagulase	98	347	369
3006	1	2170	1784	gb|U11779|	Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV30 16S-23S rRNA spacer region	87	82	387
3008	1	474	238	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	88	178	237
3008	2	451	281	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	97	120	171

TABLE 1

S aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP length	ORF nt length
3011	1	793	398	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	93	72	396
3019	1	2	235	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	97	234	234
3023	1	81	233	gb|U06451|	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	87	100	153
3029	1	90	287	gb|U51133|	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka) gene, complete cds	100	135	198
3039	1	18	164	gb|U51133|	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka) gene, complete cds	97	135	147
3039	2	70	327	gb|U51133|	Staphylococcus aureus phosphoenolpyruvate carboxykinase (pcka) gene, complete cds	77	183	258
3056	1	3	215	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	213	213
3059	1	1	261	dbj|D30690|STAN	Staphylococcus aureus genes for ORF37; HSP20; HSP70; HSP40; ORF35, complete cds	98	234	261
3073	1	27	284	gb|U06451|	Staphylococcus aureus proline permease homolog (putP) gene, complete cds	99	229	258
3074	1	2	397	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	96	250	396
3088	1	3	239	dbj|D86727|D867	Staphylococcus aureus DNA for DNA polymerase III, complete cds	95	215	237
3097	1	444	244	emb|Z48003|SAEN	S.aureus gene for DNA polymerase III	97	160	201
3102	1	307	155	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	97	142	153
3121	1	568	398	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	100	88	171
3125	1	463	233	emb|X89233|SARP	S.aureus DNA for rpoC gene	98	192	231
3133	1	2	175	emb|Z18852|SACF	S.aureus gene for clumping factor	96	154	174
3160	1	420	211	dbj|D10489|STAC	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	89	197	210
3176	1	1	378	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	96	91	378
3192	1	420	211	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	98	72	210
3210	1	3	143	gb|U76714|	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	96	141	141

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
3232	3	2106	1282	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	71	257	825
3338	1	2	394	emb|X69233|SARP	S.aureus DNA for rpoC gene	99	356	393
3543	1	392	614	gb|L11510|	Staphylococcus aureus transfer RNA sequence with two rRNAs	99	102	243
3555	1	637	320	emb|218852|SACF	S.aureus gene for clumping factor	99	307	318
3559	1	3	182	emb|X17679|SACO	Staphylococcus aureus coa gene for coagulase	100	141	180
3559	2	95	311	emb|X17679|SACO	Staphylococcus aureus coa gene for coagulase	98	174	219
3563	1	278	141	gb|U35773|	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds	100	79	138
3563	2	527	363	gb|U35773|	Staphylococcus aureus prolipoprotein diacylglyceryl transferase (lgt) gene, complete cds	98	162	165
3566	1	3	422	emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	98	175	420
3588	1	2	262	gb|L43098|	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	99	253	261
3601	1	1	350	gb|L03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	99	345	348
3600	1	758	381	emb|218852|SACF	S.aureus gene for clumping factor	72	346	378
3602	1	788	396	emb|218852|SACF	S.aureus gene for clumping factor	98	319	393
3656	1	1013	528	emb|218852|SACF	S.aureus gene for clumping factor	84	403	486
3682	1	3	236	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	231	234
3682	2	224	415	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	112	192
3693	1	758	423	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	100	229	336
3702	1	593	154	gb|L11510|	Staphylococcus aureus transfer RNA sequence with two rRNAs	96	81	240
3725	1	924	463	emb|218852|SACF	S.aureus gene for clumping factor	71	367	462
3761	1	809	450	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	85	333	360
3767	1	1	402	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	98	387	402

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name ( )	percent ident	HSP nt length	ORF nt length
3775	1	2	286	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	227	285
3786	1	456	229	dbj|D10489|STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	100	204	228
3786	2	542	366	dbj|D10489|STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	95	123	177
3798	1	3	251	emb|X17679|SACO	Staphylococcus aureus coa gene for coagulase	99	249	249
3813	1	793	398	gb|J04151|	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	98	396	396
3819	1	184	402	emb|X68425|SA23	S.aureus gene for 23S rRNA	99	161	219
3844	1	932	468	gb|U48826|	Staphylococcus aureus elastin binding protein (ebpS) gene, complete cds	87	204	465
3845	1	1	381	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	94	356	381
3856	1	798	400	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	76	192	399
3859	1	1049	573	emb|Z18852|SACF	S.aureus gene for clumping factor	85	367	477
3871	1	650	327	gb|M76716|	Staphylococcus aureus peptidoglycan hydrolase gene, complete cds	100	299	324
3876	1	2	253	dbj|D10489|STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	100	217	252
3877	1	572	288	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	97	209	285
3878	1	1	237	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	96	155	237
3888	1	3	173	emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	98	171	171
3893	1	1	183	emb|X89233|SARP	S.aureus DNA for rpoC gene	100	170	183
3893	2	181	357	emb|X89233|SARP	S.aureus DNA for rpoC gene	98	79	177
3894	1	3	485	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	450	483
3895	1	816	420	gb|J04151|	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	99	411	417
3905	1	48	239	gb|L05004|	Staphylococcus aureus dehydroquinate synthase (aroD) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	100	159	192
3905	2	188	400	gb|L05004|	Staphylococcus aureus dehydroquinate synthase (aroD) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	97	88	213

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
3910	1	3	359	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	99	278	357
3915	1	1	330	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	75	175	330
3964	1	691	347	emb|Z48003|SADN	S.aureus gene for DNA polymerase III	100	295	345
4007	1	199	390	emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	98	163	192
4036	1	3	371	dbj|D10489|STAG	Staphylococcus aureus genes for DNA gyrase A and B, complete cds	99	339	369
4046	1	692	348	emb|Z18852|SACF	S.aureus gene for clumping factor	87	221	345
4060	1	1	375	emb|Z18852|SACF	S.aureus gene for clumping factor	96	271	375
4061	1	860	432	emb|Z48003|SADN	S.aureus gene for DNA polymerase III	99	429	429
4062	1	606	304	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	75	198	303
4085	1	58	402	gb|U11786|	Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV42 16S-23S rRNA spacer region	98	127	345
4088	1	2	301	gb|L43098|	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	99	227	300
4093	1	2	277	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	99	276	276
4097	1	1	402	emb|Z18852|SACF	S.aureus gene for clumping factor	74	307	402
4116	1	22	402	gb|L05004|	Staphylococcus aureus dehydroquinate synthase (aroB) gene, 3' end cds; 3-phosphoshikimate-1-carboxyvinyltransferase (aroA) gene, complete cds; ORF3, complete cds	98	157	381
4125	1	240	401	gb|U73374|	Staphylococcus aureus type 8 capsule genes, cap8A, cap8B, cap8C, cap8D, cap8E, cap8F, cap8G, cap8H, cap8I, cap8J, cap8K, cap8L, cap8M, cap8N, cap8O, cap8P, complete cds	100	86	162
4149	1	35	247	gb|J04151|	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	99	200	213
4151	1	629	366	gb|L14017|	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	87	150	264
4154	1	754	398	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	297	357
4179	1	1	294	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	98	240	294

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match Accession	match gene name ( )	percent ident	HSP nt length	ORF nt length
4203	1	1	255	emb|X89233|SARP	S.aureus DNA for rpoC gene	99	239	255
4206	1	1	303	emb|Z18852|SACF	S.aureus gene for clumping factor	100	236	303
4206	2	195	344	emb|Z18852|SACF	S.aureus gene for clumping factor	95	65	150
4208	1	108	314	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	89	76	207
4216	1	656	330	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	98	326	327
4226	1	594	298	gb|L11530|	Staphylococcus aureus transfer RNA sequence with two rRNAs	97	132	297
4260	1	216	383	gb|U11784|	Staphylococcus aureus methicillin-resistant ATCC 33952 clone RRNV40 16S-23S rRNA spacer region	83	141	168
4272	1	355	179	emb|Z48003|SADN	S.aureus gene for DNA polymerase III	100	164	177
4276	1	4	177	emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	99	150	174
4277	1	1	270	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	265	270
4282	1	691	377	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	98	282	315
4291	1	379	191	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	183	189
4295	1	3	329	emb|X16457|SAST	Staphylococcus aureus gene for staphylocoagulase	94	144	327
4313	1	435	280	gb|L11530|	Staphylococcus aureus transfer RNA sequence with two rRNAs	100	94	156
4315	1	3	185	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	100	158	183
4315	2	101	310	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	98	75	210
4327	1	1	294	gb|L43098|	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	98	294	294
4360	1	603	319	gb|U02910|	Staphylococcus aureus ATCC 25923 16S rRNA gene, partial sequence	100	116	285
4364	1	3	146	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	95	140	144
4388	1	167	310	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	73	119	144

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	percent ident	HSP nt length	ORF nt length
4401	1	2	313	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	97	243	312
4421	1	36	281	dbj|D12572|STA2	Staphylococcus aureus rrnA gene for 23S ribosomal RNA	100	112	246
4426	1	3	293	emb|Z18852|SACF	S.aurous gene for clumping factor	85	185	291
4428	1	493	248	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	139	246
4462	1	2	271	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	99	270	270
4466	1	1	240	emb|Z18852|SACF	S.aureus gene for clumping factor	99	231	240
4469	1	1	312	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	99	265	312
4485	1	3	263	gb|L43098|	Transposon Tn5404 and insertion sequences IS1181 and IS1182 (from Staphylococcus aureus) DNA	98	259	261
4492	1	74	400	gb|M86227|	Staphylococcus aureus DNA gyrase B subunit (gyrB) RecF homologue (recF) and DNA gyrase A subunit (gyrA) gene, complete cds	85	104	327
4497	1	515	269	emb|Z18852|SACF	S.aureus gene for clumping factor	99	213	267
4529	1	2	172	emb|X64172|SARP	S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomal protein L7/L12, hypothetical protein ORF202, DNA-directed RNA polymerase beta & beta' chains	100	151	171
4547	1	1	300	emb|X62992|SAFN	S.aureus fnbB gene for fibronectin binding protein B	100	157	300
4554	1	318	160	emb|Z18852|SACF	S.aureus gene for clumping factor	84	126	159
4565	1	9	227	emb|Z18852|SACF	S.aureus gene for clumping factor	84	213	219
4569	1	79	222	emb|Z18852|SACF	S.aureus gene for clumping factor	98	127	144
4608	1	22	216	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	92	168	195
4614	1	464	234	emb|Z18852|SACF	S.aureus gene for clumping factor	86	169	231
4623	1	105	302	gb|J04151|	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	99	152	198
4632	1	18	206	gb|J03479|	S.aureus enzyme III-lac (lacF), enzyme II-lac (lacE), and phospho-beta-galactosidase (lacG) genes, complete cds	98	183	189
4646	1	1	222	emb|Z18852|SACF	S.aureus gene for clumping factor	84	100	222
4687	1	2	166	gb|J04151|	S.aureus fibronectin-binding protein (fnbA) mRNA, complete cds	98	156	165

TABLE 1

S. aureus - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name ( )	percent ident	HSP nt length	ORF nt length
4695	1	313	158	gi|1140171	Staphylococcus aureus methicillin-resistance protein (mecR) gene and unknown ORF, complete cds	75	155	156
4703	1	1	153	emb|X58434|SAPD	S.aureus pdhB, pdhC and pdhD genes for pyruvate decarboxylase, dihydrolipoamide acetyltransferase and dihydrolipoamide dehydrogenase	98	103	153

TABLE 1

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
20	6	5089	4679	gi|511839	ORF1 [Staphylococcus bacteriophage phi 11]	100	100	411
149	3	2032	1577	pir|B49703|B497	int gene activator RinA - bacteriophage phi 11	100	100	456
149	5	2109	1912	gi|166161	Bacteriophage phi-11 int gene activator [Staphylococcus actariophage phi 11]	100	100	198
349	2	558	409	gi|166159	integrase (int) [Staphylococcus bacteriophage phi 11]	100	100	150
398	1	1372	707	gi|166159	integrase (int) [Staphylococcus bacteriophage phi 11]	100	99	666
398	2	783	1001	gi|455128	excisionase (xis) [Staphylococcus bacteriophage phi 11]	100	100	219
502	4	1914	1744	gi|1204912	H. influenzae predicted coding region HI0660 [Haemophilus influenzae]	100	71	171
849	1	2	262	gi|1373002	polyprotein [Bean common mosaic virus]	100	46	261
1349	1	277	140	gi|143359	protein synthesis initiation factor 2 (infB) [Bacillus subtilis] gi|49319 IF2 gene product [Bacillus subtilis]	100	82	138
2880	1	21	308	gi|862933	protein kinase C inhibitor-I [Homo sapiens]	100	98	288
3085	1	428	216	gi|1354211	PET112-like protein [Bacillus subtilis]	100	100	213
4168	2	571	398	gi|1354211	PET112-like protein [Bacillus subtilis]	100	100	174
331	1	2	247	gi|426473	nusG gene product [Staphylococcus carnosus]	98	95	246
207	2	1272	1463	gi|460259	enolase [Bacillus subtilis]	97	90	192
331	2	395	850	gi|581638	hll protein [Staphylococcus carnosus]	97	93	456
366	1	39	215	gi|66161	Bacteriophage phi-11 int gene activator (Staphylococcus actariophage phi 11)	97	95	177
680	3	718	936	gi|426473	nusG gene product [Staphylococcus carnosus]	97	97	219
3578	1	284	144	gi|1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	97	79	141
157	1	321	518	gi|1022726	unknown [Staphylococcus haemolyticus]	96	88	198
205	33	16470	16147	gi|1165302	S10 [Bacillus subtilis]	96	91	324
3919	1	48	401	gi|971784	Clp-like ATP-dependent protease binding subunit [Bos taurus]	96	81	354
4133	1	830	417	gi|1022726	unknown [Staphylococcus haemolyticus]	96	84	414
4168	1	708	355	gi|1354211	PET112-like protein [Bacillus subtilis] .	96	95	354
4207	1	312	157	gi|602031	similar to trimethylamine DH [Mycoplasma capricolum] pir|S49950|S49950 probable trimethylamine dehydrogenase (EC .5.99.7) - Mycoplasma capricolum (SGC1) (fragment)	96	86	156

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
4227	2	152	331	gi|871784	Clp-like ATP-dependent protease binding subunit (Bos taurus)	96	81	180
4416	1	570	286	gi|1022726	unknown (Staphylococcus haemolyticus)	96	84	285
22	1	858	430	gi|511070	UreG (Staphylococcus xylosus)	95	88	429
22	7	4362	4036	gi|581787	urease gamma subunit (Staphylococcus xylosus)	95	79	327
82	6	8794	9114	pir|JG0008|JG00	ribosomal protein S7 - Bacillus stearothermophilus	95	81	321
154	9	9280	7838	gi|1354211	PET112-like protein (Bacillus subtilis)	95	92	1443
186	3	2798	2055	gi|1514656	serine O-acetyltransferase (Staphylococcus xylosus)	95	87	744
205	5	4406	4014	gi|142462	ribosomal protein S11 (Bacillus subtilis)	95	85	393
205	7	5017	4793	gi|142459	initiation factor 1 (Bacillus subtilis)	95	84	225
205	21	11365	10991	gi|1044974	ribosomal protein L14 (Bacillus subtilis)	95	93	375
259	5	7288	6644	sp|P67995|YSEA_	HYPOTHETICAL PROTEIN IN SECA 5'REGION (ORF1) (FRAGMENT).	95	85	645
302	3	795	1097	gi|40186	homologous to E.coli ribosomal protein L27 (Bacillus subtilis) i|143592 L27 ribosomal protein (Bacillus subtilis) ir|C21895|C21895 ribosomal protein L27 - Bacillus subtilis p|PU5657|RL27_BACSU 50S RIBOSOMAL PROTEIN L27 (BL30) (BL24). i|40175 L24 gene prod	95	89	303
310	1	579	1523	gi|1177684	chorismate mutase (Staphylococcus xylosus)	95	92	945
414	1	2	163	pir|C48396|C483	ribosomal protein L34 - Bacillus stearothermophilus	95	90	162
4185	2	125	277	gi|1276841	glutamate synthase (GOGAT) (Porphyra purpurea)	95	86	153
22	2	1028	723	gi|511069	UreF (Staphylococcus xylosus)	94	91	306
22	5	5046	3310	gi|410516	urease alpha subunit (Staphylococcus xylosus)	94	85	1737
60	4	815	1372	gi|666116	glucose kinase (Staphylococcus xylosus)	94	87	558
205	18	10012	9536	gi|1044978	ribosomal protein S8 (Bacillus subtilis)	94	78	477
326	4	3378	2542	gi|557492	dihydroxynapthoic acid (DHNA) synthetase (Bacillus subtilis) gi|143186 dihydroxynapthoic acid (DHNA) synthetase (Bacillus ubtilis)	94	85	837
414	3	737	955	gi|467386	thiophen and furan oxidation (Bacillus subtilis)	94	77	219
426	3	2260	1823	gi|1263908	putative (Staphylococcus epidermidis)	94	87	438
534	1	2	355	gi|633650	enzyme II(mannitol) (Staphylococcus carnosus)	94	84	354
1017	1	2	229	gi|149435	putative (Lactococcus lactis)	94	73	228
3098	1	330	184	gi|413952	ipa-28d gene product (Bacillus subtilis)	94	50	147

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3232	1	630	316	gi|1022725	unknown (Staphylococcus haemolyticus)	94	84	315
42	5	2089	2259	pir|B48396|B483	ribosomal protein L33 - Bacillus stearothermophilus	93	81	171
101	2	1745	1383	gi|155345	arsenic efflux pump protein (Plasmid pSX267)	93	82	363
205	24	12227	11865	sp|P14577|RL16_	50S RIBOSOMAL PROTEIN L16.	93	83	363
259	4	8291	5673	gi|499335	secA protein (Staphylococcus carnosus)	93	85	2619
275	1	2226	1114	gi|633650	enzyme II(mannitol) (Staphylococcus carnosus)	93	86	1113
444	6	6207	5773	gi|1022726	unknown (Staphylococcus haemolyticus)	93	81	435
491	1	152	622	gi|46912	ribosomal protein L11 (Staphylococcus carnosus)	93	88	471
607	6	1674	2033	gi|1022726	unknown (Staphylococcus haemolyticus)	93	83	360
653	1	973	488	gi|580890	translation initiation factor IF3 (AA 1-172) (Bacillus tearothermophilus)	93	77	486
1864	1	3	194	gi|306553	ribosmal protein small subunit (Homo sapiens)	93	93	192
2997	1	28	300	gi|143390	carbamyl phosphate synthetase (Bacillus subtilis)	93	82	273
3232	2	907	596	gi|1022725	unknown (Staphylococcus haemolyticus)	93	84	312
3761	2	794	621	gi|1022725	unknown (Staphylococcus haemolyticus)	93	88	174
16	1	3	374	gi|142781	putative cytoplasmic protein; putative (Bacillus subtilis) sp|P37954|UVRB_BACSU EXCINUCLEASE ABC SUBUNIT B (DNA PROTEIN) FRAGMENT).	92	83	372
31	7	5915	6124	gi|1136430	KIAA0185 protein (Homo sapiens)	92	46	210
56	19	26483	27391	gi|467401	unknown (Bacillus subtilis)	92	80	909
69	6	5882	6130	gi|530200	trophoblastin (Ovis aries)	92	53	249
145	3	2568	2038	gi|1022725	unknown (Staphylococcus haemolyticus)	92	80	531
171	3	2760	2362	gi|517475	D-amino acid transaminase (Staphylococcus haemolyticus)	92	86	399
205	12	7495	6962	gi|49189	secY gene product (Staphylococcus carnosus)	92	85	534
205	19	10812	10255	gi|1044976	ribosomal protein L5 (Bacillus subtilis)	92	82	558
219	1	710	357	gi|1303812	YqeV (Bacillus subtilis)	92	88	354
344	3	1575	1805	gi|1405474	CspC protein (Bacillus cereus)	92	85	231
699	1	20	361	gi|413999	ipa-75d gene product (Bacillus subtilis)	92	81	342
1343	1	2	160	pir|A45434|A454	ribosomal protein L19 - Bacillus stearothermophilus	92	84	159

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
1958	1	524	264	gi|407908	EIIscr (Staphylococcus xylosus)	92	80	261
3578	2	718	386	gi|1339950	large subunit of NADH-dependent glutamate synthase (Plectonema boryanum)	92	78	333
3585	1	644	324	gi|1339950	large subunit of NADH-dependent glutamate synthase (Plectonema boryanum)	92	81	321
3640	1	4	402	gi|1022726	unknown (Staphylococcus haemolyticus)	92	81	399
4362	1	14	178	gi|450688	hsdM gene of EcoprrI gene product (Escherichia coli) pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	92	76	165
4446	1	358	182	gi|1022725	unknown (Staphylococcus haemolyticus)	92	82	177
4549	1	462	232	gi|1022726	unknown (Staphylococcus haemolyticus)	92	80	231
4626	1	3	224	gi|1022725	unknown (Staphylococcus haemolyticus)	92	84	222
2	4	3980	4531	gi|535349	CodW (Bacillus subtilis)	91	74	552
28	1	2	1126	gi|1001376	hypothetical protein (Synechocystis sp.)	91	78	1125
60	5	1354	1701	gi|1226043	orf2 downstream of glucose kinase (Staphylococcus xylosus)	91	80	348
101	1	1989	1036	gi|150728	arsenic efflux pump protein (Plasmid pI258)	91	80	954
187	2	412	1194	gi|142559	ATP synthase alpha subunit (Bacillus megaterium)	91	79	783
205	22	11579	11298	gi|40149	S17 protein (AA 1-87) (Bacillus subtilis)	91	83	282
206	7	8184	10262	gi|1072418	glcA gene product (Staphylococcus carnosus)	91	83	2079
306	2	3885	2326	gi|143012	GMP synthetase (Bacillus subtilis)	91	78	1560
306	3	5319	3826	gi|467399	IMP dehydrogenase (Bacillus subtilis)	91	79	1494
310	3	2194	3207	gi|1177685	ccpA gene product (Staphylococcus xylosus)	91	81	1014
343	4	2974	3150	gi|949974	sucrose repressor (Staphylococcus xylosus)	91	82	177
480	3	1606	3042	gi|433991	ATP synthase subunit beta (Bacillus subtilis)	91	85	1437
536	3	2026	1280	gi|143366	adenylosuccinate lyase (PUR-B) (Bacillus subtilis) pir|C29326|WZBSDS adenylosuccinate lyase (EC 4.3.2.2) - Bacillus ubtilis	91	79	747
552	1	1064	615	gi|297874	fructose-bisphosphate aldolase (Staphylococcus carnosus) pir|A49943|A49943 fructose-bisphosphate aldolase (EC 4.1.2.13) - taphylococcus carnosus (strain TM300)	91	79	450
637	1	1	1536	gi|143597	CTP synthetase (Bacillus subtilis)	91	79	1536
859	1	21	359	gi|385178	unknown (Bacillus subtilis)	91	66	339

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name /	% sim	% ident	length (nt)
1327	1	339	530	gi|496558	orfX [Bacillus subtilis]	91	71	192
2515	1	466	275	gi|511070	UreG [Staphylococcus xylosus]	91	85	192
2594	1	2	202	gi|146824	beta-cystathionase [Escherichia coli]	91	75	201
3764	1	847	425	gi|1022725	unknown [Staphylococcus haemolyticus]	91	78	423
4011	1	127	495	gi|1022726	unknown [Staphylococcus haemolyticus]	91	79	369
4227	1	1	177	gi|296464	ATPase [Lactococcus lactis]	91	66	177
42	3	815	1033	gi|520401	catalase [Haemophilus influenzae]	90	86	219
51	8	3717	4607	gi|580859	OppF gene product [Bacillus subtilis]	90	74	891
129	3	5317	4001	gi|1146206	glutamate dehydrogenase [Bacillus subtilis]	90	76	1317
164	17	16628	16933	sp|P05766|RS15_	30S RIBOSOMAL PROTEIN S15 (BS18).	90	74	306
171	5	2983	2819	gi|517475	D-amino acid transaminase [Staphylococcus haemolyticus]	90	78	165
205	4	4497	3550	gi|142463	RNA polymerase alpha-core-subunit [Bacillus subtilis]	90	76	948
205	6	4748	4410	gi|1044989	ribosomal protein S13 [Bacillus subtilis]	90	73	339
205	10	7165	6404	gi|49189	secY gene product [Staphylococcus carnosus]	90	81	762
205	11	6645	6472	gi|49189	secY gene product [Staphylococcus carnosus]	90	78	174
205	27	13692	13345	gi|786157	Ribosomal Protein S19 [Bacillus subtilis]	90	79	348
205	31	15858	15496	gi|1165303	L3 [Bacillus subtilis]	90	79	363
260	5	7023	5773	gi|1161380	IcaA [Staphylococcus epidermidis]	90	78	1251
299	6	3378	3947	gi|467440	"phosphoribosylpyrophosphate synthetase [Bacillus subtilis] gi|40218 PRPP synthetase (AA 1-317) [Bacillus subtilis]	90	78	570
320	2	1025	1717	gi|312443	carbamoyl-phosphate synthase (glutamine-hydrolysing) [Bacillus aldolyticus]	90	75	693
330	4	1581	1769	gi|986963	beta-tubulin [Sporidiobolus pararoseus]	90	80	189
369	1	954	523	pir|S36762|S347	L-serine dehydratase beta chain - Clostridium sp.	90	77	432
557	1	3	188	gi|1511589	H. Jannaschii predicted coding region MJ1624 [Methanococcus jannaschii]	90	54	186
663	2	667	1200"	gi|143786	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [Bacillus subtilis] pir|JT0481|WBS tryptophan--tRNA ligase (EC 6.1.1.2) - Bacillus subtilis	90	73	534
717	1	1	261	gi|143065	hubst [Bacillus stearothermophilus]	90	79	261
745	4	1059	865	gi|1205433	H. influenzae predicted coding region HI1190 [Haemophilus influenzae]	90	81	195

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1007	1	386	565	gi|143366	adenylosuccinate lyase (PUR-B) (Bacillus subtilis) pir|C29326|WZBSDS adenylosuccinate lyase (EC 4.3.2.2) - Bacillus subtilis	90	77	180
1054	1	579	331	gi|1033122	ORF_f729 (Escherichia coli)	90	50	249
1156	1	117	707	gi|1477776	ClpP (Bacillus subtilis)	90	80	591
1180	1	408	205	gi|1377831	unknown (Bacillus subtilis)	90	74	204
1253	1	1	462	gi|40046	phosphoglucose isomerase A (AA 1-449) (Bacillus stearothermophilus) ir|S15936|NUBSSA glucose-6-phosphate isomerase (EC 5.3.1.9) A - cillus stearothermophilus	90	75	462
2951	1	3	269	gi|144816	formyltetrahydrofolate synthetase (FTHFS) (ttg start codon) (EC .3.4.3) (Moorella thermoacetica)	90	76	267
3140	1	327	166	gi|1070014	protein-dependent (Bacillus subtilis)	90	52	162
4594	1	3	233	gi|871784	Clp-like ATP-dependent protease binding subunit (Bos taurus)	90	76	231
87	1	1028	1750	gi|467327	unknown (Bacillus subtilis)	89	75	723
112	1	2	505	gi|153741	ATP-binding protein (Streptococcus mutans)	89	77	504
118	1	120	398	gi|1303804	YqoQ (Bacillus subtilis)	89	75	279
128	4	3545	3757	gi|460257	triose phosphate isomerase (Bacillus subtilis)	89	84	213
164	12	11667	12755	gi|39954	IF2 (aa 1-741) (Bacillus stearothermophilus)	89	80	1089
205	11	7875	7405	gi|216338	ORF for L15 ribosomal protein (Bacillus subtilis)	89	76	471
205	32	16152	15823	gi|1165303	L3 (Bacillus subtilis)	89	80	330
270	3	2407	2207	pir|C41902|C419	arsenate reductase (EC 1.-.-.-) - Staphylococcus xylosus plasmid pSX267	89	81	201
395	2	157	672	gi|520574	glutamate racemase (Staphylococcus haemolyticus)	89	80	516
494	1	3	839	gi|396259	protease (Staphylococcus epidermidis)	89	77	837
510	1	1	444	gi|40046	phosphoglucose isomerase A (AA 1-449) (Bacillus stearothermophilus) ir|S15936|NUBSSA glucose-6-phosphate isomerase (EC 5.3.1.9) A - cillus stearothermophilus	89	74	444
615	1	2124	1210	gi|1303812	YqeV (Bacillus subtilis)	89	74	915
841	1	18	341	gi|1165303	L3 (Bacillus subtilis)	89	80	324
1111	1	352	813	gi|47146	thermonuclease (Staphylococcus intermedius)	89	70	462
1875	1	2	256	gi|1205108	ATP-dependent protease binding subunit (Haemophilus influenzae)	89	82	255
2963	1	11	367	gi|467458	cell division protein (Bacillus subtilis)	89	83	357

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3020	1	90	362	gi|1239988	hypothetical protein (Bacillus subtilis)	89	66	273
3565	1	2	400	gi|1256635	dihydroxy-acid dehydratase (Bacillus subtilis)	89	75	399
3586	1	105	314	gi|580832	ATP synthase subunit gamma (Bacillus subtilis)	89	82	210
3629	1	794	399	gi|1009366	Respiratory nitrate reductase (Bacillus subtilis)	89	78	396
3688	1	2	400	gi|1146206	glutamate dehydrogenase (Bacillus subtilis)	89	75	399
3699	1	794	399	gi|1339950	large subunit of NADH-dependent glutamate synthase (Plectonema boryanum)	89	75	396
4016	1	428	216	gi|1009366	Respiratory nitrate reductase (Bacillus subtilis)	89	71	213
4177	1	471	301	gi|149426	putative (Lactococcus lactis)	89	76	171
4436	1	601	302	gi|1022725	unknown (Staphylococcus haemolyticus)	89	80	300
4635	1	320	162	gi|1022725	unknown (Staphylococcus haemolyticus)	89	73	159
2	2	1330	2676	gi|520754	putative (Bacillus subtilis)	88	76	1347
42	2	468	848	sp|P42321|CATA_	CATALASE (EC 1.11.1.6).	88	76	381
53	5	6389	4722	gi|474177	alpha-D-1,4-glucosidase (Staphylococcus xylosus)	88	80	1668
56	16	18018	18617	gi|467411	recombination protein (Bacillus subtilis)	88	77	600
60	3	376	843	gi|666116	glucose kinase (Staphylococcus xylosus)	88	77	468
70	2	1583	1245	gi|44095	replication initiator protein (Listeria monocytogenes)	88	74	339
82	8	11514	12719	pir|A60663|A606	translation elongation factor Tu - Bacillus subtilis	88	79	1206
103	7	4179	4391	gi|167181	serine/threonine kinase receptor (Brassica napus)	88	77	213
114	8	7732	8232	gi|1022726	unknown (Staphylococcus haemolyticus)	88	72	501
118	2	308	2011	gi|1303804	YqeQ (Bacillus subtilis)	88	77	1704
141	3	657	1136	gi|1405446	transketolase (Bacillus subtilis)	88	72	480
148	7	5871	6116	gi|1118002	dihydroptoroate synthase (Staphylococcus haemolyticus)	88	78	246
165	3	1428	2231	gi|40053	phenylalanyl-tRNA synthetase alpha subunit (Bacillus subtilis) | ir|S11730|YFBSA phenylalanine--tRNA ligase (EC 6.1.1.20) alpha cin - Bacillus subtilis	88	80	804
205	28	15027	14185	gi|1165306	L2 (Bacillus subtilis)	88	82	843
225	1	1569	898	gi|1303840	YqfS (Bacillus subtilis)	88	78	672
235	1	2	1975	gi|452309	valyl-tRNA synthetase (Bacillus subtilis)	88	76	1974

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
339	3	2060	1566	gi|1118002	dihydropteroate synthase (Staphylococcus haemolyticus)	88	73	495
443	4	4325	2928	gi|558559	pyrimidine nucleoside phosphorylase (Bacillus subtilis)	88	73	1398
532	1	3	419	gi|143797	valyl-tRNA synthetase (Bacillus stearothermophilus) sp|P11931|SYV_BACST VALYL-TRNA SYNTHETASE (EC 6.1.1.9) VALINE--TRNA LIGASE) (VALRS).	88	78	417
534	3	2504	2968	gi|153049	mannitol-specific enzyme-III (Staphylococcus carnosus) pir|JQ0088|JQ0088 phosphotransferase system enzyme II (EC .7.1.69), mannitol-specific, factor III - Staphylococcus carnosus sp|P17676|PTMA_STACA PTS SYSTEM, MANNITOL-SPECIFIC IIA COMPONENT EIIA-MTL) (	88	82	465
705	2	584	399	gi|710018	nitrite reductase (nirB) (Bacillus subtilis)	88	70	186
1000	2	1824	1309	gi|1022726	unknown (Staphylococcus haemolyticus)	88	78	516
1299	1	587	324	gi|401786	phosphomannomutase (Mycoplasma pirum)	88	55	264
1341	2	170	400	gi|19963	ribosomal protein L20 (AA 1-119) (Bacillus stearothermophilus) ir|S05348|R5BS20 ribosomal protein L20 - Bacillus earothermophilus	88	82	231
1386	1	41	214	pir|B47154|B471	signal recognition particle 54K chain homolog Ffh - Bacillus subtilis	88	71	174
1386	2	183	533	pir|B47154|B471	signal recognition particle 54K chain homolog Ffh - Bacillus subtilis	88	73	351
2949	1	704	399	gi|535350	CodX (Bacillus subtilis)	88	73	306
2984	1	5	169	gi|218277	O-acetylserine(thiol) lyase (Spinacia oleracea)	88	70	165
3035	1	1	138	gi|493083	dihydroxyacetone kinase (Citrobacter freundii)	88	67	138
3089	1	3	152	gi|606055	ORF_f746 (Escherichia coli)	88	88	150
3917	1	817	410	gi|143378	pyruvate decarboxylase (E-1) beta subunit (Bacillus subtilis) gi|1377836 pyruvate decarboxylase E-1 beta subunit (Bacillus ubtilis)	88	77	408
4199	1	680	342	gi|1405454	aconitase (Bacillus subtilis)	88	82	339
4201	1	734	369	gi|515938	glutamate synthase (ferredoxin) (Synechocystis sp.) pir|S46957|S46957 glutamate synthase (ferredoxin) (EC 1.4.7.1) - ynechocystis sp.	88	84	366
4274	1	1	336	gi|515938	glutamate synthase (ferredoxin) (Synechocystis sp.) pir|S46957|S46957 glutamate synthase (ferredoxin) (EC 1.4.7.1) - ynechocystis sp.	88	84	336
4308	1	794	399	gi|1146206	glutamate dehydrogenase (Bacillus subtilis)	88	71	396
2	5	4570	6000	gi|535350	CodX (Bacillus subtilis)	87	70	1431
52	8	6781	6482	gi|1064791	function umknown (Bacillus subtilis)	87	66	300

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name ( )	% sim	% ident	length (nt)
73	3	1584	2480	gi|142992	|glycerol kinase (glpK) (EC 2.7.1.30) [Bacillus subtilis] pir|B45868|B45868 |glycerol kinase (EC 2.7.1.30) - Bacillus subtilis sp|P18157|GLPK_BACSU GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL -PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK).	87	72	897
98	12	8813	9100	gi|467433	|unknown [Bacillus subtilis]	87	62	288
124	4	4265	2988	gi|556886	|serine hydroxymethyltransferase [Bacillus subtilis] pir|S49363|S49363 |serine hydroxymethyltransferase - Bacillus subtilis	87	77	1278
124	6	4457	4032	gi|556883	|unknown [Bacillus subtilis]	87	66	426
148	5	3741	4559	gi|467460	|unknown [Bacillus subtilis]	87	70	819
164	13	12710	13810	gi|39954	|IF2 (aa 1-741) [Bacillus stearothermophilus]	87	72	1101
177	2	1104	2126	gi|467385	|unknown [Bacillus subtilis]	87	78	1023
199	1	1982	1158	gi|143527	|iron-sulfur protein [Bacillus subtilis]	87	77	825
199	2	4717	2933	pir|A27763|A277	|succinate dehydrogenase (EC 1.3.99.1) flavoprotein - Bacillus subtilis	87	80	1785
205	23	11782	11543	gi|1044972	|ribosomal protein L29 [Bacillus subtilis]	87	78	240
205	25	13275	12607	gi|1165309	|S3 [Bacillus subtilis]	87	75	669
222	1	2033	1107	gi|1177249	|rec233 gene product [Bacillus subtilis]	87	70	927
236	3	1635	1333	gi|1146198	|ferredoxin [Bacillus subtilis]	87	80	303
246	5	2585	2292	gi|467373	|ribosomal protein S18 [Bacillus subtilis]	87	77	294
260	2	4189	3422	gi|1161382	|IcaC (Staphylococcus epidermidis]	87	72	768
320	3	1696	2391	gi|312443	|carbamoyl-phosphate synthase (glutamine-hydrolyzing) [Bacillus aldolyticus]	87	80	696
380	4	1165	1383	gi|142570	|ATP synthase c subunit [Bacillus firmus]	87	80	219
414	4	900	1073	gi|467386	|thiophen and furan oxidation [Bacillus subtilis]	87	77	174
425	2	1003	794	gi|1046166	|pilin repressor [Mycoplasma genitalium]	87	69	210
448	1	1255	722	gi|405134	|acetate kinase [Bacillus subtilis]	87	75	534
480	1	1	711	gi|142559	|ATP synthase alpha subunit [Bacillus megaterium]	87	79	711
481	1	2	352	sp|Q06797|RL1_B	|50S RIBOSOMAL PROTEIN L1 (BL1).	87	72	351
677	2	359	955	gi|460911	|fructose-bisphosphate aldolase [Bacillus subtilis]	87	78	597
677	3	934	1284	gi|460911	|fructose-bisphosphate aldolase [Bacillus subtilis]	87	78	351
876	1	3	452	gi|1146247	|asparaginyl-tRNA synthetase [Bacillus subtilis]	87	79	450

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
1376	1	426	214	gi|1065555	F46H6.4 gene product (Caenorhabditis elegans)	87	75	213
2206	1	3	374	gi|215098	excisionase (Bacteriophage 154a)	87	72	372
2938	1	3	290	gi|508979	GTP-binding protein (Bacillus subtilis)	87	69	288
3081	2	126	308	gi|467399	IMP dehydrogenase (Bacillus subtilis)	87	72	183
1535	1	3	401	gi|1405454	aconitase (Bacillus subtilis)	87	80	399
4238	1	547	275	gi|b03769	HutU protein, urocanase (Bacillus subtilis)	87	73	273
4	8	10427	8736	gi|603769	HutU protein, urocanase (Bacillus subtilis)	86	72	1692
22	6	4190	3738	gi|410515	urease beta subunit (Staphylococcus xylosus)	86	73	453
54	2	2480	1572	gi|289287	UDP-glucose pyrophosphorylase (Bacillus subtilis)	86	70	909
124	3	2336	1713	gi|556887	uracil phosphoribosyltransferase (Bacillus subtilis) pir|S49364|S49364 uracil phosphoribosyltransferase - Bacillus subtilis	86	74	624
148	3	1349	3448	gi|467458	cell division protein (Bacillus subtilis)	86	75	2100
148	4	3638	3859	gi|467460	unknown (Bacillus subtilis)	86	73	222
152	3	1340	2086	gi|1377835	pyruvate decarboxylase E-1 alpha subunit (Bacillus subtilis)	86	75	747
164	18	17347	19467	gi|1184680	polynucleotide phosphorylase (Bacillus subtilis)	86	72	2121
180	2	554	1159	gi|143467	ribosomal protein S4 (Bacillus subtilis)	86	80	606
205	3	2966	2592	gi|142464	ribosomal protein L17 (Bacillus subtilis)	86	77	375
205	26	13364	12990	gi|40107	ribosomal protein L22 (Bacillus stearothermophilus) ir|S10612|S10612 ribosomal protein L22 - Bacillus earothermophilus	86	75	375
246	7	3463	3140	gi|467375	ribosomal protein S6 (Bacillus subtilis)	86	70	324
299	3	1196	1540	gi|39656	spoVG gene product (Bacillus megaterium)	86	70	345
299	7	3884	4345	gi|467440	'phosphoribosylpyrophosphate synthetase (Bacillus subtilis) gi|40218 PRPP synthetase (AA 1-317) (Bacillus subtilis)	86	78	462
304	5	2170	2523	gi|666983	putative ATP binding subunit (Bacillus subtilis)	86	65	354
310	2	1487	1678	gi|1177684	chorismate mutase (Staphylococcus xylosus)	86	71	192
337	5	2086	3409	gi|487434	isocitrate dehydrogenase (Bacillus subtilis)	86	78	1320
339	2	1489	1109	gi|1118003	dihydroneopterin aldolase (Staphylococcus haemolyticus)	86	77	381
358	2	2124	3440	gi|1146219	28.2% of identity to the Escherichia coli GTP-binding protein Era; putative (Bacillus subtilis)	86	73	1317

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% identity	length (nt)
404	2	1015	2058	gi|1303817	YqfA (Bacillus subtilis)	86	78	1044
581	2	661	452	gi|40056	phoP gene product (Bacillus subtilis)	86	71	210
642	2	338	1075	gi|1176399	EpiF (Staphylococcus epidermidis)	86	72	738
770	1	622	347	gi|143328	phoP protein (put.); putative (Bacillus subtilis)	86	69	276
865	1	1777	890	gi|1146247	asparaginyl-tRNA synthetase (Bacillus subtilis)	86	74	888
868	2	963	1133	gi|1002911	transmembrane protein (Saccharomyces corevisiae)	86	69	171
904	1	1	162	gi|1303912	YqhW (Bacillus subtilis)	86	72	162
989	1	35	433	gi|1303993	YqkL (Bacillus subtilis)	86	76	399
1212	1	296	150	gi|414014	ipa-90d gene product (Bacillus subtilis)	86	70	147
1323	1	2	148	gi|40041	pyruvate dehydrogenase (lipoamide) (Bacillus stearothermophilus) ir|S10798|DEBSPF pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) pha chain - Bacillus stearothermophilus	86	75	147
3085	2	540	310	gi|1354211	PET112-like protein (Bacillus subtilis)	86	86	231
1847	1	1	228	gi|296464	ATPase (Lactococcus lactis)	86	63	228
4487	1	476	240	gi|1022726	unknown (Staphylococcus haemolyticus)	86	73	237
4583	1	372	187	gi|1022725	unknown (Staphylococcus haemolyticus)	86	79	186
25	5	4287	5039	gi|1502421	3-ketoacyl-acyl carrier protein reductase (Bacillus subtilis)	85	64	753
56	21	30627	29395	gi|1408507	pyrimidine nucleoside transport protein (Bacillus subtilis)	85	69	1233
68	2	332	1192	gi|467376	unknown (Bacillus subtilis)	85	74	861
73	2	880	1707	gi|142992	glycerol kinase (glpK) (EC 2.7.1.30) (Bacillus subtilis) pir|B45868|B45868 glycerol kinase (EC 2.7.1.30) - Bacillus subtilis sp|P18157|GLPK_BACSU GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL -PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK).	85	72	828
106	4	1505	3490	gi|143766	(thrSv) (EC 6.1.1.3) (Bacillus subtilis)	85	74	1986
128	2	1153	2202	gi|311924	glyceraldehyde-3-phosphate dehydrogenase (Clostridium pasteurianum) pir|S34254|S34254 glyceraldehyde-3-phosphate dehydrogenase (EC .2.1.12) - Clostridium pasteurianum	85	75	1050
129	4	6466	5252	gi|1064807	ORTHININE AMINOTRANSFERASE (Bacillus subtilis)	85	73	1215
138	6	3475	5673	gi|1072419	glcB gene product (Staphylococcus carnosus)	85	74	2199
189	1	2	169	gi|467385	unknown (Bacillus subtilis)	85	65	168

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
205	15	8624	8106	gi|1044981	ribosomal protein S5 [Bacillus subtilis]	85	75	519
205	20	10928	10596	pir|A02819|R5BS	ribosomal protein L24 - Bacillus stearothermophilus	85	72	333
220	6	6490	6101	gi|48980	sacA gene product [Bacillus subtilis]	85	66	390
231	4	4877	3159	gi|1002520	HutS [Bacillus subtilis]	85	70	1719
243	9	8013	8783	gi|414011	ipa-87r gene product [Bacillus subtilis]	85	72	771
249	2	5894	3186	gi|1405454	acamitase [Bacillus subtilis]	85	73	2709
302	1	140	475	gi|40173	homolog of E.coli ribosomal protein L21 [Bacillus subtilis] ir|S18439|S18439 Ribosomal protein L21 - Bacillus subtilis p|P26908|RL21_BACSU 50S RIBOSOMAL PROTEIN L21 (BL20).	85	72	336
333	1	5445	2968	gi|442360	ClpC adenosine triphosphatase [Bacillus subtilis]	85	69	2478
364	6	6082	8196	gi|871784	Clp-like ATP-dependent protease binding subunit [Bos taurus]	85	68	2115
448	2	1992	1339	gi|405134	acetate kinase [Bacillus subtilis]	85	68	654
747	1	1251	853	gi|1373157	orf-X; hypothetical protein; Method: conceptual translation supplied by author [Bacillus subtilis]	85	73	399
886	2	159	467	gi|541768	hemin permease [Yersinia enterocolitica]	85	55	309
1089	1	1208	606	pir|B47154|B471	signal recognition particle 54K chain homolog Ffh - Bacillus subtilis	85	71	603
1163	1	816	409	gi|304155	diaminopimalate decarboxylase [Bacillus methanolicus] sp|P41022|DCDA_BACMT DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20) DAP DECARBOXYLASE).	85	62	408
1924	1	487	251	gi|215098	excisionase [Bacteriophage 154a]	85	73	237
2932	1	776	390	gi|1041099	Pyruvate kinase [Bacillus licheniformis]	85	71	387
3030	1	3	275	gi|42370	pyruvate formate-lyase (AA 1-760) [Escherichia coli] ir|S01788|S01788 formate C-acetyltransferase (EC 2.3.1.54) - charichia coli	85	74	273
3111	1	595	299	gi|63568	11mb deformity protein [Gallus gallus]	85	85	297
3778	1	630	316	gi|391840	beta-subunit of HDT [Pseudomonas fragi]	85	67	315
3835	1	1	387	gi|1204472	type I restriction enzyme ECOR124/3 I M protein [Haemophilus influenzae]	85	56	387
4042	1	3	386	gi|18178	formate acetyltransferase [Chlamydomonas reinhardtii] ir|S24997|S24997 formate C-acetyltransferase (EC 2.3.1.54) - lamydomonas reinhardtii	85	70	384
4053	1	35	340	gi|1204472	type I restriction enzyme ECOR124/3 I M protein [Haemophilus influenzae]	85	56	306
4108	1	2	181	gi|1072418	glcA gene product [Staphylococcus carnosus]	85	61	180
4300	1	575	330	gi|151932	fructose enzyme II [Rhodobacter capsulatus]	85	59	246

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name /)	% sim	% ident	length (nt)
4392	1	627	355	gi|1022725	unknown (Staphylococcus haemolyticus)	85	74	273
4408	1	2	235	gi|871784	clp-like ATP-dependent protease binding subunit (Bos taurus)	85	62	234
4430	1	578	291	gi|1009366	Respiratory nitrate reductase (Bacillus subtilis)	85	68	288
4555	1	2	253	gi|450688	hsdM gene of EcoprrI gene product (Escherichia coli) pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	85	52	252
4611	1	481	242	gi|1256635	dihydroxy-acid dehydratase (Bacillus subtilis)	85	65	240
4	10	10061	10591	gi|46982	fosB gene product (Staphylococcus epidermidis)	84	68	531
13	2	1348	1172	gi|142450	ahrC protein (Bacillus subtilis)	84	56	177
16	4	1803	4652	gi|1277198	DNA repair protein (Deinococcus radiodurans)	84	67	2850
22	3	1515	1128	gi|511069	UreF (Staphylococcus xylosus)	84	73	408
23	7	5055	5306	gi|603320	Yer082p (Saccharomyces cerevisiae)	84	61	252
53	11	11597	11145	gi|1303948	YqiW (Bacillus subtilis)	84	68	453
53	12	14059	12770	gi|142613	branched chain alpha-keto acid dehydrogenase E2 (Bacillus subtilis) gi|1303944 BfmBB (Bacillus subtilis)	84	71	1290
70	1	1332	982	gi|46647	ORF (repE) (Staphylococcus aureus)	84	68	351
73	4	2512	4311	gi|142993	glycerol-3-phosphate dehydrogenase (glpD) (EC 1.1.99.5) (Bacillus subtilis)	84	74	1800
98	7	4324	6096	gi|467427	methionyl-tRNA synthetase (Bacillus subtilis)	84	66	1773
100	9	9501	8680	gi|1340128	ORF1 (Staphylococcus aureus)	84	78	822
117	3	1934	3208	gi|1237019	Srb (Bacillus subtilis)	84	68	1275
148	6	4720	5670	gi|467462	cysteine synthetase A (Bacillus subtilis)	84	69	951
152	4	2064	2456	gi|143377	pyruvate decarboxylase (E-1) alpha subunit (Bacillus subtilis) pir|B36718|DEBSPA pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain - Bacillus subtilis	84	70	393
169	7	3614	3861	gi|1001342	hypothetical protein (Synechocystis sp.)	84	66	228
171	4	2992	2657	gi|517475	D-amino acid transaminase (Staphylococcus haemolyticus)	84	71	336
186	6	6941	6216	gi|467475	unknown (Bacillus subtilis)	84	70	726
205	9	6261	5692	gi|216340	ORF for adenylate kinase (Bacillus subtilis)	84	71	570
224	2	915	1391	gi|288269	beta-fructofuranosidase (Staphylococcus xylosus)	84	70	477

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name ( )	% sim	% ident	length (nt)
251	1	92	388	gi|1303790	YqeI (Bacillus subtilis)	84	65	297
282	3	1526	2836	gi|143040	glutamate-1-semialdehyde 2,1-aminotransferase (Bacillus subtilis) pir|D42728|D42728 glutamate-1-semialdehyde 2,1-aminomutase (EC .4.3.8) - Bacillus subtilis	84	75	1311
307	5	3138	2959	gi|1070014	protein-dependent (Bacillus subtilis)	84	62	180
320	4	2343	4229	gi|143390	carbamyl phosphate synthetase (Bacillus subtilis)	84	70	1887
372	1	3	296	gi|1022725	unknown (Staphylococcus haemolyticus)	84	70	294
413	2	2201	1341	gi|1256146	YbbQ (Bacillus subtilis)	84	65	861
439	1	3	392	gi|1046173	osmotically inducible protein (Mycoplasma genitalium)	84	53	390
461	3	1362	2270	gi|40211	threonine synthase (thrC) (AA 1-352) (Bacillus subtilis) ir|A25364|A25364 threonine synthase (EC 4.2.99.2) - Bacillus btilis	84	69	909
487	1	3	299	gi|1144531	integrin-like protein alpha Intlp (Candida albicans)	84	46	297
491	2	624	905	pir|S08564|R3BS	ribosomal protein S9 - Bacillus stearothermophilus	84	69	282
491	3	816	1033	pir|S08564|R3BS	ribosomal protein S9 - Bacillus stearothermophilus	84	77	198
548	1	3	341	gi|431231	uracil permease (Bacillus caldolyticus)	84	74	339
728	2	2701	1748	gi|912445	DNA polymerase (Bacillus caldotenax)	84	68	954
769	1	3	257	gi|1510953	cobalamin biosynthesis protein N (Methanococcus jannaschii)	84	38	255
954	1	308	156	gi|1405454	aconitase (Bacillus subtilis)	84	57	153
957	1	3	395	gi|143402	recombination protein (ttg start codon) (Bacillus subtilis) gi|1303923 RecN (Bacillus subtilis)	84	68	393
975	1	3	452	gi|885934	ClpB (Synechococcus sp.)	84	70	450
1585	1	3	257	gi|510140	ligoendopeptidase F (Lactococcus lactis)	84	56	255
2954	1	3	323	gi|603769	HutU protein, urocanase (Bacillus subtilis)	84	73	321
2996	1	650	348	gi|18178	formato acetyltransferase (Chlamydomonas reinhardtii) ir|S24997|S24997 formate C-acetyltransferase (EC 2.3.1.54) - lamydomonas reinhardtii	84	65	303
3766	1	737	375	gi|517205	67 kDa Myosin-crossreactive streptococcal antigen (Streptococcus yogenes)	84	72	363
4022	1	2	169	gi|1146206	glutamate dehydrogenase (Bacillus subtilis)	84	54	168
4058	1	620	312	gi|151932	fructose enzyme II (Rhodobacter capsulatus)	84	71	309
4108	2	106	351	gi|1072418	glcA gene product (Staphylococcus carnosus)	84	77	246

TABLE 2

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S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
4183	1	3	308	gi|603769	HutU protein, urocanase (Bacillus subtilis)	84	72	306
4726	1	55	234	gi|146208	glutamate synthase large subunit (EC 2.6.1.53) (Escherichia coli) pir|A29617|A29617 glutamate synthase (NADPH) (EC 1.4.1.13) large hain - Escherichia coli	84	73	180
22	4	2043	1576	gi|393297	urease accessory protein (Bacillus sp.)	83	64	468
53	13	14722	13745	gi|142612	branched chain alpha-keto acid dehydrogenase E1-beta (Bacillus ubtilis)	83	68	978
57	16	13357	12872	gi|143132	lactate dehydrogenase (AC 1.1.1.27) (Bacillus caldolyticus) pir|B29704|B29704 L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus aldolyticus	83	66	486
66	3	3119	2274	gi|1303894	YqhM (Bacillus subtilis)	83	63	846
66	5	6118	4643	gi|1212730	YqhK (Bacillus subtilis)	83	68	1476
70	3	1864	1523	gi|44095	replication initiator protein (Listeria monocytogenes)	83	73	342
90	1	377	1429	gi|155571	alcohol dehydrogenase I (adhA) (EC 1.1.1.1) (Zymomonas mobilis) pir|A35260|A35260 alcohol dehydrogenase (EC 1.1.1.1) I - Zymomonas obilis	83	70	1053
95	2	708	2162	gi|506381	phospho-beta-glucosidase (Bacillus subtilis)	83	70	1455
137	1	68	694	gi|467391	initiation protein of replicaton (Bacillus subtilis)	83	77	627
140	4	3209	2742	gi|634107	kdpB (Escherichia coli)	83	65	468
142	3	3468	2989	gi|1212776	lumazine synthase (b-subunit) (Bacillus amyloliquefaciens)	83	69	480
161	12	5749	6696	gi|903307	ORF75 (Bacillus subtilis)	83	64	948
164	9	9880	11070	gi|49316	ORF2 gene product (Bacillus subtilis)	83	66	1191
164	14	14148	14546	gi|580902	ORF6 gene product (Bacillus subtilis)	83	60	399
170	2	3144	2467	gi|520844	orf4 (Bacillus subtilis)	83	64	678
186	2	2029	1370	gi|289284	cysteinyl-tRNA synthetase (Bacillus subtilis)	83	72	660
205	14	7822	7607	gi|216337	ORF for L30 ribosomal protein (Bacillus subtilis)	83	74	216
237	6	3683	4540	gi|1510488	imidazoleglycerol-phosphate synthase (cyclase) (Methanococcus jannaschii)	83	60	858
301	1	985	638	gi|467419	unknown (Bacillus subtilis)	83	65	348
302	4	1421	2743	gi|508979	GTP-binding protein (Bacillus subtilis)	83	68	1323
321	4	3933	3571	gi|39844	fumarase (citG) (aa 1-462) (Bacillus subtilis)	83	68	363
367	1	2	352	gi|1039479	ORFU (Lactococcus lactis)	83	54	351

TABLE 2

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
387	1	3	662	gi|806281	DNA polymerase I (Bacillus stearothermophilus)	83	70	660
527	2	916	1566	gi|396259	protease (Staphylococcus epidermidis)	83	67	651
533	1	355	179	gi|142455	alanine dehydrogenase (EC 1.4.1.1) (Bacillus stearothermophilus) pir|B34261|B34261 alanine dehydrogenase (EC 1.4.1.1) - Bacillus tearothermophilus	83	66	177
536	4	1617	1438	gi|143366	adenylosuccinate lyase (PUR-B) (Bacillus subtilis) ; tr|C29326|WZBSDS adenylosuccinate lyase (EC 4.3.2.2) - Bacillus ubtilis	83	67	180
652	1	2	859	gi|520753	DNA topoisomerase I (Bacillus subtilis)	83	72	858
774	2	200	361	gi|1522665	M. jannaschii predicted coding region MJECL28 (Methanococcus jannaschii)	83	58	162
897	1	120	296	gi|1064807	ORTHININE AMINOTRANSFERASE (Bacillus subtilis)	83	76	177
1213	1	3	491	gi|289288	lexA (Bacillus subtilis)	83	67	489
2529	1	296	150	gi|143786	tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Bacillus subtilis) pir|JT0481|YWBS tryptophan--tRNA ligase (EC 6.1.1.2) - Bacillus ubtilis	83	69	147
2973	1	649	326	gi|1109687	ProZ (Bacillus subtilis)	83	58	324
1009	1	720	366	gi|882532	ORF_o294 (Escherichia coli)	83	65	363
3035	2	45	305	gi|950062	hypothetical yeast protein 1 (Mycoplasma capricolum) pir|S48578|S48578 hypothetical protein - Mycoplasma capricolum SGC3) (fragment)	83	59	261
1906	1	67	309	gi|1353197	thioredoxin reductase (Eubacterium acidaminophilum)	83	61	243
4458	1	540	271	gi|397526	clumping factor (Staphylococcus aureus)	83	78	270
4570	1	444	223	gi|1022726	unknown (Staphylococcus haemolyticus)	83	74	222
4654	1	97	261	gi|1072419	glcB gene product (Staphylococcus carnosus)	83	79	165
16	2	295	1191	gi|153854	uvs402 protein (Streptococcus pneumoniae)	82	67	897
16	3	1193	1798	gi|153854	uvs402 protein (Streptococcus pneumoniae)	82	70	606
38	12	9644	8724	gi|1204400	N-acetylneuraminate lyase (Haemophilus influenzae)	82	58	921
42	4	988	2019	gi|841192	catalase (Bacteroides fragilis)	82	70	1032
51	6	2590	3489	gi|143607	sporulation protein (Bacillus subtilis)	82	69	900
56	11	12270	13925	gi|39431	oligo-1,6-glucosidase (Bacillus cereus)	82	60	1656
56	15	17673	18014	gi|467410	unknown (Bacillus subtilis)	82	66	342
61	2	881	3313	gi|143148	transfer RNA-Leu synthetase (Bacillus subtilis)	82	70	2433

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
82	7	9162	11318	gi|48240	elongation factor G (AA 1-691) [Thermus aquaticus thermophilus] ir|S15928|EFTWG translation elongation factor G - Thermus aquaticus p|P13551|EFG_THETH ELONGATION FACTOR G (EF-G).	82	64	2157
85	2	5470	3260	gi|143369	phosphoribosylformyl glycinamidine synthetase II (PUR-Q) [Bacillus ubtilis]	82	66	2211
102	6	3662	5380	gi|1256635	dihydroxy-acid dehydratase [Bacillus subtilis]	82	65	1719
117	4	3242	3493	pir|A47154|A471	orf1 5' of Ffh - Bacillus subtilis	82	53	252
128	6	4377	5933	gi|460258	phosphoglycerate mutase [Bacillus subtilis]	82	66	1557
129	2	1229	2182	gi|403373	glycerophosphoryl diester phosphodiesterase [Bacillus subtilis] pir|S37251|S37251 glycerophosphoryl diester phosphodiesterase - acillus subtilis	82	62	954
170	1	2	1441	gi|1377831	unknown [Bacillus subtilis]	82	67	1440
177	1	3	1094	gi|467386	thiophen and furan oxidation [Bacillus subtilis]	82	65	1092
184	4	3572	4039	gi|153566	ORF (19K protein) [Enterococcus faecalis]	82	59	468
189	8	4455	4225	gi|1001878	CspL protein [Listeria monocytogenes]	82	73	231
206	19	21166	20707	gi|473916	lipopeptide antibiotics iturin A [Bacillus subtilis] sp|P39144|LP14_BACSU LIPOPEPTIDE ANTIBIOTICS ITURIN A AND SURFACTIN IOSYNTHESIS PROTEIN.	82	50	660
221	2	805	1722	gi|517205	67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]	82	63	918
223	4	3866	3651	gi|439619	[Salmonella typhimurium IS200 insertion sequence from SARA17, artial.], gene product [Salmonella typhimurium]	82	69	216
260	3	5207	4296	gi|1161381	icaB [Staphylococcus epidermidis]	82	61	912
315	3	4864	2855	gi|143397	quinol oxidase [Bacillus subtilis]	82	67	2010
321	10	8520	7945	gi|142981	ORF5; This ORF includes a region (aa23-103) containing a potential ron-sulphur centre homologous to a region of Rhodospirillum ruhrum nd Chromatium vinosum; putative [Bacillus stearothermophilus] pir|PQ0299|PQ0299 hypothetical protein 5 (gldA 3' region) -	82	62	576
331	3	1055	1342	gi|436574	ribosomal protein L1 [Bacillus subtilis]	82	71	288
370	2	262	618	gi|1303793	YqeL [Bacillus subtilis]	82	59	357
404	4	3053	4024	gi|1303821	YqfE [Bacillus subtilis]	82	68	972
405	4	4440	3073	gi|1303913	YqhX [Bacillus subtilis]	82	67	1368
436	3	4096	2864	gi|149521	tryptophan synthase beta subunit [Lactococcus lactis] pir|S35129|S35129 tryptophan synthase (EC 4.2.1.20) beta chain - actococcus lactis subsp. lactis	82	67	1233

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name ( )	% sim	% ident	length (nt)
441	4	3394	2573	gi|142952	glyceraldehyde-3-phosphate dehydrogenase (Bacillus tearothermophilus)	82	67	822
444	12	10415	11227	gi|1204354	spore germination and vegetative growth protein (Haemophilus influenzae)	82	67	813
446	1	3	191	gi|143387	aspartate transcarbamylase (Bacillus subtilis)	82	66	189
462	3	1007	1210	gi|142521	deoxyribodipyrimidine photolyase (Bacillus subtilis) pir|A37192|A37192 uvrB protein - Bacillus subtilis sp|P14951|UVRC_BACSU EXCINUCLEASE ABC SUBUNIT C.	82	64	204
537	1	1560	784	gi|853767	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (Bacillus subtilis)	82	61	777
680	2	407	700	gi|426472	secE gene product (Staphylococcus carnosus)	82	69	294
724	2	565	386	gi|143373	phosphoribosyl aminoimidazole carboxy formyl ormyltransferase/inosine monophosphate cyclohydrolase (PUR-H(J)) Bacillus subtilis)	82	68	180
763	1	422	213	gi|467458	cell division protein (Bacillus subtilis)	82	35	210
818	1	564	283	gi|1064787	function unknown (Bacillus subtilis)	82	69	282
858	1	175	1176	gi|143043	uroporphyrinogen decarboxylase (Bacillus subtilis) pir|B47045|B47045 uroporphyrinogen decarboxylase (EC 4.1.1.37) - acillus subtilis	82	71	1002
895	1	3	599	gi|1027507	ATP binding protein (Borrelia burgdorfori)	82	72	597
939	1	10	399	gi|143795	transfer RNA-Tyr synthetase (Bacillus subtilis)	82	60	390
961	1	1	306	gi|577647	gamma-hemolysin (Staphylococcus aureus)	82	69	306
1192	1	307	155	gi|146974	NH3-dependent NAD synthetase (Escherichia coli)	82	71	153
1317	1	49	375	gi|407908	EIIscr (Staphylococcus xylosus)	82	72	327
1341	1	1	150	gi|39962	ribosomal protein L35 (AA 1-66) (Bacillus stearothermophilus) ir|S05347|R5BS35 ribosomal protein L35 - Bacillus earothermophilus	82	68	150
2990	2	567	349	gi|534855	ATPase subunit epsilon (Bacillus stearothermophilus) sp|P42009|ATPE_BACST ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34).	82	47	219
3024	1	45	224	gi|467402	unknown (Bacillus subtilis)	82	64	180
3045	1	276	139	gi|467335	ribosomal protein L9 (Bacillus subtilis)	82	60	138
3045	2	558	400	gi|467335	ribosomal protein L9 (Bacillus subtilis)	82	82	159
3091	1	474	238	gi|499335	secA protein (Staphylococcus carnosus)	82	78	237
3107	1	416	210	gi|546918	orfY 3' of comK (Bacillus subtilis, E26, Peptide Partial, 140 aa) pir|S43612|S43612 hypothetical protein Y - Bacillus subtilis sp|P40398|YHXD_BACSU HYPOTHETICAL PROTEIN IN COMK 3'REGION (ORFY) FRAGMENT).	82	64	207

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match geno name	% sim	% ident	length (nt)
4332	1	2	319	gi|42086	nitrate reductase alpha subunit (Escherichia coli) p|P09152|NARG_ECOLI RESPIRATORY NITRATE REDUCTASE 1 ALPHA CHAIN (EC 7.99.4). (SUB 2-1247)	82	75	318
23	3	3275	2574	gi|1199573	spsB (Sphingomonas sp.)	81	64	702
42	1	638	321	gi|466778	lysine specific permease (Escherichia coli)	81	59	318
48	5	4051	4350	gi|1045937	M. genitalium predicted coding region MG246 (Mycoplasma genitalium)	81	62	300
51	4	3578	2579	pir|S16649|S166	dciAC protein - Bacillus subtilis	81	55	1002
53	2	364	1494	gi|1303961	YqjJ (Bacillus subtilis)	81	67	1131
53	8	9419	7971	gi|146930	6-phosphogluconate dehydrogenase (Escherichia coli)	81	66	1449
54	9	10757	10119	gi|143016	permease (Bacillus subtilis)	81	65	639
54	10	13360	11786	gi|143015	gluconate kinase (Bacillus subtilis)	81	64	1575
57	17	13983	13366	pir|A25805|A258	L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus subtilis	81	74	618
81	2	2708	2217	gi|1222302	NifU-related protein (Haemophilus influenzae)	81	54	492
86	1	745	374	gi|414017	ipa-93d gene product (Bacillus subtilis)	81	70	372
103	6	6438	4861	gi|971342	nitrate reductase beta subunit (Bacillus subtilis) sp|P42176|NARH_BACSU NITRATE REDUCTASE BETA CHAIN (EC 1.7.99.4).	81	64	1578
120	15	10845	12338	gi|1524392	GbsA (Bacillus subtilis)	81	67	1494
128	5	3676	4413	gi|143319	triose phosphate isomerase (Bacillus megaterium)	81	64	738
131	9	10308	9280	gi|299163	alanine dehydrogenase (Bacillus subtilis)	81	68	1029
143	6	6088	5471	gi|439619	(Salmonella typhimurium IS200 insertion sequence from SARA17, artial.), geno product (Salmonella typhimurium)	81	61	618
169	1	43	825	gi|897795	30S ribosomal protein (Pediococcus acidilactici) sp|P49668|RS2_PEDAC 30S RIBOSOMAL PROTEIN S2.	81	65	783
230	1	450	226	gi|1125826	short region of weak similarity to tyrosine-protein kinase receptors in a fibronectin type III-like domain (Caenorhabditis elegans)	81	54	225
233	5	2000	2677	gi|467404	unknown (Bacillus subtilis)	81	63	678
241	2	3081	2149	gi|16510	succinate--CoA ligase (GDP-forming) (Arabidopsis thaliana) ir|S30579|S30579 succinate--CoA ligase (GDP-forming) (EC 6.2.1.4) pha chain - Arabidopsis thaliana (fragment)	81	69	933
256	1	1	981	pir|S09411|S094	spoIIIE protein - Bacillus subtilis	81	65	981
259	3	3752	2691	sp|P28367|RF2_B	PROBABLE PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2) (FRAGMENT).	81	65	1062

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name (')	% sim	% ident	length (nt)
275	2	1728	3581	gi|726480	L-glutamino-D-fructose-6-phosphate amidotransferase [Bacillus ubtilis]	81	68	1854
285	1	1466	735	gi|1204844	H. influenzae predicted coding region HI0594 [Haemophilus influenzae]	81	63	732
296	1	99	1406	gi|467328	adenylosuccinate synthetase [Bacillus subtilis]	81	67	1308
302	9	5590	5889	gi|147485	queA [Escherichia coli]	81	64	300
317	2	1137	1376	gi|154961	resolvase [Transposon Tn917]	81	54	240
343	2	1034	1342	gi|405955	yeeD [Escherichia coli]	81	60	309
360	2	1404	2471	gi|1204570	aspartyl-tRNA synthetase [Haemophilus influenzae]	81	67	1068
364	5	6251	5706	gi|1206652	methylated-DNA--protein-cysteine methyltransferase [Haemophilus influenzae]	81	63	546
372	2	1707	1135	gi|467016	unknown [Bacillus subtilis]	81	65	573
392	1	43	603	pir|S09411|S094	spoIIIE protein - Bacillus subtilis	81	65	561
404	9	5252	6154	gi|606745	Bex [Bacillus subtilis]	81	65	903
426	2	1727	1119	gi|39453	Manganese superoxide dismutase [Bacillus caldotenax] ir|S22053|S22053 superoxide dismutase (EC 1.15.1.1) (Mn) - Bacillus idotenax	81	66	609
480	7	6653	5889	pir|C37040|C370	hypothetical protein 1f (ompH 3' region) - Salmonella typhimurium (fragment)	81	57	237
625	3	1105	2070	gi|1262360	protein kinase PknB [Mycobacterium leprae]	81	56	966
754	2	504	1064	gi|1303902	YqhU [Bacillus subtilis]	81	71	561
842	1	86	430	gi|1405446	transketolase [Bacillus subtilis]	81	68	345
953	1	798	400	gi|1205429	dipeptide transport ATP-binding protein [Haemophilus influenzae]	81	57	399
961	2	252	401	gi|487686	synergohymanotropic toxin [Staphylococcus intermedius] pir|S44944|S44944 synergohymenotropic toxin - Staphylococcus ntermedius	81	72	150
1035	1	1	189	gi|1046138	M. genitalium predicted coding region MG423 [Mycoplasma genitalium]	81	43	189
1280	1	670	449	gi|559164	helicase [Autographa californica nuclear polyhedrosis virus] op|P24307|VI41_NPVAC HELICASE.	81	43	222
1371	1	68	241	gi|1322245	mevalonate pyrophosphate decarboxylase [Rattus norvegicus]	81	62	174
1715	1	475	239	gi|537137	ORF_f188 [Escherichia coli]	81	58	237
1908	1	2	325	gi|439619	[Salmonella typhimurium IS200 insertion sequence from SARA17, artial.], gene product [Salmonella typhimurium]	81	68	324
1940	1	3	401	gi|296464	ATPase [Lactococcus lactis]	81	69	399

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% identity	length (nt)
3954	1	1	318	gi|1224069	amidase [Moraxella catarrhalis]	81	68	318
4049	1	337	170	gi|603768	HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis] gi|603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis]	81	68	168
4209	1	1	324	gi|403373	glycerophosphoryl diester phosphodiesterase [Bacillus subtilis] pir|S37251|S37251 glycerophosphoryl diester phosphodiesterase - acillus subtilis	81	58	324
4371	1	627	322	gi|216677	indolepyruvate decarboxylase [Enterobacter cloacae] pir|S16013|S16013 indolepyruvate decarboxylase (EC 4.1.1.-) - nterobacter cloacae	81	72	306
4387	1	19	228	gi|460689	TVG [Thermoactinomyces vulgaris]	81	59	210
4191	1	581	306	gi|1524193	unknown [Mycobacterium tuberculosis]	81	67	276
4425	1	3	341	gi|143015	gluconate kinase [Bacillus subtilis]	81	66	339
9	1	1593	847	gi|1064786	function unknown [Bacillus subtilis]	80	62	747
17	1	544	311	gi|559164	helicase [Autographa californica nuclear polyhedrosis virus] sp|P24307|V143_NPVAC HELICASE.	80	40	234
45	2	1159	2448	gi|1109684	ProV [Bacillus subtilis]	80	63	1290
45	5	4032	4733	gi|1109687	ProZ [Bacillus subtilis]	80	55	702
54	8	10266	9502	gi|563952	gluconate permease [Bacillus licheniformis]	80	62	765
62	12	8852	7545	gi|854655	Na/H antiporter system [Bacillus alcalophilus]	80	62	1308
62	14	8087	8683	gi|559713	ORF [Homo sapiens]	80	68	597
67	16	13781	14122	gi|305002	ORF_f356 [Escherichia coli]	80	65	342
70	13	11495	10296	gi|1303995	YqkN [Bacillus subtilis]	80	64	1200
98	9	6336	7130	gi|467428	unknown [Bacillus subtilis]	80	68	795
98	10	7294	7833	gi|467430	unknown [Bacillus subtilis]	80	64	540
98	11	7820	8737	gi|467431	high level kasgamycin resistance [Bacillus subtilis]	80	61	918
109	16	14154	14813	gi|580875	ipa-57d gene product [Bacillus subtilis]	80	63	660
112	15	14294	16636	gi|1072361	pyruvate-formate-lyase [Clostridium pasteurianum]	80	65	2343
139	1	1448	726	gi|506699	CapC [Staphylococcus aureus]	80	58	723
139	2	2179	1448	gi|506698	CapB [Staphylococcus aureus]	80	59	732
174	4	3271	2870	gi|1146242	aspartate 1-decarboxylase [Bacillus subtilis]	80	61	402

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
177	3	2102	2842	gi|467385	unknown [Bacillus subtilis]	80	70	741
184	6	6124	5912	gi|161953	85-kDa surface antigen [Trypanosoma cruzi]	80	46	213
186	4	5368	3875	gi|289282	glutamyl-tRNA synthetase [Bacillus subtilis]	80	65	1494
205	10	15796	15140	gi|40103	ribosomal protein L4 [Bacillus stearothermophilus]	80	66	657
207	1	140	1315	gi|460259	enolase [Bacillus subtilis]	80	67	1176
211	3	1078	1590	gi|410131	ORFX7 [Bacillus subtilis]	80	61	513
235	2	1962	2255	gi|143797	valyl-tRNA synthetase [Bacillus stearothermophilus] sp|P11931|SYV_BACST VALYL-TRNA SYNTHETASE (EC 6.1.1.9) VALINE--TRNA LIGASE) (VALRS).	80	55	294
239	1	1	1263	gi|143000	proton glutamate symport protein [Bacillus stearothermophilus] pir|S26247|S26247 glutamate/aspartate transport protein - Bacillus tearothermophilus	80	59	1263
272	5	2724	2461	gi|709993	hypothetical protein [Bacillus subtilis]	80	54	264
301	3	1446	1111	gi|467418	unknown [Bacillus subtilis]	80	58	336
310	4	5697	4501	gi|1177686	acuC gene product [Staphylococcus xylosus]	80	67	1197
310	6	5258	7006	gi|348053	acetyl-CoA synthetase [Bacillus subtilis]	80	67	1749
310	7	7410	9113	gi|1103865	formyl-tetrahydrofolate synthetase [Streptococcus mutans]	80	67	1704
325	3	1114	1389	gi|310325	outer capsid protein [Rotavirus sp.]	80	40	276
337	1	1268	636	gi|537049	ORF_o470 [Escherichia coli]	80	55	633
374	2	929	1228	gi|1405448	YneF [Bacillus subtilis]	80	70	300
375	5	3062	3331	gi|467448	unknown [Bacillus subtilis]	80	68	270
388	1	267	587	gi|1064791	function unknown [Bacillus subtilis]	80	65	321
394	1	9	659	gi|304976	matches PS00017: ATP_GTP_A and PS00301: EFACTOR_GTP; similar to longation factor G, TetM/TetO tetracycline-resistance proteins Escherichia coli]	80	65	651
456	1	625	1263	gi|1146183	putative [Bacillus subtilis]	80	65	639
475	1	1	654	gi|288269	beta-fructofuranosidase [Staphylococcus xylosus]	80	66	654
544	2	1449	2240	gi|529754	speC [Streptococcus pyogenes]	80	50	792
622	4	1623	1871	gi|1483545	unknown [Mycobacterium tuberculosis]	80	65	249
719	1	1	1257	gi|1064791	function unknown [Bacillus subtilis]	80	68	1257
739	1	107	838	gi|666983	putative ATP binding subunit [Bacillus subtilis]	80	61	732

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name ( )	% sim	% ident	length (nt)
745	2	581	414	gi|1511600	coenzyme PQQ synthesis protein III [Methanococcus jannaschii]	80	61	168
822	1	17	679	gi|410141	ORFX17 [Bacillus subtilis]	80	68	663
827	2	991	836	gi|1205301	leukotoxin secretion ATP-binding protein [Haemophilus influenzae]	80	54	156
1044	1	3	149	gi|60632	vp2 [Marburg virus]	80	55	147
1220	2	571	413	pir|A61072|EPSG	gallidermin precursor - Staphylococcus gallinarum	80	74	159
2519	1	75	275	gi|147556	dpj [Escherichia coli]	80	45	201
2947	1	503	279	gi|1184680	polynucleotide phosphorylase [Bacillus subtilis]	80	62	225
3120	1	2	226	gi|517205	67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogenes]	80	65	225
3191	1	294	148	gi|151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	80	59	147
3560	2	285	434	gi|217130	photosystem I core protein B [Synechococcus vulcanus]	80	70	150
3655	1	47	346	gi|415855	deoxyribose aldolase [Mycoplasma hominis]	80	56	300
3658	2	324	584	gi|551531	2-nitropropane dioxygenase [Williopsis saturnus]	80	54	261
3769	1	798	400	gi|1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	80	68	399
3781	1	692	348	gi|166412	NADH-glutamate synthase [Medicago sativa]	80	62	345
3988	1	48	287	gi|1204696	fructose-permease IIBC component [Haemophilus influenzae]	80	69	240
4030	1	571	287	gi|1009366	Respiratory nitrate reductase [Bacillus subtilis]	80	60	285
4092	1	547	275	gi|1370207	orf6 [Lactobacillus sake]	80	69	273
4103	1	680	342	gi|39956	IIGlc [Bacillus subtilis]	80	65	339
4231	1	692	348	gi|289287	UDP-glucose pyrophosphorylase [Bacillus subtilis]	80	65	345
4265	1	595	299	gi|603768	HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis] gi|603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis]	80	63	297
4504	1	498	250	gi|1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	80	68	249
2	6	5998	6798	g |535351	CodY [Bacillus subtilis]	79	63	801
4	7	8295	7051	gi|603768	HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis] gi|603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis]	79	64	1245
25	6	5273	5515	pir|A36728|A367	acyl carrier protein - Rhizobium meliloti	79	65	243

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
59	2	1173	1424	gi|147923	threonine dehydratase 2 (EC 4.2.1.16) [Escherichia coli]	79	75	252
60	1	1	204	gi|666115	orf1 upstream of glucose kinase [Staphylococcus xylosus] pir|S52351|S52351 hypothetical protein 1 - Staphylococcus xylosus	79	60	204
81	1	3002	1590	gi|466082	ppol; D1696_C2_109 [Mycobacterium leprae]	79	64	1413
85	7	7023	6505	gi|143364	phosphoribosyl aminoimidazole carboxylase I (PUR-E) [Bacillus subtilis]	79	60	519
89	6	5660	4554	gi|144906	product homologous to E.coli thioredoxin reductase: J.Biol.Chem. 1988) 263:9015-9019, and to P52a protein of alkyl hydroperoxide reductase from S.typhimurium: J.Biol.Chem. (1990) 265:10535-10540; pon reading frame A [Clostridium pasteurianum]	79	35	1107
102	11	7489	8571	gi|143093	ketol-acid reductoisomerase [Bacillus subtilis] sp|P37253|ILVC_BACSU KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86) ACETOHYDROXY-ACID ISOMEROREDUCTASE) (ALPHA-KETO-BETA-HYDROXYLACIL REDUCTOISOMERASE).	79	64	1083
102	14	11190	12563	gi|149428	putativo [Lactococcus lactis]	79	65	1374
127	9	7792	9372	gi|458688	PrfC/RF3 [Dichelobacter nodosus]	79	68	1581
139	3	2540	1983	gi|506697	CapA [Staphylococcus aureus]	79	55	558
144	2	1644	1156	gi|1498296	peptido methionine sulfoxido reductase [Streptococcus pneumoniae]	79	47	489
148	2	529	1098	gi|467457	hypoxanthine-guanine phosphoribosyltransferase [Bacillus subtilis] gi|467457 hypoxanthine-guanine phosphoribosyltransferase [Bacillus subtilis]	79	59	570
150	1	965	591	gi|755602	unknown [Bacillus subtilis]	79	61	375
176	1	1039	587	gi|297874	fructose-bisphosphate aldolase [Staphylococcus carnosus] pir|A49943|A49943 fructose-bisphosphate aldolase (EC 4.1.2.13) - taphylococcus carnosus (strain TM300)	79	65	453
186	7	7584	6874	gi|1314298	ORF5; putative Sms protein; similar to Sms proteins from Haemophilus influenzae and Escherichia coli [Listeria monocytogones]	79	64	711
205	16	8687	8498	gi|1044980	ribosomal protein L18 [Bacillus subtilis]	79	70	390
211	1	1	519	gi|1303994	YqkM [Bacillus subtilis]	79	62	519
223	2	4183	2801	gi|488430	alcohol dehydrogenase 2 [Entamoeba histolytica]	79	60	1383
243	8	8915	7896	gi|580883	ipa-88d gene product [Bacillus subtilis]	79	60	1020
279	4	3721	4329'	gi|413930	ipa-6d gene product [Bacillus subtilis]	79	59	609
300	1	11	1393	gi|403372	glycerol 3-phosphate permease [Bacillus subtilis]	79	62	1383
307	3	2930	1935	gi|950062	hypothetical yeast protein 1 (Mycoplasma capricolum) pir|S48578|S48578 hypothetical protein - Mycoplasma capricolum SGC3) (fragment)	79	60	996

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
352	6	10106	8886	gi|216854	P47K (Pseudomonas chlororaphis)	79	59	1221
412	1	1153	578	gi|143177	putative (Bacillus subtilis)	79	51	576
481	3	621	1124	gi|786163	Ribosomal Protein L10 (Bacillus subtilis)	79	66	504
516	1	702	352	gi|805090	NisF (Lactococcus lactis)	79	48	351
525	2	2457	1426	gi|143371	phosphoribosyl aminoimidazole synthetase (PUR-M) (Bacillus subtilis) pir|H29326|AJBSCL phosphoribosylformylglycinamidine cyclo-ligase EC 6.3.3.1) - Bacillus subtilis	79	61	1032
538	4	3448	2825	gi|1370207	orf6 (Lactobacillus sake)	79	67	624
570	1	2	421	gi|476160	arginine permease substrate-binding subunit (Listeria monocytogenes)	79	61	420
645	8	2663	3241	gi|153898	transport protein (Salmonella typhimurium)	79	62	579
683	1	75	374	gi|1064795	function unknown (Bacillus subtilis)	79	62	300
816	3	4700	3987	gi|1407784	orf-1; novel antigen (Staphylococcus aureus)	79	62	714
2929	1	3	401	gi|1524397	glycine betaine transporter OpuD (Bacillus subtilis)	79	61	399
2937	1	357	202	pir|S52915|S529	nitrate reductase alpha chain - Bacillus subtilis (fragment)	79	58	156
2940	1	768	385	gi|149429	putative (Lactococcus lactis)	79	72	384
2946	1	570	286	gi|143267	2-oxoglutarate dehydrogenase (odhA; EC 1.2.4.2) (Bacillus subtilis)	79	61	285
2999	1	3	212	gi|710020	nitrite reductase (nirB) (Bacillus subtilis)	79	59	210
3022	1	514	332	gi|450686	3-phosphoglycerate kinase (Thermotoga maritima)	79	61	183
3064	1	3	314	gi|1204436	pyruvate formate-lyase (Haemophilus influenzae)	79	60	312
3083	1	2	220	gi|1149662	hypD gene product (Clostridium perfringens)	79	56	219
3126	1	701	411	gi|1339950	large subunit of NADH-dependent glutamate synthase (Plectonema boryanum)	79	55	291
3181	1	607	326	gi|1339950	large subunit of NADH-dependent glutamate synthase (Plectonema boryanum)	79	59	282
3345	1	3	476	gi|871784	Clp-like ATP-dependent protease binding subunit (Bos taurus)	79	63	474
3718	1	536	270	pir|C36889|C368	leuB protein, inactive - Lactococcus lactis subsp. lactis (strain IL1403)	79	71	267
3724	2	159	401	gi|1009366	Respiratory nitrate reductase (Bacillus subtilis)	79	64	243
3836	1	608	312	gi|1524193	unknown (Mycobacterium tuberculosis)	79	65	297
3941	1	2	334	gi|415855	deoxyribose aldolase (Mycoplasma hominis)	79	54	333
4113	1	3	341	gi|143015	gluconate kinase (Bacillus subtilis)	79	63	339

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name ( )	% sim	% ident	length (nt)
4501	1	406	209	gi|1022726	unknown (Staphylococcus haemolyticus)	79	66	198
4612	1	2	238	gi|460689	TVG (Thermoactinomyces vulgaris)	79	58	237
2	1	2	1213	gi|520753	DNA topoisomerase I (Bacillus subtilis)	78	64	1212
8	2	2266	1220	gi|216151	DNA polymerase (gene L; ttg start codon) (Bacteriophage SPO2) gi|579197 SPO2 DNA polymerase (aa 1-668) (Bacteriophage SPO2) pir|A21498|DJBPS2 DNA-directed DNA polymerase (EC 2.7.7.7) - phage PO2	78	72	1047
9	2	1340	1089	gi|1064787	function unknown (Bacillus subtilis)	78	57	252
32	8	6803	7702	gi|146974	NH3-dependent NAD synthetase (Escherichia coli)	78	63	900
36	4	2941	3138	gi|290503	glutomate permease (Escherichia coli)	78	53	198
53	15	17684	16221	gi|1303941	YqiV (Bacillus subtilis)	78	58	1464
57	14	10520	12067	gi|1072418	glcA gene product (Staphylococcus carnosus)	78	65	1548
66	7	6798	5812	gi|1212729	YqhJ (Bacillus subtilis)	78	67	987
67	4	4029	4376	gi|466612	nikA (Escherichia coli)	78	71	348
91	9	10058	10942	gi|467380	stage 0 sporultion (Bacillus subtilis)	78	50	885
102	12	8574	10130	gi|149426	putative (Lactococcus lactis)	78	61	1557
112	6	3540	4463	gi|854234	cymG gene product (Klebsiella oxytoca)	78	56	924
124	2	1888	1061	gi|405622	unknown (Bacillus subtilis)	78	60	828
130	3	1805	2260	gi|1256636	putative (Bacillus subtilis)	78	71	456
133	1	751	377	gi|168060	lamB (Emericella nidulans)	78	59	375
166	4	7125	6163	gi|451216	Mannosephosphate Isomerase (Streptococcus mutans)	78	63	963
186	1	1586	795	gi|289284	cysteinyl-tRNA synthetase (Bacillus subtilis)	78	63	792
195	4	2749	2315	gi|1353874	unknown (Rhodobacter capsulatus)	78	58	435
199	3	4279	3623	gi|143525	succinate dehydrogenase cytochrome b-558 subunit (Bacillus subtilis) pir|A29843|DEBSSC succinate dehydrogenase (EC 1.3.99.1) cytochrome 558 - Bacillus subtilis	78	57	657
199	4	7209	5557	gi|142521	deoxyribodipyrimidine photolyase (Bacillus subtilis) pir|A37192|A37192 uvrB protein - Bacillus subtilis sp|P14951|UVRC_BACSU EXCINUCLEASE ABC SUBUNIT C.	78	62	1653
223	3	3831	3523	gi|439596	(Escherichia coli IS200 insertion sequence from ECOR63, partial.), ene product (Escherichia coli)	78	67	309

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name ( )	% sim	% ident	length (nt)
299	4	1865	2149	gi|467439	temperature sensitive cell division [Bacillus subtilis]	78	62	285
321	9	7734	7315	gi|142979	ORF3 is homologous to an ORF downstream of the spoT gene of E.coli; RF3 [Bacillus stearothermophilus]	78	55	420
352	4	3714	3944	gi|349050	actin 1 [Pneumocystis carinii]	70	42	231
352	5	7592	6093	gi|903587	NADH dehydrogenase subunit 5 [Bacillus subtilis] sp|P39755|NDHP_BACSU NADH DEHYDROGENASE SUBUNIT 5 (EC 1.6.5.3) NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5).	78	58	1500
376	1	2	583	gi|551693	dethiobiotin synthase [Bacillus sphaericus]	78	34	582
424	2	1595	1768	gi|1524117	alpha-acetolactate decarboxylase [Lactococcus lactis]	78	68	174
450	1	1914	988	gi|1030068	NAD(P)H oxidoreductase, isoflavone reductase homologue [Solanum tuberosum]	78	63	927
558	1	762	562	gi|1511588	bifunctional protein [Methanococcus jannaschii]	78	60	201
670	3	1152	1589	gi|1122759	unknown [Bacillus subtilis]	78	64	438
714	1	64	732	gi|143460	37 kd minor sigma factor (rpoF, sig8; ttg start codon) [Bacillus subtilis]	78	57	669
814	1	3	368	gi|1377833	unknown [Bacillus subtilis]	78	59	366
981	1	1381	692	gi|143802	GerC2 [Bacillus subtilis]	78	64	690
995	2	978	727	gi|296947	uridine kinase [Escherichia coli]	78	64	252
1045	1	3	401	gi|1407784	orf-1; novel antigen [Staphylococcus aureus]	78	61	399
1163	2	368	186	gi|410117	diaminopimelate decarboxylase [Bacillus subtilis]	78	54	183
2191	1	794	399	gi|215098	excisionase [Bacteriophage 154a]	78	65	396
2933	1	2	181	gi|1204436	pyruvate formate-lyase [Haemophilus influenzae]	78	73	180
3041	2	139	317	gi|624632	GltL [Escherichia coli]	78	53	189
3501	1	105	401	gi|763186	3-ketoacyl-coA thiolase [Saccharomyces cerevisiae]	78	55	297
3709	1	3	230	gi|460689	fVG [Thermoactinomyces vulgaris]	78	58	228
3974	1	528	265	gi|558839	unknown [Bacillus subtilis]	78	65	264
3980	1	3	401	gi|39956	ITGlc [Bacillus subtilis]	78	62	399
4056	1	647	354	gi|1256635	dihydroxy-acid dehydratase [Bacillus subtilis]	78	55	294
4114	1	630	316	pir|S09372|S093	hypothetical protein - Trypanosoma brucei	78	62	315
4185	1	3	179	gi|1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	78	58	177

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name ( )	% sim	% ident	length (nt)
4235	1	655	329	gi|558839	unknown (Bacillus subtilis)	78	60	327
4352	1	541	302	gi|603768	HutI protein, imidazolone-5-propionate hydrolase (Bacillus subtilis) gi|603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis]	78	63	240
4368	1	612	307	gi|1353678	heavy-metal transporting P-type ATPase (Proteus mirabilis)	78	59	306
4461	1	428	216	gi|1276841	glucanate synthase (GOGAT) (Porphyra purpurea)	78	36	213
4530	1	474	238	gi|39956	IIGlc (Bacillus subtilis)	78	65	237
3	2	2969	2073	gi|1109684	proV (Bacillus subtilis)	77	56	897
12	2	2426	1965	gi|467335	ribosomal protein L9 (Bacillus subtilis)	77	59	462
27	1	2	388	gi|121728	YqhI (Bacillus subtilis)	77	63	387
39	2	590	1252	gi|40054	phenylalanyl-tRNA synthetase beta subunit (AA 1-804) (Bacillus btilis)	77	60	663
42	6	2704	2931	gi|606241	30S ribosomal subunit protein S14 (Escherichia coli) sp|P02370|RS14_ECOLI 30S RIBOSOMAL PROTEIN S14. (SUB 2-101)	77	65	228
46	18	15459	16622	gi|297798	mitochondrial formate dehydrogenase precursor (Solanum tuberosum) pir|JQ2272|JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, itochondrial - potato	77	55	1164
100	4	4562	4002	gi|1340128	ORF1 (Staphylococcus aureus)	77	54	561
102	8	5378	5713	gi|1311482	acetolactate synthase (Thermus aquaticus)	77	57	336
109	7	4742	5383	gi|710637	Unknown (Bacillus subtilis)	77	56	642
117	1	2	1228	gi|1237015	ORF4 (Bacillus subtilis)	77	53	1227
124	10	8323	7688	gi|405819	thymidine kinase (Bacillus subtilis)	77	63	636
147	3	1146	985	gi|849027	hypothetical 15.9-kDa protein (Bacillus subtilis)	77	37	162
152	10	7354	7953	gi|1205583	spermidine/putrescine transport ATP-binding protein (Haemophilus influenzae)	77	55	600
169	2	1004	1282	gi|473825	'elongation factor EF-Ts' (Escherichia coli)	77	58	279
184	2	380	1147	gi|216314	esterase (Bacillus stearothermophilus)	77	60	768
189	7	3296	3868	gi|853809	ORF3 (Clostridium perfringens)	77	48	573
193	1	132	290	gi|1303788	YqeH (Bacillus subtilis)	77	54	159
195	8	8740	8414	gi|1499620	M. jannaschii predicted coding region MJ0798 (Methanococcus jannaschii)	77	44	327
205	8	5428	5204	gi|216340	ORF for adenylate kinase (Bacillus subtilis)	77	61	225

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match Acession	match gene name	% sim	% ident	length (nt)
205	29	14795	14502	gi|786155	Ribosomal Protein L23 [Bacillus subtilis]	77	62	294
211	5	1908	2084	gi|410132	ORFX8 [Bacillus subtilis]	77	47	177
217	5	3478	4416	gi|496254	fibronectin/fibrinogen-binding protein [Streptococcus pyogenes]	77	54	939
232	1	267	998	gi|1407784	orf-1; novel antigen [Staphylococcus aureus]	77	57	732
233	2	1819	1346	gi|467408	unknown [Bacillus subtilis]	77	61	474
243	3	2661	2299	gi|516155	unconventional myosin [Sus scrofa]	77	32	363
299	1	68	769	gi|467436	unknown [Bacillus subtilis]	77	54	702
301	4	1468	1283	gi|950071	ATP-bind. pyrimidine kinase [Mycoplasma capricolum] pir|S48605|S48605 hypothetical protein - Mycoplasma capricolum SGC3) (fragment)	77	48	186
302	5	2741	3211	gi|508980	pheB [Bacillus subtilis]	77	57	471
302	7	3835	4863	gi|147783	ruvB protein [Escherichia coli]	77	60	1029
307	9	5402	4797	gi|1070015	protein-dependent [Bacillus subtilis]	77	60	606
312	1	99	1391	gi|143165	malic enzyme (EC 1.1.1.38) [Bacillus stearothermophilus] pir|A33307|DEBSXS malate dehydrogenase oxaloacetate-decarboxylating) (EC 1.1.1.38) - Bacillus tearothermophilus	77	62	1293
312	2	1541	2443	gi|1399855	carboxyltransferase beta subunit [Synechococcus PCC7942]	77	58	903
321	5	5666	4596	gi|39844	fumarase (citG) (aa 1-462) [Bacillus subtilis]	77	65	1071
354	1	47	568	gi|1154634	YmaB [Bacillus subtilis]	77	57	522
365	1	2	1021	gi|143374	phosphoribosyl glycinamide synthetase (PUR-D; gtg start codon) Bacillus subtilis]	77	62	1020
374	1	1	708	gi|1405446	transketolase [Bacillus subtilis]	77	61	708
385	1	1128	565	gi|533099	endonuclease III [Bacillus subtilis]	77	63	564
392	2	594	1940	gi|556014	UDP-N-acetyl muramate-alanine ligase [Bacillus subtilis] sp|P40778|MURC_BACSU UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC .3.2.8) (UDP-N- ACETYLMURANOYL-L-ALANINE SYNTHETASE) (FRAGMENT).	77	65	1347
405	5	4079	3570	gi|1303912	YqhW [Bacillus subtilis]	77	64	510
487	4	1302	1472	gi|432427	ORF1 gene product [Acinetobacter calcoaceticus]	77	48	171
522	1	2	562	pir|A01179|SYBS	tyrosine--tRNA ligase (EC 6.1.1.1) - Bacillus stearothermophilus	77	63	561

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
523	2	1587	1351	gi|1387979	44% identity over 302 residues with hypothetical protein from Synechocystis sp, accession D64006_CD; expression induced by environmental stress; some similarity to glycosyl transferases; two potential membrane-spanning helices [Bacillus subtil	77	48	237
536	2	983	612	gi|143366 -	adenylosuccinate lyase (PUR-B) [Bacillus subtilis] pir|C29326|WZBSDS adenylosuccinate lyase (EC 4.3.2.2) - Bacillus ubtilis	77	61	372
548	2	339	872	gi|143387	aspartate transcarbamylase [Bacillus subtilis]	77	56	534
597	1	2	481	gi|904198	hypothetical protein [Bacillus subtilis]	77	33	480
633	2	1747	1313	gi|387577	ORF1A [Bacillus subtilis]	77	64	435
642	1	85	360	gi|46971	epiP gene product [Staphylococcus epidermidis]	77	61	276
659	1	125	1219	gi|1072381	glutamyl-aminopeptidase [Lactococcus lactis]	77	62	1095
670	4	1587	1820	gi|1122760	unknown [Bacillus subtilis]	77	58	234
789	1	2	391	gi|1377823	aminopeptidase [Bacillus subtilis]	77	65	390
815	1	10	573	gi|1303861	YqgN [Bacillus subtilis]	77	49	564
899	1	1	225	gi|1204844	H. influenzae predicted coding region HI0594 [Haemophilus influenzae]	77	55	225
1083	1	3	188	gi|460828	B969 [Saccharomyces cerevisiae]	77	66	186
1942	1	415	209	gi|160047	p101/acidic basic repeat antigen (Plasmodium falciparum] pir|A29232|A29232 101K malaria antigen precursor - Plasmodium alciparum (strain Camp)	77	38	207
2559	1	1	171	gi|1499034	M. jannaschii predicted coding region MJ0255 [Methanococcus jannaschii]	77	61	171
2933	2	243	401	gi|42370	pyruvate formate-lyase (AA 1-760) [Escherichia coli] ir|S01788|S01788 formate C-acetyltransferase (EC 2.3.1.54) - cherichia coli	77	72	159
2966	1	56	292	gi|1524397	glycine betaine transporter OpuD [Bacillus subtilis]	77	45	237
2976	1	614	309	gi|40003	oxoglutarate dehydrogenase (NADP+) [Bacillus subtilis] p|P23129|ODO1_BACSU 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE).	77	60	306
2979	2	678	400	gi|1204354	spore germination and vegetative growth protein [Haemophilus influenzae]	77	61	279
2988	1	601	377	gi|438465	Probable operon with orfP. Possible alternative initiation codon, atgs 2151-2153. Homology with acetyltransferases.; putative Bacillus subtilis]	77	55	225
2990	1	331	167	gi|142562	ATP synthase epsilon subunit [Bacillus megaterium] pir|B28599|PWBSEM H+-transporting ATP synthase (EC 3.6.1.34) psilon chain - Bacillus megaterium	77	63	165
3032	1	3	389	gi|488430	alcohol dehydrogenase 2 [Entamoeba histolytica]	77	56	387
3057	1	1	195	gi|468764	mocR gene product [Rhizobium meliloti]	77	50	195

TABLE 2

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
4008	1	726	400	gi|603768	HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis] gi|603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis]	77	52	327
4048	1	703	386	gi|216278	gramicidin S synthetase 1 [Bacillus brevis]	77	55	318
4110	1	3	368	pir|S52915|S529	nitrate reductase alpha chain - Bacillus subtilis (fragment]	77	61	366
4115	1	1	348	gi|517205	67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus yogones]	77	65	348
4225	1	590	297	gi|1322245	mevalonate pyrophosphate decarboxylase [Rattus norvegicus]	77	60	294
4611	2	494	327	gi|508979	GTP-binding protein [Bacillus subtilis]	77	57	168
466A	1	361	182	pir|S52915|S529	nitrate reductase alpha chain - Bacillus subtilis (fragment)	77	61	180
25	1	2	1627	gi|1150620	HmsA [Streptococcus pneumoniae]	76	58	1626
38	5	1488	2537	pir|A43577|A435	regulatory protein pfoR - Clostridium perfringens	76	57	1050
52	5	2962	4041	gi|1161061	dioxygonase [Methylobacterium extorquons]	76	62	1080
56	20	27389	27955	gi|467402	unknown [Bacillus subtilis]	76	56	567
57	15	12046	12219	gi|1206040	weak similarity to keratin [Caenorhabditis elegans]	76	40	174
91	2	1062	2261	gi|475715	acetyl coenzyme A acetyltransferase (thiolase) [Clostridium cotobutylicum]	76	57	1200
98	2	818	1624	gi|467422	unknown [Bacillus subtilis]	76	62	807
98	5	2965	3228	gi|897793	y98 gene product [Pediococcus acidilactici]	76	52	264
98	8	5922	6326	gi|467427	methionyl-tRNA synthetase [Bacillus subtilis]	76	53	405
104	3	1322	1885	gi|216151	DNA polymerase (gene L; ttg start codon) [Bacteriophage SPO2] gi|579197 SPO2 DNA polymerase (aa 1-648) [Bacteriophage SPO2) pir|A21498|DJBPS2 DNA-directed DNA polymerase (EC 2.7.7.7) - phage PO2	76	63	564
124	9	8134	7055	gi|853776	peptide chain release factor 1 [Bacillus subtilis] pir|S55437|S55437 peptide chain release factor 1 - Bacillus ubtilis	76	58	1080
164	5	2832	3311	gi|1204976	prolyl-tRNA synthetase [Haemophilus influenzae]	76	53	480
168	2	2617	1841	gi|1177253	putative ATP-binding protein of ABC-type [Bacillus subtilis]	76	58	777
189	2	163	888	gi|467384	unknown [Bacillus subtilis]	76	63	726
235	3	2253	3518	gi|142936	folyl-polyglutamate synthetase [Bacillus subtilis] pir|B40646|B40646 folC - Bacillus subtilis	76	53	1266
236	1	335	925	gi|1146197	putative [Bacillus subtilis]	76	54	591
237	8	5323	5541	gi|1279261	F11G3.6 [Caenorhabditis elegans]	76	47	219

TABLE 2

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
263	5	5490	4585	gi|1510348	dihydrodipicolinate synthase (Methanococcus jannaschii)	76	49	906
304	3	1051	1794	gi|666982	putative membrane spanning subunit (Bacillus subtilis) pir|S52382|S52382 probable membrane spanning protein - Bacillus subtilis	76	60	744
312	4	3611	4624	gi|143312	6-phospho-1-fructokinase (gtg start codon; EC 2.7.1.11) (Bacillus tenarothermophilus)	76	56	1014
343	1	2	1036	gi|405956	yeeE (Escherichia coli)	76	59	1035
347	1	409	1701	gi|396304	acetylornithine deacetylase (Escherichia coli)	76	72	1293
358	1	672	1907	gi|1146215	39.0% identity to the Escherichia coli S1 ribosomal protein; putative (Bacillus subtilis)	76	58	1236
371	1	1	222	gi|537084	alternate gene name mgt; CG Site No. 497 (Escherichia coli) pir|S56460|S56460 mgtA protein - Escherichia coli	76	61	222
379	4	4331	4858	gi|143268	dihydrolipoamide transsuccinylase (odhB; EC 2.3.1.61) (Bacillus subtilis)	76	61	528
404	5	4022	4492	gi|1303823	YqfG (Bacillus subtilis)	76	60	471
411	1	2	307	gi|486025	ORF YKL027w (Saccharomyces cerevisiae)	76	55	306
472	3	4356	2854	gi|1405464	AlsT (Bacillus subtilis)	76	57	1503
546	1	273	995	gi|153821	streptococcal pyrogenic exotoxin type C (speC) precursor Streptococcus pyogenes)	76	36	723
588	1	1054	557	gi|1002520	MutS (Bacillus subtilis)	76	61	498
591	1	16	735	gi|885934	ClpB (Synechococcus sp.)	76	44	720
602	2	175	798	gi|1486422	OppD homologue (Rhizobium sp.)	76	52	624
619	2	547	290	gi|330613	major capsid protein (Human cytomegalovirus)	76	47	258
660	4	2568	3302	gi|904199	hypothetical protein (Bacillus subtilis)	76	55	735
677	1	452	228	gi|40177	spo0F gene product (Bacillus subtilis)	76	58	225
962	1	24	206	gi|142443	adenylosuccinate synthetase (Bacillus subtilis) sp|P29726|PURA_BACSU ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) IMP--ASPARTATE LIGASE).	76	67	183
978	1	1158	580	gi|1511333	M. jannaschii predicted coding region MJ1322 (Methanococcus jannaschii)	76	56	579
997	1	486	244	gi|467154	No definition line found (Mycobacterium leprae)	76	38	243
1563	1	529	266	gi|1303984	YqkG (Bacillus subtilis)	76	52	264
2184	1	361	182	gi|506706	CapJ (Staphylococcus aureus)	76	38	180
2572	1	1	387	gi|153898	transport protein (Salmonella typhimurium)	76	65	387

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
2942	1	29	400	gi|710020	nitrite reductase (nirB) [Bacillus subtilis]	76	59	372
2957	1	377	216	gi|1511251	hypothetical protein (SP:P42404) [Methanococcus jannaschii]	76	47	162
2980	1	554	279	gi|1405464	AlsT [Bacillus subtilis]	76	53	276
3015	1	649	326	gi|408115	ornithine acetyltransferase [Bacillus subtilis]	76	61	324
3124	1	13	174	gi|882705	ORF_o401 [Escherichia coli]	76	65'	162
3179	1	3	161	gi|168477	ferredoxin-dependant glutamate synthase [Zea mays] pir|A38596|A38596 glutamate synthase (ferredoxin) (EC 1.4.7.1) - maize	76	53	159
3789	1	2	379	gi|39956	IIGlc [Bacillus subtilis]	76	55	378
3892	1	3	314	gi|1510398	ferripyochelin binding protein [Methanococcus jannaschii]	76	52	312
3928	1	798	400	gi|143016	permease [Bacillus subtilis]	76	59	399
4159	1	757	386	sp|P80544|MRSP_	METHICILLIN-RESISTANT SURFACE PROTEIN (FRAGMENTS).	76	66	372
4204	1	17	331	gi|296464	ATPase [Lactococcus lactis]	76	56	315
4398	1	494	249	gi|987255	Menkes disease gene [Homo sapiens]	76	48	246
4506	1	2	313	gi|216746	D-lactate dehydrogenase [Lactobacillus plantarum]	76	47	312
4546	1	477	247	gi|1339950	large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	76	61	231
4596	1	379	191	gi|560027	cellulose synthase [Acetobacter xylinum]	76	70	189
4	5	5257	4337	gi|882532	ORF_o294 [Escherichia coli]	75	59	921
6	1	164	952	gi|40960	OTCase [Escherichia coli]	75	56	789
12	3	5935	3944	gi|467336	unknown [Bacillus subtilis]	75	57	1992
23	18	18272	17310	gi|1296433	O-acetylserine sulfhydrylase B [Alcaligenes eutrophus]	75	55	963
25	3	2356	3393	gi|1502419	PlsX [Bacillus subtilis]	75	56	1038
36	8	5765	6037	gi|1256517	unknown [Schizosaccharomyces pombe]	75	45	273
46	13	11186	12058	gi|48972	nitrate transporter [Synechococcus sp.]	75	46	873
51	7	3474	3677	gi|143607	sporulation protein [Bacillus subtilis]	75	61	204
53	16	16850	16590	gi|143402	recombination protein (ttg start codon), [Bacillus subtilis] gi|1303923 RocN [Bacillus subtilis]	75	51	261
74	3	3572	2568	gi|1204847	ornithine carbamoyltransferase [Haemophilus influenzae]	75	61	1005

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
85	3	4628	3930	gi|143368	phosphoribosylformyl glycinamidino synthetase I (PUR-L; gtg start odon) (Bacillus subtilis)	75	63	699
85	5	5588	4878	gi|143367	phosphoribosyl aminoidazole succinocarboxamide synthetase (PUR-C; tg start codon) (Bacillus subtilis)	75	55	711
85	8	6625	7530	gi|1303916	YqiA (Bacillus subtilis)	75	53	906
87	3	2340	3590	gi|1064813	homologous to sp:PHOR_BACSU (Bacillus subtilis)	75	56	1251
87	6	6084	6896	gi|1064810	function unknown (Bacillus subtilis)	75	61	813
108	2	1844	1503	gi|1001824	hypothetical protein (Synechocystis sp.)	75	51	342
110	3	1748	3727	gi|1147593	putative ppGpp synthetase (Streptomyces coelicolor)	75	55	1980
110	7	4153	5252	gi|1177251	ciwD gene product (Bacillus subtilis)	75	75	900
120	14	11266	10649	gi|1524394	ORF-2 upstream of gbsAB operon (Bacillus subtilis)	75	55	618
121	5	2050	4221	gi|1154632	NrdE (Bacillus subtilis)	75	54	2172
124	1	283	143	gi|405622	unknown (Bacillus subtilis)	75	56	141
128	1	81	1139	gi|143316	(gapl gene products (Bacillus megaterium)	75	48	1059
130	8	5760	5903	gi|1256654	54.8% identity with Neisseria gonorrhoese regulatory protein PilB; putative (Bacillus subtilis)	75	62	144
136	2	4480	3185	gi|467403	seryl-tRNA synthetase (Bacillus subtilis)	75	54	1296
161	10	5439	5798	gi|1001195	hypothetical protein (Synechocystis sp.)	75	55	360
172	4	3819	2995	gi|755153	ATP-binding protein (Bacillus subtilis)	75	52	825
179	1	2024	1107	gi|143037	porphobilinogen deaminase (Bacillus subtilis)	75	58	918
195	10	9529	9374	sp|P25745|YCFR_	HYPOTHETICAL PROTEIN IN PURB 5'REGION (ORF-15) (FRAGMENT).	75	60	156
200	4	2605	4596	gi|142440	ATP-dependent nuclease (Bacillus subtilis)	75	56	1992
206	3	6900	5620	gi|1256135	YbbF (Bacillus subtilis)	75	53	1281
216	2	159	389	gi|1052800	unknown (Schizosaccharomyces pombe)	75	58	231
229	1	29	847	gi|1205958	branched chain aa transport system II carrior protein (Haemophilus influenzae)	75	49	819
230	2	518	1714	gi|971337	nitrite extrusion protein (Bacillus subtilis)	75	53	1197
231	1	2240	1122	gi|1002521	MutL (Bacillus subtilis)	75	54	1119
233	3	1314	1859	gi|467405	unknown (Bacillus subtilis)	75	59	546

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
269	1	325	164	gi|1511246	methyl coenzyme M reductase system, component A2 [Methanococcus jannaschii]	75	50	162
292	1	1389	772	gi|1511604	M. jannaschii predicted coding region MJ1651 [Methanococcus jannaschii]	75	46	618
304	4	1773	2261	gi|1205328	surfactin [Haemophilus influenzae]	75	55	489
312	3	2437	3387	gi|285621	undefined open reading frame [Bacillus stearothermophilus]	75	62	951
312	5	4622	6403	gi|1041097	Pyruvate Kinase [Bacillus psychrophilus]	75	57	1782
319	1	353	877	gi|1212728	YqhI [Bacillus subtilis]	75	54	525
320	5	4321	5031	gi|1070361	OMP decarboxylase [Lactococcus lactis]	75	56	711
320	6	5010	5642	gi|143394	OMP-PRPP transferase [Bacillus subtilis]	75	60	633
337	4	1519	2088	gi|487433	citrate synthase II [Bacillus subtilis]	75	58	570
394	2	669	1271	gi|304976	matches PS00017: ATP_GTP_A and PS00301: EFACTOR_GTP; similar to longation factor G, TetM/TetO tetracycline-resistance proteins Escherichia coli]	75	51	603
423	1	127	570	gi|1183839	unknown [Pseudomonas aeruginosa]	75	59	444
433	2	1603	1929	gi|149211	acetolactate synthase [Klebsiella pneumonica]	75	63	327
446	2	176	1540	gi|312441	dihydroorotase [Bacillus caldolyticus]	75	62	1365
486	1	494	249	gi|1149682	potF gene product [Clostridium perfringens]	75	55	246
496	1	3	794	gi|143582	spoIIIEA protein [Bacillus subtilis]	75	59	792
498	2	824	1504	gi|143328	phoP protein (put.); putative [Bacillus subtilis]	75	47	681
499	2	1061	1624	gi|1387979	44% identity over 302 residues with hypothetical protein from Synechocystis sp, accession D64006_CD; expression induced by environmental stress; some similarity to glycosyl transferases; two potential membrane-spanning helices [Bacillus subtil	75	51	564
568	1	641	453	pir|JC4110|JC41	triacylglycerol lipase (EC 3.1.1.3) 2 - Mycoplasma mycoides subsp. mycoides (SGC3)	75	50	189
613	2	430	233	gi|330993	tegument protein [Saimiriine herpesvirus 2]	75	75	198
621	1	1	525	gi|529754	speC [Streptococcus pyogenes]	75	43	525
642	5	1809	2474	gi|1176401	EpiG [Staphylococcus epidermidis]	75	51	666
646	2	454	657	gi|172442	ribonuclease P [Saccharomyces cerevisiae]	75	37	204
657	1	3	347	gi|882541	ORF_o236 [Escherichia coli]	75	47	345
750	1	1662	832	gi|46971	epiP gene product [Staphylococcus epidermidis]	75	57	831

TABLE 2

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
754	1	2	481	gi|1303901	YqhT (Bacillus subtilis)	75	57	480
763	2	563	393	gi|1205145	multidrug resistance protein (Haemophilus influenzae)	75	51	171
775	1	961	482	pir|B36889|D36889	leuA protein, inactive - Lactococcus lactis subsp. lactis (strain IL1403)	75	63	480
793	1	1	180	gi|143316	(gap) gene products (Bacillus megaterium)	75	57	180
800	1	318	160	gi|509411	NFRA protein (Azorhizobium caulinodans)	75	34	159
811	1	1117	560	gi|143434	Rho Factor (Bacillus subtilis)	75	60	558
940	1	493	329	gi|1276985	arginase (Bacillus caldovelox)	75	50	165
971	2	37	252	gi|1001373	hypothetical protein (Synechocystis sp.)	75	58	216
1059	1	384	232	gi|726480	L-glutamine-D-fructose-6-phosphate amidotransferase (Bacillus ubtilis)	75	67	153
1109	2	219	374	gi|143331 | pir|A27650|A27650 | sp|P23545|PHOR_BACSU	alkaline phosphatase regulatory protein (Bacillus subtilis) regulatory protein phoR - Bacillus subtilis ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN HOR (EC 2.7.3.-).	75	53	156
1268	1	271	137	gi|304135 | sp|Q07908|ARGJ_BACST	ornithine acetyltransferase (Bacillus stearothermophilus) GLUTAMATE N-ACETYLTRANSFERASE (EC 2.3.1.35) ORNITHINE ACETYLTRANSFERASE) (ORNITHINE TRANSACETYLASE) (OATASE) / MINO-ACID ACETYLTRANSFERASE (EC 2.3.1.1) (N-ACETYLGLUTAMATE YNTHA	75	63	135
1500	1	324	163	gi|1205488	excinuclease ABC subunit B (Haemophilus influenzae)	75	57	162
1529	1	798	400	gi|1002521	MutL (Bacillus subtilis)	75	54	399
3010	1	770	387	gi|1204435	pyruvate formate-lysse activating enzyme (Haemophilus influenzae)	75	54	384
3105	1	1	180	gi|1041097	Pyruvate Kinase (Bacillus psychrophilus)	75	57	180
3117	1	45	212	gi|899317 | pir|S49111|S49111	peptide synthetase module (Microcystis aeruginosa) probable amino acid activating domain - icrocystis aeruginosa (fragment) (SUB 144-528)	75	42	168
3139	2	139	345	gi|145294	adenine phosphoribosyl-transferase (Escherichia coli)	75	66	207
3880	1	618	310	gi|1009366	Respiratory nitrate reductase (Bacillus subtilis)	75	58	309
3911	1	48	401	gi|433991	ATP synthase subunit beta (Bacillus subtilis)	75	68	354
3957	1	2	379	pir|D36889|D36889	3-isopropylmalate dehydratase (EC 4.2.1.33) chain leuC - Lactococcus lactis subsp. lactis (strain IL1403)	75	65	378
4005	1	5	259	gi|216746	D-lactate dehydrogenase (Lactobacillus plantarum)	75	48	255
4080	1	71	333	gi|415855	deoxyribose aldolase (Mycoplasma hominis)	75	59	261

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	% match gene name	% sim	% ident	length (nt)
4111	1	1	339	gi|149435	putative (Lactococcus lactis)	75	57	339
4136	1	602	303	gi|450648	hsdM gene of Ecoprri gene product (Escherichia coli) pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	75	56	300
4144	1	668	336	gi|48972	nitrate transporter (Synechococcus sp.)	75	49	333
4237	1	664	374	gi|1339950	large subunit of NADH-dependent glutamate synthase (Plectonema boryanum)	75	55	291
4306	2	73	318	gi|294260	major surface glycoprotein (Pneumocystis carinii)	75	68	246
4343	1	715	359	gi|1204652	methylated-DNA--protein-cysteine methyltransferase (Haemophilus influenzae)	75	52	357
4552	1	620	312	gi|396464	ATPase (Lactococcus lactis)	75	55	309
38	9	5776	6126	gi|443793	NupC (Escherichia coli)	74	50	351
50	8	6910	6221	gi|1239988	hypothetical protein (Bacillus subtilis)	74	55	690
56	9	10770	12221	gi|1000451	TreP (Bacillus subtilis)	74	57	1452
64	2	2266	1622	gi|41015	aspartate-tRNA ligase (Escherichia coli)	74	57	645
66	6	5063	4848	gi|1212729	YqhJ (Bacillus subtilis)	74	47	216
67	18	14334	14897	gi|1510631	endoglucanase (Methanococcus jannaschii)	74	52	564
102	15	12561	13136	gi|149429	putative (Lactococcus lactis)	74	67	576
102	16	13121	14419	gi|149435	putative (Lactococcus lactis)	74	57	1299
108	4	4873	3902	gi|39478	ATP binding protein of transport ATPases (Bacillus firmus) tr|S15406|S15406 ATP-binding protein - Bacillus firmus p|P26906|YATR_BACFI HYPOTHETICAL ATP-BINDING TRANSPORT PROTEIN.	74	59	972
116	5	8574	7093	gi|1205430	dipeptide transport system permease protein (Haemophilus influenzae)	74	49	1482
120	7	4342	4803	gi|146970	ribonucleoside triphosphate reductase (Escherichia coli) pir|A47331|A47331 anaerobic ribonucleotide reductase - Escherichia oli	74	58	462
121	7	5961	6581	gi|1107528	ttg start (Campylobacter coli)	74	51	621
128	3	2320	3531	gi|143318	phosphoglycerate kinase (Bacillus megaterium)	74	57	1212
130	7	5237	5791	gi|1256653	DNA-binding protein (Bacillus subtilis)	74	60	555
136	3	6745	5150	gi|143076	histidase (Bacillus subtilis)	74	58	1596
145	2	664	1368	gi|407773	devA gene product (Anabaena sp.)	74	45	705
152	1	552	277	gi|1377883	unknown (Bacillus subtilis)	74	54	276

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	aapqh gene name	% aim	% ident	length (nt)
164	10	11064	11375	gi|580900	ORF3 gene product [Bacillus subtilis]	74	52	312
175	2	3109	2624	gi|642656	unknown [Rhizobium meliloti]	74	34	486
175	9	6064	5612	gi|854656	Na/H antiporter system ORF2 [Bacillus alcalophilus]	74	46	453
195	11	11346	10339	gi|1204430	hypothetical protein (SP:P25745) [Haemophilus influenzae]	74	55	1008
205	17	9619	9059	gi|1044979	ribosomal protein L6 [Bacillus subtilis]	74	64	561
236	7	5574	6710	gi|1146207	putative [Bacillus subtilis]	74	63	1137
241	3	4521	3334	gi|694121	malate thiokinase [Methylobacterium extorquens]	74	52	1188
246	6	3305	2799	gi|467374	single strand DNA binding protein [Bacillus subtilis]	74	64	507
249	4	6551	5313	gi|1524397	glycine betaine transporter OpuD [Bacillus subtilis]	74	55	1239
261	7	4389	4081	gi|809542	CbrB protein [Erwinia chrysanthemi]	74	42	309
278	6	5714	4665	gi|1204872	ATP-binding protein [Haemophilus influenzae]	74	54	1050
309	1	1220	666	gi|1205579	hypothetical protein (GB:U14003_302) [Haemophilus influenzae]	74	53	555
315	2	1473	862	gi|143398	quinol oxidase [Bacillus subtilis]	74	57	612
320	1	1	1065	gi|143389	glutaminase of carbamoyl phosphate synthetase [Bacillus subtilis] pir[E39845|E39845 carbamoyl-phosphate synthase glutamine-hydrolyzing) (EC 6.3.5.5), pyrimidine-repressible, small hain - Bacillus subtilis	74	60	1065
380	2	382	1128	gi|534857	ATPase subunit a [Bacillus stearothermophilus]	74	56	747
405	2	1742	1311	gi|1303915	YqhZ [Bacillus subtilis]	74	65	432
433	5	2503	3270	gi|473902	alpha-acetolactate synthase [Lactococcus lactis]	74	56	768
452	1	1	942	gi|413982	ipa-58r gene product [Bacillus subtilis]	74	52	942
461	1	3	1193	gi|558494	homoserine dehydrogenase [Bacillus subtilis]	74	51	1191
461	2	1174	1407	gi|40211	threonine synthase (thrC) (AA 1-352) [Bacillus subtilis] tr|A25364|A25364 threonine synthase (EC 4.2.99.2) - Bacillus btilis	74	56	234
462	2	402	734	gi|142520	thioredoxin [Bacillus subtilis]	74	62	333
478	1	574	320	gi|1499005	glycyl-tRNA synthetase [Methanococcus jannaschii]	74	52	255
501	2	739	1740	gi|217040	acid glycoprotein [Streptococcus pyogenes]	74	58	1002
551	2	4083	2791	gi|143040	glutamato-1-semialdehydo 2,1-aminotransferaso [Bacillus subtilis] pir|D42728|D42728 glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - Bacillus subtilis	74	51	1293

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match Acession	match gene name	% sim	% ident	length (nt)
573	1	1	477	gi|1006605	hypothetical protein (Synechocystis sp.)	74	45	477
596	2	1780	1298	gi|1303853	YqgF (Bacillus subtilis)	74	55	483
618	2	2924	1758	gi|1146237	21.4% of identity to trans-acting transcription factor of Sacharomyces cerevisiae; 25% of identity to sucrose synthase of Zea mays; putative (Bacillus subtilis)	74	55	1167
659	2	1269	1595	gi|1072380	ORF3 (Lactococcus lactis)	74	62	327
724	1	373	188	gi|143374	phosphoribosyl glycinamide synthetase (PUR-D; gtg start codon) Bacillus subtilis)	74	58	186
743	2	604	1209	gi|153833	ORF1; putative (Streptococcus parasanguis)	74	50	606
836	1	2	259	gi|143458	ORF V (Bacillus subtilis)	74	47	258
989	2	443	724	gi|1303994	YqkM (Bacillus subtilis)	74	46	282
1106	1	1	492	gi|46970	epiD geno product (Staphylococcus epidermidis)	74	54	492
1135	2	373	528	gi|413948	ipa-24d gene product (Bacillus subtilis)	74	48	156
1234	1	817	452	gi|495245	recJ gene product (Erwinia chrysanthemi)	74	36	366
2586	1	2	238	gi|1149701	sbcC gene product (Clostridium perfringens)	74	62	237
2959	1	798	400	gi|1405454	aconitase (Bacillus subtilis)	74	60	399
2962	1	650	363	gi|450686	3-phosphoglycerate kinase (Thermotoga maritima)	74	58	288
2983	1	3	191	gi|1303893	YqhL (Bacillus subtilis)	74	56	189
3018	1	2	223	gi|143040	glutamate-1-semialdehyde 2,1-aminotransferase (Bacillus subtilis) pir|D42728|D42728 glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - Bacillus subtilis	74	56	222
3038	1	510	256	pir|S52915|S529	nitrate reductase alpha chain - Bacillus subtilis (fragment)	74	57	255
3062	1	374	189	gi|1107528	ttg start (Campylobacter coli)	74	51	186
4035	1	184	360	gi|1022725	unknown (Staphylococcus haemolyticus)	74	64	177
4045	1	607	305	gi|1510977	M. jannaschii predicted coding region MJ0938 (Methanococcus jannaschii)	74	41	303
4283	1	471	304	gi|520844	orf4 (Bacillus subtilis)	74	58	168
4449	1	3	221	gi|580910	peptide-synthetase ORF1 (Bacillus subtilis)	74	54	219
4587	1	458	231	gi|1370207	orf6 (Lactobacillus sake)	74	59	228

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
4603	1	29	214	gi|146208	glutamate synthase large subunit (EC 2.6.1.53) [Escherichia coli] pir|A29617|A29617 glutamate synthase (NADPH) (EC 1.4.1.13) large hain - Escherichia coli	74	60	186
4670	1	366	184	gi|1256135	YbbF [Bacillus subtilis]	74	61	183
5	10	7953	7162	gi|143727	putative [Bacillus subtilis]	73	42	792
11	2	2454	1372	gi|166338	dihydroorotate dehydrogenase [Agrocybe aegerita]	73	55	1083
14	1	2024	1020	gi|143373	phosphoribosyl aminoimidazole carboxy formyl ormyltransferase/inosine monophosphate cyclohydrolase (PUR-H(J)) Bacillus subtilis]	73	54	1005
23	5	5426	4635	gi|1468939	meso-2,3-butanediol dehydrogenase (D-acetoin forming) [Klebsiolla pneumoniae]	73	58	792
23	17	17379	16360	gi|297060	ornithine cyclodeaminase [Rhizobium meliloti]	73	37	1020
29	2	692	1273	gi|467442	stage V sporulation [Bacillus subtilis]	73	54	582
31	5	6467	4914	gi|414000	ipa-76d gene product [Bacillus subtilis]	73	55	1554
37	8	8658	7402	gi|1429259	pepT gene product [Bacillus subtilis]	73	59	1257
37	9	7738	7562	gi|168367	alpha-isopropylmalate isomerase (put.); putative [Rhizomucor ircinolloides]	73	52	177
38	7	3931	4896	gi|405885	yeiN [Escherichia coli]	73	58	966
44	6	5041	4238	gi|580895	unknown [Bacillus subtilis]	73	53	804
44	11	7767	8306	gi|42009	moaB gene product [Escherichia coli]	73	50	540
45	3	2439	3080	gi|1109685	ProW [Bacillus subtilis]	73	47	642
54	13	14036	13794	gi|413931	ipa-7d gene product [Bacillus subtilis]	73	61	243
59	4	1430	2248	gi|147923	threonine dehydratase 2 (EC 4.2.1.16) [Escherichia coli]	73	53	819
65	1	1458	730	gi|677944	AppF [Bacillus subtilis]	73	56	729
80	2	1375	860	gi|580932	murD gene product [Bacillus subtilis]	73	53	516
102	13	10124	11179	gi|580891	3-isopropylmalate dehydrogenase (AA 1 - 365) [Bacillus subtilis] pir|A26522|A26522 3-isopropylmalate dehydrogenase (EC 1.1.1.85) - acillus subtilis	73	55	1056
109	2	3493	2600	gi|1510849	M. jannaschii predicted coding region MJ0775 [Methanococcus jannaschii]	73	40	894
120	8	4782	5756	gi|146970	ribonucleoside triphosphate reductase [Escherichia coli] pir|A47331|A47331 anaerobic ribonucleotide reductase - Escherichia oli	73	56	975
120	9	5726	6223	gi|1204333	anaerobic ribonucleoside-triphosphate reductase [Haemophilus influenzae]	73	62	498

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
132	5	4151	4363	gi|871048	HPSN2 - heavy chain potential motor protein (Giardia intestinalis)	73	43	213
140	6	5952	4324	gi|634107	kdpB (Escherichia coli)	73	59	1629
142	6	7060	5919	gi|410125	riboflavin gene product (Bacillus subtilis)	73	57	1122
149	4	1866	1717	gi|460892	heparin binding protein-44, HBP-44 (mice, Peptide, 360 aa) pir|JX0281|JX0281 heparin-binding protein-44 precursor - mouse gi|220434 ORF (Mus musculus) (SUB 2-360)	73	53	150
158	1	1	1431	gi|882504	ORF_f560 (Escherichia coli)	73	57	1431
174	6	5352	4525	gi|1146240	ketopantoate hydroxymethyltransferase (Bacillus subtilis)	73	55	828
175	8	5537	5178	gi|854657	Na/H antiporter system ORF3 (Bacillus alcalophilus)	73	56	360
186	5	6593	5493	gi|467477	unknown (Bacillus subtilis)	73	48	1101
249	6	6283	5729	gi|1524397	glycine betaine transporter OpuD (Bacillus subtilis)	73	56	555
265	4	1873	2280	gi|39848	U3 (Bacillus subtilis)	73	41	408
270	1	328	582	gi|780461	220 kDa polyprotein (African swine fever virus)	73	53	255
278	4	4283	3618	gi|1208965	hypothetical 23.3 kd protein (Escherichia coli)	73	49	666
279	3	4984	3593	gi|1185288	isochorismate synthase (Bacillus subtilis)	73	58	1392
291	4	1207	1575	gi|1511440	glutamino--fructose-6-phosphate transaminase (Methanococcus jannaschii)	73	63	369
299	2	735	1166	gi|467437	unknown (Bacillus subtilis)	73	58	432
299	5	2050	3234	gi|467439	temperature sensitive cell division (Bacillus subtilis)	73	53	1185
334	1	1237	728	gi|536655	ORF YBR244w (Saccharomyces cerevisiae)	73	43	510
336	2	1827	1036	gi|790943	urea amidolyase (Bacillus subtilis)	73	51	792
374	3	1389	1874	gi|1405451	YneJ (Bacillus subtilis)	73	55	486
433	4	1916	2554	gi|473902	alpha-acetolactato synthase (Lactococcus lactis)	73	54	639
509	2	1795	1028	gi|467483	unknown (Bacillus subtilis)	73	56	768
513	1	1709	918	gi|1146220	NAD+ dependent glycerol-3-phosphate dehydrogenase (Bacillus subtilis)	73	56	792
533	2	239	733	gi|1510605	hypothetical protein (SP:P42297) (Methanococcus jannaschii)	73	44	495
546	2	1148	2815	gi|41748	hsdM protein (AA 1-520) (Escherichia coli)	73	52	1668
549	1	762	382	gi|1314847	CinA (Bacillus subtilis)	73	57	381
567	1	1346	675	gi|410137	ORFX13 (Bacillus subtilis)	73	58	672

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
716	2	654	1112	gi|1256623	exodeoxyribonuclease [Bacillus subtilis]	73	56	459
772	1	3	677	gi|142010	Shows 70.2% similarity and 48.6% identity to the EnvM protein of almonella typhimurium [Anabaena sp.]	73	57	675
774	1	3	209	gi|409286	BmrU [Bacillus subtilis]	73	52	207
782	1	1	402	gi|143320	[gap] gene products [Bacillus megaterium]	73	56	402
789	2	451	762	gi|1063246	low homology to P14 protein of Haemophilus influenzae and 14.2 kDa protein of Escherichia coli [Bacillus subtilis]	73	56	312
796	1	3	911	gi|853754	ABC transporter [Bacillus subtilis]	73	58	909
806	3	1209	949	gi|143786	tryptophanyl-tRNA synthetase (EC 6.1.1.2) [Bacillus subtilis] pir|JT0401|YWBS tryptophan--tRNA ligase (EC 6.1.1.2) - Bacillus ubtilis	73	51	261
816	2	4839	3097	gi|41748	hsdM protein (AA 1-520) [Escherichia coli]	73	52	1743
839	1	798	400	gi|886906	argininosuccinate synthetase [Streptomyces clavuligerus] pir|S57659|S57659 argininosuccinate synthase [EC 6.3.4.5] - treptomyces clavuligerus	73	59	399
857	1	3	290	gi|348052	acetoin utilization protein [Bacillus subtilis]	73	50	288
1008	1	790	398	gi|40100	rodC (tagJ) polypeptide (AA 1-746) [Bacillus subtilis] tr|S06049|S06049 rodC protein - Bacillus subtilis p|P13485|MAGF_BACSU TECHOIC ACID BIOSYNTHESIS PROTEIN F.	73	41	393
1018	1	1	213	gi|529357	No definition line found (Caenorhabditis elegans) sp|P46975|STT3_CAEEL OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT ONOLOG.	73	53	213
1031	1	3	491	gi|142706	comG1 gene product [Bacillus subtilis]	73	51	489
1174	1	395	204	gi|1149513	alphaia subunit of laminin 5 [Homo sapiens]	73	60	192
1175	1	655	329	gi|473817	'ORF' [Escherichia coli]	73	57	327
1187	1	3	209	gi|580870	ipa-37d gosA gene product [Bacillus subtilis]	73	52	207
1206	1	72	245	gi|144816	formyltetrahydrofolate synthetase (FTHFS) (ttg start codon) (EC .3.4.3) [Moorella thermoacetica]	73	43	174
1454	1	423	241	gi|1213253	unknown [Schizosaccharomyces pombe]	73	53	183
1469	1	517	260	gi|1303787	YqeG [Bacillus subtilis]	73	55	258
1761	1	374	189	gi|9135	Hsc26An gene product [Drosophila simulans]	73	34	186
1849	1	467	243	gi|162307	DNA topoisomerase II [Trypanosoma cruzi]	73	60	225
2055	1	2	400	gi|559381	P47K protein [Rhodococcus erythropolis]	73	34	399
2556	1	2	244	gi|145925	fecB [Escherichia coli]	73	62	243

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
2947	2	549	400	gi|1184680	polynucleotide phosphorylase [Bacillus subtilis]	73	51	150
2956	1	746	375	gi|143397	quinol oxidase [Bacillus subtilis]	73	58	372
3037	1	655	329	gi|143091	acetolactate synthase [Bacillus subtilis]	73	55	327
3115	1	385	194	gi|323866	overlapping out-of-phase protein [Eggplant mosaic virus] sp|P20129|V70K_EPMV 70 KD PROTEIN.	73	53	192
3603	2	700	527	gi|1439521	glutaryl-CoA dehydrogenase precursor [Mus musculus]	73	48	174
3743	1	798	400	gi|450688	hsdM gene of Ecoprri gene product [Escherichia coli] pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli [SUB 40-520]	73	54	399
3752	1	640	359	gi|1524193	unknown [Mycobacterium tuberculosis]	73	59	282
3852	1	2	181	gi|216746	D-lactate dehydrogenase [Lactobacillus plantarum]	73	68	180
3914	1	475	239	pir|S13490|S134	Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Chicken (fragment)	73	53	237
3914	2	570	343	gi|528991	unknown [Bacillus subtilis]	73	38	228
4069	1	2	316	gi|40003	oxoglutarate dehydrogenase (NADP+) [Bacillus subtilis] p|P23129|ODO1_BACSU 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE).	73	55	315
4165	1	715	365	gi|1439521	glutaryl-CoA dehydrogenase precursor [Mus musculus]	73	48	351
4196	1	1	177	gi|809660	deoxyribose-phosphate aldolase [Bacillus subtilis] pir|S49455|S49455 deoxyribose-phosphate aldolase (EC 4.1.2.4) - acillus subtilis	73	60	177
4202	1	572	378	gi|528991	unknown [Bacillus subtilis]	73	38	195
4314	1	2	193	gi|436797	N-acyl-L-amino acid amidohydrolase [Bacillus stearothermophilus] sp|P37112|AMA_BACST N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC .5.1.14) (AMINOACYLASE).	73	47	192
4393	1	3	263	gi|216267	ORF2 [Bacillus megaterium]	73	47	261
35	2	903	1973	gi|1146196	phosphoglycerate dehydrogenase [Bacillus subtilis]	72	53	1071
38	22	19094	17877	gi|602031	similar to trimethylamine DH [Mycoplasma capricolum] pir|S49950|S49950 probable trimethylamine dehydrogenase (EC .5.99.7) - Mycoplasma capricolum (SGC3) (fragment)	72	54	1218
38	23	18134	19162	gi|413968	ipa-44d gene product [Bacillus subtilis]	72	54	1029
44	19	11895	12953	gi|516272	unknown [Bacillus subtilis]	72	49	1059
48	7	6248	7117	gi|43499	pyruvate synthase [Halobacterium halobium]	72	49	870
50	7	6563	5691	gi|1205399	proton glutamate symport protein [Haemophilus influenzae]	72	53	873

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
53	9	10521	9259	gi|1303956	YqjE [Bacillus subtilis]	72	52	1263
56	23	29549	29995	gi|467471	unknown [Bacillus subtilis]	72	47	447
69	4	5298	4123	gi|1354775	pfoS/R [Treponema pallidum]	72	46	1176
69	5	4377	4982	gi|904198	hypothetical protein [Bacillus subtilis]	72	43	606
73	1	2	856	gi|142997	glycerol uptake facilitator [Bacillus subtilis]	72	59	855
98	13	9371	10258	gi|467435	unknown [Bacillus subtilis]	72	50	888
127	1	1	1593	gi|217144	alanine carrier protein [thermophilic bacterium PS3] pir|A45111|A45111 alanine transport protein - thermophilic acterium PS-3	72	56	1593
131	1	5197	2600	gi|153952	polymerase III polymerase subunit (dnaE) [Salmonella typhimurium] pir|A45915|A45915 DNA-directed DNA polymerase (EC 2.7.7.7) III lpha chain - Salmonella typhimurium	72	53	2598
141	4	1040	1978	gi|1405446	transketolase [Bacillus subtilis]	72	54	939
149	8	2819	2535	gi|606234	secY [Escherichia coli]	72	44	285
149	17	5472	5265	gi|1304472	DNA polymerase [Unidentified phycodnavirus clone OTU6]	72	55	228
154	1	1	210	gi|1205620	ferritin like protein [Haemophilus influenzae]	72	40	210
155	1	2207	1320	gi|391610	farnesyl diphosphate synthase [Bacillus stearothermophilus] pir|JX0257|JX0257 geranyltranstransferase (EC 2.5.1.10) - Bacillus tearothermophilus	72	57	888
180	1	2	328	gi|433630	A180 [Saccharomyces cerevisiae]	72	62	327
184	3	1145	3553	gi|1205110	virulence associated protein homolog [Haemophilus influenzae]	72	49	2409
195	2	1923	1279	gi|1001730	hypothetical protein [Synechocystis sp.]	72	45	645
206	13	14646	15869	gi|1064807	ORTHININE AMINOTRANSFERASE [Bacillus subtilis]	72	50	1224
209	2	462	932	gi|1206666	hypothetical protein (GB:X73124_53) [Haemophilus influenzae]	72	60	471
215	2	764	522	gi|881513	insulin receptor homolog [Drosophila melanogaster] pir|S57245|S57245 insulin receptor homolog - fruit fly (Drosophila elanogaster) [SUB 46-2146]	72	63	243
224	1	2	790	gi|949974	sucrose repressor [Staphylococcus xylosus]	72	54	789
233	1	1526	765	gi|1408493	homologous to SwissProt:YIDA_ECOLI hypothetical protein [Bacillus subtilis]	72	52	762
240	1	220	1485	gi|537049	ORF_o470 [Escherichia coli]	72	52	1266
245	1	3	1340	gi|1206578	hypothetical protein (GB:U06949_1) [Haemophilus influenzae]	72	46	1338

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
259	2	2108	1245	gi|1340128	ORF1 [Staphylococcus aureus]	72	59	864
304	2	285	1094	gi|1205330	glutamine-binding periplasmic protein [Haemophilus influenzae]	72	52	810
307	10	5326	5039	gi|1070015	protein-dependent [Bacillus subtilis]	72	53	288
315	1	517	260	gi|143399	quinol oxidase [Bacillus subtilis]	72	55	258
316	11	9622	9308	gi|1204465	hypothetical protein (SP:P27857) [Haemophilus influenzae]	72	58	315
337	3	926	1609	gi|487433	citrate synthase II [Bacillus subtilis]	72	55	684
364	7	12538	10693	gi|1510643	ferrous iron transport protein B [Methanococcus jannaschii]	72	53	2046
409	2	340	1263	gi|1402944	orfRH1 gene product [Bacillus subtilis]	72	49	924
441	3	2177	1590	gi|312379	highly conserved among eubacteria [Clostridium acetobutylicum] pir|S34312|S34312 hypothetical protein V - Clostridium cotobutylicum	72	48	588
453	6	2654	2505	pir|S00601|BXSA	antibacterial protein 3 - Staphylococcus haemolyticus	72	70	150
460	1	2	625	gi|1016162	ABC transporter subunit [Cyanophora paradoxa]	72	51	624
463	1	3253	1628	gi|666014	The polymorphysm (RFLP) of this gene is associated with susceptibility to essential hypertension. The SA gene product has light homology to acetyl-CoA synthetase [Homo sapiens]	72	60	1626
480	4	3047	3466	gi|433992	ATP synthase subunit epsilon [Bacillus subtilis]	72	53	420
502	1	1086	586	gi|310859	ORF2 [Synechococcus sp.]	72	50	501
519	1	81	1184	gi|1303704	YrkE [Bacillus subtilis]	72	54	1104
559	1	3	746	gi|1107530	ceuD gene product [Campylobacter coli]	72	56	744
575	1	1142	573	gi|1303866	YqgS [Bacillus subtilis]	72	56	570
671	1	2	592	gi|1204497	protein-export membrane protein [Haemophilus influenzae]	72	44	591
679	2	295	1251	gi|563258	virulence-associated protein E [Dicholobacter nodosus]	72	52	957
687	2	295	957	gi|1146214	44% identical amino acids with the Escherichia coli smbA suprasa; putative [Bacillus subtilis]	72	49	663
837	1	1	435	gi|1146183	putative [Bacillus subtilis]	72	54	435
868	1	150	788	gi|1377842	unknown [Bacillus subtilis]	72	55	639
922	1	130	432	gi|1088269	unknown protein [Azotobacter vinelandii]	72	58	303
941	1	2	238	gi|153929	NADPH-sulfite reducatase flavoprotein component [Salmonella typhimurium]	72	49	237
980	1	840	421	gi|853767	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis]	72	59	420

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
1209	1	383	213	gi|144735	neurotoxin type B (Clostridium botulinum)	72	44	171
1469	2	671	474	gi|1205458	hypothetical protein (GB:D26562_47) (Haemophilus influonzae)	72	63	198
1956	1	727	365	gi|154409	hexosephosphate transport protein (Salmonella typhimurium) pir|B41853|B41853 hexose phosphate transport system regulatory rotein uhpB - Salmonella typhimurium	72	44	363
2101	1	3	401	gi|1303950	YqiY (Bacillus subtilis)	72	50	399
2503	1	569	399	gi|149713	formate dehydrogenase (Methanobacterium formicicum) pir|A42712|A42712 formate dehydrogenase (EC 1.2.1.2) - othanobacterium formicicum	72	56	171
2967	1	3	155	gi|1212729	YqhJ (Bacillus subtilis)	72	46	153
3004	1	367	185	gi|665999	hypothetical protein (Bacillus subtilis)	72	55	183
3109	1	278	141	gi|413968	ipa-44d gene product (Bacillus subtilis)	72	45	138
3171	1	3	287	gi|515938	glutamate synthase (ferredoxin) (Synochocystis sp.) pir|S46957|S46957 glutamate synthase (ferrodoxin) (EC 1.4.7.1) - ynechocystis sp.	72	52	285
3771	1	26	367	gi|1408501	homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus (Bacillus subtilis)	72	63	342
3951	1	1	222	gi|1500409	M. jannaschii predicted coding region MJ1519 (Methanococcus jannaschii)	72	38	222
4190	1	721	362	gi|39956	IIGlc (Bacillus subtilis)	72	57	360
4444	1	3	347	gi|1009366	Respiratory nitrate reductase (Bacillus subtilis)	72	55	345
6	2	951	1200	gi|537095	ornithine carbamoyltransferase (Escherichia coli)	71	55	270
11	15	11350	10859	gi|532309	25 kDa protein (Escherichia coli)	71	47	492
19	2	1248	2435	gi|1244574	D-alanine:D-alanine ligase (Enterococcus hirae)	71	52	1188
21	2	898	1488	gi|149629	anthranilate synthase component 2 (Leptospira biflexa) pir|C32840|C32840 anthranilate synthase (EC 4.1.3.27) component II Leptospira biflexa	71	45	591
34	1	1	567	gi|1303983	YqkP (Bacillus subtilis)	71	59	567
37	3	3192	2806	gi|1209681	glutamate-rich protein (Bacillus firmus)	71	50	387
38	18	12250	12462	gi|927645	arginyl endopeptidase (Porphyromonas gingivalis)	71	50	213
39	3	1246	4431	pir|S09411|S094	spoIIIE protein - Bacillus subtilis	71	49	3186
53	14	15770	14760	gi|142611	branchod chain alpha-koto acid dehydrogenase E1-alpha (Bacillus ubtilis)	71	58	1011
54	11	13461	12625	gi|143014	gnt repressor (Bacillus subtilis)	71	46	837

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
57	7	7152	5860	gi|508175	EIIC domain of PTS-dependent Gat transport and phosphorylation Escherichia coli	71	48	1293
57	18	13897	14334	gi|1063247	high homology to flavohemoprotein (Haemoglobin-like protein) of Alcaligenes eutrophus and Saccharomyces cerevisiae (Bacillus subtilis)	71	56	438
62	16	9831	10955	gi|1303926	YqiG (Bacillus subtilis)	71	54	1125
70	12	8505	8966	gi|147198	phnE protein (Escherichia coli)	71	38	462
86	5	2394	2089	gi|904205	hypothetical protein (Bacillus subtilis)	71	51	306
96	7	7601	8269	gi|709991	hypothetical protein (Bacillus subtilis)	71	49	669
100	6	4822	5931	gi|1060848	Opine dehydrogenase (Arthrobacter sp.)	71	45	1110
103	1	1062	532	gi|143089	iep protein (Bacillus subtilis)	71	41	531
109	18	15312	15695	gi|413985	ipa-61d gene product (Bacillus subtilis)	71	57	384
113	1	630	316	gi|663254	probable protein kinase (Saccharomyces cerevisiae)	71	57	315
114	5	6598	5603	gi|143156	membrane bound protein (Bacillus subtilis)	71	40	996
133	2	3087	1723	gi|1303913	YqhX (Bacillus subtilis)	71	53	1365
149	19	6335	5895	gi|529650	G40P (Bacteriophage SPP1)	71	51	441
154	5	3635	3087	gi|425488	repressor protein (Streptococcus sobrinus)	71	47	549
164	11	11354	11689	gi|49318	ORF4 gene product (Bacillus subtilis)	71	52	336
169	5	1936	2745	gi|1403403	unknown (Mycobacterium tuberculosis)	71	56	810
193	2	272	1234	gi|1303788	YqoH (Bacillus subtilis)	71	49	963
205	1	1743	895	gi|1215694	GlnQ (Mycoplasma pneumoniae)	71	46	849
233	4	1849	2022	gi|633732	ORF1 (Campylobacter jejuni)	71	50	174
237	7	4501	5169	gi|149384	HisIE (Lactococcus lactis)	71	54	669
272	4	2848	2273	gi|709993	hypothetical protein (Bacillus subtilis)	71	48	576
274	2	618	1496	gi|143035	NAD(P)H:glutamyl-transfer RNA reductase (Bacillus subtilis) pir|A35252|A35252 5-aminolevulinate synthase (EC 2.3.1.37) - acillus subtilis	71	53	879
276	5	3349	2720	gi|303562	ORF210 (Escherichia coli)	71	50	630
287	1	136	660	gi|110634	20 kDa protein (Streptococcus gordonii)	71	53	525
288	6	3322	2771	gi|1256625	putative (Bacillus subtilis)	71	47	552

TABLE 2

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
301	6	3492	2461	gi|467417	similar to lysine decarboxylase (Bacillus subtilis)	71	57	1032
306	4	6607	5222	gi|1256618	transport protein (Bacillus subtilis)	71	56	1386
307	2	1536	925	gi|632683	orfC (Mycoplasma capricolum)	71	45	612
310	5	5793	5146	gi|348052	acetoin utilization protein (Bacillus subtilis)	71	51	648
322	1	2	1303	gi|1001819	hypothetical protein (Synechocystis sp.)	71	46	1302
333	4	4171	3995	gi|467473	unknown (Bacillus subtilis)	71	57	177
350	2	548	922	gi|551879	ORF 1 (Lactococcus lactis)	71	55	375
375	4	1860	3071	gi|467447	unknown (Bacillus subtilis)	71	57	1212
380	5	1560	2102	gi|142557	ATP synthase b subunit (Bacillus megaterium)	71	43	543
414	2	251	637	gi|580904	homologous to E.coli rnpA (Bacillus subtilis)	71	49	387
424	1	335	1354	gi|581305	L-lactate dehydrogenase (Lactobacillus plantarum)	71	57	1020
436	4	3701	3270	pir|PN0501|PN05	phosphoribosylanthranilate isomerase (EC 5.3.1.24) - Bacillus subtilis (fragment)	71	66	432
482	1	3	1280	gi|410142	ORFX18 (Bacillus subtilis)	71	49	1278
525	3	2272	1844	gi|143370	phosphoribosylpyrophosphate amidotransferase (PUR-F; EC 2.4.2.14) Bacillus subtilis)	71	56	429
529	4	2739	2047	gi|606150	ORF_f309 (Escherichia coli)	71	43	691
563	1	22	969	gi|1237015	ORF4 (Bacillus subtilis)	71	53	948
581	1	506	255	gi|1301730	T25G3.2 (Caenorhabditis elegans)	71	47	252
612	2	1068	913	gi|153968	fimbriae 2 (Salmonella typhimurium)	71	55	156
613	1	1	654	gi|466778	lysine specific permease (Escherichia coli)	71	50	654
618	1	1243	623	gi|1146238	poly(A) polymerase (Bacillus subtilis)	71	52	621
630	1	1170	586	gi|1486243	unknown (Bacillus subtilis)	71	53	585
691	1	1126	641	gi|289260	comE ORF1 (Bacillus subtilis)	71	51	486
694	2	149	427	gi|12971	NADH dehydrogenase subunit V (AA 1-605) (Gallus gallus) ir|S10197|S10197 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain - chicken mitochondrion (SGC1)	71	47	279
715	2	169	777	gi|1303830	YqfL (Bacillus subtilis)	71	53	609
746	2	1473	970	gi|1377843	unknown (Bacillus subtilis)	71	52	504

TABLE 2

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
748	1	1437	802	gi|1405459	YnaS (Bacillus subtilis)	71	49	636
753	1	1018	524	gi|1510389	H. jannaschii predicted coding region MJ0296 (Methanococcus jannaschii)	71	53	495
761	1	3	215	gi|475972	pentafunctional enzyme (Pneumocystis carinii)	71	47	213
783	1	1203	703	gi|536655	ORF YBR244w (Saccharomyces cerevisiae)	71	52	501
800	3	1292	987	gi|1204326	tRNA delta(2)-isopentenylpyrophosphate transferase (Haemophilus influenzae)	71	48	306
806	1	116	286	gi|1419075	cbiN gene product (Methanobacterium thermoautotrophicum)	71	50	171
931	1	973	488	gi|893358	PgsA (Bacillus subtilis)	71	56	486
1041	1	2	262	gi|1408507	pyrimidine nucleoside transport protein (Bacillus subtilis)	71	45	261
1070	1	2	172	gi|709993	hypothetical protein (Bacillus subtilis)	71	46	171
1176	1	57	365	gi|151259	HMG-CoA reductase (EC 1.1.1.88) (Pseudomonas mevalonii) pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	71	49	309
1181	1	366	184	gi|46971	epiP gene product (Staphylococcus epidermidis)	71	50	183
1281	1	3	290	gi|153016	ORF 419 protein (Staphylococcus aureus)	71	50	288
1348	1	456	229	gi|602683	orfC (Mycoplasma capricolum)	71	48	228
2002	1	756	379	gi|1008177	ORF YJL046w (Saccharomyces cerevisiae)	71	48	378
2119	1	2	217	gi|1046088	arginyl-tRNA synthetase (Mycoplasma genitalium)	71	50	216
2418	1	3	320	gi|1499771	H. jannaschii predicted coding region MJ0936 (Methanococcus jannaschii)	71	57	318
2961	1	2	187	gi|312443	carbamoyl-phosphate synthase (glutamine-hydrolysing) (Bacillus aldolyticus)	71	57	186
2999	2	67	306	gi|710020	nitrite reductase (nirB) (Bacillus subtilis)	71	43	240
3033	1	2	184	gi|2262335	YmaA (Bacillus subtilis)	71	57	183
3584	1	3	338	gi|401716	beta-isopropylmalate dehydrogenase (Neurospora crassa)	71	55	336
3715	2	743	399	gi|563952	gluconate permease (Bacillus licheniformis)	71	59	345
3785	1	770	387	gi|47382	acyl-CoA-dehydrogenase (Streptomyces purpurascens)	71	57	384
3875	1	541	272	gi|1001541	hypothetical protein (Synechocystis sp.)	71	38	270
4135	1	637	320	gi|142695	S-adenosyl-L-methionine:uroporphyrinogen III methyltransferase Bacillus megaterium	71	52	318
4249	1	63	239	gi|1205363	deoxyribose aldolase (Haemophilus influenzae)	71	63	177
4508	1	530	267	gi|1197667	vitellogenin (Anolis pulchellus)	71	46	264

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
6	3	1237	2721	gi|1321788	arginine ornithine antiporter (Clostridium perfringens)	70	54	1485
11	11	6572	7486	gi|216854	P47K (Pseudomonas chlororaphis)	70	41	915
12	1	2890	1481	gi|467330	replicative DNA helicase (Bacillus subtilis)	70	49	1410
15	1	1756	893	gi|451216	Mannosephosphate Isomerase (Streptococcus mutans)	70	46	864
15	2	1277	1050	gi|476092	unknown (Bacillus subtilis)	70	50	228
17	2	2132	1350	gi|145402	choline dehydrogenase (Escherichia coli)	70	52	783
21	1	2	925	gi|149516	anthranilate synthase alpha subunit (Lactococcus lactis) pir|S35124|S35124 anthranilate synthase (EC 4.1.3.27) alpha chain - actococcus lactis subsp. lactis	70	50	924
25	7	5580	6251	gi|1389549	ORF3 (Bacillus subtilis)	70	52	672
33	6	6071	7423	gi|1303875	YqhB (Bacillus subtilis)	70	51	1353
36	2	959	1594	gi|500755	methyl purine glycosylase (Mus musculus)	70	47	636
38	8	4901	5860	gi|1408507	pyrimidine nucleoside transport protein (Bacillus subtilis)	70	44	960
44	8	5312	5989	gi|1006620	hypothetical protein (Synechocystis sp.)	70	49	678
46	10	8950	10020	gi|1403126	czcD gene product (Alcaligenes eutrophus)	70	45	1071
52	2	2727	1900	gi|1486247	unknown (Bacillus subtilis)	70	53	828
52	6	4048	4656	gi|244501	esterase II•carboxylesterase (EC 3.1.1.1) (Pseudomonas fluorescens, eptido, 218 aa)	70	50	609
56	8	8460	9962	gi|1339951	small subunit of NADH-dependent glutamate synthase (Plectonema boryanum)	70	51	1503
62	1	48	290	gi|142702	A competence protein 2 (Bacillus subtilis)	70	47	243
64	1	1080	541	gi|1204377	molybdopterin biosynthesis protein (Haemophilus influenzae)	70	47	540
70	5	5139	3595	gi|1204834	2',3'-cyclic-nucleotide 2'-phosphodiesterase (Haemophilus influenzae)	70	47	1545
91	4	7793	5466	gi|886471	methionine synthase (Catharanthus roseus)	70	56	2328
96	5	8754	7255	pir|B39096|B390	alkaline phosphatase (EC 3.1.3.1) III precursor - Bacillus subtilis	70	54	1500
110	2	767	1300	gi|145294	adanine phosphoribosyl-transferase (Escherichia coli)	70	51	534
116	6	7026	7976	gi|143607	sporulation protein (Bacillus subtilis)	70	50	951
121	8	6401	6988	gi|1107528	ttg start (Campylobacter coli)	70	45	588
131	8	6842	7936	gi|1150454	prolidase PepQ (Lactobacillus delbrueckii)	70	48	1095

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match Accession	match gene name	% sim	% ident	length (nt)
135	1	2	1489	gi|311309	putative membrane-bound protein with four times repitition of ro-Ser-Ala at the N-terminus; function unknown [Alcaligenes utrophus]	70	49	1488
138	3	418	714	gi|904181	hypothetical protein [Bacillus subtilis]	70	46	297
164	8	9344	9874	gi|49315	ORF1 gene product [Bacillus subtilis]	70	47	531
164	16	15626	16618	gi|1205212	hypothetical protein (GB:D10483_18) [Haemophilus influenzae]	70	50	993
205	2	2735	1803	gi|1215695	peptide transport system protein SapF homolog; SapF homolog [Mycoplasma pneumoniae]	70	47	933
209	3	910	1386	gi|1204665	hypothetical protein (GB:X73124_26) [Haemophilus influenzae]	70	48	477
246	3	340	756	gi|215098	excisionase [Bacteriophage 154a]	70	46	417
263	7	7876	6749	gi|142540	aspartokinase II [Bacillus sp.]	70	51	1128
268	3	3212	4117	gi|1340128	ORF1 [Staphylococcus aureus]	70	50	906
302	6	3201	3827	gi|147782	ruvA protein (gtg start) [Escherichia coli]	70	46	627
302	10	5879	7051	pir|C38530|C385	queuine tRNA-ribosyltransferase (EC 2.4.2.29) - Escherichia coli	70	55	1173
313	1	2520	1414	gi|1205934	aminopeptidase a/i [Haemophilus influenzae]	70	46	1107
355	2	379	669	gi|1070013	protein-dependent [Bacillus subtilis]	70	48	291
403	1	1255	629	gi|733147	GumF [Xanthomonas campestris]	70	33	627
444	10	8770	9273	gi|1204752	high affinity ribose transport protein [Haemophilus influenzae]	70	52	504
449	1	2	1243	gi|619724	MgtE [Bacillus firmus]	70	44	1242
472	1	637	320	gi|727145	open reading frame; putative [Bacillus amyloliquofaciens] pir|B29091|B29091 hypothetical protein (bglA region) - Bacillus myloliquofaciens (fragment)	70	41	318
480	2	727	1608	gi|142560	ATP synthase gamma subunit [Bacillus megaterium]	70	44	882
524	1	2	307	gi|602292	RCH2 protein [Brassica napus]	70	45	306
525	1	823	413	gi|143372	phosphoribosyl glycinamide formyltransferase (PUR-N) [Bacillus ubtilis]	70	52	411
565	4	3625	2552	gi|881434	ORFP [Bacillus subtilis]	70	51	1074
607	4	829	1284	gi|511524	hypothetical protein (SP:P37002) [Methanococcus jannaschii]	70	50	456
633	1	1383	703	gi|431231	uracil permease [Bacillus caldolyticus]	70	53	681
646	3	1683	1309	gi|467340	unknown [Bacillus subtilis]	70	49	375
663	1	830	417	gi|1303873	YvjZ [Bacillus subtilis]	70	40	414

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
681	1	1488	781	gi|1001678	hypothetical protein (Synechocystis sp.)	70	53	708
708	1	2	448	sp|P33940|YOJH_	HYPOTHETICAL 54.3 KD PROTEIN IN ECO-ALKB INTERGENIC REGION.	70	51	447
725	1	51	722	gi|1001644	hypothetical protein (Synechocystis sp.)	70	46	672
776	1	1371	787	gi|145165	putative (Escherichia coli)	70	47	585
834	1	250	783	gi|552971	NADH dehydrogenase (ndhF) (Vicia faba)	70	47	534
865	2	1585	1379	gi|1204636	ATP-dependent helicase (Haemophilus influenzae)	70	45	207
894	1	535	269	gi|467364	DNA binding protein (probable) (Bacillus subtilis)	70	41	267
919	1	3	317	gi|1314847	CinA (Bacillus subtilis)	70	40	315
944	1	3	572	gi|709991	hypothetical protein (Bacillus subtilis)	70	46	570
988	2	772	605	gi|142441	ORF 3; putative (Bacillus subtilis)	70	50	168
1055	1	3	335	gi|529755	speC (Streptococcus pyogenes)	70	37	333
1093	1	2	904	gi|853754	ABC transporter (Bacillus subtilis)	70	49	903
1109	1	2	310	gi|1001827	hypothetical protein (Synechocystis sp.)	70	42	309
1220	1	468	235	pir|S23416|S234	epiB protein - Staphylococcus epidermidis	70	40	234
1279	1	73	348	gi|153015	FemA protein (Staphylococcus aureus)	70	47	276
1316	1	195	542	sp|P31776|PBPA_	PENICILLIN-BINDING PROTEIN 1A (PBP-1A) (PENICILLIN-BINDING PROTEIN A).	70	50	348
1537	2	232	402	gi|1146181	putative (Bacillus subtilis)	70	50	171
1574	1	451	272	gi|219630	endothelin-A receptor (Homo sapiens)	70	47	180
1640	1	690	346	gi|1146243	22.4% identity with Escherichia coli DNA-damage inducible protein ...; putative (Bacillus subtilis)	70	46	345
2504	1	2	286	gi|495179	transmembrane protein (Lactococcus lactis)	70	51	285
3061	1	564	301	gi|508175	EIIC domain of PTS-dependant Gat transport and phosphorylation Escherichia coli)	70	44	264
3128	1	2	199	gi|1340096	unknown (Mycobacterium tuberculosis)	70	51	198
3218	1	3	488	gi|515938	glutamate synthase (ferredoxin) (Synechocystis sp.) pir|S46957|S46957 glutamate synthase (ferredoxin) (EC 1.4.7.1) - ynechocystis sp.	70	50	486
3323	1	794	399	gi|1154891	ATP binding protein (Phormidium laminosum)	70	52	396
3679	1	599	399	gi|529385	chromosome condensation protein (Caenorhabditis elegans)	70	30	201

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3841	1	706	398	gi|1208965	hypothetical 23.3 kd protein [Escherichia coli]	70	47	309
1929	1	3	401	gi|149435	putative [Lactococcus lactis]	70	49	399
4044	1	595	374	gi|602033	similar to trimethylamine DH [Mycoplasma capricolum] pir|S49930|S49930 probable trimethylamine dehydrogenase (EC .5.99.7) - Mycoplasma capricolum (SGC3) (fragment)	70	40	222
4329	1	558	280	gi|1339951	small subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	70	49	279
4422	1	576	289	gi|296464	ATPase [Lactococcus lactis]	70	57	288
4647	1	361	200	gi|166412	NADH-glutamate synthase [Medicago sativa]	70	59	162
16	8	7571	9031	gi|1499620	H. jannaschii predicted coding region MJ0798 [Methanococcus jannaschii]	69	44	1461
16	9	9080	10033	gi|1353197	chloredoxin reductase [Eubacterium acidaminophilum]	69	54	954
30	1	1452	727	gi|1204910	hypothetical protein (GB:U14003_302) [Haemophilus influenzae]	69	52	726
38	4	1023	1298	gi|407773	devA gene product [Anabaena sp.]	69	41	276
44	9	5987	6595	gi|1205920	molybdate uptake system hydrophilic membrane-bound protein [Haemophilus influenzae]	69	45	609
62	15	9104	9475	gi|305178	unknown [Bacillus subtilis]	69	40	372
66	4	2402	2803	gi|1303893	YqhL [Bacillus subtilis]	69	51	402
67	15	14124	13627	gi|149647	ORF2 [Listeria monocytogenes]	69	37	498
67	17	14033	14382	gi|305002	ORF_f356 [Escherichia coli]	69	49	330
67	19	15130	15807	gi|1109684	ProV [Bacillus subtilis]	69	45	678
78	3	1447	2124	gi|1256633	putative [Bacillus subtilis]	69	53	678
78	4	4513	3725	gi|1103958	YqjO [Bacillus subtilis]	69	32	789
85	4	4521	4213	pir||E29326|E293	hypothetical protein (pur operon) - Bacillus subtilis	69	32	309
86	6	3253	2654	gi|973332	OrfC [Bacillus subtilis]	69	50	600
95	1	96	710	gi|786468	4All antigen, spore tail membrane antigenputative sucrose-specific hosphotransferase enzyme II homolog [mice, toxic, Peptide Partial, 72 aa]	69	43	615
100	7	6023	7426	gi|1205355	Na+/H+ antiporter [Haemophilus influenzae]	69	39	1404
102	2	2678	1650	gi|561690	sialoglycoprotease [Pasteurella haemolytica]	69	47	1029
103	8	12241	9537	gi|1009366	Respiratory nitrate reductase [Bacillus subtilis]	69	54	2705
103	11	14987	12552	gi|710020	nitrite reductase (nirB) [Bacillus subtilis]	69	51	2436

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
112	11	8708	10168	gi|154111	hexosephosphate transport protein (Salmonella typhimurium) pir|D41853|D41853 hexose phosphate transport system protein uhpT - almonella typhimurium	69	51	1461
112	16	16644	17414	gi|1204435	pyruvate formate-lyase activating enzyme (Haemophilus influenzae)	69	50	771
113	2	33	953	gi|290509	o307 (Escherichia coli)	69	43	921
114	2	1537	1058	pir|A42771|A427	reticulocyte-binding protein 1 - Plasmodium vivax	69	39	480
121	6	4309	5310	gi|154633	NrdF (Bacillus subtilis)	69	53	1002
125	2	267	854	gi|413931	lpa-7d gene product (Bacillus subtilis)	69	43	588
149	27	10666	10400	pir|S28089|S280	hypothetical protein A - yeast (Zygosaccharomyces bisporus) plasmid pSD1	69	39	267
161	1	1598	813	gi|1205538	hypothetical protein (GB:U14003_302) (Haemophilus influenzae)	69	47	786
165	4	2222	4633	gi|40054	phenylalanyl-tRNA synthetase beta subunit (AA 1-804) (Bacillus btilis)	69	52	2412
169	3	1210	1761	gi|296031	elongation factor Ts (Spirulina platensis)	69	45	552
175	12	8686	8339	gi|732682	FimE protein (Escherichia coli)	69	69	348
190	2	484	1671	sp|P17731|HIS8_	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9) (IMIDAZOLE ACETOL-PHOSPHATE TRANSAMINASE).	69	48	1188
206	1	5551	2777	gi|41750	hsdR protein (AA 1-1033) (Escherichia coli)	69	49	2775
206	4	6038	5796	gi|1256135	YbbF (Bacillus subtilis)	69	48	243
249	1	636	319	gi|1405456	YmuP (Bacillus subtilis)	69	50	318
302	8	4820	5776	gi|1001768	hypothetical protein (Synechocystis sp.)	69	48	957
324	2	7384	3893	gi|1256798	pyruvate carboxylase (Rhizobium etli)	69	53	3492
351	3	2098	1808	gi|1491664	T04H1.4 (Caenorhabditis elegans)	69	30	291
369	3	2075	2305	gi|336458	ORF (Balaenoptera acutorostrata)	69	61	231
392	3	1999	2424	gi|556015	ORF1 (Bacillus subtilis)	69	45	426
410	1	87	779	gi|155611	phosphoglyceromutase (Zymomonas mobilis)	69	58	693
421	1	2085	1129	gi|1276985	arginase (Bacillus caldovelox)	69	54	957
444	8	6713	7741	gi|1221782	purine synthesis repressor (Haemophilus influenzae)	69	40	1029
453	1	828	415	gi|1122758	unknown (Bacillus subtilis)	69	57	414
469	2	3286	2246	gi|1458228	mutY homolog (Homo sapiens)	69	44	1041

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
509	3	1730	1371	gi|49224	URF 4 [Synechococcus sp.]	69	39	360
520	5	3023	2823	gi|726427	similar to D. melanogaster MST101-2 protein (PIR:S34154) Caenorhabditis elegans]	69	39	201
531	1	26	760	gi|509672	repressor protein [Bacteriophage Tuc2009]	69	33	735
589	1	107	253	gi|169101	17.9 kDa heat shock protein (hsp17.9) [Pisum sativum]	69	52	147
594	2	597	1391	gi|142783	DNA photolyase [Bacillus firmus]	69	48	795
604	4	2476	2114	gi|413930	ipa-6d gene product [Bacillus subtilis]	69	45	363
607	1	2	313	gi|1236103	W08D2.3 [Caenorhabditis elegans]	69	47	312
607	2	590	312	gi|536715	ORF YBR275c [Saccharomyces cerevisiae]	69	39	279
734	1	864	433	gi|467327	unknown [Bacillus subtilis]	69	44	432
759	1	3	338	gi|1009367	Respiratory nitrate reductase [Bacillus subtilis]	69	50	336
761	2	392	586	gi|3508	Leucyl-tRNA synthetase (cytoplasmic) [Saccharomyces cerevisiae] |1370340 ORF YPL160w [Saccharomyces cerevisiae]	69	46	195
802	1	72	1013	gi|143044	ferrochelatase [Bacillus subtilis]	69	55	942
816	1	2573	1368	gi|1510268	restriction modification system S subunit [Methanococcus jannaschii]	69	45	1206
838	2	133	387	gi|1255371	coded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase [Caenorhabditis elegans]	69	46	255
851	2	745	1005	gi|288998	secA gene product [Antithamnion sp.]	69	39	261
867	1	535	269	gi|1070014	protein-dependent [Bacillus subtilis]	69	47	267
995	1	954	478	gi|1205569	transcription elongation factor [Haemophilus influenzae]	69	53	477
999	1	1009	506	gi|899256	predicted trithorax protein [Drosophila virilis]	69	21	504
1127	1	1315	659	gi|1205434	H. influenzae predicted coding region HI1191 [Haemophilus influenzae]	69	56	657
1138	1	248	460	gi|1510646	M. jannaschii predicted coding region MJ0568 [Methanococcus jannaschii]	69	48	213
2928	1	3	401	gi|290503	glutamate permease [Escherichia coli]	69	41	399
3090	1	444	223	gi|1206987	DNA polymerase III, alpha chain [Haemophilus influenzae]	69	36	222
3817	1	2	400	gi|1483199	peptide-synthetase [Amycolatopsis mediterranei]	69	45	399
3833	1	667	335	gi|1524193	unknown [Mycobacterium tuberculosis]	69	46	333

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match geno name	% sim	% ident	length (nt)
4079	1	747	400	gi|546918	orfY 3' of comK (Bacillus subtilis, E26, Peptide Partial, 140 aa) pir|S43612|S43612 hypothetical protein Y - Bacillus subtilis sp|P40398|YHXD_BACSU HYPOTHETICAL PROTEIN IN COMK 3'REGION (ORFY) FRAGMENT).	69	64	348
4115	2	215	400	gi|517205	67 kDa Myosin-crossreactive streptococcal antigen (Streptococcus pyogenes)	69	59	186
4139	1	1	333	gi|1208451	hypothetical protein (Synechocystis sp.)	69	36	333
4258	1	457	230	gi|496158	restriction-modification enzyme subunit M1 (Mycoplasma pulmonis) pir|S49395|S49395 HsdM1 protein - Mycoplasma pulmonis (SGC3)	69	43	228
4317	1	90	374	gi|413967	ipa-43d gene product (Bacillus subtilis)	69	44	285
4465	1	3	293	gi|396296	similar to phosphotransferase system enzyme II (Escherichia coli) sp|P32672|PTWC_ECOLI PTS SYSTEM, FRUCTOSE-LIKE-2 IIC COMPONENT PHOSPHOTRANSFERASE ENZYME II, C COMPONENT).	69	49	291
3	1	2302	1193	gi|1109685	ProW (Bacillus subtilis)	68	46	1110
15	4	2592	2076	gi|807973	unknown (Saccharomyces cerevisiae)	68	45	519
31	8	6328	8772	gi|290642	ATPase (Enterococcus hirae)	68	48	2445
40	2	1115	750	gi|606342	ORF_o622; reading frame open far upstream of start; possible ramashift, linking to previous ORF (Escherichia coli)	68	55	166
46	9	6886	8415	gi|155276	aldehyde dehydrogenase (Vibrio cholerae)	68	44	1530
48	3	3643	3404	gi|285608	241k polyprotein (Apple stem grooving virus)	68	47	240
48	4	3536	4132	gi|1045937	M. genitalium predicted coding region MG246 (Mycoplasma genitalium)	68	39	597
53	10	11671	10685	gi|1303952	YqjA (Bacillus subtilis)	68	46	987
70	9	7346	8155	gi|147198	phnE protein (Escherichia coli)	68	40	810
89	4	1899	2966	gi|145173	35 kDa protein (Escherichia coli)	68	43	1068
108	1	2187	1150	gi|38722	precursor (aa -20 to 381) (Acinetobacter calcoaceticus) ir|A29277|A29277 aldose 1-epimerase (EC 5.1.3.3) - Acinetobacter lwoffii	68	57	1038
112	5	2666	3622	gi|153724	MalC (Streptococcus pneumoniae)	68	55	957
116	7	7865	8638	gi|143608	sporulation protein (Bacillus subtilis)	68	48	774
118	3	2484	3698	gi|1303805	YqeR (Bacillus subtilis)	68	46	1215
120	2	1424	1594	sp|P38038|CYSJ_	SULFITE REDUCTASE (NADPH) FLAVOPROTEIN ALPHA-COMPONENT (EC 1.8.1.2) (SIR-FP).	68	45	171
129	1	1	1011	gi|396307	argininosuccinate lyase (Escherichia coli)	68	50	1011

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
132	3	1867	2739	gi|216267	ORF2 [Bacillus megaterium]	68	48	873
134	2	848	1012	gi|147545	DNA recombinase [Escherichia coli]	68	50	165
141	2	372	614	gi|872116	act (stress inducible protein) [Glycine max]	68	36	243
149	7	2454	2260	gi|145774	hsp70 protein (dnaK gene) [Escherichia coli]	68	48	195
155	2	1776	1534	gi|216583	ORF1 [Escherichia coli]	68	36	243
158	3	1826	3289	sp|P33940|YOJH_	HYPOTHETICAL 54.3 KD PROTEIN IN ECO-ALKB INTERGENIC REGION.	68	51	1464
169	6	2749	3318	gi|1403402	unknown [Mycobacterium tuberculosis]	68	46	570
175	10	9158	7365	gi|1072195	phaA gene product [Rhizobium meliloti]	68	51	1794
188	7	4184	5434	gi|1173843	3-ketoacyl-ACP synthase II [Vibrio harveyi]	68	48	1251
189	3	907	1665	gi|467383	DNA binding protein (probable) [Bacillus subtilis]	68	55	759
206	5	7683	6709	gi|1256138	YbbI [Bacillus subtilis]	68	48	975
206	8	10425	12176	gi|452687	pyruvate decarboxylase [Saccharomyces cerevisiae]	68	48	1752
212	8	3421	3648	gi|1369941	c1 gene product [Bacteriophage 81]	68	39	228
214	8	5457	6482	gi|1420467	ORF YOR196c [Saccharomyces cerevisiae]	68	45	1026
237	4	2507	3088	gi|149381	HisH [Lactococcus lactis]	68	46	582
243	5	5540	4542	gi|1235684	mevalonate pyrophosphate decarboxylase [Saccharomyces cerevisiae]	68	47	999
262	1	3	164	gi|150974	4-oxalocrotonate tautomerase [Pseudomonas putida]	68	42	162
262	2	1984	1118	gi|1147744	PSR [Enterococcus hirae]	68	49	867
276	6	3702	3139	sp|P30750|ABC_E	ATP-BINDING PROTEIN ABC (FRAGMENT).	68	50	564
306	6	6345	5725	gi|1256617	adenine phosphoribosyltransferase [Bacillus subtilis]	68	53	621
333	3	4599	3850	gi|467473	unknown [Bacillus subtilis]	68	45	750
365	6	5017	4838	gi|1130643	T22B3.3 [Caenorhabditis elegans]	68	45	180
376	2	549	1646	gi|1277026	DAPA aminotransferase [Bacillus subtilis]	68	51	1098
405	1	1741	872	gi|1303917	YqiB [Bacillus subtilis]	68	47	870
406	2	853	539	gi|1511513	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	68	44	315
426	6	3558	3391	gi|624632	GltL [Escherichia coli]	68	48	168
438	1	108	329	gi|146923	nitrogenase reductase [Escherichia coli]	68	43	222

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
443	1	476	240	gi|535810	hippuricase (Campylobacter jejuni)	68	42	237
443	2	518	1015	gi|1204742	H. influenzae predicted coding region HI0491 (Haemophilus influenzae)	68	48	498
443	5	4447	3779	gi|809660	deoxyribose-phosphate aldolase (Bacillus subtilis) pir|S49455|S49455 deoxyribose-phosphate aldolase (EC 4.1.2.4) - acillus subtilis	68	55	669
476	2	240	1184	gi|571345	unknown, similar to E.coli cardiolipin synthase (Bacillus subtilis) sp|P45860|YWIE_BACSU HYPOTHETICAL 58.2 PROTEIN IN NARI-ACDA INTERGENIC REGION.	68	45	945
486	2	1876	1046	gi|147328	transport protein (Escherichia coli)	68	41	831
517	3	1764	2084	gi|:523809	orf2 (Bacteriophage A2)	68	64	321
572	1	2	571	sp|P39237|YO5L_	HYPOTHETICAL 6.8 KD PROTEIN IN NRDC-TK INTERGENIC REGION.	68	47	570
646	1	914	459	gi|413982	ipa-58r gene product (Bacillus subtilis)	68	52	456
659	3	1668	1901	gi|1107541	C33D9.8 (Caenorhabditis elegans)	68	36	234
864	5	1510	1716	gi|145774	hsp70 protein (dnaK gene) (Escherichia coli)	68	48	207
920	1	860	432	gi|1510416	hypothetical protein (SP:P31666) (Methanococcus jannaschii)	68	54	429
952	1	1096	611	gi|(33456	reductase (Leishmania major)	68	46	486
970	1	91	402	gi|1354775	ptoS/R (Treponema pallidum)	68	46	312
1028	1	1064	534	gi|470117	diaminopimelate decarboxylase (Bacillus subtilis)	68	47	531
1029	1	428	216	gi|1135714	Plasmodium falciparum mRNA for asparagine-rich antigen (clone 17C1) (Plasmodium falciparum)	68	31	213
1058	1	692	348	gi|:81649	epiC gene product (Staphylococcus epidermidis)	68	46	345
1096	2	665	465	gi|143434	Rho Factor (Bacillus subtilis)	68	43	201
1308	1	2	694	gi|1.69939	group B oligopeptidase.PepB (Streptococcus agalactiae)	68	50	693
1679	1	2	238	gi|:17205	67 kDa Myosin-crossreactive streptococcal antigen (Streptococcus yogonos)	68	53	237
2039	1	3	383	gi|153898	transport protein (Salmonella typhimurium)	68	51	381
2077	1	3	326	pir|C33496|C334	hisC homolog - Bacillus subtilis	68	47	324
2112	1	613	374	gi|64884	lamin LIII (Xenopus laevis)	68	50	240
2273	1	793	398	gi|581688	epiB gene product (Staphylococcus epidermidis)	68	45	396
2348	1	2	385	gi|216869	branched-chain amino acid transport carrier (Pseudomonas aeruginosa) pir|A38534|A38534 branched-chain amino acid transport protein braZ Pseudomonas aeruginosa	68	41	384

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
2955	1	768	400	gi|904179	hypothetical protein [Bacillus subtilis]	68	49	369
2981	1	572	288	gi|508979	GTP-binding protein [Bacillus subtilis]	68	48	285
3014	1	584	294	gi|1524394	ORF-2 upstream of gbsAB operon [Bacillus subtilis]	68	45	291
3082	1	336	169	gi|1204696	fructose-permease IIBC component [Haemophilus influenzae]	68	53	168
3108	1	103	258	gi|217855	heat-shock protein [Arabidopsis thaliana]	68	48	156
3639	1	919	461	gi|1510490	nitrate transport permease protein [Methanococcus jannaschii]	68	47	459
3657	1	1	330	gi|155369	PTS enzyme-II fructose [Xanthomonas campestris]	68	48	330
3823	1	780	391	gi|603768	HutI protein, imidazolone-5-propionate hydrolase [Bacillus subtilis] gi|603768 HutI protein, imidazolone-5-propionate hydrolase Bacillus subtilis]	68	54	390
3982	1	2	277	gi|149435	putative [Lactococcus lactis]	68	47	276
4051	1	1	342	gi|450688	hsdM gene of EcoprrI gene product [Escherichia coli] pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli [SUB 40-520]	68	48	342
4089	1	12	209	gi|1353678	heavy-metal transporting P-type ATPase [Proteus mirabilis]	68	47	198
4143	1	47	187	gi|603769	HutU protein, urocanase [Bacillus subtilis]	68	55	141
4148	1	2	352	gi|450688	hsdM gene of EcoprrI gene product [Escherichia coli] pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli [SUB 40-520]	68	51	351
4173	1	2	382	gi|1041097	Pyruvate Kinase [Bacillus psychrophilus]	68	48	381
4182	1	498	250	gi|413968	ipa-44d gene product [Bacillus subtilis]	68	50	249
4362	2	148	318	gi|450688	hsdM gene of EcoprrI gene product [Escherichia coli] pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli [SUB 40-520]	68	44	171
5	11	9493	8300	gi|143727	putative [Bacillus subtilis]	67	46	1194
31	11	10318	9833	gi|216746	D-lactate dehydrogenase [Lactobacillus plantarum]	67	41	486
32	3	3560	3155	gi|1098557	renal sodium/dicarboxylate cotransporter [Homo sapiens]	67	46	1596
32	5	4945	4145	gi|1510720	prephenate dehydratase [Methanococcus jannaschii]	67	51	801
36	5	5350	4268	gi|[illegible]66216	45% identity with the product of the ORF6 gene from the Erwinia herbicola carotenoid biosynthesis cluster; putative [Bacillus subtilis]	67	58	1083
44	7	4492	5304	gi|1006621	hypothetical protein [Synechocystis sp.]	67	43	813

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
56	7	3943	8481	gi|334131	glutamate synthase large subunit precursor (Azospirillum brasilonse) pir|B46602|B46602 glutamate synthase (NADPH) (EC 1.4.1.13) alpha hain - Azospirillum brasilonse	67	52	4539
56	12	13923	14678	gi|1000453	TreR (Bacillus subtilis)	67	48	756
62	8	5092	4757	gi|1113949 |	orf3 (Bacillus, C-125, alkali-sensitive mutant 18224, Peptide Mutant, 112 aa)	67	45	336
62	10	7570	6338	gi|654655	Na/H antiporter system (Bacillus alcalophilus)	67	49	1233
99	3	2119	3321	gi|1200349	hypothetical protein (GB:GB:D90212_3) (Haemophilus influenzae)	67	50	1203
102	9	5695	7176	gi|149432	putative (Lactococcus lactis)	67	51	1482
103	13	14549	14049	gi|1408497	LP9D gene product (Bacillus subtilis)	67	48	501
109	15	14821	13982	gi|413976	ipa-52r gene product (Bacillus subtilis)	67	49	840
109	17	14811	15194	gi|413983	ipa-59d gene product (Bacillus subtilis)	67	29	384
121	4	1713	2153	gi|1262335	YmaA (Bacillus subtilis)	67	54	441
122	1	1	1149	gi|143047	ORFB (Bacillus subtilis)	67	35	1149
124	5	4060	3518	gi|556885	Unknown (Bacillus subtilis)	67	47	543
131	2	4584	3589	gi|1046081	hypothetical protein (GB:D26105_10) (Mycoplasma genitalium)	67	30	996
140	3	2899	2297	gi|146549	kdpC (Escherichia coli)	67	45	603
142	4	5409	4198	gi|1212775	GTP cyclohydrolase II (Bacillus amyloliquefaciens)	67	55	1212
147	5	2913	2374	gi|1303709	YrkJ (Bacillus subtilis)	67	64	540
152	8	6341	6673	gi|1377841	unknown (Bacillus subtilis)	67	48	333
161	4	2720	3763	gi|496319	SphX (Synechococcus sp.)	67	47	1044
163	6	1989	3428	gi|595681	2-oxoglutarate/malate translocator (Spinacia oleracea)	67	47	1440
193	3	1351	1626	gi|1511101	shikimate 5-dehydrogenase (Methanococcus jannaschii)	67	53	276
200	2	917	2179	gi|142439	ATP-dependent nuclease (Bacillus subtilis)	67	48	1263
206	10	12445	12801	sp|P37347|YECD_	HYPOTHETICAL 21.8 KD PROTEIN IN ASPS 5'REGION.	67	47	357
206	11	13047	14432	gi|732813	branched-chain amino acid carrier (Lactobacillus delbrueckii)	67	46	1386
208	2	1321	809	gi|1033037	100 kDa heat shock protein (Hsp100) (Leishmania major)	67	36	513
238	3	1039	2052	gi|809542	ChrB protein (Erwinia chrysanthemi)	67	42	1014

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
246	2	176	367	gi|215098	excisionase (Bacteriophage 154a)	67	37	192
276	2	2260	1412	gi|303560	ORF271 (Escherichia coli)	67	50	849
297	6	2223	3056	gi|142784	CtaA protein (Bacillus firmus)	67	46	834
307	7	5220	4186	gi|1070013	protein-dependent (Bacillus subtilis)	67	43	1035
316	1	36	1028	gi|1161061	dioxygenase (Methylobacterium extorquens)	67	52	993
324	3	5650	5030	gi|1469784	putative cell division protein FtsW (Enterococcus hirae)	67	49	621
336	1	524	264	gi|173122	urea amidolyase (Saccharomyces cerevisiae)	67	45	261
340	1	1	1084	sp|P30053|SYHI_S	HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA LIGASE) (HISRS).	67	47	1287
364	3	4890	3592	gi|151259	HMG-CoA reductase (EC 1.1.1.88) (Pseudomonas mevalonii) pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	67	46	1299
365	3	2940	2113	gi|1296823	orf2 gene product (Lactobacillus helveticus)	67	47	828
367	2	325	918	gi|1039479	ORFU (Lactococcus lactis)	67	47	594
395	3	666	1271	gi|1204516	hypothetical protein (GB:U00014_4) (Haemophilus influenzae)	67	55	606
415	1	1800	901	gi|482579	CG Site No. 29739 (Escherichia coli)	67	46	900
419	1	1799	903	gi|520752	putative (Bacillus subtilis)	67	48	897
474	1	2	796	gi|486906	arginino succinate synthetase (Streptomyces clavuligerus) pir|S57659|S57659 arginino succinate synthase (EC 6.3.4.5) - streptomyces clavuligerus	67	49	795
485	2	1921	2226	gi|143434	Rho Factor (Bacillus subtilis)	67	43	306
596	1	1728	865	gi|1303853	YqgF (Bacillus subtilis)	67	47	864
700	1	433	218	gi|1204628	hypothetical protein (SP:P21498) (Haemophilus influenzae)	67	47	216
806	2	249	647	gi|677947	AppC (Bacillus subtilis)	67	51	399
828	2	340	900	gi|777761	IrrA (Synechococcus sp.)	67	37	561
833	1	1407	916	gi|142996	regulatory protein (Bacillus subtilis)	67	41	492
856	1	1555	779	gi|780224	2K970.2 (Caenorhabditis elegans)	67	38	777
888	1	1614	850	gi|437315	TTG start codon (Bacillus licheniformis)	67	40	765
1034	1	1190	597	gi|1205113	hypothetical protein (GB:L19201_15) (Haemophilus influenzae)	67	45	594
1062	1	636	319	gi|1303850	YqgC (Bacillus subtilis)	67	41	318
1067	1	918	460	pir|A32950|A329	probable reductase protein - Leishmania major	67	54	459

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
1158	1	3	293	gi|1001369	hypothetical protein (Synechocystis sp.)	67	44	291
2181	1	3	302	gi|1510416	hypothetical protein (SP:P31466) (Methanococcus jannaschii)	67	48	300
3000	1	1	507	gi|517205	67 kDa Myosin-crossreactive streptococcal antigen (Streptococcus pyogenes)	67	56	507
3066	1	464	234	gi|308861	GTG start codon (Lactococcus lactis)	67	46	231
3087	1	454	251	gi|1205366	oligopeptide transport ATP-binding protein (Haemophilus influenzae)	67	44	204
3101	1	2	256	gi|1531541	uroporphyrinogen III methyltransferase (Zea mays)	67	55	255
3598	1	728	393	gi|151259	HMG-CoA reductase (EC 1.1.1.88) (Pseudomonas mevalonii) pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	67	56	336
3765	2	584	366	gi|557489	menD (Bacillus subtilis)	67	45	219
3788	1	658	398	pir|S52915|S529	nitrate reductase alpha chain - Bacillus subtilis (fragment)	67	45	261
3883	1	2	265	gi|704397	cystathionine beta-lyase (Arabidopsis thaliana)	67	46	264
3926	1	2	340	gi|1483199	peptide-synthetase (Amycolatopsis mediterranei)	67	44	339
4417	1	82	396	gi|1205337	ribonucleotide transport ATP-binding protein (Haemophilus influenzae)	67	46	315
2	3	3075	3989	gi|535348	CodV (Bacillus subtilis)	66	42	915
15	6	2273	2542	gi|46491	SmtB (Synechococcus PCC7942)	66	37	270
31	9	8059	7826	gi|292046	mucin (*Homo sapiens*)	66	44	234
31	10	9034	9258	gi|1204545	mercury scavenger protein (Haemophilus influenzae)	66	48	225
32	6	6347	5253	gi|998342	inducible nitric oxide synthase (Gallus gallus)	66	47	1095
44	13	8856	10124	gi|1510751	molybdenum cofactor biosynthesis moeA protein (Methanococcus jannaschii)	66	46	1269
48	2	1276	2868	gi|150209	ORF 1 (Mycoplasma mycoides)	66	40	1593
58	8	7178	8428	gi|665999	hypothetical protein (Bacillus subtilis)	66	47	1251
62	7	5143	4370	gi|1072398	phaD gene product (Rhizobium meliloti)	66	40	774
70	14	11693	10998	gi|809660	deoxyribose-phosphate aldolase (Bacillus subtilis) pir|S49455|S49455 deoxyribose-phosphate aldolase (EC 4.1.2.4) - acillus subtilis	66	55	696
76	1	1	1305	gi|142440	ATP-dependent nuclease (Bacillus subtilis)	66	42	1305
91	6	9236	8205	gi|704397	cystathionine beta-lyase (Arabidopsis thaliana)	66	40	1032
102	5	3810	3265	gi|1204323	hypothetical protein (SP:P31805) (Haemophilus influenzae)	66	41	546

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
103	4	3418	2732	gi|971344	nitrate reductase gamma subunit (Bacillus subtilis) sp|P42177|NARI_BACSU NITRATE REDUCTASE GAMMA CHAIN (EC 1.7.99.4). gi|1009369 Respiratory nitrate reductase (Bacillus subtilis) (SUB -160)	66	48	687
109	6	4243	4674	gi|170886	glucosamine-6-phosphate deaminase (Candida albicans) pir|A46652|A46652 glucosamine-6-phosphate isomerase (EC 5.3.1.10) - yeast (Candida albicans)	66	45	432
112	17	17491	17712	gi|1323179	ORF YGR111w (Saccharomyces cerevisiae)	66	33	222
116	2	4667	2637	gi|1491813	gamma-glutamyltranspeptidase (Bacillus subtilis)	66	43	2031
150	5	3189	2989	gi|1146224	putative (Bacillus subtilis)	66	30	201
172	5	3264	3662	gi|755152	highly hydrophobic integral membrane protein (Bacillus subtilis) sp|P42953|TAGG_BACSU TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN AGG.	66	41	399
174	5	4592	3723	gi|1146241	pantothenate synthetase (Bacillus subtilis)	66	49	870
175	4	3209	2880	gi|642655	unknown (Rhizobium meliloti)	66	29	330
175	11	8743	7994	gi|854655	Na/H antiporter system (Bacillus alcalophilus)	66	43	750
190	5	7079	5727	gi|451072	di-tripeptide transporter (Lactococcus lactis)	66	40	1353
195	15	13919	13713	gi|1322411	unknown (Mycobacterium tuberculosis)	66	42	207
217	3	2822	2595	gi|1143542	alternative stop codon (Rattus norvegicus)	66	36	228
233	9	7133	6135	gi|1458327	F08F3.4 gene product (Caenorhabditis elegans)	66	47	999
238	1	41	1041	gi|809541	CbrA protein (Erwinia chrysanthemi)	66	42	999
241	1	2102	1053	gi|153067	peptidoglycan hydrolase (Staphylococcus aureus)	66	53	1050
261	1	1178	648	gi|1510859	M. jannaschii predicted coding region MJ0790 (Methanococcus jannaschii)	66	40	531
263	3	3731	2973	gi|1205865	tetrahydrodipicolinate N-succinyltransferase (Haemophilus influenzae)	66	47	759
272	8	6548	5484	gi|882101	high affinity nickel transporter (Alcaligenes eutrophus) sp|P23516|HOXN_ALCEU HIGH-AFFINITY NICKEL TRANSPORT PROTEIN.	66	44	1065
276	3	2805	2106	gi|1208965	hypothetical 23.3 kd protein (Escherichia coli)	66	47	702
278	2	2830	1784	gi|1488662	phosphatase-associated protein (Bacillus subtilis)	66	48	1047
278	3	3830	2952	gi|303560	ORF271 (Escherichia coli)	66	45	879
279	2	3894	2218	gi|1185289	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1- carboxylate synthase (Bacillus subtilis)	66	48	1677
288	4	2535	2275	gi|1256625	putative (Bacillus subtilis)	66	42	261
292	2	1133	942	gi|1511604	M. jannaschii predicted coding region MJ1651 (Methanococcus jannaschii)	66	30	192

TABLE 2

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
294	1	1116	559	gi|216314	asterase (Bacillus stearothermophilus)	66	45	558
297	4	2913	1978	gi|994794	cytochrome a assembly facto (Bacillus subtilis) sp|P24009|COXX_BACSU PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR.	66	45	936
316	4	2051	2682	gi|1107839	alginate lyase (Pseudomonas aeruginosa)	66	40	630
338	4	2460	2302	gi|520750	biotin synthetase (Bacillus sphaericus)	66	58	159
339	1	1214	785	gi|467468	7, 8-dihydro-6-hydroxymethylpterin-pyrophosphokinase (Bacillus ubtilis)	66	52	480
363	1	3	863	gi|581649	epiC gene product (Staphylococcus epidermidis)	66	47	861
366	2	232	483	gi|1103505	unknown (Schizosaccharomyces pombe)	66	53	252
367	4	2468	1845	sp|P20692|TYRA_	PREPHENATE DEHYDROGENASE (EC 1.3.1.12) (PDH).	66	50	624
372	3	2150	1599	gi|467416	unknown (Bacillus subtilis)	66	38	552
378	1	212	1009	gi|147309	purine nucleoside phosphorylase (Escherichia coli)	66	50	798
401	1	1	462	gi|388263	p-aminobenzoic acid synthase (Streptomyces griseus) pir|JN0531|JN0531 p-aminobenzoic acid synthase - Streptomyces griseus	66	46	462
404	7	4826	5254	gi|606744	cytidine deaminase (Bacillus subtilis)	66	51	429
411	2	1738	1103	gi|1460081	unknown (Mycobacterium tuberculosis)	66	44	636
420	1	2	541	gi|1046024	Na+ ATPase subunit J (Mycoplasma genitalium)	66	49	540
431	1	1	858	gi|1500008	M. jannaschii predicted coding region MJ1154 (Methanococcus jannaschii)	66	50	858
443	7	5679	5299	gi|852076	MrgA (Bacillus subtilis)	66	46	381
444	3	3405	2413	gi|153047	lysostaphin (ttg start codon) (Staphylococcus simulans) pir|A25081|A25881 lysostaphin precursor - Staphylococcus simulans sp|P10547|LSTP_STASI LYSOSTAPHIN PRECURSOR (EC 3.5.1.-).	66	51	993
561	1	956	480	gi|1204905	DNA-3-methyladenine glycosidase I (Haemophilus influenzae)	66	45	477
562	3	1066	1383	gi|1046082	M. genitalium predicted coding region MG372 (Mycoplasma genitalium)	66	52	318
576	1	11	724	gi|305014	ORF_o234 (Escherichia coli)	66	43	714
577	3	1190	903	gi|1001353	hypothetical protein (Synechocystis sp.)	66	52	288
584	1	2	331	sp|P24204|YEBA_	HYPOTHETICAL 46.7 KD PROTEIN IN HSBB-RUVB INTERGENIC REGION (ORFU).	66	48	330
592	1	1410	706	gi|928839	ORF266; putative (Lactococcus lactis phage BK5-T)	66	51	705
601	1	1433	720	gi|1488695	novel antigen; orf-2 (Staphylococcus aureus)	66	55	714

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
619	3	468	845	gi|746573	similar to M. musculus transport system membrane protein, Nramp PIR:A40739) and S. cerevisiae SMF1 protein (PIR:A45154) Caenorhabditis elegans)	66	45	378
706	2	561	355	gi|804808	unknown protein (Rattus norvegicus)	66	46	207
734	2	673	512	gi|1519085	phosphatidylcholine binding immunoglobulin heavy chain IgM variable region (Mus musculus)	66	60	162
740	1	3	317	gi|1209272	argininosuccinate lyase (Campylobacter jejuni)	66	42	315
764	1	310	747	gi|435296	alkaline phosphatase like protein (Lactococcus lactis) pir|S39339|S39339 alkaline phosphatase-like protein - Lactococcus actis	66	42	438
852	1	338	171	gi|536955	CG Site No. 361 (Escherichia coli)	66	43	168
886	1	3	158	gi|289272	ferrichrome-binding protein (Bacillus subtilis)	66	44	156
889	1	462	232	gi|833061	HCMVUL27 (AA 1-642) (Human cytomegalovirus)	66	66	231
893	1	2	247	gi|149008	putative (Helicobacter pylori)	66	45	246
900	1	1425	733	gi|580842	F3 (Bacillus subtilis)	66	51	693
906	2	2300	1473	gi|790945	aryl-alcohol dehydrogenase (Bacillus subtilis)	66	53	828
947	1	79	549	gi|410117	diaminopimelate decarboxylase (Bacillus subtilis)	66	47	471
950	1	1100	552	gi|48713	orf145 (Staphylococcus aureus)	66	35	549
955	2	89	475	gi|1204390	uridine kinase (uridine monophosphokinase) (Haemophilus influenzae)	66	50	387
981	2	1308	997	gi|457146	rhoptry protein (Plasmodium yoelii)	66	38	312
986	1	25	315	gi|305002	ORF_f356 (Escherichia coli)	66	31	291
1057	1	3	203	gi|1303853	YqgF (Bacillus subtilis)	66	40	201
1087	1	1	294	gi|575933	unknown (Saccharomyces cerevisiae)	66	53	294
1105	1	1	231	gi|1045799	methylgalactoside permease ATP-binding protein (Mycoplasma genitalium)	66	46	231
1128	1	2	574	gi|1001493	hypothetical protein (Synechocystis sp.)	66	46	573
1150	1	498	250	gi|1499034	H. jannaschii predicted coding region MJ0255 (Methanococcus jannaschii)	66	40	249
1180	2	707	453	gi|21908	DNA polymerase (g43) (Bacteriophage T4)	66	46	255
1208	1	1123	587	gi|1256653	DNA-binding protein (Bacillus subtilis)	66	58	537
1342	1	1	402	gi|1208474	hypothetical protein (Synechocystis sp.)	66	53	402
1761	2	589	398	gi|21811	tail fiber protein (Bacteriophage T3)	66	50	192

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1983	1	499	251	gi|1045935	DNA helicase II (Mycoplasma genitalium)	66	40	249
2103	2	176	400	gi|929798	precursor for the major merozoite surface antigens (Plasmodium alciparum)	66	46	225
2341	1	373	188	gi|1256623	exodeoxyribonuclease (Bacillus subtilis)	66	38	186
2458	1	325	164	gi|1019410	unknown (Schizosaccharomyces pombe)	66	47	162
2505	1	468	235	gi|1510394	putative transcriptional regulator (Methanococcus jannaschii)	66	39	234
2525	1	558	280	gi|1000695	cytotoxin L (Clostridium sordellii)	66	44	279
2935	1	3	275	gi|765073	autolysin (Staphylococcus aureus)	66	47	273
3005	1	114	305	gi|1205784	heterocyst maturation protein (Haemophilus influenzae)	66	46	192
3048	1	80	277	gi|1303813	YqeW (Bacillus subtilis)	66	42	198
3071	1	1	189	gi|1070014	protein-dependent (Bacillus subtilis)	66	41	189
3081	1	404	225	gi|984212	unknown (Schizosaccharomyces pombe)	66	44	180
3090	2	580	386	gi|1204987	DNA polymerase III, alpha chain (Haemophilus influenzae)	66	48	195
3318	1	1	387	gi|1009366	Respiratory nitrate reductase (Bacillus subtilis)	66	49	387
3739	1	798	400	gi|1109684	ProV (Bacillus subtilis)	66	47	399
3796	1	402	202	gi|853760	acyl-CoA dehydrogenase (Bacillus subtilis)	66	60	201
1924	1	595	347	gi|563952	gluconate permease (Bacillus licheniformis)	66	46	249
4240	1	3	350	gi|151259	HMG-CoA reductase (EC 1.1.1.88) (Pseudomonas mevalonii) pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	66	51	348
4604	1	7	234	pir|A26713|BHHC	hemocyanin subunit II - Atlantic horseshoe crab	66	46	228
4	9	8845	9750	gi|145646	cynR (Escherichia coli)	65	35	906
6	5	2708	3565	gi|887824	ORF_o310 (Escherichia coli)	65	47	858
13	1	1993	998	gi|143402	recombination protein (ttg start codon) (Bacillus subtilis) gi|1303923 RecN (Bacillus subtilis)	65	44	996
15	7	2693	3524	gi|1403126	czcD gene product (Alcaligenes eutrophus)	65	38	1032
18	3	1908	1372	gi|349187	acyltransferase (Saccharomyces cerevisiae)	65	50	537
21	3	1467	2492	gi|149518	phosphoribosyl anthranilate transferase (Lactococcus lactis) pir|S35126|S35126 anthranilate phosphoribosyltransferase (EC .4.2.18) - Lactococcus lactis subsp. lactis	65	52	1026
25	4	3374	4312	gi|1502420	malonyl-CoA:Acyl carrier protein transacylase (Bacillus subtilis)	65	44	939

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt.)
27	2	390	626	gi|1212729	YqhJ [Bacillus subtilis]	65	45	237
31	12	11040	10387	gi|509245	D-hydroxyisocaproate dehydrogenase (Lactobacillus delbrueckii)	65	41	654
38	24	19172	19528	gi|547: .	H-protein (Flaveria cronquistii)	65	41	357
44	2	790	1746	gi|405882	yeiK (Escherichia coli)	65	46	957
44	12	9356	8832	gi|1205905	molybdenum cofactor biosynthesis protein (Haemophilus influenzae)	65	50	525
45	8	6635	7588	gi|491074	ApbA protein (Salmonella typhimurium)	65	46	954
51	2	580	1503	gi|580897	OppB gene product (Bacillus subtilis)	65	45	924
52	1	225	953	gi|1205518	NAD(P)H-flavin oxidoreductase (Haemophilus influenzae)	65	45	729
55	4	1339	1058	pir|A44459|A444	troponin T beta TnT-S - rabbit	65	41	282
67	9	7421	8272	gi|143607	sporulation protein (Bacillus subtilis)	65	42	852
73	5	4446	5375	gi|1204896	lysophospholipase L2 (Haemophilus influenzae)	65	37	930
74	1	954	478	gi|1204844	H. influenzae predicted coding region HI0594 (Haemophilus influenzae)	65	50	477
77	1	2	757	gi|1046082	M. genitalium predicted coding region MG372 (Mycoplasma genitalium)	65	46	756
77	2	795	1433	gi|1222116	permease (Haemophilus influenzae)	65	37	639
81	3	4728	3454	gi|1001708	hypothetical protein (Synechocystis sp.)	65	49	1275
91	7	8548	8357	gi|1399263	cystathionine beta-lyase (Emericella nidulans)	65	40	192
98	3	1608	1988	gi|467423	unknown (Bacillus subtilis)	65	38	381
98	4	2250	2987	gi|467424	unknown (Bacillus subtilis)	65	45	738
102	3	2598	2119	gi|1511532	N-terminal acetyltransferase complex, subunit ARD1 (Methanococcus jannaschii)	65	39	480
102	4	3647	2862	gi|1204637	H. influenzae predicted coding region HI0388 (Haemophilus influenzae)	65	32	786
103	9	10851	9841	gi|142695	S-adenosyl-L-methionine:uroporphyrinogen III methyltransferase Bacillus megaterium	65	47	1011
103	10	10439	10119	gi|710021	nitrite reductase (nirD) (Bacillus subtilis)	65	51	321
106	2	262	1140	gi|39881	ORF 311 (AA 1-311) (Bacillus subtilis)	65	44	879
109	5	3909	4268	gi|1204399	glucosamine-6-phosphate deaminase protein (Haemophilus influenzae)	65	44	360
109	10	7165	8595	gi|536955	CG Site No. 361 (Escherichia coli)	65	41	1431

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
110	4	3688	3915	gi|407881	stringent response-like protein [Streptococcus equisimilis] pir|S39975|S39975 stringent response-like protein - Streptococcus equisimilis	65	45	228
110	5	3882	4295	gi|407880	ORF1 [Streptococcus equisimilis]	65	50	414
110	6	4231	4380	gi|1139574	Orf2 [Streptomyces griseus]	65	56	150
112	10	9218	8640	gi|1204571	H. influenzae predicted coding region HI0318 [Haemophilus influenzae]	65	52	579
112	12	12049	11288	gi|710496	transcriptional activator protein [Bacillus brevis]	65	32	762
125	1	2	202	gi|1151158	repeat organellar protein [Plasmodium chabaudi]	65	39	201
126	1	3	422	gi|37589	precursor [Homo sapiens]	65	46	420
127	11	10711	12658	gi|1064809	homologous to sp|MTRA_ECOLI [Bacillus subtilis]	65	41	1926
143	8	7541	7004	gi|216513	mutator mutT (AT-GC transversion) [Escherichia coli]	65	56	540
145	5	3587	3838	gi|1209768	D02_orf569 [Mycoplasma pneumoniae]	65	27	252
150	4	3482	2841	gi|1146225	putative [Bacillus subtilis]	65	37	642
166	1	3858	1948	gi|148304	beta-1,4-N-acetylmuramoylhydrolase [Enterococcus hirae] pir|A42296|A42296 lysozyme 2 (EC 3.2.1.-) precursor - Enterococcus hirae (ATCC 9790)	65	50	1911
188	6	3195	4178	gi|151943	ORF3; putative [Rhodobacter capsulatus]	65	46	984
189	9	4982	4785	gi|58812	ORF IV (AA 1-489) [Figwort mosaic virus]	65	40	198
195	6	7908	5272	gi|145220	alanyl-tRNA synthetase [Escherichia coli]	65	49	2637
195	7	10599	8104	gi|882711	exonuclease V alpha-subunit [Escherichia coli]	65	38	2496
206	16	16896	18191	gi|408115	ornithine acetyltransferase [Bacillus subtilis]	65	53	1296
217	6	3844	3215	gi|1205974	5'guanylate kinase [Haemophilus influenzae]	65	41	630
220	4	5265	3751	gi|580920	rodD (gtaA) polypeptide (AA 1-673) [Bacillus subtilis] pir|S06048|S06048 probable rodD protein - Bacillus subtilis sp|P13484|TAGP_BACSU PROBABLE POLY(GLYCEROL-PHOSPHATE) LPHA-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TECHOIC ACID BIOSYNTHESIS HOTEIN E).	65	40	1515
236	5	2327	3709	gi|1146200	DNA or RNA helicase, DNA-dependent ATPase [Bacillus subtilis]	65	46	1383
237	3	1902	2513	gi|149379	HisBd [Lactococcus lactis]	65	46	612
241	4	4968	4195	gi|1205308	ribonuclease HII (EC 31264) (RNASE HII) [Haemophilus influenzae]	65	50	774
252	1	1278	940	gi|1204989	hypothetical protein (OB:U00022_9) [Haemophilus influenzae]	65	40	339
261	5	4780	3794	gi|145927	fecD [Escherichia coli]	65	43	987

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
274	1	3	278	gi|496558	ortX (Bacillus subtilis)	65	42	276
301	2	982	815	gi|.67418	unknown (Bacillus subtilis)	65	45	168
307	4	3586	2864	gi|1070014	protein-dependent (Bacillus subtilis)	65	40	723
335	2	2246	1399	gi|146913	N-acetylglucosamine transport protein (Escherichia coli) pir|B29895|MQEC2N phosphotransferase system enzyme II (EC 2.7.1.69), N-acetylglucosamine-specific - Escherichia coli sp|P09323|PTAA_ECOLI PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC IIABC OMPONENT (EIIA	65	50	888
338	5	4120	3170	gi|1277029	biotin synthase (Bacillus subtilis)	65	49	951
343	3	1490	2800	gi|143264	membrane-associated protein (Bacillus subtilis)	65	48	1311
344	4	2761	2531	gi|1050540	tRNA-glutamine synthetase (Lupinus luteus)	65	34	231
358	3	3421	3621	gi|1146220	NAD+ dependent glycerol-3-phosphate dehydrogenase (Bacillus subtilis)	65	47	201
364	1	238	699	gi|1340128	ORF1 (Staphylococcus aureus)	65	51	462
379	1	1	576	gi|143331	alkaline phosphatase regulatory protein (Bacillus subtilis) pir|A27650|A27650 regulatory protein phoR - Bacillus subtilis sp|P23545|PHOR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN HOR (EC 2.7.3.-).	65	40	576
379	3	3666	4346	gi|143268	dihydrolipoamide transsuccinylase (odhB; EC 2.3.1.61) (Bacillus ubtilis)	65	50	681
428	1	187	483	gi|1420465	ORF YOR195w (Saccharomyces cerevisiae)	65	45	297
438	2	272	838	gi|143498	dcuS procein (Bacillus subtilis)	65	38	567
444	11	9280	10215	gi|1204756	;ribokinase (Haemophilus influenzae)	65	47	936
449	2	1241	1531	gi|599848	Na/H antiporter homolog (Lactococcus lactis)	65	41	291
478	2	1452	865	gi|1045942	glycyl-tRNA synthetase (Mycoplasma genitalium)	65	39	588
479	1	1032	517	gi|1498192	putative (Pseudomonas aeruginosa)	65	40	516
480	6	4312	5637	gi|415662	UDP-N-acetylglucosamine 1-carboxyvinyl transferase (Acinetobacter alcoaceticus)	65	48	1326
484	1	2	430	gi|146551	transmembrane protein (KdpD) (Escherichia coli)	65	44	429
499	1	54	932	gi|603456	reductase (Leishmania major)	65	53	879
505	1	914	459	gi|1518853	OafA (Salmonella typhimurium)	65	39	456
571	2	1509	883	gi|49399	open reading frame upstream glnE (Escherichia coli) tr|S37754|S37754 hypothecical protein XE (glnE 5' region) - cherichia coli	65	44	627
611	2	506	270	gi|10961	RAP-2 (Plasmodium falciparum)	65	40	237

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% identity	length (nt)
705	1	564	283	gi|710020	nitrite reductase (nirB) [Bacillus subtilis]	65	52	282
712	1	1	177	gi|289272	ferrichrome-binding protein [Bacillus subtilis]	65	37	177
712	2	196	354	gi|289272	ferrichrome-binding protein [Bacillus subtilis]	65	37	159
743	1	2	631	gi|310631	ATP binding protein [Streptococcus gordonii]	65	45	630
749	2	393	779	gi|467374	single strand DNA binding protein [Bacillus subtilis]	65	29	387
762	1	1698	850	gi|160399	multidrug resistance protein [Plasmodium falciparum]	65	48	849
788	1	85	315	gi|1129096	unknown protein [Bacillus sp.]	65	35	231
850	1	1	408	gi|1006604	hypothetical protein [Synechocystis sp.]	65	37	408
908	1	1	444	gi|1199546	2362 [Saccharomyces cerevisiae]	65	46	444
925	1	1	174	gi|1256653	DNA-binding protein [Bacillus subtilis]	65	54	174
1031	1	26	232	gi|238657	AppCcytochrome d oxidase, subunit I homolog [Escherichia coli, K12, aptide, 514 aa]	65	47	207
1037	1	414	262	gi|1491813	gamma-glutamyltranspeptidase [Bacillus subtilis]	65	46	153
1053	1	348	175	gi|642655	unknown [Rhizobium meliloti]	65	34	174
1149	1	1399	752	gi|1162980	ribulose-5-phosphate 3-epimerase [Spinacia oleracea]	65	48	648
1214	1	881	495	gi|1205959	lactam utilization protein [Haemophilus influenzae]	65	45	387
1276	1	476	276	pir|S35493|S354	site-specific DNA-methyltransferase StsI (EC 2.1.1.-) - Streptococcus sanguis	65	35	201
1276	2	900	577	gi|473794	'ORF' [Escherichia coli]	65	34	324
2057	1	272	138	gi|631699	TraH [Yersinia enterocolitica]	65	21	135
2321	1	336	169	gi|1045789	hypothetical protein (GB:U14003_76) [Mycoplasma genitalium]	65	41	168
2974	1	590	297	gi|152052	enantiomerase-selective amidase [Rhodococcus sp.]	65	45	294
3031	1	306	154	pir|JQ1024|JQ10	hypothetical 30K protein (DmRP140 5' region) - fruit fly (Drosophila melanogaster)	65	35	153
3069	1	3	278	gi|144906	product homologous to E.coli thioredoxin reductase: J.Biol.Chem. 1988) 263:9015-9019, and to F52a protein of alkyl hydroperoxide eductase from S.typhimurium: J.Biol.Chem. (1990) 265:10535-10540; pen reading frame A [Clostridium pasteurianum]	65	46	276
3146	1	282	142	gi|49315	ORF1 gene product [Bacillus subtilis]	65	47	141
3170	1	679	341	gi|1507711	indolepyruvate decarboxylase [Erwinia herbicola]	65	44	339

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3546	1	1	303	gi|450688	hsdM gene of EcoprrI gene product (Escherichia coli) pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	65	42	303
3782	1	2	328	gi|166412	NADH-glutamate synthase (Medicago sativa)	65	42	327
3990	1	374	189	gi|1009366	Respiratory nitrate reductase (Bacillus subtilis)	65	53	186
4032	1	613	308	gi|1323127	ORF YGR087c (Saccharomyces cerevisiae)	65	50	306
4278	2	726	364	gi|1197667	vitellogenin (Anolis pulchellus)	65	42	363
19	4	4259	5518	gi|145727	deaD (Escherichia coli)	64	45	1260
19	6	7639	6926	gi|1016232	ycf27 gene product (Cyanophora paradoxa)	64	36	714
20	8	7053	6454	gi|765073	autolysin (Staphylococcus aureus)	64	47	600
31	13	12706	11537	gi|414009	ipa-85d gene product (Bacillus subtilis)	64	45	1170
33	4	2388	4364	gi|1204696	fructose-permease IIBC component (Haemophilus influenzae)	64	47	1977
36	3	1871	3013	gi|290503	glutamate permease (Escherichia coli)	64	40	1143
37	6	4065	4409	gi|39815	orf 2 gene product (Bacillus subtilis)	64	46	345
45	9	7852	8760	gi|1230585	nucleotide sugar epimerase (Vibrio cholerae O139)	64	53	909
53	3	1540	1899	gi|1303961	YqjJ (Bacillus subtilis)	64	50	360
56	6	4793	3855	gi|457514	gltC (Bacillus subtilis)	64	45	939
56	24	30002	30247	gi|470331	similar to zinc fingers (Caenorhabditis elegans)	64	42	246
62	4	2759	2421	gi|642655	unknown (Rhizobium meliloti)	64	28	339
85	6	7178	6027	gi|457702	5-aminoimidazole ribonucleotide-carboxilase (Pichia methanolica) pir|S39112|S39112 phosphoribosylaminoimidazole carboxylase (EC .1.1.21) - yeast (Pichia methanolica)	64	46	1152
96	9	9251	10030	gi|1511513	ABC transporter, probable ATP-binding subunit (Methanococcus jannaschii)	64	42	780
100	1	1	600	gi|765073	autolysin (Staphylococcus aureus)	64	44	600
106	5	3868	4854	gi|466778	lysine specific permease (Escherichia coli)	64	46	987
123	2	838	554	gi|467484	unknown (Bacillus subtilis)	64	47	285
127	8	7514	7810	gi|210061	serotype-specific antigen (African horse sickness virus) pir|S27891|S27891 capsid protein VP2 - African horse sickness virus	64	28	297
131	7	7134	6721	gi|1511160	M. jannaschii predicted coding region MJ1163 (Methanococcus jannaschii)	64	46	414

TABLE 2

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
142	5	5465	4817	gi|1173517	riboflavin synthase alpha subunit (Actinobacillus pleuropneumoniae)	64	44	639
143	1	709	356	pir|A32950|A329	probable reductase protein - Leishmania major	64	52	354
149	10	3555	3295	gi|398151	major surface antigen MSG2 (Pneumocystis carinii)	64	44	261
154	4	3134	2307	gi|984587	DinP (Escherichia coli)	64	50	828
161	5	3855	4880	gi|903304	ORF72 (Bacillus subtilis)	64	37	1026
165	1	33	791	gi|467483	unknown (Bacillus subtilis)	64	38	759
175	6	6355	4714	gi|1072398	phaD gene product (Rhizobium meliloti)	64	42	1512
188	3	2042	2500	gi|1001961	MHC class II analog (Staphylococcus aureus)	64	45	459
195	14	13667	13446	gi|396380	No definition line found (Escherichia coli)	64	47	222
206	15	16429	16938	gi|304134	argC (Bacillus stearothermophilus)	64	49	510
215	1	560	282	gi|142359	ORF 6 (Azotobacter vinelandii)	64	39	279
243	7	7818	6928	gi|414014	ipa-90d gene product (Bacillus subtilis)	64	49	891
258	2	1330	845	gi|664754	P17 (Listeria monocytogenes)	64	38	486
259	1	462	232	gi|1499663	M. jannaschii predicted coding region MJ0837 (Methanococcus jannaschii)	64	52	231
263	6	6565	5567	gi|142828	aspartate semialdehyde dehydrogenase (Bacillus subtilis) sp|Q04797|DHAS_BACSU ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (EC .2.1.11) (ASA DEHYDROGENASE).	64	48	999
271	1	3	1163	gi|467091	hflX; B2235_C2_202 (Mycobacterium leprae)	64	44	1161
280	1	173	1450	gi|1303839	YqfR (Bacillus subtilis)	64	43	1278
293	1	2532	1267	gi|147345	primosomal protein n' (Escherichia coli)	64	45	1266
295	2	742	1488	gi|459266	Potential membrane spanning protein (Staphylococcus hominis) pir|S42932|S42932 potential membrane spanning protein - taphylococcus hominis	64	39	747
301	5	1625	1446	gi|580835	lysine decarboxylase (Bacillus subtilis)	64	35	180
315	4	5064	3949	gi|143396	quinol oxidase (Bacillus subtilis)	64	45	1116
321	1	1264	635	gi|710696	transcriptional activator protein (Bacillus brevis)	64	41	630
333	5	4520	4239	gi|1314295	ORF2; putative 19 kDa protein (Listeria monocytogenes)	64	43	282
342	1	1	549	gi|142940	ftsA (Bacillus subtilis)	64	38	549
353	3	2878	2324	gi|537049	ORF_o470 (Escherichia coli)	64	44	555

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
379	2	827	3658	pir|S25295|A328	oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) - Bacillus subtilis	64	47	2832
404	6	4429	4839	pir|A36933|A369	diacylglycerol kinase homolog - Streptococcus mutans	64	35	411
407	1	2020	1133	gi|969026	OrfX (Bacillus subtilis)	64	41	888
425	1	1109	591	gi|1146177	phosphotransferase system glucose-specific enzyme II (Bacillus subtilis)	64	44	519
443	6	4082	4798	gi|147309	purine nucleoside phosphorylase (Escherichia coli)	64	51	717
450	2	1035	1604	gi|606376	ORF_o162 (Escherichia coli)	64	38	570
470	5	1680	6107	gi|1369948	host interacting protein (Bacteriophage B1)	64	45	4428
486	4	1911	1471	gi|1205582	spermidine/putrescine transport system permease protein (Haemophilus influenzae)	64	35	441
497	1	2217	1159	sp|P36929|FMU_E	FMU PROTEIN.	64	38	1059
501	1	3	410	gi|142450	ahrC protein (Bacillus subtilis)	64	38	408
514	1	3	290	gi|1204496	H. influenzae predicted coding region HI0238 (Haemophilus influenzae)	64	34	288
551	4	3162	3323	gi|1204511	bacterioferritin comigratory protein (Haemophilus influenzae)	64	41	162
603	4	759	956	gi|755823	NADH dehydrogenase F (Streptogyna americana)	64	35	198
653	2	940	746	gi|1213234	dicarboxylic amino acids Dip5p permease (Saccharomyces cerevisiae)	64	41	195
660	3	3801	2257	sp|P46133|YDAH_	HYPOTHETICAL PROTEIN IN OGT 5'REGION (FRAGMENT).	64	39	1545
695	1	11	502	gi|1001383	hypothetical protein (Synechocystis sp.)	64	41	492
702	1	3	752	gi|142865	DNA primase (Bacillus subtilis)	64	46	750
826	1	1	339	gi|971336	arginyl tRNA synthetase (Bacillus subtilis)	64	50	339
838	1	1831	917	gi|1354775	pfoS/R (Treponema pallidum)	64	41	915
864	3	675	944	gi|39833	cyclomaltodextrin glucanotransferase (Bacillus stearothermophilus) i|39835 cyclomaltodextrin glucanotransferase (Bacillus earothermophilus)	64	47	270
887	1	3	677	gi|153002	enterotoxin type E precursor (Staphylococcus aureus) pir|A28179|A28179 enterotoxin E precursor - Staphylococcus aureus sp|P12993|ETXE_STAAU ENTEROTOXIN TYPE E PRECURSOR (SEE).	64	46	675
928	2	1172	963	gi|311976	fibrinogen-binding protein (Staphylococcus aureus) pir|S34270|S34270 fibrinogen-binding protein - Staphylococcus aureus	64	41	210
1049	2	800	606	gi|1049115	Rap60 (Bacillus subtilis)	64	42	195
1067	2	999	748	gi|1151072	HhdA precursor (Haemophilus ducreyi)	64	50	252

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
1120	1	50	202	gi|142439	ATP-dependent nuclease (Bacillus subtilis)	64	30	153
1125	1	751	377	gi|581648	epiB gene product (Staphylococcus epidermidis)	64	44	375
1688	1	402	214	pir|A01365|TVMS	transforming protein K-ras - mouse	64	47	189
2472	1	2	358	gi|487282	Na+ -ATPase subunit J (Enterococcus hirae)	64	36	357
2989	1	520	356	gi|304134	argC (Bacillus stearothermophilus)	64	50	165
3013	1	630	352	gi|551699	cytochrome oxidase subunit I (Bacillus firmus)	64	51	279
3034	1	546	274	gi|1204349	hypothetical protein (GB:GB:D90212_3) (Haemophilus influenzae)	64	50	273
3197	1	613	308	gi|1009366	Respiratory nitrate reductase (Bacillus subtilis)	64	46	306
3303	1	90	362	gi|1107839	alginate lyase (Pseudomonas aeruginosa)	64	43	273
3852	2	82	288	gi|216746	D-lactate dehydrogenase (Lactobacillus plantarum)	64	42	207
3868	1	1	312	gi|149435	putative (Lactococcus lactis)	64	48	312
3918	1	660	331	gi|5532	acetyl-CoA acyltransferase (Yarrowia lipolytica)	64	46	330
4000	1	112	378	gi|994688	unknown (Saccharomyces cerevisiae)	64	44	267
4009	1	81	368	gi|39372	grsB gene product (Bacillus brevis)	64	41	288
4166	1	2	349	gi|149435	putative (Lactococcus lactis)	64	46	348
4366	1	2	307	gi|216267	ORF2 (Bacillus megaterium)	64	44	306
4457	1	2	400	gi|1197667	vitellogenin (Anolis pulchellus)	64	43	399
11	3	1539	2438	gi|438228	ORF C (Staphylococcus aureus)	63	32	900
24	7	5611	5423	gi|1369943	a1 gene product (Bacteriophage B1)	63	34	189
29	1	1	390	gi|467441	expressed at the end of exponential growyh under condtions in which he enzymes of the TCA cycle are repressed (Bacillus subtilis) gi|467441 expressed at the end of exponential growyh under ondtions in which the enzymes of the TCA cycle are repressed Bacil	63	43	390
31	6	6329	5712	gi|496943	ORF (Saccharomyces cerevisiae)	63	47	618
44	23	14669	15019	pir|A04446|QQEC	hypothetical protein F-92 - Escherichia coli	63	36	351
48	6	4403	6250	gi|43498	pyruvate synthase (Halobacterium halobium)	63	42	1848
50	5	3869	4738	gi|413967	ipa-43d gene product (Bacillus subtilis)	63	43	870
53	6	6764	5742	gi|474176	regulator protein (Staphylococcus xylosus)	63	49	1023

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	Match acession	match gene name	% alm	% ident	length (nt)
56	14	15880	17607	gi|467409	DNA polymerase III subunit [Bacillus subtilis]	63	44	1728
57	11	7945	7376	gi|537036	ORF_o158 [Escherichia coli]	63	39	570
62	3	2479	2114	gi|142656	unknown [Rhizobium meliloti]	63	41	366
70	8	6562	7353	gi|1399821	PhoC [Rhizobium meliloti]	63	46	792
75	2	223	927	gi|149376	HisG [Lactococcus lactis]	63	45	705
78	5	4912	4403	gi|413950	lpa-26d gene product [Bacillus subtilis]	63	42	510
91	5	9076	7220	gi|466997	metH2; B2126-C1_157 [Mycobacterium leprae]	63	41	1857
91	8	10566	9448	gi|1204344	cystathionine gamma-synthase [Haemophilus influenzae]	63	45	1119
120	1	21	1508	gi|882657	sulfite reductase (NADPH) flavoprotein beta subunit [Escherichia coli]	63	46	1488
120	4	2722	4125	gi|665994	hypothetical protein [Bacillus subtilis]	63	34	1404
127	7	6064	7566	gi|40162	murE gene product [Bacillus subtilis]	63	44	1503
149	6	2321	2106	gi|148503	dnaK [Erysipelothrix rhusiopathiae]	63	40	216
149	26	10445	10170	gi|4870	ORF 2, has similarity to DNA polymerase [Saccharomyces kluyveri] r|S15961|S15961 hypothetical protein 2 - yeast (Saccharomyces yvori) plasmid pSKL	63	42	276
164	2	507	1298	gi|145476	CDP-diglyceride synthetase [Escherichia coli]	63	44	792
166	6	9909	8164	gi|151932	fructose enzyme II [Rhodobacter capsulatus]	63	41	1746
169	4	1704	1886	gi|152886	elongation factor Ts (tsf) [Spiroplasma citri]	63	48	183
188	5	3145	2951	gi|1334547	GIY COI 114 grp IB protein [Podospora anserina]	63	42	195
195	13	11767	12804	gi|606100	ORF_o335 [Escherichia coli]	63	40	1038
201	2	607	2283	gi|433534	arginyl-tRNA synthetase [Corynebacterium glutamicum] pir|A49936|A49936 arginine--tRNA ligase (EC 6.1.1.19) - corynebacterium glutamicum	63	46	1677
206	14	15893	16489	gi|580828	N-acetyl-glutamate-gamma-semialdehyde dehydrogenase [Bacillus subtilis]	63	49	597
220	5	7769	5766	gi|216334	secA protein [Bacillus subtilis]	63	42	2004
221	1	74	907	gi|677945	AppA [Bacillus subtilis]	63	42	834
227	3	944	1708	gi|1510558	cobyric acid synthase [Methanococcus jannaschii]	63	46	765
261	2	804	1070	gi|486511	ORF YKR054c [Saccharomyces cerevisiae]	63	45	267
269	2	3606	1960	gi|148221	DNA-dependent ATPase, DNA helicase [Escherichia coli] pir|JS0137|BVECRQ recQ protein - Escherichia coli	63	42	1647

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
278	R	7417	6176	gi|699273	cystathionine gamma-synthase [Mycobacterium leprae] sp|P46807|METB_MYCLE CYSTATHIONINE GAMMA-SYNTHASE (EC 4.2.99.9) O-SUCCINYLHOMOSERINE (THIOL)-LYASE).	63	41	1242
287	2	738	1733	gi|405133	putative [Bacillus subtilis]	63	38	996
295	1	2	748	gi|1239983	hypothetical protein [Bacillus subtilis]	63	41	747
328	3	2148	3134	gi|45302	carrier protein (AA 1 - 437) [Pseudomonas aeruginosa] ir|S11497|S11497 branched-chain amino acid transport protein braB - eudomonas aeruginosa	63	36	987
362	2	1626	1216	sp|P35136|SERA_	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95) (PGDH).	63	38	411
404	1	326	1051	gi|1303816	YqeZ [Bacillus subtilis]	63	35	726
405	3	2101	1715	gi|1303914	YqhY [Bacillus subtilis]	63	42	387
406	1	451	227	gi|142152	sulfate permease (gtg start codon) [Synechococcus PCC6301] pir|A30301|GRYCS7 sulfate transport protein - Synechococcus sp. PCC 7942)	63	43	225
415	2	1048	2718	gi|1205402	transport ATP-binding protein [Haemophilus influenzae]	63	41	1671
426	4	3575	2679	gi|393268	29-kiloDalton protein [Streptococcus pneumoniae] sp|P42362|P29K_STRPN 29 KD MEMBRANE PROTEIN IN PSAA 5'REGION ORF1).	63	39	897
505	3	1347	2195	gi|1418999	orf4 [Lactobacillus sake]	63	40	849
507	1	2	574	gi|546917	comK [Bacillus subtilis, E26, Peptide, 192 aa]	63	35	573
562	2	146	1084	gi|43985	nifS-like gene [Lactobacillus delbrueckii]	63	45	939
675	1	427	215	gi|1510994	serine aminotransferase [Methanococcus jannaschii]	63	29	213
686	1	3	230	gi|517356	nitrate reductase (NADH) [Lotus japonicus]	63	52	228
701	1	3	392	gi|881940	NorQ protein [Paracoccus denitrificans]	63	41	390
720	1	2	400	gi|47168	open reading frame (Streptomyces lividans)	63	35	399
779	1	571	287	gi|1261932	unknown [Mycobacterium tuberculosis]	63	41	285
907	1	22	321	gi|149445	ORF1 [Lactococcus lactis]	63	27	300
972	1	794	399	gi|1511235	M. jannaschii predicted coding region MJ1232 [Methanococcus jannaschii]	63	27	396
1085	1	1154	618	gi|1204277	hypothetical protein (GB:U00019_14) [Haemophilus influenzae]	63	38	537
1094	1	3	542	gi|790943	urea amidolyase [Bacillus subtilis]	63	39	540
1108	1	3	482	pir|S49892|S498	regulation protein - Bacillus subtilis	63	44	480
1113	1	1231	617	gi|493017	endocarditis specific antigen [Enterococcus faecalis]	63	45	615

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
1300	1	3	695	|sp|P33940|YOJH_	HYPOTHETICAL 54.3 KD PROTEIN IN ECO-ALKB INTERGENIC REGION.	63	46	693
1325	1	1	204	|gi|928989	p100 protein (Borrelia burgdorferi)	63	30	204
1814	1	3	245	|gi|1303914	YqhY (Bacillus subtilis)	63	34	243
2021	1	498	250	|pir|C33496|C334	hisC homolog - Bacillus subtilis	63	46	249
2325	1	2	193	|gi|436132	|product is similar to TnpA of transposon Tn554 from Staphylococcus aureus (Clostridium butyricum)	63	40	192
2335	1	1	195	|gi|1184298	flagellar MS-ring protein (Borrelia burgdorferi)	63	47	195
2406	1	451	227	|gi|1041785	rhoptry protein (Plasmodium yoelii)	63	33	225
2961	2	136	360	|gi|312443	carbamoyl-phosphate synthase (glutamine-hydrolysing) (Bacillus aldolyticus)	63	52	225
2965	1	1	402	|gi|1407784	orf-1; novel antigen (Staphylococcus aureus)	63	50	402
2987	1	583	293	|gi|1224069	amidase (Moraxella catarrhalis)	63	35	291
2994	1	266	135	|gi|836646	phosphoribosylformimino-praic ketoisomerase (Rhodobacter phaeroides)	63	51	132
3043	1	440	252	|gi|1480237	phenylacetaldehyde dehydrogenase (Escherichia coli)	63	40	189
3078	1	609	400	|gi|1487982	intrinsic membrane protein (Mycoplasma hominis)	63	36	210
3139	1	2	217	|gi|439126	glutamate synthase (NADPH) (Azospirillum brasilense) pir|A49916|A49916 glutamate synthase (NADPH) (EC 1.4.1.13) - zospirillum brasilense	63	47	216
1625	1	791	198	|gi|623073	ORF160; putative (Bacteriophage LL-H)	63	48	396
3658	1	1	399	|gi|1303697	YrkA (Bacillus subtilis)	63	37	399
3659	1	3	395	|gi|1256135	YbbF (Bacillus subtilis)	63	48	393
3783	1	720	361	|gi|1256902	Pyruvate decarboxylase isozyme 2 (Swiss Prot. accession number P16467) (Saccharomyces cerevisiae)	63	34	360
3900	1	338	171	|sp|P10537|AMYB_	BETA-AMYLASE (EC 3.2.1.2) (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE).	63	54	168
4309	1	3	176	|pir|A37967|A379	neural cell adhesion molecule Ng-CAM precursor - chicken	63	57	174
4367	1	1	195	|gi|1121932	Por6p gene product (Pichia pastoris)	63	30	195
4432	1	1	312	|gi|151259	|HMG-CoA reductase (EC 1.1.1.88) (Pseudomonas mevalonii) pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC.1.1.1.88) Pseudomonas sp.	63	51	312
4468	1	6	308	|gi|296464	ATPase (Lactococcus lactis)	63	36	303
33	3	1411	2400	|gi|153675	tagatose 6-P kinase (Streptococcus mutans)	62	44	990
36	9	5985	6218	|gi|1490521	DHSH3 (Homo sapiens)	62	51	234

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
37	1	2	721	gi|1107531	ceuE gene product (Campylobacter coli)	62	33	720
38	15	10912	11589	gi|1222058	H. influenzae predicted coding region HIN1279 (Haemophilus influenzae)	62	38	678
38	25	19526	20329	gi|695280	ORF2 (Alcaligenes eutrophus)	62	41	804
57	2	2523	1780	gi|171234	orf1 (Haemophilus influenzae)	62	55	744
57	9	6646	6350	gi|508174	EIIB domain of PTS-dependent Gat transport and phosphorylation Escherichia coli	62	35	297
58	1	2	559	gi|755152	highly hydrophobic integral membrane protein (Bacillus subtilis) sp|P42953|TAGG_BACSU TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN AGG.	62	34	558
67	10	8250	9014	gi|470683	Shows similarity with ATP-binding proteins from other ABC-transport perons. Swiss Prot Accession Numbers P24137, P08007, P04285, P24136 Escherichia coli	62	34	765
69	8	8315	7494	gi|46816	actVA 4 gene product (Streptomyces coelicolor)	62	44	822
80	3	1793	1320	gi|39993	UDP-N-acetylmuramoylalanine--D-glutamate ligase (Bacillus subtilis)	62	43	474
87	7	7034	9205	gi|217191	5'-nucleotidase precursor (Vibrio parahaemolyticus)	62	48	2172
100	3	4051	3089	gi|1511047	phosphoglycerate dehydrogenase (Methanococcus jannaschii)	62	42	963
102	1	2	520	gi|153655	mismatch repair protein (Streptococcus pneumoniae) pir|C28667|C28667 DNA mismatch repair protein hexA - Streptococcus neumoniae	62	34	519
112	2	466	1068	gi|153741	ATP-binding protein (Streptococcus mutans)	62	37	603
114	7	6855	7562	gi|1204866	L-fucose operon activator (Haemophilus influenzae)	62	38	708
116	4	6823	5633	gi|677947	AppC (Bacillus subtilis)	62	37	1191
124	8	6855	6004	gi|853777	product similar to E.coli PRFA2 protein (Bacillus subtilis) pir|S55438|S55438 ywkE protein - Bacillus subtilis sp|P45873|HEMK_BACSU POSSIBLE PROTOPORPHYRINOGEN OXIDASE (EC .3.3.-).	62	44	852
148	1	24	554	gi|467456	unknown (Bacillus subtilis)	62	50	531
149	20	7591	6725	gi|1205807	replicative DNA helicase (Haemophilus influenzae)	62	41	867
163	3	1503	1153	gi|40067	X gene product (Bacillus sphaericus)	62	42	351
164	15	14673	15632	gi|42219	P35 gene product (AA 1 - 314) (Escherichia coli)	62	38	960
165	2	1166	1447	gi|403936	phenylalanyl-tRNA synthetase alpha subunit (Gly294 variant) unidentified cloning vector)	62	38	282
166	2	2084	5089	gi|308861	GTG start codon (Lactococcus lactis)	62	44	3006
171	1	1225	614	gi|1046053	hypothetical protein (SP:P32049) (Mycoplasma genitalium)	62	41	612

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
181	1	2521	1310	gi|143045	hemY (Bacillus subtilis)	62	45	1212
200	1	3	956	gi|142439	ATP-dependent nuclease (Bacillus subtilis)	62	32	954
237	2	935	1966	gi|41695	hisC protein (Escherichia coli)	62	44	1032
261	3	4008	2605	gi|143121	ORF A; putative (Bacillus firmus)	62	42	1404
299	8	4477	4719	gi|467441	expressed at the end of exponential growyh under condtions in which he enzymes of the TCA cycle are repressed (Bacillus subtilis) gi|467441 expressed at the end of exponential growyh under ondtions in which the enzymes of the TCA cycle are repressed Bacil	62	47	243
304	6	5018	3819	gi|153015	FemA protein (Staphylococcus aureus)	62	43	1200
324	1	2	262	gi|142717	cytochrome aa3 controlling protein (Bacillus subtilis) pir|A33960|A33960 cta protein - Bacillus subtilis sp|P12946|CTAA_BACSU CYTOCHROME AA3 CONTROLLING PROTEIN.	62	30	261
325	2	269	1207	gi|581088	methionyl-tRNA formyltransferase (Escherichia coli)	62	39	939
332	6	4894	4631	gi|1499960	uridine 5'-monophosphate synthase (Methanococcus jannaschii)	62	36	264
355	1	2	370	gi|145925	fecB (Escherichia coli)	62	32	369
365	8	6628	6804	gi|413943	ipa-19d gene product (Bacillus subtilis)	62	54	177
369	2	2744	1626	pir|A43577|A435	regulatory protein pfoR - Clostridium perfringens	62	42	1119
370	1	34	264	gi|40665	beta-glucosidase (Clostridium thermocellum)	62	37	231
415	3	2709	3176	gi|1205401	transport ATP-binding protein (Haemophilus influenzae)	62	35	468
429	1	1578	790	gi|1046024	Na+ ATPase subunit J (Mycoplasma genitalium)	62	40	789
444	2	704	1369	gi|581510	nodulation gene; integral membrane protein; homology to Rhizobium eguminosarum nodI (Rhizobium loti)	62	37	666
477	2	751	1869	pir|A48440|A484	ring-infected erythrocyte surface antigen 2, RESA-2 - Plasmodium falciparum	62	44	1119
485	1	241	1707	gi|17934	betaine aldehyd dehydrogenase (Beta vulgaris)	62	43	1467
487	3	1141	1311	gi|149445	ORF1 (Lactococcus lactis)	62	31	171
494	2	1134	1313	gi|166835	ribulose bisphosphate carboxylase/oxygenase activase (Arabidopsis haliona)	62	37	180
518	1	193	882	gi|153491	O-methyltransferase (Streptomyces glaucescens)	62	39	690
534	2	369	2522	gi|1480429	putative transcriptional regulator (Bacillus stearothermophilus)	62	35	2154
551	6	4371	4820	gi|511113	ferric uptake regulation protein (Campylobacter jejuni)	62	37	450
574	1	1	570	gi|153000	enterotoxin B (Staphylococcus aurous)	62	43	570

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
590	2	344	1171	gi|40367	[ORFC [Clostridium acetobutylicum]	62	37	828
655	1	396	830	gi|147195	[phnB protein [Escherichia coli]	62	44	435
656	1	2	478	gi|1205451	[cell division inhibitor [Haemophilus influenzae]	62	36	477
676	1	692	348	gi|1511613	[methyl coenzyme M reductase system, component A2 [Methanococcus jannaschii]	62	36	345
687	1	493	248	gi|49272	[Asparaginase [Bacillus licheniformis]	62	48	246
700	2	267	944	gi|1205822	[hypothetical protein (GB:X75627_4) [Haemophilus influenzae]	62	40	678
840	2	1715	1041	gi|1045865	[M. genitalium predicted coding region MG181 [Mycoplasma genitalium]	62	36	675
864	4	898	1491	gi|1144332	[deoxyuridine nucleotidohydrolase [Homo sapiens]	62	38	594
916	1	35	400	gi|413931	[ipa-7d gene product [Bacillus subtilis]	62	45	366
1071	1	1	771	gi|1510649	[aspartokinase I [Methanococcus jannaschii]	62	40	771
1084	1	19	609	gi|688011	[Agx-1 antigen [human, infertile patient, testis, Peptide, 505 aa]	62	39	591
1103	1	3	203	gi|581261	[ORF homologous to E.coli motB [Herpetosiphon aurantiacus] pir|S14030|S14030 [Hypothetical protein - Herpetosiphon aurantiacus (fragment)]	62	51	201
1217	1	463	233	gi|460025	[ORF2, putative [Streptococcus pneumoniae]	62	41	231
1533	1	644	414	gi|413968	[ipa-44d gene product [Bacillus subtilis]	62	44	231
1537	1	3	257	gi|1510641	[alanyl-tRNA synthetase [Methanococcus jannaschii]	62	29	255
2287	1	3	161	gi|485956	[mycC gene product [Proteus mirabilis]	62	45	159
2386	1	3	245	gi|285708	[nontoxic component [Clostridium botulinum]	62	31	243
2484	1	331	167	gi|142092	[DNA-repair protein (recA) [Anabaena variabilis]	62	35	165
2490	1	798	400	gi|581648	[epiB gene product [Staphylococcus epidermidis]	62	42	399
3016	1	596	300	gi|710022	[uroporphyrinogen III [Bacillus subtilis]	62	51	297
3116	1	1	213	gi|466883	[nifS; B1496_C2_193 [Mycobacterium leprae]	62	44	213
3297	1	823	413	gi|475715	[acetyl coenzyme A acetyltransferase (thiolase) [Clostridium cetobutylicum]	62	42	411
3609	1	31	276	gi|1408501	[homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus [Bacillus subtilis]	62	48	246
3665	2	584	402	gi|151259	[HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir[A44756]A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	62	40	183
3733	1	3	374	gi|1352197	[thioredoxin reductase [Eubacterium acidaminophilum]	62	42	372

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3898	1	1	237	gi|153675	tagatose 6-P kinase (Streptococcus mutans)	62	45	237
4027	1	283	143	gi|330705	homologue to gene 30 (aa 1-59); putative (Bovine herpesvirus 4)	62	43	141
4109	1	727	365	gi|41748	hsdN protein (AA 1-520) (Escherichia coli)	62	45	363
4303	1	1	303	gi|1303813	YqeW (Bacillus subtilis)	62	43	303
4380	1	530	267	gi|1215684	mevalonate pyrophosphate decarboxylase (Saccharomyces cerevisiae)	62	55	264
4494	1	2	256	gi|510692	enterotoxin H (Staphylococcus aureus)	62	34	255
4598	1	411	223	gi|763513	ORF4; putative (Streptomyces violaceoruber)	62	45	189
4624	1	1	222	gi|41748	hsdM protein (AA 1-520) (Escherichia coli)	62	45	222
5	5	4288	3912	gi|928831	ORF95; putative (Lactococcus lactis phage BK5-T)	61	36	357
11	1	320	162	pir|C33356|C333	prothymosin alpha homolog (clone 32) - human (fragment)	61	33	159
16	11	10991	11938	gi|1205391	hypothetical protein (SP:P33995) (Haemophilus influenzae)	61	44	948
32	1	281	801	gi|1066504	exo-beta 1,3 gluconase (Cochliobolus carbonum)	61	50	519
38	3	616	1107	gi|510864	glutamine transport ATP-binding protein Q (Methanococcus jannaschii)	61	41	492
45	4	3082	4038	gi|1109686	ProX (Bacillus subtilis)	61	45	957
48	8	7118	7504	gi|498839	ORF2 (Clostridium perfringens)	61	33	387
51	9	4605	5570	gi|388269	traC (Plasmid pAD1)	61	42	966
60	6	1689	2243	gi|1205893	hypothetical protein (GB:U00011_3) (Haemophilus influenzae)	61	32	555
62	9	5559	5122	gi|854656	Na/H antiporter system ORF2 (Bacillus alcalophilus)	61	38	438
67	5	4330	5646	gi|466612	nikA (Escherichia coli)	61	36	1317
74	2	2400	1504	gi|1204846	carbamate kinase (Haemophilus influenzae)	61	40	897
85	1	2198	1101	gi|1498756	amidophosphoribosyltransferase PurF (Rhizobium etli)	61	41	1098
86	4	1995	1582	gi|1499931	M. jannaschii predicted coding region MJ1083 (Methanococcus jannaschii)	61	44	414
97	1	74	649	gi|1518679	orf (Bacillus subtilis)	61	44	576
99	2	2454	1990	gi|413958	lpa-3dd gene product (Bacillus subtilis)	61	38	465
124	7	6223	5123	gi|556881	Similar to Saccharomyces cerevisiae SUA5 protein (Bacillus subtilis) pir|S49358|S49358 ipc-29d protein - Bacillus subtilis sp|P39153|YMLC_BACSU HYPOTHETICAL 37.0 KD PROTEIN IN SPOIIR-GLYC INTERGENIC REGION.	61	46	1101
125	4	1668	2531	gi|1491643	ORFA gene product (Chloroflexus aurantiacus)	61	43	864

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
132	1	1250	627	pir|PQ0259|PQ02	hypothetical protein I - Enterococcus faecalis plasmid pAM-beta-1 (fragment)	61	43	624
149	9	3617	3075	gi|1144332	deoxyuridine nucleotidohydrolase (Homo sapiens)	61	40	543
149	22	8690	7869	gi|160047	p101/acidic basic repeat antigen (Plasmodium falciparum) pir|A29232|A29232 101K malaria antigen precursor - Plasmodium alciparum (strain Camp)	61	35	822
168	3	1915	2361	gi|1499694	HIT protein, member of the HIT-family (Methonococcus jannaschii)	61	41	447
171	9	9675	7948	gi|467446	similar to SpoVB (Bacillus subtilis)	61	38	1728
174	3	1042	2340	gi|216374	glutaryl 7-ACA acylase precursor (Bacillus laterosporus)	61	49	1299
190	4	5034	4111	gi|409286	bmrU (Bacillus subtilis)	61	37	924
216	1	2	190	gi|415861	eukaryotic initiation factor 2 beta (eIF-2 beta) (Oryctolagus uniculus)	61	29	189
227	7	4161	5048	gi|216341	ORF for methionine amino peptidase (Bacillus subtilis)	61	41	888
238	4	1959	3047	gi|409543	CbrC protein (Erwinia chrysanthemi)	61	38	1089
247	1	2	694	gi|537231	ORF_f579 (Escherichia coli)	61	38	693
247	2	678	1034	gi|142226	chvD protein (Agrobacterium tumefaciens)	61	40	357
257	2	3523	2627	gi|699379	glvr-1 protein (Mycobacterium leprae)	61	40	897
268	2	3419	3051	gi|40364	ORFA1 (Clostridium acetobutylicum)	61	41	369
275	4	4621	4827	gi|1204848	hypothetical protein (GP:H87049_57) (Haemophilus influenzae)	61	36	207
277	1	1	1845	gi|784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	45	1845
278	9	8003	7032	gi|467462	cysteine synthetase A (Bacillus subtilis)	61	43	972
278	10	9878	8535	gi|1205919	Na+ and Cl- dependent gamma-aminobutryic acid transporter (Haemophilus influenzae)	61	38	1344
283	1	1	366	gi|755607	polyA polymerase (Bacillus subtilis)	61	36	366
288	2	1918	1496	gi|388108	cell wall enzyme (Enterococcus faecalis)	61	43	423
291	1	86	334	gi|454265	FBP3 (Petunia hybrida)	61	38	249
318	1	1104	694	gi|290531	similar to beta-glucoside transport protein (Escherichia coli) sp|P31451|PTIB_ECOLI PTS SYSTEM, ARBUTIN-LIKE IIB COMPONENT PHOSPHOTRANSFERASE ENZYME II, B COMPONENT) (EC 2.7.1.69).	61	47	411
330	2	1912	1190	gi|1001805	hypothetical protein (Synechocystis sp.)	61	41	723

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name ( )	% sim	% ident	length (nt)
385	2	1513	1025	gi|533098	DnaD protein (Bacillus subtilis)	61	42	489
426	1	794	399	gi|1303853	YqqF (Bacillus subtilis)	61	44	396
438	3	810	1421	gi|1293660	AbaA2 (Streptomyces coelicolor)	61	36	612
454	1	1580	792	gi|733522	phosphatidylinositol-4,5-diphosphate 3-kinase (Dictyostelium isoldoum)	61	30	789
464	2	784	560	gi|1122120	(C53)37.5 gene product (Caenorhabditis elegans)	61	38	225
470	8	6077	7357	gi|623073	ORF360; putative (Bacteriophage LL-H)	61	47	1281
509	1	554	279	gi|467484	unknown (Bacillus subtilis)	61	45	276
555	3	1916	1296	gi|141800	anthranilate synthase glutamine amidotransferase (Acinetobacter alcoaceticus)	61	42	621
569	1	1711	857	gi|467090	B2235_C2_195 (Mycobacterium leprae)	61	47	855
585	2	961	803	sp|P36686|SURE_	SURVIVAL PROTEIN SURE HOMOLOG (FRAGMENT).	61	33	159
592	3	1694	1422	gi|1221602	Immunity repressor protein (Haemophilus influenzae)	61	32	273
603	1	43	357	gi|507738	Hmp (Vibrio parahaemolyticus)	61	33	315
669	1	2467	1235	gi|1146243	22.4% identity with Escherichia coli DNA-damage inducible protein ...; putative (Bacillus subtilis)	61	37	1233
675	3	805	1101	gi|403373	glycerophosphoryl diester phosphodiesterase (Bacillus subtilis) pir|S37251|S37251 glycerophosphoryl diester phosphodiesterase - acillus subtilis	61	36	297
703	1	1656	829	gi|537181	ORF_f470 (Escherichia coli)	61	32	828
728	1	1628	816	gi|806281	DNA polymerase I (Bacillus stearothermophilus)	61	39	813
821	1	61	318	gi|709992	hypothetical protein (Bacillus subtilis)	61	38	258
856	2	2313	1567	gi|609310	portal protein gp3 (Bacteriophage HK97)	61	40	747
923	1	1081	542	gi|143213	putative (Bacillus subtilis)	61	38	540
1124	1	59	370	gi|1107541	(C)3D9.8 (Caenorhabditis elegans)	61	26	312
1492	1	548	276	gi|406397	unknown (Mycoplasma genitalium)	61	32	273
1602	1	46	318	gi|733522	phosphatidylinositol-4,5-diphosphate 3-kinase (Dictyostelium isoldeus)	61	34	273
2500	1	577	290	gi|1045964	hypothetical protein (GB:U14003_297) (Mycoplasma genitalium)	61	31	288
2968	1	2	808	gi|397526	clumping factor (Staphylococcus aureus)	61	55	807
3076	1	3	248	gi|1169373	ORF 1 (Lactococcus lactis)	61	41	246

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3609	2	207	401	gi|1408501	homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus (Bacillus subtilis)	61	39	195
3662	1	1477	740	gi|1303813	YqeW (Bacillus subtilis)	61	42	738
3672	1	2	442	gi|784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	50	441
3724	1	2	220	gi|1009366	Respiratory nitrate reductase (Bacillus subtilis)	61	41	219
3728	1	3	398	gi|677943	AppD (Bacillus subtilis)	61	46	396
3884	1	3	401	gi|784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	47	399
3971	1	3	383	gi|784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	45	381
4038	1	661	359	gi|13399?0	large subunit of NADH-dependent glutamate synthase (Plectonema boryanum)	61	24	303
4041	1	546	274	gi|413953	ipa-29d gene product (Bacillus subtilis)	61	48	273
4047	1	1	402	gi|528991	unknown (Bacillus subtilis)	61	42	402
4102	1	1	345	gi|976025	HrsA (Escherichia coli)	61	46	345
4155	1	1	336	gi|784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	50	336
4268	1	463	233	gi|450688	hsdM gene of EcoprrI gene product (Escherichia coli) pir|S30037|S30037 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	61	38	231
4374	1	542	273	gi|784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	50	270
4389	1	2	172	gi|147516	ribokinase (Escherichia coli)	61	35	171
4621	1	2	268	gi|784897	beta-N-acetylhexosaminidase (Streptococcus pneumoniae) pir|A56390|A56390 mannosyl-glycoprotein ndo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - treptococcus pneumoniae	61	47	267
4663	1	27	227	gi|976025	HrsA (Escherichia coli)	61	50	201
4	6	6663	5536	gi|1408501	homologous to N-acyl-L-amino acid amidohydrolase of Bacillus stearothermophilus (Bacillus subtilis)	60	43	1128

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
11	6	3426	3725	gi|410748	ring-infected erythrocyte surface antigen [Plasmodium falciparum] pir|A25526|A25526 ring-infected erythrocyte surface antigen precursor - Plasmodium falciparum (strain FC27/Papua New Guinea) sp|P13830|RESA_PLAFF RING-INFECTED ERYTHROCYTE SURFACE ANTIGEN RE	60	24	300
11	14	11035	10313	gi|1217651	carbonyl reductase (NADPH) [Rattus norvegicus]	60	28	723
16	12	11917	12930	gi|1001453	hypothetical protein [Synechocystis sp.]	60	37	1014
33	1	26	469	gi|388109	regulatory protein [Enterococcus faecalis]	60	41	444
37	13	10414	9834	gi|1336656	OrfI [Bacillus subtilis]	60	40	981
39	4	4364	4522	gi|4872	ORF 4 [Saccharomyces kluyveri]	60	47	159
41	1	2047	1025	gi|142822	D-alanine racemase cds [Bacillus subtilis]	60	39	1023
43	4	2474	3607	gi|468046	para-nitrobenzyl esterase [Bacillus subtilis]	60	40	1134
44	10	6756	7769	gi|414234	thiF [Escherichia coli]	60	52	1014
45	10	8874	9074	gi|343949	var1(40.0) [Saccharomyces cerevisiae]	60	44	201
56	18	27842	26430	gi|468764	mocR gene product [Rhizobium meliloti]	60	35	1413
60	2	173	388	gi|1303864	YqgQ [Bacillus subtilis]	60	33	216
63	2	357	1619	gi|467124	ureD; B229_C1_234 [Mycobacterium leprae]	60	43	1263
69	1	787	395	gi|518853	OafA [Salmonella typhimurium]	60	36	393
88	1	1	1188	gi|1480429	putative transcriptional regulator [Bacillus stearothermophilus]	60	30	1188
92	6	4735	3881	gi|349227	transmembrane protein [Escherichia coli]	60	37	855
92	7	5996	4923	gi|466613	nikB [Escherichia coli]	60	38	1074
93	1	949	476	gi|1510925	coenzyme F420-reducing hydrogenase, beta subunit [Methanococcus jannaschii]	60	27	474
96	6	7866	7618	gi|972715	hypothetical protein [Mycobacterium paratuberculosis]	60	30	213
98	6	3212	4069	gi|467425	unknown [Bacillus subtilis]	60	42	858
102	10	7158	7430	gi|143092	acetolactate synthase small subunit [Bacillus subtilis] sp|P37252|ILVN_BACSU ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC 4.1.3.18) (ALAS) (ACETOHYDROXY-ACID SYNTHASE SMALL SUBUNIT) (ALS).	60	37	273
109	11	9127	10515	gi|1255259	o-succinylbenzoic acid (OSB) CoA ligase [Staphylococcus aureus]	60	28	1389
109	12	10499	11656	gi|141954	beta-ketothiolase [Alcaligenes eutrophus]	60	41	1158
119	2	4630	3134	gi|524280	unknown [Mycobacterium tuberculosis]	60	45	1497

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
121	9	6957	7646	gi|1107529	ceuC gene product (Campylobacter coli)	60	35	690
140	7	7704	6013	gi|146547	kdpA (Escherichia coli)	60	45	1692
145	1	2	703	gi|1460077	unknown (Mycobacterium tuberculosis)	60	23	702
150	3	2809	2216	gi|1146230	putative (Bacillus subtilis)	60	40	594
157	2	1389	961	gi|1303975	YqjX (Bacillus subtilis)	60	30	429
158	5	5125	4769	gi|1449288	unknown (Mycobacterium tuberculosis)	60	36	357
159	1	511	257	gi|580932	murD gene product (Bacillus subtilis)	60	43	255
160	1	159	1187	gi|1204532	hypothetical protein (GB:L19201_29) (Haemophilus influenzae)	60	34	1029
161	14	8249	7866	gi|1496003	ORF3; PepV; putative oligoendopeptidase based on homology with Lactococcus lactis PepF (GenBank Accession Number Z32522) (Caldicellulosiruptor saccharolyticus)	60	34	384
172	3	1331	2110	gi|485280	28.2 kDa protein (Streptococcus pneumoniae)	60	33	780
173	2	4082	2460	gi|1524397	glycine betaine transporter OpuD (Bacillus subtilis)	60	41	1623
173	4	5963	4953	gi|1100737	NADP dependent leukotriene b4 12-hydroxydehydrogenase (Sus scrofa)	60	44	1011
198	1	3	995	gi|413943	ipa-19d gene product (Bacillus subtilis)	60	42	993
201	4	3641	4573	sp|P37028|YADT_	HYPOTHETICAL 29.4 KD PROTEIN IN HEML-PFS INTERGENIC REGION PRECURSOR.	60	37	933
203	1	3269	2415	gi|927798	D9719.34p; CAI: 0.14 (Saccharomyces cerevisiae)	60	43	855
206	9	12234	12515	sp|P37347|YECD_	HYPOTHETICAL 21.8 KD PROTEIN IN ASPS 5'REGION.	60	47	282
212	4	1213	1410	gi|332711	hemagglutinin-neuraminidase fusion protein (Human parainfluenza irus 3)	60	34	198
214	1	65	1153	gi|1204366	hypothetical protein (GB:U14003_130) (Haemophilus influenzae)	60	36	1089
237	1	2	937	gi|149377	HisD (Lactococcus lactis)	60	40	936
241	6	5696	4998	gi|1046160	hypothetical protein (GB:U00021_5) (Mycoplasma genitalium)	60	37	699
260	6	5919	6485	gi|431950	similar to a B.subtilis gene (GB: BACHEMEHY_5) (Clostridium asteurianum)	60	35	567
264	1	2432	1218	gi|397526	clumping factor (Staphylococcus aureus)	60	53	1215
267	1	3	1409	gi|148316	NaH-antiporter protein (Enterococcus hirae)	60	27	1407
275	3	3804	4595	pir|F36AR9|F368	leuD 3'-region hypothetical protein - Lactococcus lactis subsp. lactis (strain IL1403)	60	35	792
291	3	860	1198	gi|1208889	coded for by C. elegans cDNA yk130e12.5; contains C2H2-type zinc fingers (Caenorhabditis elegans)	60	33	339

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
307	6	3421	3176	gi|1070014	protein-dependent [Bacillus subtilis]	60	36	246
316	8	4957	5823	gi|413952	ipa-28d gene product [Bacillus subtilis]	60	41	867
328	4	2996	3484	gi|1204484	membrane-associated component, branched amino acid transport system [Haemophilus influenzae]	60	39	489
332	5	4887	4363	gi|1205449	colicin V production protein (pur regulon) [Haemophilus influenzae]	60	37	525
357	1	1062	532	gi|887842	single-stranded DNA-specific exonuclease [Escherichia coli]	60	41	531
375	2	96	362	gi|1057	adenylyl cyclase gene product [Saccharomyces kluyveri] r|JQ1145|OYBYK adenylate cyclase (EC 4.6.1.1) - yeast ccharomyces kluyveri]	60	47	267
397	1	66	416	gi|709999	Glucarate dehydratase [Bacillus subtilis]	60	37	351
409	1	2	163	gi|499700	glycogen phosphorylase [Saccharomyces cerevisiae]	60	35	162
453	4	914	1237	gi|1196899	unknown protein [Staphylococcus aureus]	60	36	324
453	7	3838	3620	sp|P12222|YCF1_	HYPOTHETICAL 226 KD PROTEIN (ORF 1901).	60	31	219
470	2	622	945	pir|S30702|S307	integrin homolog - yeast (Saccharomyces cerevisiae)	60	31	324
500	1	118	606	gi|467407	unknown [Bacillus subtilis]	60	36	489
503	3	752	982	gi|167835	myosin heavy chain [Dictyostelium discoideum]	60	34	231
505	4	2238	3563	gi|1510732	NADH oxidase [Methanococcus jannaschii]	60	26	1326
523	1	3	1043	gi|143331	alkaline phosphatase regulatory protein [Bacillus subtilis] pir|A27650|A27650 regulatory protein phoR - Bacillus subtilis sp|P23545|PHOR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN HOR (EC 2.7.3.-).	60	41	1041
543	1	1	465	gi|1511103	cobalt transport ATP-binding protein O [Methanococcus jannaschii]	60	40	465
545	1	1	726	gi|1498192	putative [Pseudomonas aeruginosa]	60	40	726
556	1	2	1054	gi|1477402	tex gene product [Bordetella pertussis]	60	42	1053
578	1	974	489	gi|1205129	H. influenzae predicted coding region HI0882 [Haemophilus influenzae]	60	42	486
594	1	1	624	gi|1212755	adenylyl cyclase [Aeromonas hydrophila]	60	45	624
604	1	3	530	gi|145925	fecB [Escherichia coli]	60	42	528
620	1	926	465	gi|1205483	bicyclomycin resistance protein [Haemophilus influenzae]	60	33	462
630	2	871	1122	gi|1486242	unknown [Bacillus subtilis]	60	41	252
645	2	574	425	gi|1205136	serine hydroxymethyltransferase (serine methylase) [Haemophilus influenzae]	60	28	150

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% idant	length (nt)
684	1	1082	843	gi|1205538	hypothetical protein (GB:U14003_302) [Haemophilus influenzae]	60	39	240
786	1	967	485	gi|1402944	orfRM1 gene product [Bacillus subtilis]	60	46	483
844	1	588	346	gi|790943	urea amidolyase [Bacillus subtilis]	60	40	243
851	1	1	726	gi|159661	GMP reductase [Ascaris lumbricoides]	60	41	726
871	1	1746	874	gi|1001493	hypothetical protein [Synechocystis sp.]	60	39	873
896	1	1558	839	gi|604926	NADH dehydrogenase, subunit 5 [Schizophyllum commune] sp|P50368|NU5M_SCHCO NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC .6.5.3).	60	39	720
908	2	448	753	gi|662880	novel hemolytic factor [Bacillus cereus]	60	31	306
979	1	2	595	gi|1429255	putative; orf1 [Bacillus subtilis]	60	30	594
1078	1	669	502	gi|581055	inner membrane copper tolerance protein [Escherichia coli] gi|871029 disulphide isomerase like protein [Escherichia coli] pir|S47295|S47295 inner membrane copper tolerance protein - echerichia coli	60	40	168
1112	1	1150	620	gi|407885	ORF3 [Streptomyces griseus]	60	30	531
1135	1	484	275	gi|1171407	Vps8p [Saccharomyces cerevisiae]	60	36	210
1146	1	17	562	gi|1239981	hypothetical protein [Bacillus subtilis]	60	36	546
1291	1	716	360	pir|S57530|S575	carboxyl esterase - Acinetobacter calcoaceticus	60	30	357
1332	1	336	169	gi|1222056	aminotransferase [Haemophilus influenzae]	60	44	168
1429	1	3	146	gi|1205619	ferritin like protein [Haemophilus influenzae]	60	39	144
1722	1	570	286	gi|240052	dihydroflavonol-4-reductase, DFR [Hordeum vulgare=barley, cv. Gula, optido, 354 aa]	60	36	285
2350	1	385	200	gi|497626	ORF 1 [Plasmid pAQ1]	60	20	186
2936	1	519	310	gi|508981	prephenate dehydratase [Bacillus subtilis]	60	48	210
3027	1	568	302	gi|1146199	putative [Bacillus subtilis]	60	37	267
3084	1	20	208	gi|1407784	orf-1; novel antigen [Staphylococcus aureus]	60	51	189
3155	1	2	226	gi|1046097	cytadherence-accessory protein [Mycoplasma genitalium]	60	34	225
3603	1	368	186	gi|510108	mitochondrial long-chain enoyl-CoA hydratase/3-hydroxycyl-CoA dehydrogenase alpha-subunit [Rattus norvegicus]	60	42	183
3665	1	486	244	gi|151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii] pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	60	42	243
3747	1	3	146	gi|474192	iucC gene product [Escherichia coli]	60	36	144

TABLE 2

S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3912	1	3	335	gi|488695	noval antigen; orf-2 [Staphylococcus aureus]	60	44	333
4072	1	3	272	gi|405879	yeiH [Escherichia coli]	60	33	270
4134	1	510	352	gi|780656	chemoreceptor protein [Rhizobium leguminosarum bv. viciae] gi|780656 chemoreceptor protein (Rhizobium leguminosarum bv. iciae)	60	28	159
4207	2	677	402	gi|602031	similar to trimethylamine DH [Mycoplasma capricolum] pir|S49950|S49950 probable trimethylamine dehydrogenase (EC 1.5.99.7) - Mycoplasma capricolum (SGC3) (fragment)	60	41	276
4243	1	127	324	gi|859317	peptide synthetase module [Microcystis aeruginosa] pir|S49111|S49111 probable amino acid activating domain - Microcystis aeruginosa (fragment) (SUB 144-528)	60	42	198
4310	1	624	313	gi|308980	phaB [Bacillus subtilis]	60	28	312
4345	1	343	173	gi|510108	mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit [Rattus norvegicus]	60	42	171
4382	1	498	280	gi|47382	acyl-CoA-dehydrogenase [Streptomyces purpuracons]	60	48	219
4474	1	53	223	gi|510108	mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit [Rattus norvegicus]	60	42	171
23	4	4518	3523	gi|426446	VipB protein [Salmonella typhi]	59	39	996
33	2	707	1483	pir|S48604|S486	hypothetical protein - Mycoplasma capricolum (SGC3) (fragment)	59	33	777
33	5	4651	5853	gi|6721	F59B2.3 [Caenorhabditis elegans]	59	33	1203
17	2	1328	2299	gi|143813	ORF2 [Bacillus subtilis]	59	37	910
38	21	16784	16593	gi|912576	BIP [Phaeodactylum tricornutum]	59	40	192
52	3	2648	2349	gi|536972	ORF_o90a [Escherichia coli]	59	44	300
54	12	14181	13402	gi|483940	transcription regulator [Bacillus subtilis]	59	37	780
57	3	4397	3339	gi|508176	Gat-1-P-DH, NAD dependent [Escherichia coli]	59	40	1059
66	1	986	495	gi|1303901	YqhT [Bacillus subtilis]	59	34	492
67	7	6552	7460	gi|912461	nlkC [Escherichia coli]	59	37	909
70	7	5383	6366	gi|1399822	PhoD precursor [Rhizobium meliloti]	59	46	984
78	1	1	1449	gi|971345	unknown, similar to E.coli cardiolipin synthase [Bacillus subtilis] sp|P45860|YWIE_BACSU HYPOTHETICAL 58.2 PROTEIN IN NARI-ACDA INTERGENIC REGION.	59	39	1449
82	10	14329	15534	gi|490328	LORF F [unidentified]	59	44	1206

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
89	2	1602	958	gi|642801	unknown (Saccharomyces cerevisiae)	59	32	645
96	4	4940	5473	gi|1333802	protein of unknown function (Rhodobacter capsulatus)	59	33	534
98	1	2	820	gi|467421	similar to B. subtilis DnaH (Bacillus subtilis)	59	34	819
119	1	166	1557	gi|143122	ORF B; putative (Bacillus firmus)	59	36	1392
120	10	6214	6756	gi|15354	ORF 55.9 (Bacteriophage T4)	59	39	543
120	16	12476	13510	gi|1086575	BotA (Rhizobium meliloti)	59	44	1035
123	1	386	195	gi|984737	catalase (Campylobacter jejuni)	59	38	192
130	1	370	645	gi|1256634	25.8% identity over 120 aa with the Synenococcus sp. MpeV protein; putative (Bacillus subtilis)	59	31	276
131	4	5278	5712	gi|1510655	hypothetical protein (SP:P42297) (Methanococcus jannaschii)	59	39	435
164	1	3	509	gi|1001342	hypothetical protein (Synechocystis sp.)	59	41	507
164	4	1529	2821	gi|1205165	hypothetical protein (SP:P37764) (Haemophilus influenzae)	59	35	1293
164	19	19643	21376	gi|1001381	hypothetical protein (Synechocystis sp.)	59	34	1734
173	3	4727	3717	gi|1184121	auxin-induced protein (Vigna radiata)	59	50	1011
179	2	2218	1688	gi|143036	unidentified gene product (Bacillus subtilis)	59	33	531
195	12	12669	11503	gi|762778	NifS gene product (Anabaena azollae)	59	41	1167
201	5	4702	5670	gi|1510240	hemin permease (Methanococcus jannaschii)	59	32	969
201	7	5719	6315	gi|1511456	M. jannaschii predicted coding region MJ1437 (Methanococcus jannaschii)	59	34	597
209	1	102	461	gi|1204666	hypothetical protein (GB:X73124_53) (Haemophilus influenzae)	59	42	360
214	3	1050	2234	gi|551531	2-nitropropane dioxygenase (Williopsis saturnus)	59	36	1185
214	5	3293	4135	gi|1303709	YrkJ (Bacillus subtilis)	59	32	843
217	2	3381	2167	gi|290489	dfp (CG Site No. 18430) (Escherichia coli)	59	44	1215
237	5	3078	3785	gi|149382	HisA (Lactococcus lactis)	59	38	708
251	2	376	960	gi|1303791	YqeJ (Bacillus subtilis)	59	34	585
286	1	1621	812	gi|146551	transmembrane protein (kdpD) (Escherichia coli)	59	31	810
316	5	4978	3860	gi|405879	yoiH (Escherichia coli)	59	32	1119
370	3	600	761	gi|1303794	YqeH (Bacillus subtilis)	59	35	162

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% identity	length (nt)
382	1	1009	506	gi|547513	orf3 [Haemophilus influenzae]	59	34	504
391	3	1620	1273	gi|152901	ORF 3 [Spirochaeta aurantia]	59	37	348
406	3	2805	1705	gi|709992	hypothetical protein [Bacillus subtilis]	59	34	1101
426	5	3802	3245	gi|1204610	iron(III) dicitrate transport ATP-binding protein FECE [Haemophilus influenzae]	59	36	558
429	2	1513	1148	gi|1064809	homologous to sp:HTRA_ECOLI [Bacillus subtilis]	59	42	366
460	2	708	1301	gi|466882	ppsI; B1496_C2_189 [Mycobacterium leprae]	59	37	594
461	4	2212	3135	gi|1498295	homoserine kinase homolog [Streptococcus pneumoniae]	59	37	924
473	1	2929	1607	gi|147989	trigger factor [Escherichia coli]	59	40	1323
480	8	5862	6110	gi|1205311	(3R)-hydroxymyristol acyl carrier protein dehydrase [Haemophilus influenzae]	59	40	249
521	1	14	1354	pir|A25620|A256	staphylocoagulase - Staphylococcus aureus (fragment)	59	32	1341
534	4	2994	4073	gi|153746	mannitol-phosphate dehydrogenase [Streptococcus mutans] pir|C44798|C44798 mannitol-phosphate dehydrogenase MtlD - treptococcus mutans	59	36	1080
535	1	1	954	gi|1469939	group B oligopeptidase PepB [Streptococcus agalactiae]	59	33	954
551	3	2836	3186	gi|1204511	bacterioferritin comigratory protein [Haemophilus influenzae]	59	45	351
573	2	449	940	gi|386681	ORF YAL022 [Saccharomyces cerevisiae]	59	36	492
650	1	5	748	gi|396400	similar to eukaryotic Na+/H+ exchangers [Escherichia coli] sp|P32703|YJCE_ECOLI HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS NTERGENIC REGION (O549).	59	30	744
664	1	566	285	gi|1262748	LukF-PV like component [Staphylococcus aureus]	59	33	282
670	1	3	455	gi|1122758	unknown [Bacillus subtilis]	59	42	453
674	3	543	929	gi|293033	integrase [Bacteriophage phi-LC3]	59	46	387
758	1	349	176	gi|1500472	M. jannaschii predicted coding region MJ1577 [Methanococcus jannaschii]	59	37	174
771	2	2270	1461	gi|522150	bromoperoxidase BPO-A1 [Streptomyces aureofociens] sp|P33912|BPA1_STRAU NON-HAEM BROMOPEROXIDASE BPO-A1 (EC 1.11.1.-) BROMIDE PEROXIDASE) (BPO1). (SUB 2-275)	59	44	810
825	1	2191	1097	gi|397526	clumping factor (Staphylococcus aureus) .	59	47	1095
1052	2	1094	723	gi|289262	comE ORF3 [Bacillus subtilis]	59	36	372
1152	1	373	188	gi|1276668	ORF238 gene product [Porphyra purpurea]	59	37	186

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
1198	1	492	247	gi|142439	ATP-dependent nuclease (Bacillus subtilis)	59	26	246
1441	1	468	235	gi|1045942	glycyl-tRNA synthetase (Mycoplasma genitalium)	59	37	234
2103	1	1	186	gi|459250	triacylglycerol lipase (Galactomyces geotrichum)	59	33	186
2205	1	793	398	gi|1303794	YqeN (Bacillus subtilis)	59	38	396
2578	1	484	284	gi|258003	insulin-like growth factor binding protein complex acid-labile ubunit (rats, liver, Peptide, 603 aa)	59	48	201
2967	2	145	348	gi|1212730	YqhK (Bacillus subtilis)	59	44	204
3012	1	3	248	gi|773571	neurofilament protein NF70 (Helix aspersa)	59	31	246
3544	1	3	401	gi|1055218	crotonase (Clostridium acetobutylicum)	59	42	399
3548	1	3	401	gi|1055218	crotonase (Clostridium acetobutylicum)	59	42	399
3580	1	698	351	gi|1055218	crotonase (Clostridium acetobutylicum)	59	42	348
3720	1	722	363	gi|1408494	homologous to penicillin acylase (Bacillus subtilis)	59	36	360
4171	1	3	296	gi|1055218	crotonase (Clostridium acetobutylicum)	59	42	294
4305	1	618	310	gi|1524193	unknown (Mycobacterium tuberculosis)	59	39	309
18	1	1242	622	gi|146913	N-acetylglucosamine transport protein (Escherichia coli) pir|B29895|WQEC2N phosphotransferase system enzyme II (EC 7.1.69), N-acetylglucosamine-specific - Escherichia coli sp|P09323|PTAA_ECOLI PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC IIABC OMPONENT (EIIA	58	43	621
20	7	7020	5845	gi|50502	collagen alpha chain precursor (AA -27 to 1127) (Mus musculus)	58	50	1176
21	5	3234	3626	gi|1054860	phosphoribosyl anthranilate isomerase (Thermotoga maritima)	58	32	393
23	2	2841	1669	gi|1276880	EpsG (Streptococcus thermophilus)	58	29	1173
23	10	9301	8090	pir|A31133|A311	diaminopimelate decarboxylase (EC 4.1.1.20) - Pseudomonas aeruginosa	58	37	1212
38	29	22555	22884	gi|973249	vestitone reductase (Medicago sativa)	58	37	330
44	1	2	406	gi|289272	ferrichrome-binding protein (Bacillus subtilis)	58	33	405
45	1	1	552	gi|29464	embryonic myosin heavy chain (1085 AA) (Homo sapiens) ir|S12460|S12460 myosin beta heavy chain - human	58	33	552
55	2	759	538	gi|158852	glucose regulated protein (Echinococcus multilocularis)	58	32	222
62	13	8493	8068	gi|975353	kinase-associated protein B (Bacillus subtilis)	58	35	426
63	3	1553	1717	gi|166926	(Arabidopsis thaliana unidentified mRNA sequence, complete cds.), ene product (Arabidopsis thaliana)	58	35	165

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
67	13	12017	11229	gi|1228083	NADH dehydrogenase subunit 2 (Chorthippus parallelus)	58	41	789
96	8	8208	9167	gi|709992	hypothetical protein (Bacillus subtilis)	58	42	960
107	2	2065	1364	gi|806327	Escherichia coli hrpA gene for A protein similar to yeast PRP16 and RP22 (Escherichia coli)	58	37	702
112	7	4519	5613	gi|155588	glucose-fructose oxidoreductase (Zymomonas mobilis) pir|A42289|A42289 glucose-fructose oxidoreductase (EC 1.1.-.-) recursor - Zymomonas mobilis	58	38	1095
114	6	7318	6503	gi|1377843	unknown (Bacillus subtilis)	58	38	816
143	2	2261	1395	pir|A45605|A456	mature-parasite-infected erythrocyte surface antigen MESA - Plasmodium falciparum	58	31	867
151	2	717	950	gi|1370261	unknown (Mycobacterium tuberculosis)	58	31	234
154	6	6015	4627	gi|1209277	pCTHom1 gene product (Chlamydia trachomatis)	58	41	1389
154	16	14281	13541	gi|146613	DNA ligase (EC 6.5.1.2) (Escherichia coli)	58	39	741
155	3	2269	1892	gi|1303917	YqiB (Bacillus subtilis)	58	34	378
174	1	1056	529	gi|904198	hypothetical protein (Bacillus subtilis)	58	26	528
189	4	1533	1769	gi|467383	DNA binding protein (probable) (Bacillus subtilis)	58	25	237
201	3	2669	3307	gi|1511453	endonuclease III (Methanococcus jannaschii)	58	34	639
208	1	2	238	gi|1276729	phycobilisome linker polypeptide (Porphyra purpurea)	58	29	237
220	11	14575	13058	gi|397526	clumping factor (Staphylococcus aureus)	58	51	1518
231	3	1629	1474	gi|1002520	HutS (Bacillus subtilis)	58	45	156
233	6	4201	3497	gi|1463023	No definition line found (Caenorhabditis elegans)	58	39	705
243	10	9303	10082	gi|537207	ORF_f277 (Escherichia coli)	58	32	780
257	1	331	1143	gi|1340128	ORF1 (Staphylococcus aureus)	58	44	813
302	2	460	801	gi|40174	ORF X (Bacillus subtilis)	58	34	342
307	11	6984	6127	gi|1303842	YqfU (Bacillus subtilis)	58	30	858
321	3	1914	2747	gi|1239996	hypothetical protein (Bacillus subtilis)	58	41	834
342	4	2724	3497	gi|454838	ORF 6; putative (Pseudomonas aeruginosa)	58	41	774
348	1	1	663	gi|467478	unknown (Bacillus subtilis)	58	36	663
401	2	384	605	gi|143407	para-aminobenzoic acid synthase, component I (pab) (Bacillus ubtilis)	58	53	222

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
437	1	325	1554	gi|1303866	YqgS (Bacillus subtilis)	58	35	1230
445	1	105	1442	gi|581583	protein A (Staphylococcus aureus)	58	32	1338
453	3	789	965	gi|1009455	unknown (Schizosaccharomyces pombe)	58	34	177
453	5	2748	2047	gi|537214	yjjG gene product (Escherichia coli)	58	40	702
479	2	731	1444	gi|1256621	26.7% of identity in 165 aa to a Thermophilic bacterium hypothetical protein 6; putative (Bacillus subtilis)	58	36	714
490	1	909	547	gi|580920	rodD (gtaA) polypeptide (AA 1-673) (Bacillus subtilis) pir|S06048|S06048 probable rodD protein - Bacillus subtilis sp|P13484|TAGE_BACSU PROBABLE POLY(GLYCEROL-PHOSPHATE) LPHA-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TECHOIC ACID BIOSYNTHESIS ROTEIN E).	58	36	363
517	1	1	1164	sp|P47264|Y018_	HYPOTHETICAL HELICASE MG018.	58	30	1164
517	6	4182	4544	gi|453422	orf268 gene product (Mycoplasma hominis)	58	29	363
546	3	2802	4019	gi|886052	restriction modification system S subunit (Spiroplasma citri) gi|886052 restriction modification system S subunit (Spiroplasma itri)	58	37	1218
562	1	3	179	gi|43831	nifS protein (AA 1-400) (Klebsiella pneumoniae)	58	34	177
600	2	1347	1156	gi|1183839	unknown (Pseudomonas aeruginosa)	58	48	192
604	2	1231	1001	gi|1001353	hypothetical protein (Synechocystis sp.)	58	41	231
619	1	1	504	gi|903748	integral membrane protein (Homo sapiens)	58	43	504
625	1	2	364	gi|1208474	hypothetical protein (Synechocystis sp.)	58	43	363
635	1	1492	755	gi|1510995	transaldolase (Methanococcus jannaschii)	58	41	738
645	1	1	846	gi|677882	ileal sodium-dependent bile acid transporter (Rattus norvegicus) gi|677882 ileal sodium-dependent bile acid transporter (Rattus orvegicus)	58	33	846
645	3	906	1556	gi|1239999	hypothetical protein (Bacillus subtilis)	58	41	651
665	1	771	532	gi|1204262	hypothetical protein (GB:L10328_61) (Haemophilus influenzae)	58	39	240
674	1	635	327	gi|498817	ORF8; homologous to small subunit of phage terminases (Bacillus ubtilis)	58	39	309
675	2	1312	806	gi|42181	osmC gene product (Escherichia coli)	58	28	507
745	1	618	310	gi|1205432	coenzyme PQQ synthesis protein III (pqqIII) (Haemophilus influenzae)	58	32	309
799	2	242	1174	gi|1204669	collagenase (Haemophilus influenzae)	58	36	933
800	2	1096	614	gi|171963	tRNA isopentenyl transferase (Saccharomyces cerevisiae) sp|P07804|MOD5_YEAST TRNA ISOPENTENYLTRANSFERASE (EC 2.5.1.8) ISOPENTENYL-DIPHOSPHATE: TRNA ISOPENTENYLTRANSFERASE) (IPP RANSFERASE) (IPPT).	58	37	483

TABLE 2

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
854	1	1108	605	gi|466778	lysine specific permease (Escherichia coli)	58	44	504
885	1	481	242	gi|861199	protoporphyrin IX Mg-chelatase subunit precursor (Hordeum vulgare)	58	33	240
891	1	3	527	gi|1293660	AbsA2 (Streptomyces coelicolor)	58	31	525
942	1	931	467	gi|405567	traH (Plasmid pSK41)	58	30	465
1002	1	952	521	gi|577649	proLUKH (Staphylococcus aureus)	58	34	432
1438	1	1	261	gi|581558	isoleucyl tRNA synthetase (Staphylococcus aureus) sp|P41368|SYIP_STAAU ISOLEUCYL-TRNA SYNTHETASE, MUPIROCIN RESISTANT EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS) (MUPIROCIN RESISTANCE ROTEIN).	58	30	261
1442	1	2	463	gi|971394	similar to Acc.No. D26185 (Escherichia coli)	58	34	462
1873	1	480	241	gi|1339951	small subunit of NADH-dependent glutamate synthase (Plectonema boryanum)	58	38	240
1876	1	3	158	gi|529216	No definition line found (Caenorhabditis elegans) sp|P46503|YLX7_CAEEL HYPOTHETICAL 7.3 KD PROTEIN F23F12.7 IN HROMOSOME III.	58	33	156
1989	1	108	401	gi|1405458	YneR (Bacillus subtilis)	58	29	294
2109	1	3	401	gi|1001801	hypothetical protein (Synechocystis sp.)	58	31	399
2473	1	288	145	gi|510140	ligoendopeptidase F (Lactococcus lactis)	58	38	144
2523	1	452	228	gi|644873	catabolic dehydroquinate dehydratase (Acinetobacter calcoaceticus)	58	37	225
3041	1	2	211	gi|1205367	oligopeptide transport ATP-binding protein (Haemophilus influenzae)	58	39	210
3094	1	3	263	gi|1185288	isochorismate synthase (Bacillus subtilis)	58	38	261
3706	1	3	383	gi|456614	mevalonate kinase (Arabidopsis thaliana)	58	48	381
3854	1	1	402	gi|808869	human gcp372 (Homo sapiens)	58	32	402
4082	1	51	224	gi|508551	ribulose-1,5 bisphosphate carboxylase large subunit -methyltransferase (Pisum sativum)	58	37	174
4278	1	3	206	gi|180189	cerebellar-degeneration-related antigen (CDR34) (Homo sapiens) gi|182737 cerebellar degeneration-associated protein (Homo sapiens) pir|A29770|A29770 cerebellar degeneration-related protein - human	58	37	204
19	7	7818	7363	gi|1001516	hypothetical protein (Synechocystis sp.)	57	31	456
23	11	9663	8872	gi|606066	ORF_f256 (Escherichia coli)	57	29	792
31	1	4801	2402	gi|153146	ORF3 (Streptomyces coelicolor)	57	32	2400
38	14	11611	10796	gi|144859	ORF B (Clostridium perfringens)	57	31	816
46	14	12063	13046	gi|1001319	hypothetical protein (Synechocystis sp.)	57	25	984

TABLE 2

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S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
51	3	1411	1187	pir|B33856|B338	hypothetical 80K protein - Bacillus sphaericus	57	38	225
54	1	1	453	gi|684950	staphylococcal accessory regulator A (Staphylococcus aureus)	57	31	453
75	1	3	239	gi|1000470	C27B7.7 (Caenorhabditis elegans)	57	42	237
92	5	3855	3061	gi|143607	sporulation protein (Bacillus subtilis)	57	35	795
96	3	4006	4773	gi|144297	acetyl esterase (XynC) (Caldocellum saccharolyticum) pir|B37202|B37202 acetylesterase (EC 3.1.1.6) (XynC) - Caldocellum saccharolyticum	57	34	768
107	3	1480	2076	gi|460955	TagE (Vibrio cholerae)	57	42	597
109	8	5340	5933	gi|1438846	Unknown (Bacillus subtilis)	57	41	594
112	9	6679	7701	gi|1486250	unknown (Bacillus subtilis)	57	33	1023
114	4	6384	4108	gi|871456	putative alpha subunit of formate dehydrogenase (Methanobacterium hermoautotrophicum)	57	37	2277
126	2	430	1053	gi|288301	ORF2 gene product (Bacillus megaterium)	57	37	624
131	5	6537	6277	gi|1511160	M. jannaschii predicted coding region MJ1163 (Methanococcus jannaschii)	57	38	261
133	3	2668	2201	gi|1303912	YqhW (Bacillus subtilis)	57	40	468
133	4	3383	2784	gi|1221884	(urea?) amidolyase (Haemophilus influenzae)	57	37	600
147	4	2164	1694	gi|467469	unknown (Bacillus subtilis)	57	33	471
160	2	1293	1060	gi|558604	chitin synthase 2 (Neurospora crassa)	57	28	234
163	8	5687	4764	gi|145580	rarD gene product (Escherichia coli)	57	38	924
168	6	4336	5325	gi|39702	33kDa lipoprotein (Bacillus subtilis)	57	32	990
170	5	3297	3455	gi|603404	Yer164p (Saccharomyces cerevisiae)	57	37	159
221	6	8026	6809	gi|1136221	carboxypeptidase (Sulfolobus solfataricus)	57	32	1218
228	3	1348	1791	gi|288969	fibronectin binding protein (Streptococcus dysgalactiae) pir|S33850|S33850 fibronectin-binding protein - Streptococcus ysgalactiae	57	32	444
263	4	4411	3686	gi|1185002	dihydrodipicolinate reductase (Pseudomonas syringae pv. tabaci)	57	42	726
276	1	494	255	gi|396380	No definition line found (Escherichia coli)	57	40	240
283	2	335	1324	gi|773349	BirA protein (Bacillus subtilis)	57	32	990
297	1	469	236	gi|1334820	reading frame V (Cauliflower mosaic virus)	57	46	234
342	3	1993	2805	gi|1206431	hypothetical protein (SP:PJ3644) (Haemophilus influenzae)	57	35	813

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
375	6	3340	3741	gi|385177	cell division protein [Bacillus subtilis]	57	26	402
433	6	3286	4011	gi|1524117	alpha-acetolactate decarboxylase [Lactococcus lactis]	57	40	726
470	3	903	1145	gi|804819	protein serine/threonine kinase [Toxoplasma gondii]	57	30	243
487	5	1391	1723	gi|507323	ORF1 [Bacillus stearothermophilus]	57	28	333
498	1	274	852	gi|1334549	NADH-ubiquinone oxidoreductase subunit 4L [Podospora anserina]	57	34	579
503	1	343	173	gi|1502283	organic cation transporter OCT2 [Rattus norvegicus]	57	30	171
505	2	1619	1284	gi|466884	B1496_C2_194 [Mycobacterium leprae]	57	40	336
519	2	1182	2549	gi|1303707	YrkH [Bacillus subtilis]	57	34	1368
522	2	3234	1945	gi|1064809	homologous to sp:HTRA_ECOLI [Bacillus subtilis]	57	36	1290
538	2	909	1415	gi|153179	phosphorinothyrcin n-acetyltransferase [Streptomyces coelicolor] pir|JH0246|JH0246 phosphinothricin N-acetyltransferase (EC 2.3.1.-) Streptomyces coelicolor	57	40	507
547	1	968	486	gi|467340	unknown [Bacillus subtilis]	57	50	483
599	1	1062	532	sp|P20692|TYRA_	PREPHENATE DEHYDROGENASE (EC 1.3.1.12) (PDH).	57	41	531
620	2	757	572	gi|1107894	unknown [Schizosaccharomyces pombe]	57	38	186
622	2	1600	1130	gi|173028	thioredoxin II [Saccharomyces cerevisiae]	57	39	471
625	2	362	1114	gi|1262366	hypothetical protein [Mycobacterium leprae]	57	34	753
680	1	1	204	gi|143544	RNA polymerase sigma-30 factor [Bacillus subtilis] pir|A28625|A28625 transcription initiation factor sigma H - acillus subtilis	57	30	204
690	1	3	629	gi|466520	poeR [Salmonella typhimurium]	57	29	627
696	1	2	433	gi|413972	ipa-48r gene product [Bacillus subtilis]	57	33	432
704	1	36	638	gi|1499931	M. jannaschii predicted coding region MJ1083 [Methanococcus jannaschii]	57	36	603
732	1	2316	1621	gi|1418599	orf4 [Lactobacillus sake]	57	37	696
746	1	451	227	gi|392973	Rab3 [Aplysia californica]	57	42	225
757	1	20	466	gi|43979	L.curvatus small cryptic plasmid gene for rep protein [Lactobacillus rvatus]	57	45	447
862	1	2	295	gi|1303827	YqfI [Bacillus subtilis]	57	21	294
1049	1	907	455	gi|1510108	ORF-1 [Agrobacterium tumefaciens]	57	35	453
1117	1	1387	695	gi|896286	NH2 terminus uncertain [Leishmania tarentolae]	57	28	693

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name ( )	% sim	% ident	length (nt)
1136	1	2	322	gi|1303853	YqgF (Bacillus subtilis)	57	38	321
1144	2	1033	611	gi|310083	voltage-activated calcium channel alpha-1 subunit (Rattus orvegicus)	57	46	423
1172	1	1472	738	gi|1511146	H. jannaschii predicted coding region MJ1143 (Methanococcus jannaschii)	57	28	735
1500	2	746	558	gi|142780	putative membrane protein; putative (Bacillus subtilis)	57	35	189
1676	1	659	399	gi|313777	uracil permease (Escherichia coli)	57	31	261
2481	1	2	400	gi|1237015	ORF4 (Bacillus subtilis)	57	23	399
3099	1	3	230	gi|1204540	isochorismate synthase (Haemophilus influenzae)	57	39	228
3122	1	360	181	gi|882472	ORF_o464 (Escherichia coli)	57	40	180
3560	1	2	361	gi|153490	tetracenomycin C resistance and export protein (Streptomyces lavcocono)	57	37	360
3850	1	856	434	gi|155588	glucose-fructose oxidoreductase (Zymomonas mobilis) pir|A42289|A42289 glucose-fructose oxidoreductase (EC 1.1.-.-) rocursor - Zymomonas mobilis	57	40	423
3931	1	704	354	gi|413953	ipa-29d gene product (Bacillus subtilis)	57	36	351
3993	1	1	384	gi|151259	HMG-CoA reductase (EC 1.1.1.88) (Pseudomonas mevalonii) pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	57	39	384
4065	1	793	398	pir|JV0037|RDEC	nitrate reductase (EC 1.7.99.4) alpha chain - Escherichia coli	57	31	396
4100	1	596	300	gi|1086633	T06C10.5 gene product (Caenorhabditis elegans)	57	47	297
4163	1	571	287	gi|21512	patatin (Solanum tuberosum)	57	50	285
4267	2	631	335	gi|1000365	SpoIIIAG (Bacillus subtilis)	57	38	297
4358	1	3	302	gi|298032	EF (Streptococcus suis)	57	32	300
4389	2	108	290	gi|405894	1-phosphofructokinase (Escherichia coli)	57	37	183
4399	1	2	232	gi|1481603	Pristinamycin I synthase 1 (Streptomyces pristinaespiralis)	57	35	211
4481	1	572	288	gi|405879	yeiH (Escherichia coli)	57	44	285
4486	1	512	258	gi|515938	glutamate synthase (ferredoxin) (Synechocystis sp.) pir|S46957|S46957 glutamate synthase (ferredoxin) (EC 1.4.7.1) - ynechocystis sp.	57	42	255
4510	1	481	242	gi|1205301	leukotoxin secretion ATP-binding protein (Haemophilus influenzae)	57	38	240
4617	1	468	256	gi|1511222	restriction modification enzyme, subunit M1 (Methanococcus jannaschii)	57	35	213
4	11	12201	11524	gi|149204	histidine utilization repressor C (Klebsiella aerogenes) pir|A36730|A36730 hutG protein - Klebsiella pneumoniae (fragment) sp|P19452|HUTG_KLEAE FORMIMINOGLUTAMASE (EC 3.5.3.8) FORMIMINOGLUTAMATE HYDROLASE) (HISTIDINE UTILIZATION PROTEIN G) FRAGMENT).	56	31	678

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name ( )	% sim	% ident	length (nt)
22	8	4248	5177	gi|1322222	RACH1 (Homo sapiens)	56	33	930
38	28	21179	22264	gi|1480705	lipoate-protein ligase (Mycoplasma capricolum)	56	34	1086
44	3	1861	2421	gi|490320	Y gene product (unidentified)	56	31	561
44	15	10103	10606	gi|1205099	hypothetical protein (GB:L19201_1) (Haemophilus influenzae)	56	39	504
50	6	4820	5161	gi|209931	fiber protein (Human adenovirus type 5)	56	48	342
53	4	2076	2972	gi|623476	transcriptional activator (Providencia stuartii) sp|P43463|AARP_PROST TRANSCRIPTIONAL ACTIVATOR AARP.	56	30	897
67	6	5656	6594	gi|466613	nikB (Escherichia coli)	56	32	939
89	3	2364	1810	gi|482922	protein with homology to pail repressor of B.subtilis (Lactobacillus elbrueckii)	56	39	555
96	1	203	913	gi|145594	cAMP receptor protein (crp) (Escherichia coli)	56	35	711
109	21	18250	17846	gi|1204367	hypothetical protein (GB:U14003_278) (Haemophilus influenzae)	56	27	405
112	8	5611	6678	gi|155588	glucose-fructose oxidoreductase (Zymomonas mobilis) pir|A42289|A42289 glucose-fructose oxidoreductase (EC 1.1.-.-) recursor - Zymomonas mobilis	56	40	1068
131	3	6404	5100	gi|619724	MgtE (Bacillus firmus)	56	30	1305
134	2	65	232	gi|413948	ipa-24d gene product (Bacillus subtilis)	56	31	168
138	4	823	1521	gi|580868	ipa-22r gene product (Bacillus subtilis)	56	31	699
146	2	740	447	gi|1046009	M. genitalium predicted coding region MG309 (Mycoplasma genitalium)	56	37	294
149	2	1639	1067	gi|945380	terminase small subunit (Bacteriophage LL-H)	56	35	573
163	1	2	223	gi|143947	glucamine synthetase (Bacteroides fragilis)	56	30	222
166	5	6745	6449	gi|405792	ORF154 (Pseudomonas putida)	56	26	297
187	1	31	393	gi|311237	H(+)-transporting ATP synthase (Zea mays)	56	30	363
190	1	2	373	gi|1109686	ProX (Bacillus subtilis)	56	35	372
191	8	11538	9943	gi|581070	acyl coenzyme A synthetase (Escherichia coli)	56	35	1596
195	1	1291	647	gi|1510242	collagenase (Methanococcus jannaschii)	56	34	645
230	3	2323	2072	gi|40363	heat shock protein (Clostridium acetobutylicum)	56	39	252
238	5	3383	3775	gi|1477533	sarA (Staphylococcus aureus)	56	31	393
270	2	813	1712	gi|765073	autolysin (Staphylococcus aureus)	56	41	900

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name ( )	% sim	% ident	length (nt)
290	1	3221	1632	gi|547513	orf3 (Haemophilus influenzae)	56	34	1590
297	5	1140	1373	gi|1511556	M. jannaschii predicted coding region MJ1561 (Methanococcus jannaschii)	56	40	234
321	2	2947	1799	gi|1001801	hypothetical protein (Synechocystis sp.)	56	31	1149
359	2	1279	641	gi|46336	nolI gene product (Rhizobium meliloti)	56	26	639
371	2	360	1823	gi|145304	L-ribulokinase (Escherichia coli)	56	39	1464
391	4	1762	2409	gi|1001634	hypothetical protein (Synechocystis sp.)	56	34	648
402	1	380	192	gi|1438904	5-HT4L receptor (Homo sapiens)	56	48	189
416	4	2480	2109	gi|1408486	HS74A gene product (Bacillus subtilis)	56	31	372
424	3	1756	2334	gi|142471	acetolactate decarboxylase (Bacillus subtilis)	56	32	579
457	1	1907	1017	gi|1205194	formamidopyrimidine-DNA glycosylase (Haemophilus influenzae)	56	36	891
458	2	2423	1812	gi|15466	terminase (Bacteriophage SPP1)	56	37	612
504	2	2152	1283	gi|1142681	Lpp38 (Pasteurella haemolytica)	56	38	870
511	1	1	1284	gi|217049	brnQ protein (Salmonella typhimurium)	56	37	1284
604	3	1099	1701	gi|467109	rim; 30S Ribosomal protein S18 alanine acetyltransferase; 229_C1_170 (Mycobacterium leprae)	56	43	603
660	5	3547	3774	gi|1229106	ZK930.1 (Caenorhabditis elegans)	56	30	228
707	1	35	400	gi|153929	NADPH-sulfite reducatase flavoprotein component (Salmonella typhimurium)	56	38	366
709	2	1385	1095	gi|1510801	hydrogenase accessory protein (Methanococcus jannaschii)	56	38	291
718	1	1	495	gi|413948	ipa-24d gene product (Bacillus subtilis)	56	35	495
744	1	87	677	gi|928836	repressor protein (Lactococcus lactis phage BK5-T)	56	35	591
790	1	776	399	gi|1511513	ABC transporter, probable ATP-binding subunit (Methanococcus jannaschii)	56	33	378
795	1	3	407	gi|1205382	cell division protein (Haemophilus influenzae)	56	34	405
813	1	19	930	gi|1222161	permease (Haemophilus influenzae)	56	28	912
855	1	3	515	gi|1256621	26.7% of identity in 165 aa to o Thermophilic bacterium hypothetical protein 6; putative (Bacillus subtilis)	56	33	513
968	1	2	466	gi|547513	orf3 (Haemophilus influenzae)	56	37	465
973	2	1049	732	gi|886022	MexR (Pseudomonas aeruginosa)	56	31	318
1203	1	5	223	gi|184251	HHG-1 (Homo sapiens)	56	34	219

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
1976	1	452	237	gi|9806	lysine-rich aspartic acid-rich protein [Plasmodium chabaudi] r|S22183|S22183 lysine/aspartic acid-rich protein - Plasmodium baudi	56	33	216
2161	1	2	400	gi|1237015	ORF4 [Bacillus subtilis]	56	27	399
2958	1	362	183	gi|466685	No definition line found [Escherichia coli]	56	26	180
2979	1	421	212	gi|1204354	spore germination and vegetative growth protein [Haemophilus influenzae]	56	40	210
2994	2	526	326	gi|836646	phosphoribosylformimino-praic ketoisomerase [Rhodobacter phaeroides]	56	29	201
3026	1	179	328	gi|143306	penicillin V amidase [Bacillus sphaericus]	56	30	150
3189	1	289	146	gi|1166604	Similar to aldehyde dehydrogenase [Caenorhabditis elegans]	56	37	144
3770	1	63	401	gi|1129145	acetyl-CoA C-acyltransferase [Mangifera indica]	56	43	339
4054	2	720	361	gi|1205355	Na+/H+ antiporter [Haemophilus influenzae]	56	31	360
4145	1	1	324	gi|726095	long-chain acyl-CoA dehydrogenase [Mus musculus]	56	36	324
4200	1	505	254	gi|155588	glucose-fructose oxidoreductase [Zymomonas mobilis] pir|A42289|A42289 glucose-fructose oxidoreductase (EC 1.1.-.-) precursor - Zymomonas mobilis	56	40	252
4273	1	675	355	gi|308861	GTG start codon [Lactococcus lactis]	56	33	321
1	3	4095	3436	gi|5341	Putative orf YCLX8c, len:192 [Saccharomyces cerevisiae] r|S53591|S53591 hypothetical protein - yeast (Saccharomyces cerevisiae)	55	25	660
11	12	9377	8505	gi|216773	haloacetate dehalogenase H-1 [Moraxella sp.]	55	32	873
12	4	5133	4534	gi|467337	unknown [Bacillus subtilis]	55	26	600
19	5	5404	5844	gi|1001719	hypothetical protein [Synechocystis sp.]	55	25	441
23	13	14087	12339	gi|474190	iucA gene product [Escherichia coli]	55	30	1749
32	7	5368	6888	gi|1340096	unknown [Mycobacterium tuberculosis]	55	37	1521
34	3	2569	1808	gi|1303968	YqjQ [Bacillus subtilis]	55	39	762
34	5	3960	3412	gi|1303962	YqjK [Bacillus subtilis]	55	33	549
36	1	1291	647	gi|606045	ORF_o118 [Escherichia coli]	55	27	645
36	6	6220	5243	gi|1001341	hypothetical protein [Synechocystis sp.]	55	31	978
47	3	3054	3821	gi|1001819	hypothetical protein [Synechocystis sp.]	55	21	768
49	1	2065	1127	gi|403373	glycerophosphoryl diester phosphodiesterase [Bacillus subtilis] pir|S37251|S37251 glycerophosphoryl diester phosphodiesterase - acillus subtilis	55	36	939

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
67	11	8966	9565	gi|153053	norA1199 protein [Staphylococcus aureus]	55	23	600
75	3	881	1273	gi|21698	L-histidinol: NAD+ oxidoreductase (EC 1.1.1.23) (aa 1-434) [Escherichia coli]	55	33	393
82	9	15387	14194	gi|1136221	carboxypeptidase [Sulfolobus solfataricus]	55	35	1194
87	4	3517	4917	gi|1068812	function unknown [Bacillus subtilis]	55	26	1401
88	2	1172	1636	gi|882463	protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia coli]	55	35	465
92	1	127	516	gi|1377832	unknown [Bacillus subtilis]	55	36	390
100	2	836	2035	gi|1170274	[xanthin epoxidase (Nicotiana plumbaginifolia)	55	36	1200
100	5	5137	4658	gi|396660	[unknown open reading frame [Buchnera aphidicola]	55	29	480
108	3	4266	2986	gi|1499866	[M. jannaschii predicted coding region MJ1024 [Methanococcus jannaschii]	55	31	1281
114	3	2616	1834	gi|1511367	[formate dehydrogenase, alpha subunit [Methanococcus jannaschii]	55	29	783
144	3	1805	1476	gi|1100787	[unkown [Saccharomyces cerevisiae]	55	35	330
165	5	6212	5508	gi|1045884	[M. genitalium predicted coding region MG199 [Mycoplasma genitalium]	55	27	705
189	5	2205	2576	gi|142569	[ATP synthase a subunit [Bacillus firmus]	55	35	372
191	6	9136	6857	gi|559411	[B0272.3 [Caenorhabditis elegans]	55	39	2280
194	2	364	636	gi|1145768	[K7 kinesin-like protein [Dictyostelium discoideum]	55	34	273
209	4	1335	1676	gi|473357	[thi4 gene product [Schizosaccharomyces pombe]	55	35	342
211	2	1693	1145	gi|410130	[ORFX6 [Bacillus subtilis]	55	37	549
213	2	644	1372	gi|633692	[TrgA [Yersinia enterocolitica]	55	28	729
214	7	4144	5481	gi|1001793	[hypothetical protein [Synechocystis sp.]	55	30	1338
221	7	11473	9197	gi|466520	[pocR [Salmonella typhimurium]	55	32	2277
233	8	5908	4817	gi|1237063	[unknown [Mycobacterium tuberculosis]	55	38	1092
236	4	1375	2340	gi|1146199	[putative [Bacillus subtilis]	55	32	966
243	2	380	1885	gi|459907	[mercuric reductase [Plasmid pI258]	55	29	1506
258	1	786	394	gi|455006	[orf6 [Rhodococcus fascians]	55	36	393
281	1	126	938	gi|1408493	[homologous to SwissProt:YIDA_ECOLI hypothetical protein [Bacillus subtilis]	55	35	813
316	3	1323	2102	gi|1486447	[LuxA homologue [Rhizobium sp.]	55	30	780
326	5	2968	2744	gi|1296824	[proline iminopeptidase [Lactobacillus helveticus]	55	36	225

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	Length (nt)
351	2	2322	1429	gi|1204820	hydrogen peroxide-inducible activator (Haemophilus influenzae)	55	28	894
353	4	2197	2412	gi|1272475	chitin synthase (Emericella nidulans)	55	50	216
380	1	14	379	gi|142554	ATP synthase 1 subunit (Bacillus megaterium)	55	37	366
383	1	462	232	gi|39272	ferrichrome-binding protein (Bacillus subtilis)	55	36	231
386	1	3	938	gi|1510251	DNA helicase, putative (Methanococcus jannaschii)	55	30	936
410	2	1208	1891	gi|1205144	multidrug resistance protein (Haemophilus influenzae)	55	27	684
483	2	411	833	gi|413934	ips-10r gene product (Bacillus subtilis)	55	26	423
529	3	1777	1433	gi|1606150	ORF_f309 (Escherichia coli)	55	33	345
555	1	1088	585	gi|143407	para-aminobenzoic acid synthase, component I (pabB) (Bacillus subtilis)	55	28	504
565	1	402	202	gi|1223961	CDP-tyvelose epimerase (Yersinia pseudotuberculosis)	55	41	201
582	1	751	452	gi|1256643	20.2k identity with NADH dehydrogenase of the Leishmania major mitochondrion; putative (Bacillus subtilis)	55	36	300
645	5	2260	2057	gi|210824	fusion protein F (Bovine respiratory syncytial virus) pir|JQ1481|VGNZBA fusion glycoprotein precursor - bovine respiratory syncytial virus (strain A51908)	55	25	204
672	2	957	2216	gi|1511333	M. jannaschii predicted coding region MJ1322 (Methanococcus jannaschii)	55	36	1260
730	1	955	479	gi|537007	ORF_f379 (Escherichia coli)	55	30	477
737	1	1859	945	gi|536963	CG Site No. 18166 (Escherichia coli)	55	30	915
742	2	228	572	gi|304160	product unknown (Bacillus subtilis)	55	38	345
817	2	1211	903	gi|1136289	histidine kinase A (Dictyostelium discoideum)	55	29	309
819	1	582	355	gi|558073	polymorphic antigen (Plasmodium falciparum)	55	22	228
832	2	1152	724	gi|40367	ORFC (Clostridium acetobutylicum)	55	32	429
840	1	769	386	gi|1205875	pseudouridylate synthase I (Haemophilus influenzae)	55	39	384
1021	1	23	529	gi|48563	beta-lactamase (Yersinia enterocolitica)	55	38	507
1026	1	60	335	gi|47804	Opp C (AA1-301) (Salmonella typhimurium)	55	26	276
1525	1	1	282	gi|1477533	sarA (Staphylococcus aureus)	55	29	282
1814	2	224	985	gi|1046078	M. genitalium predicted coding region MG369 (Mycoplasma genitalium)	55	38	762
3254	1	427	254	gi|413968	ips-44d gene product (Bacillus subtilis)	55	30	174

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3695	1	686	345	gi|216773	haloacetate dehalogenase H-1 (Moraxella sp.)	55	32	342
3721	1	1	312	gi|42029	ORF1 gene product (Escherichia coli)	55	31	312
3799	1	3	272	gi|42029	ORF1 gene product (Escherichia coli)	55	38	270
3889	1	22	423	gi|1129145	acetyl-CoA C-acyltransferase (Mangifera indica)	55	45	402
3916	1	2	385	gi|529754	speC (Streptococcus pyogenes)	55	38	384
3945	1	4	198	gi|476252	phase 1 flagellin (Salmonella enterica)	55	36	195
4074	1	488	246	gi|42029	ORF1 gene product (Escherichia coli)	55	38	243
4184	1	2	343	gi|1524267	unknown (Mycobacterium tuberculosis)	55	28	342
4284	1	14	208	gi|1100774	ferredoxin-dependent glutamate synthase (Synechocystis sp.)	55	36	195
4457	2	644	378	gi|180189	cerebellar-degeneration-related antigen (CDR34) (Homo sapiens) gi|182737 cerebellar degeneration-associated protein (Homo sapiens) pir|A29770|A29770 cerebellar degeneration-related protein - human	55	38	267
4514	1	2	244	gi|216773	haloacetate dehalogenase H-1 (Moraxella sp.)	55	32	243
4599	1	432	217	gi|1129145	acetyl-CoA C-acyltransferase (Mangifera indica)	55	42	216
4606	1	416	210	gi|386120	myosin alpha heavy chain (S2 subfragment) (rabbits, masseter, peptide Partial, 234 aa)	55	27	207
5	8	5348	4932	gi|536069	ORF YBL047c (Saccharomyces cerevisiae)	54	27	417
12	7	7166	6165	gi|1205504	homoserine acetyltransferase (Haemophilus influenzae)	54	30	1002
23	16	17086	15326	gi|474192	iucC gene product (Escherichia coli)	54	31	1761
35	1	2	979	gi|48054	small subunit of soluble hydrogenase (AA 1-384) (Synechococcus sp.) ir|S06919|HQYCSS soluble hydrogenase (EC 1.12.-.-) small chain - nechococcus sp. (PCC 6716)	54	36	978
37	11	9437	8667	gi|537207	ORF_f277 (Escherichia coli)	54	38	771
37	12	8165	8332	gi|1160967	palmitoyl-protein thioesterase (Homo sapiens)	54	37	168
46	15	13025	13804	gi|438473	protein is hydrophobic, with homology to E. coli ProW; putative Bacillus subtilis)	54	28	780
56	2	203	736	gi|1256139	YbbJ (Bacillus subtilis)	54	34	534
57	13	11117	10179	gi|1151248	inosine-uridine preferring nucleoside hydrolase (Crithidia fasciculata)	54	32	939
66	2	516	1133	gi|1335781	Cap (Drosophila melanogaster)	54	29	618
70	10	8116	8646	gi|1399823	PhoE (Rhizobium meliloti)	54	31	531

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% identity	length (nt)
70	15	12556	11801	sp|P02983|TCR_S	TETRACYCLINE RESISTANCE PROTEIN.	54	29	756
87	5	4915	5706	gi|1064811	function unknown (Bacillus subtilis)	54	33	792
92	4	3005	2289	gi|1205366	oligopeptide transport ATP-binding protein (Haemophilus influenzae)	54	33	717
103	2	2596	1556	gi|710495	protein kinase (Bacillus brevis)	54	33	1041
105	2	3585	2095	gi|143727	putative (Bacillus subtilis)	54	30	1491
112	4	2337	2732	gi|153724	HaiC (Streptococcus pneumoniae)	54	41	396
127	2	1720	2693	gi|144297	acetyl esterase (XynC) (Caldocellum saccharolyticum) pir|B37202|B37202 acetylesterase (EC 3.1.1.6) (XynC) - Caldocellum saccharolyticum	54	34	774
138	5	1600	3306	gi|42473	pyruvate oxidase (Escherichia coli)	54	36	1707
152	2	525	1172	gi|1377834	unknown (Bacillus subtilis)	54	23	648
161	9	4831	5469	gi|903305	ORF73 (Bacillus subtilis)	54	28	639
161	13	6694	7251	gi|1511039	phosphate transport system regulatory protein (Methanococcus jannaschii)	54	32	558
164	6	3263	4543	gi|1204976	prolyl-tRNA synthetase (Haemophilus influenzae)	54	34	1281
164	20	21602	22243	gi|143582	spoIIIEA protein (Bacillus subtilis)	54	32	642
171	6	5683	4250	gi|436965	(malA) gene products (Bacillus stearothermophilus) pir|S43914|S43914 hypothetical protein 1 - Bacillus tearothermophilus	54	37	1434
206	18	19208	19720	gi|1240016	R09E10.3 (Caenorhabditis elegans)	54	38	513
218	2	1090	1905	gi|467378	unknown (Bacillus subtilis)	54	26	816
220	1	1322	663	gi|1353761	myosin II heavy chain (Naegleria fowleri)	54	22	660
220	13	12655	13059	pir|S00485|S004	gene 11-1 protein precursor - Plasmodium falciparum (fragments)	54	35	405
221	3	2030	3709	gi|1303813	YqeW (Bacillus subtilis)	54	34	1680
272	7	5055	4219	gi|62964	arylamine N-acetyltransferase (AA 1-290) (Gallus gallus) ir|S06652|XYCHY3 arylamine N-acetyltransferase (EC 2.3.1.5) (clone NAT-3) - chicken	54	33	837
316	7	4141	4701	gi|682769	mccE gene product (Escherichia coli)	54	31	561
316	10	6994	8742	gi|413951	lpa-27d gene product (Bacillus subtilis)	54	28	1749
338	3	3377	2214	gi|490328	LORF F (unidentified)	54	28	1164
341	4	3201	3614	gi|171959	myosin-like protein (Saccharomyces cerevisiae)	54	25	414

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
346	1	1820	912	gi|396400	similar to eukaryotic Na+/H+ exchangers [Escherichia coli] sp|P32703|YJCE_ECOLI HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS NTERGENIC REGION (0549).	54	34	909
348	2	623	1351	gi|537109	ORF_f343a [Escherichia coli]	54	34	729
378	2	1007	1942	sp|P02983|TCR_S	TETRACYCLINE RESISTANCE PROTEIN.	54	31	936
408	6	4351	5301	gi|474190	iucA gene product [Escherichia coli]	54	29	951
444	9	7934	8854	gi|216267	ORF2 [Bacillus megaterium]	54	32	921
461	2	2717	2229	gi|304160	product unknown [Bacillus subtilis]	54	50	489
502	2	1696	1133	gi|1205015	hypothetical protein (SP:P10120) [Haemophilus influenzae]	54	38	564
505	6	6262	5357	gi|1500558	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase [Methanococcus jannaschii]	54	41	906
550	1	2736	1522	gi|40100	rodC (tag3) polypeptide (AA 1-746) [Bacillus subtilis] ir|S06049|S06049 rodC protein - Bacillus subtilis p|P13485|TAGF_BACSU TECHOIC ACID BIOSYNTHESIS PROTEIN F.	54	35	1215
551	5	3305	4279	gi|950197	unknown [Corynebacterium glutamicum]	54	34	975
558	2	1356	958	gi|485090	No definition line found [Caenorhabditis elegans]	54	32	399
580	1	91	936	gi|331906	fused envelope glycoprotein precursor [Friend spleen focus-forming virus]	54	45	846
603	3	554	757	gi|1322423	ORF YGR234w [Saccharomyces cerevisiae]	54	36	204
617	1	25	249	gi|219959	ornithine transcarbamylase [Homo sapiens]	54	40	225
622	3	1097	1480	gi|1303873	YqgZ [Bacillus subtilis]	54	25	384
623	1	3	404	gi|1063250	low homology to P20 protein of Bacillus lichiniformis and bleomycin acetyltransferase of Streptomyces verticillus [Bacillus subtilis]	54	45	402
689	1	1547	1011	gi|552446	NADH dehydrogenase subunit 4 [Apis mellifera ligustica] pir|S52968|S52968 NADH dehydrogenase chain 4 - honeybee itochondrion (SGC4)	54	30	537
725	2	686	1441	gi|987096	sensory protein kinase [Streptomyces hygroscopicus]	54	26	756
956	1	1	249	pir|S30782|S307	integrin homolog - yeast [Saccharomyces cerevisiae]	54	24	249
978	2	1137	859	gi|1301994	ORF YNL091w [Saccharomyces cerevisiae]	54	33	279
1314	1	3	281	gi|1001108	hypothetical protein [Synechocystis sp.]	54	33	279
2450	1	1	228	gi|1045057	ch-TOG [Homo sapiens]	54	32	228
2934	1	1	387	gi|580870	ipa-37d qoxA gene product [Bacillus subtilis]	54	36	387
2970	1	499	251	sp|P37134P|YECE_	HYPOTHETICAL PROTEIN IN ASPS 5'REGION (FRAGMENT).	54	42	249

TABLE 2

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S aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3002	1	1	309	gi|44027	Tma protein (Lactococcus lactis)	54	33	309
3561	1	9	464	gi|151259	HMG-CoA reductase (EC 1.1.1.88) (Pseudomonas mevalonii) pir|A44756|A44756 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) Pseudomonas sp.	54	35	456
3572	1	72	401	gi|450688	hsdM gene of Ecoprrl gene product (Escherichia coli) pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	54	36	330
3829	1	798	400	gi|1322245	mevalonate pyrophosphate decarboxylase (Rattus norvegicus)	54	29	399
3909	1	1	273	gi|29865	CENP-E (Homo sapiens)	54	30	273
3921	1	3	209	pir|S24325|S243	glucan 1,4-beta-glucosidase (EC 3.2.1.74) - Pseudomonas fluorescens subsp. cellulosa	54	34	207
4438	1	566	285	gi|1196657	unknown protein (Mycoplasma pneumoniae)	54	30	282
4459	1	3	272	gi|1046081	hypothetical protein (GB:D26185_10) (Mycoplasma genitalium)	54	38	270
4564	1	3	221	gi|216267	ORF2 (Bacillus megaterium)	54	38	219
23	12	12538	10685	gi|474192	iucC gene product (Escherichia coli)	53	35	1854
23	14	14841	13579	gi|42029	ORF1 gene product (Escherichia coli)	53	32	1263
24	3	4440	3940	gi|1369947	c2 gene product (Bacteriophage B1)	53	36	501
26	4	3818	4618	gi|1486267	unknown (Bacillus subtilis)	53	37	801
38	6	2856	3998	gi|405880	yeii (Escherichia coli)	53	40	1143
38	10	9380	7806	gi|1399954	thyroid sodium/iodide symporter NIS (Rattus norvegicus)	53	29	1575
56	10	12324	12100	pir|A54592|A545	110k actin filam... -associated protein - chicken	53	32	225
57	6	5047	4583	pir|A00361|DEZP	alcohol dehydrogenase (EC 1.1.1.1) - fission yeast (Schizosaccharomyces pombe)	53	39	465
57	12	10515	8932	gi|1480429	putative transcriptional regulator (Bacillus stearothermophilus)	53	30	1584
67	12	9496	10218	gi|1511555	quinolone resistance norA protein protein (Methanococcus jannaschii)	53	31	723
69	3	3125	2382	gi|1087017	arabinogalactan-protein, AGP (Nicotiana alata, cell-suspension culture filtrate, Peptide, 461 aa)	53	30	744
79	1	3	1031	gi|1523802	glucanase (Anabaena variabilis)	53	32	1029
80	1	673	338	gi|452428	ATPase 3 (Plasmodium falciparum)	53	36	336
88	4	1910	2524	gi|537034	ORF_o488 (Escherichia coli)	53	25	615
88	5	2467	3282	gi|537034	ORF_o488 (Escherichia coli)	53	29	816

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
92	8	5870	5505	gi|399598	amphotropic murine retrovirus receptor [Rattus norvegicus]	53	33	366
94	5	4417	3239	gi|173038	tropomyosin (TPM1) [Saccharomyces cerevisiae]	53	25	1179
99	5	4207	5433	sp|P28246|BCR_E	BICYCLOMYCIN RESISTANCE PROTEIN (SULFONAMIDE RESISTANCE PROTEIN).	53	30	1227
120	3	1639	2262	gi|576655	ORF1 [Vibrio anguillarum]	53	35	624
120	11	7257	8897	gi|1524397	glycine betaine transporter OpuD [Bacillus subtilis]	53	33	1641
127	6	6893	5685	gi|1256630	putative [Bacillus subtilis]	53	32	1209
147	2	255	557	gi|581648	epiB gene product [Staphylococcus epidermidis]	53	34	303
158	4	4705	4256	gi|151004	mucoidy regulatory protein AlgR [Pseudomonas aeruginosa] pir|A32802|A32802 regulatory protein algR - Pseudomonas aeruginosa sp|P26275|ALGR_PSEAE POSITIVE ALGINATE BIOSYNTHESIS REGULATORY ROTEIN.	53	32	450
171	7	5717	5421	gi|1510669	hypothetical protein (GP:D64044_18) [Methanococcus jannaschii]	53	34	297
191	9	13087	11483	gi|298085	acetoacetate decarboxylase [Clostridium acetobutylicum] pir|B49346|B49346 butyrate--acetoacetate CoA-transferase (EC .8.3.9) small chain - Clostridium acetobutylicum sp|P33752|CTFA_CLOAB BUTYRATE-ACETOACETATE COA-TRANSFERASE SUBUNIT (EC 2.8.3.9) (COAT A)	53	31	1605
203	5	3763	4326	gi|143456	rpoE protein (ttg start codon) [Bacillus subtilis]	53	29	564
206	17	18204	18971	gi|304136	acetylglutamate kinase [Bacillus stearothermophilus] sp|Q07905|ARGB_BACST ACETYLGLUTAMATE KINASE (EC 2.7.2.8) (NAG KNASE) (AGK) (N-ACETYL-L-GLUTAMATE 5-PHOSPHOTRANSFERASE).	53	36	768
212	10	4021	4221	gi|9878	protein kinase [Plasmodium falciparum]	53	28	201
231	2	1580	1350	gi|537506	paramyosin [Dirofilaria immitis]	53	34	231
272	6	2719	3249	pir|A33141|A331	hypothetical protein (gtfD 3' region) - Streptococcus mutans	53	34	531
308	3	927	2576	gi|606292	ORF_o696 [Escherichia coli]	53	33	1650
320	7	5645	5884	gi|160596	RNA polymerase III largest subunit [Plasmodium falciparum] sp|P27625|RPC1_PLAFA DNA-DIRECTED RNA POLYMERASE III LARGEST UBUNIT (EC 2.7.7.6).	53	33	240
327	1	218	901	gi|854601	unknown [Schizosaccharomyces pombe]	53	31	684
341	2	212	2500	gi|633732	ORF1 [Campylobacter jejuni]	53	31	2289
351	1	763	383	sp|P31675|YAEM_	HYPOTHETICAL 42.7 KD PROTEIN IN TBPA-LEUD INTERGENIC REGION (ORF104).	53	32	381
433	7	5087	4731	gi|1001961	MHC class II analog [Staphylococcus aureus]	53	30	357
454	2	1240	980	pir|A60328|A603	40K cell wall protein precursor (sr 5' region) - Streptococcus mutans (strain OMZ175, serotype f)	53	27	261

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	Match gene name	% sim	% Ident	length (nt)
470	4	1123	1761	gi|516826	rat GCP160 (Rattus rattus)	53	30	639
483	1	432	217	gi|1480429	putative transcriptional regulator (Bacillus stearothermophilus)	53	33	216
544	1	516	1259	gi|46587	ORF 1 (AA 1 - 121) (1 is 2nd base in codon) (Staphylococcus aureus) ir|S15765|S15765 hypothetical protein 1 (hlb 5' region) - aphylococcus aureus (fragment)	53	38	744
558	10	3957	3754	gi|15140	res gene (Bacteriophage P1)	53	32	204
603	2	319	620	gi|507738	Hmp (Vibrio parahaemolyticus)	53	26	282
693	1	1669	941	gi|153123	toxic shock syndrome toxin-1 precursor (Staphylococcus aureus) pir|A24606|XCSAS1 toxic shock syndrome toxin-1 precursor - taphylococcus aureus	53	38	729
766	1	2	673	gi|687600	orfA2; orfA2 forms an operon with orfA1 (Listeria monocytogenes)	53	43	672
781	1	667	335	gi|1204551	pilin biogenesis protein (Haemophilus influonsae)	53	26	333
801	1	3	545	gi|1279400	SapA protein (Escherichia coli)	53	25	543
803	1	2	910	gi|695278	lipase-like enzyme (Alcaligenes eutrophus)	53	30	909
872	1	1177	590	gi|298032	EP (Streptococcus suis)	53	30	588
910	1	2	184	gi|1044936	unknown (Schizosaccharomyces pombe)	53	29	183
943	1	794	399	gi|190508	similar to unidentified ORF near 47 minutes (Escherichia coli) sp|P31436|YICK_ECOLI HYPOTHETICAL 43.5 KD PROTEIN IN SELC-NLPA NTERGENIC REGION.	53	30	396
988	1	1004	504	gi|142441	ORF 3; putative (Bacillus subtilis)	53	28	501
1064	1	3	434	gi|305080	myosin heavy chain (Entamoeba histolytica)	53	26	432
1366	1	3	452	gi|308852	transmembrane protein (Lactococcus lactis)	53	33	450
1758	1	792	397	gi|1001774	hypothetical protein (Synechocystis sp.)	53	30	396
1897	1	1	447	gi|1303949	YqiX (Bacillus subtilis)	53	27	447
2381	1	798	400	gi|1146243	22.4% identity with Escherichia coli DNA-damage inducible protein ...; putative (Bacillus subtilis)	53	37	399
3537	1	1	327	gi|450688	hsdM gene of EcoprrI gene product (Escherichia coli) pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-320)	53	35	327
3747	2	137	397	gi|1477486	transposase (Burkholderia cepacia)	53	53	261
11	5	3049	3441	gi|868224	No definition line found (Caenorhabditis elegans)	52	33	393

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
15	5	2205	2369	gi|215966	G41 protein (gtg start codon) [Bacteriophage T4]	52	34	165
19	3	2429	3808	gi|1205379	UDP-murnac-pentapeptide synthetase [Haemophilus influenzae]	52	31	1380
24	1	6920	3462	gi|579124	predicted 86.4kd protein; 52Kd observed [Mycobacteriophage 15] pir|S30971|S30971 gene 26 protein - Mycobacterium phage L5 sp|Q05233|VG26_BPML5 MINOR TAIL PROTEIN GP26. (SUB 2-837)	52	32	3459
37	5	3015	3935	gi|1500543	P115 protein [Methanococcus jannaschii]	52	25	921
38	13	8795	9703	gi|46851	glucose kinase [Streptomyces coelicolor]	52	29	909
44	16	10617	11066	gi|42012	moaE gene product [Escherichia coli]	52	36	450
46	1	3	521	gi|1040957	NADH dehydrogenase subunit 6 [Anopheles trinkae]	52	25	519
51	10	5531	6280	gi|38269	traC [Plasmid pAD1]	52	32	750
56	5	3968	2826	gi|181949	endothelial differentiation protein (edg-1) [Homo sapiens] pir|A35300|A35300 G protein-coupled receptor edg-1 - human sp|P21453|EDG1_HUMAN PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.	52	23	1143
57	5	4850	4173	gi|304153	sorbitol dehydrogenase [Bacillus subtilis]	52	27	678
62	5	3364	2870	gi|1072399	phaE gene product [Rhizobium meliloti]	52	25	495
62	6	4445	3651	gi|46485	NADH dehydrogenase [Synechococcus PCC7942]	52	27	795
67	14	11355	12962	gi|1511365	glutamate synthase (NADPH), subunit alpha [Methanococcus jannaschii]	52	30	1608
67	21	16935	18158	gi|1204393	hypothetical protein (SP:P31122) [Haemophilus influenzae]	52	25	1224
70	4	2185	1997	gi|7227	cytoplasmic dynein heavy chain [Dictyostelium discoideum] r|A44357|A44357 dynein heavy chain, cytosolic - slime mold cyostelium discoideum)	52	36	189
96	10	10005	10664	gi|1408485	B65G gene product [Bacillus subtilis]	52	26	660
103	5	3986	3351	gi|1009368	Respiratory nitrate reductase [Bacillus subtilis]	52	42	636
109	3	4102	3350	gi|699274	lmbE gene product [Mycobacterium leprae]	52	39	753
109	19	15732	17300	gi|1526981	amino acid permease YeeF like protein [Salmonella typhimurium]	52	30	1569
121	3	1412	981	gi|732931	unknown [Saccharomyces cerevisiae]	52	32	432
125	3	865	1680	gi|1296975	puT gene product [Porphyromonas gingivalis]	52	38	816
130	2	659	1807	gi|1256634	25.8% identity over 120 aa with the Synenococcus sp. NpeV protein; putative [Bacillus subtilis]	52	36	1149
149	1	1164	583	gi|1225943	PBEX terminase [Bacillus subtilis]	52	33	582
149	14	4687	4415	gi|1510368	M. jannaschii predicted coding region MJ0272 [Methanococcus jannaschii]	52	35	273

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
167	1	216	1001	gi|146025	cell division protein [Escherichia coli]	52	43	786
188	1	120	1256	gi|474915	orf 337; translated orf similarity to SW: BCR_ECOLI bicyclomycin osistance protoin of Escherichia coli [Coxiella burnetii] pir|S40207|S40207 hypothotical protein 337 - Coxiella burnetii (SUB -338)	52	26	1137
195	9	9161	8760	gi|3028	mitochondrial outer membrane 72K protein [Neurospora crassa] r|A36682|A36682 72K mitochondrial outer membrano protein - roopora crassa	52	25	402
200	3	2065	2607	gi|142439	ATP-dependent nuclease [Bacillus subtilis]	52	35	543
203	4	2776	3684	gi|1303698	BltD [Bacillus subtilis]	52	25	909
227	8	5250	5651	gi|305080	myosin heavy chain [Entamoeba histolytica]	52	24	402
242	1	21	1424	gi|1060877	EmrY [Escherichia coli]	52	32	1404
249	5	4526	4753	pir|C37222|C372	cytochrome P450 1A1, hepatic - dog (fragment)	52	23	228
255	1	2107	1055	gi|143290	penicillin-binding protein [Bacillus subtilis]	52	28	1053
276	7	3963	3664	gi|1001610	hypothetical protein [Synechocystis sp.]	52	30	300
276	8	4456	4055	gi|416235	orf LJ [Mycoplasma capricolum]	52	26	402
289	2	1856	1449	gi|150900	GTP phosphohydrolase [Proteus vulgaris]	52	34	408
325	1	1	279	gi|1204874	polypeptide deformylase (formylmethionine deformylase) [Haemophilus influenzae]	52	33	279
340	1	2017	1010	gi|1215695	peptide transport system protein SapF homolog; SapF homolog [Mycoplasma pneumoniae]	52	33	1008
375	3	340	1878	gi|467446	similar to SpoVB [Bacillus subtilis]	52	28	1539
424	6	4104	3262	gi|1478239	unknown [Mycobacterium tuberculosis]	52	34	843
430	1	3	575	pir|A42606|A426	orfA 5' to orf405 - Saccharopolyspora erythraea (fragment)	52	28	573
444	4	4728	3712	gi|1408494	homologous to penicillin acylase [Bacillus subtilis]	52	31	1017
465	1	1802	903	gi|143331	alkoline phosphatase regulatory protein [Bacillus subtilis] pir|A27650|A27650 regulatory protein phoR - Bacillus subtilis sp|P23545|PHOR_BACSU ALKALINE PHOSPHATASE SYNTHESIS SENSOR PROTEIN HOR (EC 2.7.3.-).	52	36	900
469	5	4705	4169	gi|755152	highly hydrophobic integral membrane protein [Bacillus subtilis] sp|P42953|TAGG_BACSU TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN AGG.	52	32	537
495	1	1262	633	gi|1204607	transcription activator [Haemophilus influenzae]	52	25	630
505	7	6004	5762	gi|142440	ATP-dependent nuclease [Bacillus subtilis]	52	28	243

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
517	2	1162	1614	gi|166162	Bacteriophage phi-11 int gene activator (Staphylococcus acteriophage phi 11)	52	35	453
543	2	444	1295	gi|1215693	putative orf; GT9_orf434 (Mycoplasma pneumoniae)	52	25	852
586	1	1	336	gi|581648	epiB gene product (Staphylococcus epidermidis)	52	36	336
773	1	848	426	gi|1279769	FdhC (Methanobacterium thermoformicicum)	52	30	423
1120	2	100	330	gi|142439	ATP-dependent nuclease (Bacillus subtilis)	52	35	231
1614	1	691	347	gi|289262	comE ORF3 (Bacillus subtilis)	52	28	345
2495	1	1	324	gi|216151	DNA polymerase (gene L; ttg start codon) (Bacteriophage SPO2) gi|579197 SPO2 DNA polymerase (aa 1-648) (Bacteriophage SPO2) pir|A21498|DJBPS2 DNA-directed DNA polymerase (EC 2.7.7.7) - phage PO2	52	34	324
2931	1	566	285	gi|1256136	YbbG (Bacillus subtilis)	52	30	282
2943	1	577	320	gi|41713	hisA ORF (AA 1-245) (Escherichia coli)	52	35	258
2993	1	588	295	gi|298032	EF (Streptococcus suis)	52	34	294
3667	1	612	307	gi|849025	hypothetical 64.7-kDa protein (Bacillus subtilis)	52	36	306
3944	1	478	260	gi|1218040	BAA (Bacillus licheniformis)	52	36	219
3954	2	613	347	gi|854064	U87 (Human herpesvirus 6)	52	50	267
3986	1	90	401	gi|1205919	Na+ and Cl- dependent gamma-aminobutryic acid transporter (Haemophilus influenzae)	52	33	312
4002	1	3	389	gi|40003	oxoglutarate dehydrogenase (NADP+) (Bacillus subtilis) p|P23129|ODO1_BACSU 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 2.4.2) (ALPHA- KETOGLUTARATE DEHYDROGENASE).	52	42	387
4020	1	1	249	gi|159388	ornithine decarboxylase (Leishmania donovani)	52	47	249
4098	1	438	220	gi|409795	No definition line found (Escherichia coli)	52	32	219
4248	1	3	212	gi|965077	Adr6p (Saccharomyces cerevisiae)	52	40	210
7	1	3	575	gi|895747	putative cel operon regulator (Bacillus subtilis)	51	28	573
21	4	2479	3276	gi|1510962	indole-3-glycerol phosphate synthase (Methanococcus jannaschii)	51	32	798
22	9	5301	5966	gi|1303933	YqiN (Bacillus subtilis)	51	25	666
43	3	1516	1283	gi|1519460	Srp1 (Schizosaccharomyces pombe)	51	31	234
44	17	11042	11305	gi|42011	moaD gene product (Escherichia coli)	51	35	264
51	11	6453	6731	gi|495471	vacuolating toxin (Helicobacter pylori)	51	37	279

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
52	4	2537	2995	gi|1256652	25% identity to the E.coli regulatory protein NprA; putative [Bacillus subtilis]	51	32	459
57	10	7331	6843	gi|508173	EIIA domain of PTS-dependent Gat transport and phosphorylation Escherichia coli]	51	32	489
59	1	29	1111	gi|299163	alanine dehydrogenase [Bacillus subtilis]	51	33	1083
67	20	15791	16576	gi|1510977	M. jannaschii predicted coding region MJ0938 [Methanococcus jannaschii]	51	24	786
69	2	1559	1218	gi|467359	unknown [Bacillus subtilis]	51	34	342
71	1	3	1196	gi|298032	EF [Streptococcus suis]	51	32	1194
78	2	349	176	gi|1161242	proliferating cell nuclear antigen [Styela clava]	51	28	174
99	4	3357	4040	gi|642795	TFIID subunit TAF155 [Homo sapiens]	51	25	684
109	1	2852	1428	gi|580920	rodD (gtaA) polypeptide (AA 1-673) [Bacillus subtilis] pir|S06048|S06048 probable rodD protein - Bacillus subtilis sp|P13480|TAGE_BACSU PROBABLE POLY(GLYCEROL-PHOSPHATE) LPHA-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TECHOIC ACID BIOSYNTHESIS ROTEIN E).	51	27	1425
109	9	6007	6693	gi|1204815	hypothetical protein (SP:P32662) [Haemophilus influenzae]	51	23	687
112	3	1066	2352	pir|S05330|S053	maltose-binding protein precursor - Enterobacter aerogenes	51	42	1287
112	13	14432	12855	gi|405857	yehU [Escherichia coli]	51	29	1578
114	9	9725	8967	gi|435098	orf1 [Mycoplasma capricolum]	51	30	759
115	1	1	912	gi|1431110	ORF YML083w [Saccharomyces cerevisiae]	51	25	912
127	10	9647	10477	gi|1204314	H. influenzae predicted coding region HI0056 [Haemophilus influenzae]	51	37	831
152	9	6814	7356	gi|431929	HunI regulatory protein [Mycoplasma sp.]	51	38	543
154	2	575	1153	gi|1237044	unknown [Mycobacterium tuberculosis]	51	36	579
154	7	6587	5634	gi|409286	bmrU [Bacillus subtilis]	51	27	954
171	8	6943	6236	gi|1205484	hypothetical protein (SP:P33918) [Haemophilus influenzae]	51	32	708
184	1	1	291	gi|466886	B1696_C1_206 [Mycobacterium leprae]	51	33	291
212	5	1501	2139	pir|A45605|A456	mature-parasite-infected erythrocyte surface antigen MESA - Plasmodium falciparum	51	23	639
228	2	707	1378	gi|8204	nuclear protein [Drosophila melanogaster]	51	27	672
236	8	8137	7481	gi|49272	Asparaginase [Bacillus licheniformis]	51	31	657
243	4	4637	3546	gi|1511102	malvalonate kinase [Methanococcus jannaschii]	51	29	1092

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
257	4	3540	3373	gi|:204579	H. influenzae predicted coding region HI0326 [Haemophilus influenzae]	51	22	168
258	3	2397	1609	gi|160299	glutamic acid-rich protein [Plasmodium falciparum] pir|A54514|A54514 glutamic acid-rich protein precursor - Plasmodium falciparum	51	34	789
265	5	2419	3591	gi|580841	F1 [Bacillus subtilis]	51	32	1173
298	2	518	748	gi|1336162	SCPB [Streptococcus agalactiae]	51	34	231
316	9	5817	7049	gi|413953	ipa-28d gene product [Bacillus subtilis]	51	39	1233
332	2	3775	2057	gi|1209012	mutS [Thermus aquaticus thermophilus]	51	26	1719
364	4	3816	4991	gi|528991	unknown [Bacillus subtilis]	51	32	1176
440	2	448	684	gi|2819	transferase (GAL10) (AA 1 - 687) [Kluyveromyces lactis] r|S01407|XUKG UDPglucose 4-epimerase (EC 5.1.3.2) - yeast uyveromyces marxianus var. lactis)	51	32	237
495	2	1353	1177	gi|297861	protease G [Erwinia chrysanthemi]	51	41	177
495	3	2287	1718	gi|1513317	serine rich protein [Entamoeba histolytica]	51	25	570
506	1	840	421	gi|455320	cII protein [Bacteriophage P4]	51	33	420
600	1	1474	983	gi|587532	orf, len: 201, CAI: 0.16 [Saccharomyces cerevisiae] pir|S48818|S48818 hypothetical protein - yeast (Saccharomyces erevisiae)	51	30	492
607	3	479	934	gi|1511524	hypothetical protein (SP:P37002) [Methanococcus jannaschii]	51	40	456
686	2	127	600	gi|493017	endocarditis specific antigen [Enterococcus faecalis]	51	30	474
726	1	33	230	gi|1153851	unknown [Prochlorococcus marinus]	51	45	198
861	1	176	652	gi|410145	dehydroquinate dehydratase [Bacillus subtilis]	51	34	477
869	1	782	393	gi|40100	rodC (Lag2) polypeptide (AA 1-746) [Bacillus subtilis] ir|S06049|S06049 rodC protein - Bacillus subtilis p|P13485|TAGF_BACSU TECHOIC ACID BIOSYNTHESIS PROTEIN F.	51	23	390
1003	1	642	322	gi|1279707	hypothetical phosphoglycerate mutase [Saccharomyces cerevisiae]	51	39	321
1046	2	866	624	gi|510257	glycosyltransferase [Escherichia coli]	51	29	243
1467	1	702	352	gi|1511175	M. jannaschii predicted coding region MJ1177 [Methanococcus jannaschii]	51	32	351
2558	1	457	230	sp|P10582|DPOM_	DNA POLYMERASE (EC 2.7.7.7) (S-1 DNA ORF 3).	51	26	228
3003	1	779	399	gi|809543	CbrC protein [Erwinia chrysanthemi]	51	27	381
3604	1	1	399	pir||JC4210|JC42	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) - mouse	51	37	399
3732	1	2	316	gi|145906	acyl-CoA synthetase [Escherichia coli]	51	33	315

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3791	1	2	274	gi|1061351	semaphorin III family homolog [Homo sapiens]	51	37	273
3995	1	46	336	gi|216346	surfactin synthetase [Bacillus subtilis]	51	38	291
4193	1	612	307	gi|42749	ribosomal protein L12 (AA 1-179) [Escherichia coli] ir|S04776|XXECPL peptide N-acetyltransferase rimL (EC 2.3.1.-) - cherichia coli	51	25	306
4539	1	367	185	gi|1408494	homologous to penicillin acylase [Bacillus subtilis]	51	40	183
4562	1	442	239	gi|1458280	coded for by C. elegans cDNA cm01e7; Similar to hydroxymethylglutaryl-CoA synthase [Caenorhabditis elegans]	51	35	204
1	4	3576	4859	gi|559160	GRAIL score: null; cap site and late promoter motifs present pstream; putative [Autographa californica nuclear polyhedrosis irus]	50	44	1284
11	7	4044	5165	gi|1146207	putative [Bacillus subtilis]	50	35	1122
11	13	10509	9496	gi|1208451	hypothetical protein [Synechocystis sp.]	50	39	1014
19	1	2034	1018	gi|413966	ipa-42d gene product [Bacillus subtilis]	50	29	1017
20	11	8586	8407	gi|1323159	ORF YGR103w [Saccharomyces cerevisiae]	50	28	180
24	5	5408	4824	gi|496280	structural protein [Bacteriophage Tuc2009]	50	29	585
34	4	1926	2759	gi|1303966	YqjO [Bacillus subtilis]	50	36	834
38	30	22865	23440	gi|1072179	Similar to dihydroflavonol-4-reductase (maize, petunia, tomato) [Caenorhabditis elegans]	50	32	576
47	2	1705	2976	gi|153015	FemA protein [Staphylococcus aureus]	50	29	1272
56	13	15290	15841	gi|606096	ORF_f167; end overlaps end of o100 by 14 bases; start overlaps f174, ther starts possible [Escherichia coli]	50	30	552
57	1	2135	1077	gi|640922	xylitol dehydrogenase [unidentified hemiascomycete]	50	29	1059
58	2	628	1761	gi|143725	putative [Bacillus subtilis]	50	29	1134
88	6	4393	3884	gi|1072179	Similar to dihydroflavonol-4-reductase (maize, petunia, tomato) [Caenorhabditis elegans]	50	32	510
89	5	3700	3356	gi|1276658	ORF174 gene product [Porphyra purpurea]	50	25	345
141	1	3	239	gi|476024	carbamoyl phosphate synthetase II [Plasmodium falciparum]	50	33	237
151	1	186	626	gi|1403441	unknown [Mycobacterium tuberculosis]	50	35	441
166	7	11065	9623	gi|895747	putative cel operon regulator [Bacillus subtilis]	50	32	1443
201	6	5284	5096	gi|160229	circumsporozoite protein [Plasmodium roichenowi]	50	42	189
206	22	30784	29555	gi|1052754	LmrP integral membrane protein [Lactococcus lactis]	50	24	1230

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
211	4	1523	1927	gi|410131	ORFX7 [Bacillus subtilis]	50	29	405
214	4	2411	3295	sp|P37348|YECE_	HYPOTHETICAL PROTEIN IN ASPS 5'REGION (FRAGMENT).	50	37	885
228	7	5068	4406	gi|313580	envelope protein (Human immunodeficiency virus type 1] pir|S35835|S35835 envelope protein - human immunodeficiency virus ype 1 (fragment) (SUB 1-77)	50	35	663
272	2	3048	1723	gi|1408485	B65G gene product [Bacillus subtilis]	50	22	1326
273	2	1616	984	gi|384186	phosphoglycerate mutase [Saccharomyces corevisiae]	50	28	633
328	2	2507	1605	gi|148896	lipoprotein [Haemophilus influenzae]	50	26	903
332	4	5469	3802	gi|1526547	DNA polymerase family X [Thermus aquaticus]	50	27	1668
342	5	3473	3931	gi|456562	G-box binding factor [Dictyostelium discoideum]	50	35	459
352	1	1478	741	gi|288301	ORF2 gene product [Bacillus megaterium]	50	29	738
408	7	5299	5523	gi|11665	ORF2136 [Marchantia polymorpha]	50	27	225
420	3	650	1825	gi|757842	UDP-sugar hydrolase [Escherichia coli]	50	30	1176
464	1	1	591	gi|487282	Na+ -ATPase subunit J [Enterococcus hirae]	50	29	591
472	2	1418	864	gi|551875	BglR [Lactococcus lactis]	50	23	555
520	1	23	541	gi|567036	CapE [Staphylococcus aureus]	50	27	519
529	1	6	410	gi|1256652	25% identity to the E.coli regulatory protein MprA; putative [Bacillus subtilis]	50	34	405
534	5	7726	6059	gi|295671	selected as a weak suppressor of a mutant of the subunit AC40 of DNA ependant RNA polymerase I and III [Saccharomyces cerevisiae]	50	18	1668
647	1	2990	1497	gi|405568	TraI protein shares sequence similarity with a family of opoisomerases [Plasmid pSK41]	50	31	1494
664	3	1133	711	gi|410007	leukocidin F component [Staphylococcus aureus, MRSA No. 4, Peptide, 23 aa]	50	32	423
678	1	1	627	gi|238032	EF [Streptococcus suis]	50	29	627
755	3	947	1171	gi|150572	cytochrome c1 precursor (EC 1.10.2.2) [Paracoccus denitrificans] gi|45465 cytochrome c1 (AA 1-450) [Paracoccus denitrificans] pir|C29413|C29413 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) ytochrome c1 precursor - Paracoccus denitrificans sp|P13627|CY1	50	37	225
827	1	1363	683	gi|142020	heterocyst differentiation protein [Anabaena sp.]	50	21	681
892	1	3	752	gi|1408485	B65G gene product [Bacillus subtilis]	50	27	750
910	2	438	887	gi|1104727	tyrosine-specific transport protein [Haemophilus influenzae]	50	25	450

TABLE 2

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
933	1	524	760	gi|1205451	cell division inhibitor (Haemophilus influenzae)	50	32	237
973	1	424	236	gi|886947	orf3 gene product (Saccharomyces cerevisiae)	50	40	189
1009	1	653	429	gi|153727	M protein (group G streptococcus)	50	28	225
1027	1	511	257	gi|471934	ipa-10r gene product (Bacillus subtilis)	50	25	255
1153	2	556	326	gi|773676	nccA (Alcaligenes xylosoxydans)	50	36	231
1222	1	798	400	gi|1408485	B65G gene product (Bacillus subtilis)	50	21	399
1350	1	692	399	gi|289272	ferrichrome-binding protein (Bacillus subtilis)	50	32	294
2945	1	366	184	gi|171704	hexaprenyl pyrophosphate synthetase (COQ1) (Saccharomyces ereviaiae)	50	34	183
2968	2	1604	804	gi|397526	clumping factor (Staphylococcus aureus)	50	33	801
2998	2	657	394	gi|495696	F54E7.3 gene product (Caenorhabditis elogans)	50	40	264
3046	2	506	306	pir|S13819|S138	acyl carrier protein - Anabaena variabilis (fragment)	50	32	201
3063	1	547	275	gi|174190	lucA gene product (Escherichia coli)	50	29	273
3174	1	3	146	gi|151900	alcohol dehydrogenase (Rhodobacter sphaeroides)	50	31	144
3792	1	625	314	gi|1001423	hypothetical protein (Synechocyetis sp.)	50	35	312
3800	1	2	262	gi|144733	NAD-dependent beta-hydroxybutyryl coenzyme A dehydrogenase Clostridium acetobutylicum)	50	28	261
3946	1	173	188	gi|576765	cytochrome b (Myrmecia pilosula)	50	38	186
3984	1	578	291	sp|P37348|YECE_	HYPOTHETICAL PROTEIN IN ASPS 5'REGION (FRAGMENT).	50	37	288
37	10	8250	7885	gi|1204367	hypothetical protein (GB:U14003_278) (Haemophilus influenzae)	49	30	366
46	16	13802	14848	[r|466860	acd; B1308_F1_34 (Mycobacterium leprae)	49	24	1047
59	5	2267	3601	gi|606304	ORF_o462 (Escherichia coli)	49	27	1335
112	18	17884	18615	gi|559502	ND4 protein (AA 1 - 409) (Caenorhabditis elogans)	49	25	732
138	9	6973	7902	gi|303953	esterase (Acinetobacter calcoaceticus)	49	29	930
217	6	4401	5138	gi|496254	fibronectin/fibrinogen-binding protein (Streptococcus pyogenes)	49	31	738
220	12	11803	12657	gi|397526	clumping factor (Staphylococcus aureus)	49	31	855
228	4	1842	2492	pir|S23592|S236	hypothetical protein 9 - Plasmodium falciparum	49	24	651
268	1	5016	2614	gi|143047	ORFB (Bacillus subtilis)	49	26	2403

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
271	2	1164	1373	gi|1001257	hypothetical protein (Synechocystis sp.)	49	38	210
300	3	4340	3180	gi|1510796	hypothetical protein (GP:X91006_2) (Methanococcus jannaschii)	49	26	1161
381	1	2281	1142	gi|396301	matches PS00041: Bacterial regulatory proteins, araC family ignature (Escherichia coli)	49	29	1140
466	1	3	947	gi|1303863	YqgP (Bacillus subtilis)	49	26	945
666	1	379	191	gi|633112	ORF1 (Streptococcus sobrinus)	49	29	189
670	2	403	1014	gi|1122758	unknown (Bacillus subtilis)	49	32	612
709	1	1433	795	gi|143830	xpaC (Bacillus subtilis)	49	29	639
831	1	943	473	gi|401786	phosphomannomutase (Mycoplasma pirum)	49	29	471
1052	1	422	213	gi|1303799	YqeN (Bacillus subtilis)	49	21	210
1800	1	342	172	gi|216300	peptidoglycan synthesis enzyme (Bacillus subtilis) sp|P37585|MURG_BACSU MURG PROTEIN UPD-N-ACETYLGLUCOSAMINE--N-ACETYLMURAMYL-PENTAPEPTIDE)PYROPHOSPHORYL-UNDECAPRENOL N-ACETYLGLUCOSAMINE RANSFERASE).	49	28	171
2430	1	2	376	sp|P27434|YFGA_	HYPOTHETICAL 36.2 KD PROTEIN IN NDK-GCPE INTERGENIC REGION.	49	26	375
3096	1	542	273	gi|516360	surfactin synthetase (Bacillus subtilis)	49	25	270
32	4	3771	3100	gi|1217963	hepatocyte nuclear factor 4 gamma (HNF4gamma) (Homo sapiens)	48	36	672
38	1	1	609	gi|1205790	H. influenzae predicted coding region HI1555 (Haemophilus influenzae)	48	28	609
45	6	5021	6427	gi|1524267	unknown (Mycobacterium tuberculosis)	48	20	1407
59	14	16346	31096	gi|1197336	Lmp3 protein (Mycoplasma hominis)	48	28	14751
61	1	3	608	gi|1511555	quinolone resistance norA protein protein (Methanococcus jannaschii)	48	30	606
61	3	3311	3646	gi|1303893	YqhL (Bacillus subtilis)	48	29	336
114	1	98	415	gi|671708	su(s) homolog; similar to Drosophila melanogaster suppressor of able (su(s)) protein, Swiss-Prot Accession Number P22293 Drosophila virilis)	48	25	318
121	1	1131	610	gi|1314584	unknown (Sphingomonas S88)	48	29	522
136	1	2014	1280	gi|1205968	H. influenzae predicted coding region HI1738 (Haemophilus influenzae)	48	23	735
171	10	8220	9557	gi|1208454	hypothetical protein (Synechocystis sp.)	48	34	1338
175	1	3625	1814	gi|396400	similar to eukaryotic Na+/H+ exchangers (Escherichia coli) sp|P32703|YJCE_ECOLI HYPOTHETICAL 60.5 KD PROTEIN IN SOXR-ACS NTERGENIC REGION (O549).	48	29	1812
194	1	2	385	gi|1510493	H. jannaschii predicted coding region MJ0419 (Methanococcus jannaschii)	48	25	384

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
197	1	901	452	gi|1045714	spermidine/putrescine transport ATP-binding protein [Mycoplasma genitalium]	48	25	450
203	1	1	396	gi|940288	protein localized in the nucleoli of pea nuclei; ORF; putative Pisum sativum]	48	29	396
204	1	1163	698	gi|529202	No definition line found [Caenorhabditis elegans]	48	25	666
206	20	34815	27760	gi|511490	gramicidin S synthetase 2 [Bacillus brevis]	48	27	7056
212	1	2	166	gi|295899	nucleolin [Xenopus laevis]	48	34	165
220	10	12652	11426	gi|44073	SecY protein [Lactococcus lactis]	48	23	1227
243	6	6450	5491	gi|1184118	mevalonate kinase [Methanobacterium thermoautotrophicum]	48	30	960
264	4	5434	3308	gi|1015903	ORF YJR15C [Saccharomyces cerevisiae]	48	26	2127
484	2	388	1110	gi|146551	transmembrane protein (kdpD) [Escherichia coli]	48	18	723
441	1	1532	768	gi|142863	replication initiation protein [Bacillus subtilis] pir|B26580|B26580 replication initiation protein - Bacillus subtilis	48	23	765
444	5	3898	5298	gi|145836	putative [Escherichia coli]	48	24	1401
484	2	388	1110	gi|146551	transmembrane protein (kdpD) [Escherichia coli]	48	18	723
542	3	1425	2000	pir|S28969|S289	N-carbamoylsarcosine amidohydrolase (EC 3.5.1.59) - Arthrobacter sp.	48	27	576
566	1	3	1019	gi|153490	tetracenomycin C resistance and export protein [Streptomyces glaucescens]	48	24	1017
611	1	2	730	gi|1103507	unknown [Schizosaccharomyces pombe]	48	38	729
624	1	1255	665	gi|144859	ORF B [Clostridium perfringens]	48	26	591
846	1	1014	508	gi|537506	paramyosin [Dirofilaria immitis]	48	27	507
1020	1	66	950	gi|1499876	magnesium and cobalt transport protein [Methanococcus jannaschii]	48	30	885
1227	1	1	174	gi|493730	lipoxygenase [Pisum sativum]	48	35	174
1266	1	1	405	gi|882452	ORF_f211; alternate name yggA; orf5 of X14436 [Escherichia coli] gi|41425 ORF5 (AA 1-197) [Escherichia coli] (SUB 15-211)	48	24	405
2071	1	707	381	gi|1408486	HS74A gene product [Bacillus subtilis]	48	25	327
2398	1	463	233	gi|1500401	reverse gyrase [Methanococcus jannaschii]	48	40	231
2425	1	476	246	pir|H48563|H485	G1 protein - fowlpox virus (strain HP444) (fragment)	48	40	231
2432	1	446	225	gi|1353703	Trio [Homo sapiens]	48	33	222
2453	1	794	399	gi|142850	division initiation protein [Bacillus subtilis]	48	29	396
2998	1	469	236	gi|577569	PepV [Lactobacillus delbrueckii]	48	31	234

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
3042	1	18	280	gi|945219	mucin (Homo sapiens)	48	35	267
3686	1	1	405	gi|145836	putative (Escherichia coli)	48	25	405
4027	2	492	301	pir.S51177|S511	trans-activator protein - Equine infectious anemia virus	48	32	192
4	2	3641	2232	gi|1303989	YqkI (Bacillus subtilis)	47	24	1410
24	2	599	1084	gi|540083	PC4-1 gene product (Bradysia hygida)	47	28	486
36	10	7524	6925	gi|1209223	esterase (Acinetobacter lwoffii)	47	26	600
43	2	196	1884	gi|1403455	unknown (Mycobacterium tuberculosis)	47	27	1689
44	22	16118	15108	gi|1511555	quinolone resistance norA protein protein (Methanococcus jannaschii)	47	31	1011
69	7	7141	6710	gi|438466	Possible operon with orfG. Hydrophilic, no homologue in the atabase; putative (Bacillus subtilis)	47	29	432
81	4	5022	4279	gi|466882	pps1; B1496_C2_189 (Mycobacterium leprae)	47	24	744
120	12	9135	8863	gi|927340	D9509.27p; CAI: 0.12 (Saccharomyces cerevisiae)	47	38	273
142	1	2022	1174	gi|486143	ORF YKL094w (Saccharomyces cerevisiae)	47	32	849
168	1	2178	1093	gi|1177254	hypothetical EcsB protein (Bacillus subtilis)	47	29	1086
263	1	1884	943	gi|142822	D-alanine racemase cds (Bacillus subtilis)	47	34	942
279	1	1109	561	gi|516608	2 predicted membrane helices, homology with B. subtilis men Orf3 Rowland et. al. unpublished Accession number M74183), approximately 1 minutes on updated Rudd map; putative (Escherichia coli) sp|P37355|YFBB_ECOLI HYPOTHETICAL 26.7 KD PROTEIN IN MEND-MENB	47	31	549
345	2	2620	1676	gi|1204835	hippuricase (Haemophilus influenzae)	47	28	945
389	2	152	400	gi|456562	G-box binding factor (Dictyostelium discoideum)	47	32	249
391	1	1	831	gi|1420856	myo-inositol transporter (Schizosaccharomyces pombe)	47	19	831
404	3	2072	2773	gi|1255425	C33G8.2 gene product (Caenorhabditis elegans)	47	17	702
529	5	2145	3107	gi|1303973	YqjV (Bacillus subtilis)	47	29	963
565	2	2321	1257	gi|142824	processing protease (Bacillus subtilis)	47	28	1065
654	1	962	483	gi|243353	ORF 5' of ECRP3 (herpesvirus saimiri HVS, host-squirrel monkey, eptide, 407 aa)	47	23	480
692	1	115	633	gi|150756	40 kDa protein (Plasmid pJM1)	47	25	519
765	1	1634	819	gi|1256621	26.7% of identity in 165 aa to a Thermophilic bacterium hypothetical protein 6; putative (Bacillus subtilis)	47	28	816

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
825	2	211	1023	gi|397526	clumping factor (Staphylococcus aureus)	47	32	813
914	1	1	615	gi|558073	polymorphic antigen (Plasmodium falciparum)	47	29	615
1076	1	1	753	gi|1147557	Aspartate aminotransferase (Bacillus circulans)	47	33	753
1351	1	793	398	gi|755153	ATP-binding protein (Bacillus subtilis)	47	20	396
4192	1	3	293	gi|145836	putative (Escherichia coli)	47	24	291
5	6	4708	4361	gi|305080	myosin heavy chain (Entamoeba histolytica)	46	30	348
11	4	2777	3058	gi|603639	(Ye1040p (Saccharomyces cerevisiae)	46	28	282
46	11	10518	10300	gi|1246901	ATP-dependent DNA ligase (Candida albicans)	46	28	219
61	4	3941	7930	gi|298032	EF (Streptococcus suis)	46	35	3990
132	4	5028	4093	gi|1511057	hypothetical protein SP:P45869 (Methanococcus jannaschii)	46	25	936
170	4	4719	3652	pir|S51910|S519	G4 protein - Saurole(shania tarentolae	46	26	1068
191	7	9543	8284	gi|1041334	F54D5.7 (Caenorhabditis elegans)	46	25	1260
253	1	1	396	gi|1204449	dihydrolipoamide acetyltransferase (Haemophilus influenzae)	46	35	396
264	3	437	973	gi|180189	cerebellar-degeneration-related antigen (CDR34) (Homo sapiens) gi|182737 cerebellar degeneration-associated protein (Homo sapiens) pir|A29770|A29770 cerebellar degeneration-related protein - human	46	29	537
273	1	485	285	gi|607573	envelope glycoprotein C2V3 region (Human immunodeficiency virus type)	46	35	201
350	1	3	563	gi|537052	ORF_f286 (Escherichia coli)	46	35	561
384	1	2	862	gi|1221884	(urea?) amidolyase (Haemophilus influenzae)	46	31	861
410	4	1876	2490	gi|1110518	proton antiporter efflux pump (Mycobacterium smegmatis)	46	24	615
432	1	2663	1455	gi|1197634	orf4: putative transporter; Method: conceptual translation supplied by author (Mycobacterium smegmatis)	46	27	1209
458	1	2419	1211	gi|15470	portal protein (Bacteriophage SPP1)	46	30	1209
517	5	2477	4192	gi|1523812	orf5 (Bacteriophage A2)	46	23	1716
540	3	1512	1285	gi|215635	pacA (Bacteriophage P1)	46	30	228
587	2	649	1242	gi|537148	ORF_f181 (Escherichia coli)	46	29	594
1218	1	747	391	gi|1205456	single-stranded-DNA-specific exonuclease (Haemophilus influenzae)	46	30	357

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3585	1	1	402	gi|450688	hsdM gene of EcoprrI gene product (Escherichia coli) pir|S38437|S38437 hsdM protein - Escherichia coli pir|S09629|S09629 hypothetical protein A - Escherichia coli (SUB 40-520)	46	33	402
4176	1	673	338	gi|351460	PIM-C.1 gene product (Xenopus laevis)	46	31	336
37	7	4813	5922	gi|606064	ORF_f408 (Escherichia coli)	45	24	1110
38	16	11699	12004	gi|452192	protein tyrosine phosphatase (PTP-BAS, type 2) (Homo sapiens)	45	24	306
87	2	1748	2407	gi|1064813	homologous to sp:PHOR_BACSU (Bacillus subtilis)	45	23	660
103	12	14182	13385	gi|1001307	hypothetical protein (Synechocystis sp.)	45	22	798
112	14	14791	13811	gi|1204389	H. influenzae predicted coding region HI0131 (Haemophilus influenzae)	45	23	981
145	4	4483	3461	gi|220578	open reading frame (Mus musculus)	45	20	1023
170	6	6329	4965	gi|238657	ApoCcytochrome d oxidase, subunit I homolog (Escherichia coli, K12, eptide, 514 aa)	45	27	1365
206	2	5230	4346	gi|1220956	aminotransferase (Haemophilus influenzae)	45	27	885
228	1	60	716	gi|160299	glutamic acid-rich protein (Plasmodium falciparum) pir|A54514|A54514 glutamic acid-rich protein precursor - Plasmodium alciparum	45	23	657
288	1	2	1015	gi|1255425	C13G8.2 gene product (Caenorhabditis elegans)	45	23	1014
313	3	4339	3128	gi|581140	NADH dehydrogenase (Escherichia coli)	45	30	1212
332	1	914	459	gi|870966	P47A4.2 (Caenorhabditis elegans)	45	20	456
344	1	3	221	gi|171225	kinesin-related protein (Saccharomyces cerevisiae)	45	26	219
441	2	1501	1073	gi|142863	replication initiation protein (Bacillus subtilis) pir|B26580|B26580 replication initiation protein - Bacillus ubtilis	45	27	429
672	1	2	982	gi|1311334	M. jannaschii predicted coding region MJ1323 (Methanococcus jannaschii)	45	22	981
763	3	1345	851	gi|606180	ORF_f310 (Escherichia coli)	45	24	495
886	3	379	846	gi|726426	similar to protein kinases and C. elegans proteins F37C12.8 and 37C12.5 (Caenorhabditis elegans)	45	30	468
948	1	3	473	gi|156400	myosin heavy chain (isozyme unc-54) (Caenorhabditis elegans) pir|A37958|MWKW myosin heavy chain B - Caenorhabditis elegans sp|P02566|MYSB_CAEEL MYOSIN HEAVY CHAIN B (NHC B).	45	25	471
1158	1	2	376	gi|1441155	transmission-blocking target antigen (Plasmodium falciparum)	45	35	375
2551	1	4	285	gi|1276705	ORF287 gene product (Porphyra purpurea)	45	28	282
3967	1	42	374	gi|976025	HrsA (Escherichia coli)	45	28	333

TABLE 2

S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	matdh gene name	% sim	% ident	length (nt)
52	7	6931	5846	gi|467378	unknown (Bacillus subtilis)	44	22	1086
138	8	6475	6849	gi|173028	thioredoxin II (Saccharomyces cerevisiae)	44	28	375
221	5	7032	5617	gi|153490	tetracenomycin C resistance and export protein (Streptomyces laucescens)	44	21	1416
252	2	1331	1122	gi|1204989	hypothetical protein (GB:U00022_9) (Haemophilus influenzae)	44	30	210
263	2	3265	2093	gi|1136221	carboxypeptidase (Sulfolobus solfataricus)	44	26	1173
365	4	4963	3524	gi|1296822	orf1 gene product (Lactobacillus helveticus)	44	31	1440
543	3	1315	1833	gi|[illegible]3250	low homology to P20 protein of Bacillus lichiniformis and bleomycin acetyltransferase of Streptomyces verticillus (Bacillus subtilis)	44	24	519
544	4	3942	4892	gi|951460	FIM-C.1 gene product (Xenopus laevis)	44	32	951
792	1	1224	613	gi|205680	high molecular weight neurofilament (Rattus norvegicus)	44	28	612
46	18	11303	11911	gi|1511614	molybdopterin-guanine dinucleotide biosynthesis protein A (Methanococcus jannaschii)	43	27	609
59	8	3665	5128	gi|153490	tetracenomycin C resistance and export protein (Streptomyces laucescens)	43	21	1464
59	10	5536	7527	gi|153022	lipase (Staphylococcus epidermidis)	43	22	1992
99	1	1346	681	gi|1419051	unknown (Mycobacterium tuberculosis)	43	21	666
310	8	9402	12134	gi|397526	clumping factor (Staphylococcus aureus)	43	21	2733
432	3	2782	2303	pir|A60540|A605	sporozoite surface protein 2 - Plasmodium yoelii (fragment)	43	29	480
519	3	2547	3122	sp|Q06530|DHSU_	SULFIDE DEHYDROGENASE (FLAVOCYTOCHROME C) FLAVOPROTEIN CHAIN PRECURSOR (EC 1.8.2.-) (FC) (FCSD).	43	23	576
4	13	12053	13321	gi|295671	selected as a weak suppressor of a mutant of the subunit AC40 of DNA ependant RNA polymerase I and III (Saccharomyces cerevisiae)	42	18	1269
94	2	1768	1091	gi|501027	ORF2 (Trypanosoma brucei)	42	31	678
127	4	5791	4550	gi|42029	ORF1 gene product (Escherichia coli)	42	21	1242
297	3	1515	1036	gi|142790	ORF1; putative (Bacillus firmus)	42	25	480
344	6	4097	3525	gi|40320	ORF 2 (AA 1-203) (Bacillus thuringiensis)	42	30	573
512	1	2167	1115	gi|405957	yeeF (Escherichia coli)	42	23	1053
631	1	2434	1223	gi|580920	rodD (gtaA) polypeptide (AA 1-673) (Bacillus subtilis) pir|S06048|S06048 probable rodD protein - Bacillus subtilis sp|P13484|TAGE_BACSU PROBABLE POLY(GLYCEROL-PHOSPHATE) LPHA-GLUCOSYLTRANSFERASE (EC 2.4.1.52) (TECHOIC ACID BIOSYNTHESIS ROTEIN E).	42	24	1212

TABLE 2

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S. aureus - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match acession	match gene name	% sim	% ident	length (nt)
685	3	2359	1739	gi|1303784	YqeD (Bacillus subtilis)	42	19	621
4132	1	787	395	gi|1022910	protein tyrosine phosphatase (Dictyostelium discoideum)	42	25	393
86	2	1375	884	gi|309506	spermidine/spermine N1-acetyltransferase (Mus saxicola) pir|S43430|S43430 spermidine/spermine N1-acetyltransferase - spiny ouse (Mus saxicola)	41	30	492
191	12	14797	14075	gi|1124957	orf4 gene product (Methanosarcina barkeri)	41	22	723
212	6	2150	3127	gi|15873	observed 35.2Kd protein (Mycobacteriophage 15)	41	26	978
213	3	1263	2000	gi|633692	TrsA (Yersinia enterocolitica)	41	18	738
408	4	2625	3386	gi|1197634	orf4; putative transporter; Method: conceptual translation supplied by author (Mycobacterium smegmatis)	41	24	762
542	1	3	1103	gi|457146	rhoptry protein (Plasmodium yoelii)	41	21	1101
924	1	2	475	pir|JH0148|JH01	nucleolin - rat	41	30	474
1562	1	1	402	gi|552184	asparagine-rich antigen Pfa35-2 (Plasmodium falciparum) pir|S27826|S27826 asparagine-rich antigen Pfa35-2 - Plasmodium alciparum (fragment)	40	20	402
2395	1	518	261	pir|S42251|S422	hypothetical protein 5 - fowlpox virus	40	18	258
4077	1	3	305	gi|1055055	coded for by C. elegans cDNA yk37g1.5; coded for by C. elegans cDNA yk5c9.5; coded for by C. elegans cDNA yk1a9.5; alternatively spliced form of F52C9.8b (Caenorhabditis elegans)	39	21	303
958	1	1003	503	gi|1255425	C33G8.2 gene product (Caenorhabditis elegans)	37	25	501
59	12	8294	10636	gi|535260	STARP antigen (Plasmodium reichenowi)	36	24	2343
63	5	3550	8079	gi|298032	EF (Streptococcus suis)	36	19	4530
544	3	2507	3601	gi|1015903	ORF YJR15ic (Saccharomyces cerevisiae)	35	22	1095
63	4	1949	3574	gi|552195	circumsporozoite protein (Plasmodium falciparum) sp|P05691|CSP_PLAFL CIRCUMSPOROZOITE PROTEIN (CS) (FRAGMENT).	32	27	1626

TABLE 2

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
4	1	1234	692
4	3	1712	2278
4	4	3703	3032
4	14	11073	12585
5	2	2539	1604
5	3	1532	1771
5	7	4741	4550
5	9	7939	6422
5	12	8711	8547
6	4	2359	1982
8	1	349	176
11	8	5144	5983
11	9	5968	6498
11	10	6472	6284
11	16	10954	11271
12	5	5352	4942
12	6	4596	4862
15	3	1895	1650
16	10	11263	10835
18	2	1093	917
20	9	9125	7764
20	10	8571	8230
20	12	9201	8803
20	13	12158	10470
23	1	674	339
23	6	6138	5485
23	8	6376	5942

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
23	9	7651	6881
23	15	12618	12830
24	4	4556	4185
24	6	5642	5241
25	2	1824	2402
31	2	505	849
31	3	1177	1524
31	4	2454	3005
32	2	765	1388
32	9	7952	8575
32	10	8591	8728
32	11	9738	9379
32	12	10797	10087
34	2	1315	1049
36	7	5226	5801
36	11	7575	7261
36	12	7424	7621
37	4	3158	2964
38	2	1585	980
38	11	6425	6868
38	20	16982	16371
38	26	20253	20804
38	27	20722	21264
39	1	1	627
40	1	805	404
43	1	796	428
44	4	2674	2324

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
44	5	2484	3263
44	14	10587	10129
44	20	13724	13536
44	21	13596	13994
45	7	6575	6297
46	8	6365	6520
46	12	10449	10976
46	17	15032	15424
47	1	288	1079
48	9	7620	7778
50	1	1612	962
50	2	1621	1316
51	1	738	370
51	5	2520	2245
53	1	442	287
53	7	6705	6319
54	7	9014	8709
55	1	592	326
55	3	1052	786
56	1	1	261
56	3	1551	1228
56	4	1970	1560
56	17	19092	18712
57	4	3694	3521
57	8	5436	5822
58	9	8885	8553
59	3	1366	1509

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
59	6	3026	2802
59	7	3770	3570
59	9	4946	4563
59	11	7518	8378
59	13	10401	16403
62	2	2696	1521
62	11	5440	5757
63	1	1	336
67	1	900	1781
67	2	1774	2610
67	3	2591	3904
67	8	7110	6955
68	1	78	326
70	6	6761	5199
70	11	8935	8645
77	3	1590	1192
79	2	1509	1228
79	3	1411	1791
83	1	2	403
85	9	8300	8653
85	10	8969	8781
86	3	1426	1232
87	8	9187	9366
88	3	1620	1922
89	1	3	161
89	7	5042	4878
91	1	1098	550

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
91	3	3938	3141
92	2	449	928
92	3	1958	1467
92	9	5638	6024
94	1	661	332
94	3	2445	1813
94	4	2583	2197
96	11	10601	11050
99	6	4672	4523
99	7	5014	4784
100	8	7658	7287
102	7	4697	4368
103	3	2496	2035
104	1	2	694
104	2	699	1277
105	1	1235	693
105	3	3233	2655
105	1	3	221
106	3	1209	1355
107	1	1081	542
109	4	4025	3651
109	13	11625	11996
109	14	11981	12268
109	20	17401	17688
110	1	2	760
114	10	8764	9384
116	1	1	309

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
116	3	6273	4462
116	8	11049	9976
116	9	10313	10158
120	5	3703	3320
120	6	4270	3869
120	13	9290	9844
121	2	417	569
126	3	1050	818
127	3	2648	3196
127	5	4084	4395
131	6	6773	6438
132	2	715	1695
134	1	2	667
135	2	512	258
135	3	1124	729
138	1	3	152
138	7	6008	6463
140	1	2060	1032
140	2	2019	1513
140	5	2387	2743
142	2	1360	2388
142	7	8830	7586
143	7	7290	6502
144	1	1227	640
146	1	2	511
146	3	502	1350
146	4	3673	2540

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
146	5	2874	3071
147	1	1	339
149	11	3956	3615
149	12	4036	3785
149	13	4507	4145
149	15	4807	4610
149	16	5495	5049
149	18	5739	5491
149	21	7416	7054
149	23	9216	8521
149	24	9681	9106
149	25	10679	9897
150	2	2303	1587
154	3	1795	1508
154	8	6586	6398
154	14	12704	12147
154	15	13531	12803
156	1	315	593
157	3	1183	2232
158	2	1471	1064
159	3	452	808
161	2	876	1808
161	6	4653	4279
161	7	4803	4540
161	8	4896	4717
161	11	5817	5638
163	2	1604	840

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
163	5	2796	2344
163	7	2952	2647
163	9	4905	5132
164	3	1338	1147
166	3	5213	4854
168	4	2500	2868
168	5	3595	4158
170	3	2517	2777
171	2	2277	1450
171	11	12576	11125
172	1	3	278
172	2	1940	1149
173	1	1289	708
173	5	7001	6114
174	2	593	1105
175	3	2552	2890
175	5	3820	3335
175	7	4342	4506
182	4	5477	4986
184	5	6043	5702
188	2	1210	1755
188	4	2647	2994
189	6	2614	3019
190	3	1998	2564
191	1	1	153
191	2	950	669
191	10	11786	13019

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
191	11	12902	12363
192	1	91	426
195	3	2106	1932
195	5	2899	2606
198	2	1016	1591
201	1	170	625
203	2	783	1466
206	6	8930	7815
206	12	13947	11636
206	21	28208	27960
212	2	170	817
212	3	796	1167
212	7	3128	3436
212	9	3749	4075
213	1	1	705
214	2	1076	570
214	6	4064	3738
214	9	6600	6995
214	10	7864	7469
217	1	1927	965
218	1	178	657
218	3	1776	2156
220	2	1851	1369
220	3	3251	2262
220	7	8275	7208
220	8	10244	8661
220	9	11796	10216

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig No.	ORF ID	Start (nt)	Stop (nt)
221	4	3095	2613
221	9	11428	10757
226	1	3	659
226	2	2196	1459
226	3	1476	1961
227	1	2	487
227	2	460	975
227	4	1855	2121
227	5	2052	2345
227	6	4760	3768
227	9	5591	6367
228	5	2503	2877
228	6	2846	3526
233	7	3944	3762
236	2	809	579
238	2	1975	1391
239	2	1417	905
241	5	4495	4314
242	2	1677	1363
243	1	127	576
244	1	1291	647
244	2	3035	1962
245	2	1614	1258
246	1	69	215
246	4	738	1733
249	3	3906	3712
250	1	494	249

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
254	1	1	156
256	2	956	1144
257	3	3700	3227
260	4	4906	4580
261	4	2196	2606
261	6	3214	3681
264	2	135	439
264	5	5252	4533
264	6	4739	5107
267	2	1323	931
268	4	5140	4700
272	1	862	446
272	3	1200	1439
272	9	4691	4909
272	10	6469	6035
276	4	1746	1901
278	1	224	553
278	5	3299	3448
278	7	4849	5127
285	2	551	736
288	3	1756	1950
288	5	2055	2276
289	1	2107	1055
290	2	2234	1932
291	2	332	622
291	5	1545	2051
295	3	1606	1349

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
295	4	2728	2141
295	5	2220	2762
297	2	788	465
298	1	2	205
300	2	2380	1928
301	7	2794	2624
304	1	3	194
306	1	109	654
306	5	4036	4257
307	1	674	339
307	8	3645	3995
308	1	1	654
308	2	1120	599
308	4	2643	2332
313	2	2314	1919
314	1	10	702
316	2	982	1341
316	6	2758	3165
317	1	2	1114
317	3	4570	3458
321	6	5645	5217
321	7	6319	6140
321	8	7450	6794
322	2	827	543
326	2	165	1112
326	3	1117	1467
328	1	936	469

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
328	5	3452	3276
329	1	3	719
329	2	781	1212
329	3	1471	1833
330	1	576	289
330	3	1447	1623
332	3	2353	2204
332	7	4971	5138
333	2	3295	3128
335	1	864	433
337	2	95	526
340	2	1658	1356
341	1	3	281
341	3	2476	3192
341	5	3618	3944
341	6	3929	4558
344	5	3197	2889
345	1	1532	768
346	2	221	592
350	3	1410	1598
352	2	2178	1765
352	3	7316	4596
352	7	7967	8404
352	8	8906	9247
352	9	10171	9854
359	1	1	546
362	1	3	656

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
364	2	2158	1808
364	8	10974	10714
365	2	1612	1313
365	5	4680	4090
365	7	4980	6239
366	3	520	1719
367	3	906	1085
368	1	748	494
375	1	2	136
380	3	1351	1097
389	1	1	276
390	1	2	877
390	2	1373	1549
391	2	751	560
395	1	391	197
396	1	2132	1068
398	3	1344	1141
399	1	176	669
401	3	566	847
402	2	100	465
404	8	5561	5370
408	2	3507	3269
408	3	2875	2672
408	5	3524	4423
410	3	2111	1890
413	1	880	488
416	1	607	320

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
416	2	578	847
416	3	2195	1590
417	1	3	179
417	2	161	616
420	2	788	513
422	2	357	677
431	2	856	1407
432	2	446	1084
433	1	1	417
433	3	2311	2033
434	1	942	535
434	2	2089	1235
440	1	1	450
442	2	1269	3320
443	3	1873	1520
444	1	1	696
444	7	6761	6366
451	1	940	614
453	2	896	636
453	8	3833	4786
453	9	4718	4512
453	10	4937	4731
455	1	434	219
455	2	472	930
459	1	265	687
462	1	2	247
466	2	1494	907

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
467	1	654	349
468	1	2	250
469	1	1488	925
469	3	2386	3372
469	4	3464	3706
470	1	77	538
470	6	4098	3694
470	7	6330	5686
470	9	7351	8181
470	10	8175	9773
471	1	940	500
471	2	1562	1017
476	1	70	267
477	1	2	760
477	3	1764	2081
477	4	2066	2332
480	5	4016	4261
481	2	956	480
486	3	613	774
487	6	1795	2112
488	1	715	359
492	1	127	675
493	1	2	520
493	2	496	1242
502	3	1149	1571
504	1	690	346
505	5	4566	4150

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
511	2	1741	1232
512	2	583	747
515	1	609	812
517	4	2179	2511
520	4	2097	2360
520	6	1908	3669
527	1	1	498
528	1	637	335
529	2	1679	1104
530	7	5298	5534
536	1	308	156
538	1	1362	726
538	3	2203	2880
538	5	3531	3121
538	6	4348	3731
540	1	996	664
540	2	1495	1031
541	1	89	433
541	2	719	432
542	2	1048	1272
545	2	1012	734
551	1	2145	1129
555	2	892	704
558	3	1357	1154
558	4	1760	1458
558	5	2105	1821
558	6	2166	2020

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
558	7	2636	2322
558	8	3053	2802
558	9	3986	3453
560	1	475	921
565	3	1706	1485
571	1	308	156
571	3	994	1206
577	1	2	199
577	2	163	453
579	1	1	477
579	2	1784	1200
583	1	1988	996
585	1	946	539
587	1	22	573
588	2	1896	1372
588	3	1742	1554
590	1	47	334
592	2	1455	1141
593	1	2	775
593	2	817	1122
595	1	87	890
596	3	1593	1435
602	1	8	169
603	5	1071	1469
606	1	322	768
607	5	1444	1226
610	1	1029	541

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
612	1	3	500
616	1	991	650
617	2	736	491
622	1	36	347
625	4	2046	2549
627	1	67	210
628	1	901	452
631	3	4789	4004
634	1	1448	759
636	1	189	368
636	2	1929	1063
637	2	2323	1994
638	1	227	1081
639	1	518	261
639	2	1377	811
641	1	118	444
642	3	1615	1331
642	4	2260	1847
643	1	3	608
645	4	1534	1758
645	6	2025	2321
645	7	2940	2468
648	1	2	1045
660	1	77	601
660	2	576	872
661	1	1725	961
664	2	89	304

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
667	1	3	413
668	1	1	330
671	2	812	516
673	1	3	338
674	2	865	584
679	1	1	237
679	3	1589	1906
688	1	1236	835
688	2	1352	1077
694	1	3	143
696	2	818	432
706	1	3[illegible]	224
709	3	1183	1449
711	1	3	908
715	1	3	167
716	1	2	637
721	1	133	570
722	1	763	383
723	1	1656	829
723	2	1498	1112
727	1	2	472
729	1	268	441
731	1	130	828
735	1	2	214
736	1	3	782
738	1	2	298
742	1	3	230

TABLE 3

S. aureus - Putative coding regions of naval proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
745	3	1148	780
748	2	282	464
749	1	685	344
751	1	901	452
755	1	97	522
755	2	520	918
758	2	663	400
764	2	1033	746
767	1	1	405
768	1	2	373
771	1	1058	534
778	1	1735	902
785	1	1790	1023
787	1	1260	631
791	1	3	224
799	1	15	260
804	1	304	711
805	1	3	680
808	1	219	642
810	1	2221	1112
810	2	1774	1442
812	1	38	979
817	1	714	358
818	2	487	1104
819	2	1529	1032
819	3	1748	1419
820	1	195	1064

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
828	1	506	255
829	1	48	800
830	1	578	291
832	1	594	298
835	1	320	796
840	3	491	709
845	1	912	457
850	2	303	449
853	1	715	359
860	1	2	256
864	1	18	410
864	2	383	715
864	6	1676	1428
870	1	1	588
873	1	906	454
875	1	584	294
877	1	1661	1020
878	1	981	544
879	1	1567	785
881	1	1	243
882	1	389	604
890	1	2	508
905	1	793	398
906	1	852	544
912	1	373	188
913	1	3	290
913	2	1092	547

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
915	1	6	161
915	2	169	402
921	1	126	386
927	1	1578	808
928	1	2	385
929	1	2	400
932	1	2	400
934	1	1	384
936	1	1052	528
937	1	2	616
945	1	220	645
945	2	649	1242
946	1	1702	950
949	1	1	270
951	1	3	362
955	1	3	143
960	1	723	400
963	1	1	162
965	1	690	346
966	1	1079	606
969	1	3	302
971	1	12	170
974	1	319	161
976	1	692	348
977	1	2	211
982	1	1926	982
984	1	589	296

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig #ID	ORF ID	Start (nt)	Stop (nt)
987	1	3	467
993	1	1	525
994	1	920	549
1004	1	557	318
1014	1	624	313
1015	1	2	463
1016	1	288	145
1019	1	1205	660
1021	1	839	474
1024	1	595	299
1024	2	276	431
1030	1	673	338
1032	1	355	179
1040	1	794	399
1043	1	3	269
1044	2	115	390
1047	1	1	159
1051	1	704	354
1051	2	1233	733
1063	1	2	400
1069	1	2	148
1069	2	769	533
1075	1	707	399
1077	1	97	405
1081	1	58	438
1086	1	1	384
1087	2	246	431

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1088	1	3	374
1096	1	474	238
1098	1	1015	509
1100	1	1020	511
1100	2	1520	1158
1101	1	703	353
1102	1	385	194
1107	1	2	580
1114	1	3	422
1115	1	2	268
1119	1	22	267
1129	1	40	342
1132	1	360	181
1133	1	609	376
1144	1	446	225
1147	1	558	280
1153	1	1	153
1154	1	3	818
1159	1	1	330
1161	1	341	186
1164	1	427	254
1171	1	19	240
1171	2	108	299
1183	1	2	379
1195	1	355	179
1196	1	1	189
1200	1	33	197

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1203	2	129	464
1222	2	105	401
1232	1	1	387
1240	1	2	175
1247	1	520	311
1271	1	412	221
1286	1	2	595
1295	1	1	165
1306	1	367	185
1314	2	158	631
1316	1	58	570
1359	1	384	193
1370	1	1	402
1371	1	1	345
1374	1	710	357
1378	1	2	400
1392	1	3	413
1411	1	202	432
1433	1	311	167
1450	1	2	256
1453	1	295	149
1471	1	721	398
1477	1	869	639
1502	1	794	399
1518	1	126	449
1534	1	283	143
1546	1	3	401

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1547	1	506	255
1583	1	3	350
1587	1	3	563
1602	2	170	679
1629	1	1	402
1665	1	468	235
1760	1	625	314
1762	1	3	200
1876	2	119	286
1895	1	2	379
1931	1	798	400
1976	2	715	383
2055	2	252	401
2056	1	331	167
2150	1	523	263
2157	1	794	399
2164	1	564	283
2175	1	218	400
2212	1	492	331
2238	1	732	367
2242	1	3	167
2252	1	330	166
2252	2	622	398
2255	1	47	352
2256	1	679	341
2259	1	301	152
2421	1	296	150

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
3046	1	367	185
3049	1	553	278
3050	1	3	314
3052	1	504	253
3065	1	2	157
3070	1	357	190
3075	1	440	222
3080	1	1	285
3092	1	320	162
3093	1	411	250
3100	1	52	237
3103	1	47	298
3118	1	344	174
3123	1	2	145
3127	1	1	147
3138	1	336	169
3142	1	388	203
3144	1	664	386
3151	1	337	170
3155	2	202	384
3168	1	12	176
3205	1	288	145
3282	1	1	150
3303	2	239	400
3371	2	211	399
3558	1	2	148
3558	2	36	401

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
3046	1	367	185
3049	1	553	278
3050	1	3	314
3052	1	504	253
3065	1	2	157
3070	1	357	190
3075	1	440	222
3080	1	1	285
3092	1	320	162
3093	1	411	250
3100	1	52	237
3103	1	47	298
3118	1	344	174
3123	1	2	145
3127	1	1	147
3138	1	336	169
3142	1	388	203
3144	1	666	386
3151	1	337	170
3155	2	202	384
3168	1	12	176
3205	1	288	145
3282	1	1	150
3303	2	239	400
3371	2	211	399
3558	1	2	148
3558	2	36	401

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
3568	1	751	377
3595	1	757	380
3618	1	2	238
3618	2	130	402
3622	1	86	358
3622	2	664	398
3642	1	876	439
3649	1	781	398
3651	1	625	314
3664	1	467	637
3674	1	55	402
3677	1	619	311
3704	1	1	402
3726	1	535	269
3765	1	510	256
3779	1	554	357
3794	1	266	135
3794	2	667	377
3796	2	638	375
3801	1	474	262
3806	1	453	298
3807	1	42	389
3815	1	798	400
3827	1	3	320
3842	1	781	392
3853	1	671	399
3855	1	1	324

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
3857	1	2	235
3861	1	590	297
3865	1	695	399
3897	1	3	173
3897	2	141	400
3898	2	225	401
3921	2	103	342
3927	1	70	375
3930	1	76	234
3946	2	651	382
3951	2	105	377
3965	1	646	344
3973	1	795	400
3981	1	3	311
3998	1	3	356
4001	1	481	296
4003	1	90	335
4018	1	2	259
4018	2	186	401
4021	1	1	345
4043	1	3	344
4054	1	3	344
4066	1	1	150
4070	1	1	324
4072	2	187	390
4073	1	1	285
4077	2	127	372

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
4083	1	3	359
4090	1	27	368
4101	1	103	297
4105	1	1	306
4107	1	570	286
4119	1	629	339
4121	1	740	372
4123	1	3	230
4127	1	3	341
4128	1	2	331
4130	1	768	415
4146	1	97	381
4157	1	3	206
4186	1	505	254
4224	1	510	256
4239	1	1	348
4242	1	709	356
4252	1	589	296
4253	1	1	174
4256	1	568	323
4258	2	498	334
4267	1	284	144
4271	1	2	304
4287	1	303	163
4289	1	471	319
4302	1	153	305
4304	1	1	186

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
4304	2	96	314
4306	1	2	151
4318	1	576	289
4322	1	5	148
4331	1	439	221
4331	2	528	364
4338	1	728	399
4346	1	471	277
4367	2	117	311
4373	1	2	268
4381	1	574	326
4384	3	614	309
4397	1	9	311
4402	1	1	249
4403	1	606	328
4406	1	3	317
4411	1	2	280
4411	2	697	398
4412	1	2	364
4418	1	3	230
4424	1	601	398
4443	1	427	215
4471	1	643	323
4478	1	540	271
4482	1	50	289
4489	1	601	302
4491	1	12	206

TABLE 3

S. aureus - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
4495	1	3	179
4496	1	500	252
4500	1	130	306
4511	1	493	248
4518	1	1	246
4526	1	480	241
4527	1	2	163
4532	1	3	239
4542	1	11	175
4567	1	36	200
4573	1	1	231
4578	1	642	322
4619	1	1	160
4620	1	349	176
4662	1	1	246
4669	1	2	157
4680	1	28	183
4690	1	344	174

Table 4

ORF	SEQ ID NO	BLAST HOMOLOG	Antigenic Regions Region 1	Region 2	Region 3	Region 4
168_6	5192	lipoprotein	36-45	84-103	152-161	176-185
238_1	5193	chrA	21-39	48-58	84-95	232-249
51_2	5194	OppB gene product (B. sub	20-36	70-79	100-112	121-131
278_3	5195	lipoprotein 1	20-29	59-73	85-97	162-171
276_2	5196	lipoprotein	21-33	65-74	177-186	211-220
45_4	5197	ProX	28-37	59-69	85-100	120-129
316_8	5198	hypothetical protein	45-54	88-97	182-192	243-253
154_15	5199	unknown	31-40	48-58	79-88	95-104
228_3	5200	unknown	25-38	40-52	64-74	80-89
228_6	5201	unknown	29-41	89-101	128-143	173-184
50_1	5202	unknown	21-33	52-61	168-182	197-206
112_7	5203	iron-binding periplasmic	21-31	58-67	92-101	111-120
442_1	5204	unknown	30-39	91-100	122-137	182-192
66_2	5205	unknown	50-59	104-116	127-136	167-182
304_2	5206	Q-binding periplasmic	19-28	48-57	75-84	103-116
44_1	5207	hypothetical protein	27-36	86-95	129-138	192-201
161_4	5208	SphX	27-44	149-161	166-175	201-210
46_5	5209	cmpC (permease)	21-33	61-70	83-92	100-109
942_1	5210	traH [Plasmid pSK41]	83-92	109-118	127-142	
5_4	5211	ORF (S. aureus)	12-22	87-96	111-120	151-160
20_4	5212	peptidoglycan hydrolase (S	24-34	129-138	141-150	161-171
328_2	5213	lipoprotein (H. flu)	81-90	123-133	290-299	
520_2	5214	fibronectin binding protein	44-54	63-79	81-90	95-110
771_1	5215	emm1 gene product (S. py	30-39	65-82	96-106	112-121
999_1	5216	predicted trithorax prot. (D	7-16	120-129	157-166	
853_1	5217	ORF2136 (Marchantia polyr	43-52	88-97	102-111	
287_1	5218	psaA homolog	13-22	28-44	72-82	114-124
288_2	5219	cell wall enzyme	14-23	89-98		
596_2	5220	penicillin binding protein 2b	40-49	59-68	76-87	106-115
217_5	5221	fibronectin/fibrinogen bindi	28-37	40-49	62-71	93-111
217_6	5222	fibronectin/fibrinogen bp	10-19	31-40	54-62	73-92
528_3	5223	myosin cross reactive prote	4-13	29-47	60-73	90-99
171_11	5224	EF	20-31	91-110		
63_4	5225	penicillin binding protein 2b	12-21	59-68	95-104	
353_2	5226		46-55	62-71		
743_1	5227	29 kDa protein in fimA regi	23-32	68-79	94-103	175-184
342_4	5228	Twitching motility	10-19	48-60	83-92	111-121
69_3	5229	arabinogalactan protein	97-106	132-141	158-167	180-189
70_6	5230	nodulin	36-45	48-57	137-160	179-188
129_2	5231	glycerol diester phosphodie	8-17	41-50	55-74	97-106
58_5	5232	PBP (S. aureus)	26-35	70-79	117-126	152-161
188_3	5233	MHC class II analog (S. aure	72-81	94-103	115-124	136-145
236_6	5234	histidine kinase domain (Dic	24-33	52-67	81-94	106-121
310_8	5235	clumping factor (S. aureus)	59-71	77-86	93-102	118-127
601_1	5236	novel antigen/ORF2 (S. au	45-54	91-104	108-117	186-195
544_3	5237	ORF YJR151c (S. cerevisae	76-90	101-111	131-140	154-164
662_1	5238	MHC class II analog (S. aure	22-32	71-80	89-98	114-122
87_7	5239	5' nucleotidase precursor ('	29-45	62-71	105-114	125-137
120_1	5240	B65G gene product (B. sub	102-111			

Table 4

ORF	Antigenic Regions (cont)					
	Region 5	Region 6	Region 7	Region 8	Region 9	Region 10
168_6	244-272	303-315				
238_1	260-269	291-301	308-317			
51_2	140-152	188-208	211-220	256-266	273-283	
278_3	198-209					
276_2	255-268					
45_4	177-199	221-230	234-243	268-279	284-293	304-313
316_8						
154_15	148-157	177-187	202-211			
228_3	101-119	139-154	166-181			
228_6						
50_1						
112_7	136-149	197-211	218-229	253-273		
442_1	199-210	247-257	264-277	287-309		
66_2						
304_2	178-187	250-259				
44_1						
161_4						
46_5	131-141	162-176	206-215	243-252	264-273	285-294
942_1						
5_4	189-205	230-239	246-264	301-318	340-354	378-387
20_4	202-212	217-234	260-275	314-336	366-373	380-391
328_2						
520_2						
771_1	145-154					
999_1						
853_1						
287_1	154-164					
288_2						
596_2	121-130					
217_5	244-253	259-268	288-297	302-311		
217_6	144-158	174-183	188-197	207-216	226-242	
528_3						
171_11						
63_4						
353_2						
743_1	197-207					
342_4						
69_3	195-211					
70_6	206-215	263-272	291-301	331-340	358-371	390-414
129_2	117-127	141-157	168-183	202-211	222-231	261-270
58_5	184-203	260-269	275-299	330-344	372-381	424-433
188_3						
236_6	138-147	163-172	187-198	244-261	268-278	308-317
310_8	131-140	144-153	177-186	190-199	204-213	216-227
601_1	208-218					
544_3	170-179	184-193	224-235	274-287	327-336	352-361
662_1						
87_7						
120_1						

Table 4

ORF	Antigenic Regions (cont)					
	Region 11	Region 12	Region 13	Region 14	Region 15	Region 16
168_6						
238_1						
51_2						
278_3						
276_2						
45_4						
316_8						
154_15						
228_3						
228_6						
50_1						
112_7						
442_1						
66_2						
304_2						
44_1						
161_4						
46_5	306-315					
942_1						
5_4	393-407	416-426	456-465			
20_4	396-405	410-419	461-481			
328_2						
520_2						
771_1						
999_1						
853_1						
287_1						
288_2						
596_2						
217_5						
217_6						
528_3						
171_11						
63_4						
353_2						
743_1						
342_4						
69_3						
70_6	453-471	506-515				
129_2	296-315					
58_5						
188_3						
236_6	358-377	410-423	428-439	442-457	467-476	480-493
310_8	238-251	256-275	281-290	296-310	314-333	338-347
601_1						
544_3						
662_1						
87_7						
120_1						

Table 4

ORF	Antigenic Regions (cont)					
	Region 17	Region 18	Region 19	Region 20	Region 21	Region 22
168_6						
238_1						
51_2						
278_3						
276_2						
45_4						
316_8						
154_15						
228_3						
228_6						
50_1						
112_7						
442_1						
66_2						
304_2						
44_1						
161_4						
46_5						
942_1						
5_4						
20_4						
328_2						
520_2						
771_1						
999_1						
853_1						
287_1						
288_2						
596_2						
217_5						
217_6						
528_3						
171_11						
63_4						
353_2						
743_1						
342_4						
69_3						
70_6						
129_2						
58_5						
188_3						
236_6						
310_8	357-366	370-379	429-438	443-452	478-487	551-560
601_1						
544_3						
662_1						
87_7						
120_1						

Table 4

ORF	Antigenic Regions (cont)					
	Region 23	Region 24	Region 25	Region 26	Region 27	Region 28
168_6						
238_1						
51_2						
278_3						
276_2						
45_4						
316_8						
154_15						
228_3						
228_6						
50_1						
112_7						
442_1						
66_2						
304_2						
44_1						
161_4						
46_5						
942_1						
5_1						
20_4						
328_2						
520_2						
771_1						
999_1						
853_1						
287_1						
288_2						
596_2						
217_5						
217_6						
528_3						
171_11						
63_4						
353_2						
743_1						
342_4						
69_3						
70_6						
129_2						
58_5						
188_3						
236_6						
310_8	622-632	670-685	708-718	823-836	858-867	877-886
601_1						
544_3						
662_1						
87_7						
120_1						

Table 4

ORF	Antigenic Regions (cont)	
	Region 29	Region 30
168_6		
238_1		
51_2		
278_3		
276_2		
45_4		
316_8		
154_15		
228_3		
228_6		
50_1		
112_7		
442_1		
66_2		
304_2		
44_1		
161_4		
46_5		
942_1		
5_4		
20_4		
328_2		
520_2		
771_1		
999_1		
853_1		
287_1		
288_2		
596_2		
217_5		
217_6		
528_3		
171_11		
63_4		
353_2		
743_1		
342_4		
69_3		
70_6		
129_2		
58_5		
188_3		
236_6		
310_8		
601_1		
544_3		
662_1		
87_7		
120_1		

Table 4

ORF		BLAST HOMOLOG	Antig nic Regions Region 1	Region 2	Region 3	Region 4
46_1	5241	aldehyde dehydrogenase	8-17	36-52	83-96	112-121
63_4	5242	glycerol ester hydrolase (P.	9-26	57-73	93-107	123-133
174_6	5243	ketopantoate hydroxymeth	71-80	203-212	242-254	265-274
206_16	5244	ornithine acetyltransferase	1-10	34-43	54-63	194-210
267_1	5245	NaH-antiporter protein (E. I	120-129	332-347	398-408	
322_1	5246	acriflavin resistance protein	58-75	153-164	203-231	264-284
415_2	5247	transport ATP-binding prot	108-126	218-227	298-308	315-334
214_3	5248	2-nitropropane dioxygenase	123-136	216-233	283-292	297-306
587_3	5249	clumping factor	5-14	43-54	59-68	76-95
685_1	5250	signal peptidase	59-68	72-81	86-95	99-108
54_3	5251	fibronectin binding protein I	23-32	37-46	50-59	89-98
54_4	5252	fibronectin binding protein I	43-52	66-75	95-104	147-156
54_5	5253	fibronectin binding protein I	49-60	81-90		
54_6	5254	fibronectin binding protein I	55-71	82-97	139-158	175-186
328_1	5255	lipoprotein (H. flu)	11-20	61-70	96-105	

Table 4

ORF	Antigenic Regions (cont) Region 5	Region 6	Region 7	Region 8	Region 9	Region 10
46_1	215-242	333-352	376-385	416-432	471-487	
63_4	145-154	191-202	212-223	245-265	274-283	291-300
174_6						
206_16	239-259	275-284				
267_1						
322_1	298-319	350-359				
415_2	344-353	371-380	395-404	456-465	486-495	518-527
214_3	318-337	365-375				
587_3	106-115	142-151	156-166	173-182	186-198	204-213
685_1	113-122	130-145				
54_3	128-138	185-194	217-226	251-260	268-277	295-305
54_4	175-188	191-200	203-212	220-229		
54_5						
54_6	220-230	287-304	317-326	344-353	364-373	378-387
328_1						

Table 4

ORF	Antigenic Regions (cont)					
	Region 11	Region 12	Region 13	Region 14	Region 15	Region 17
46_1						
63_4	306-315	319-328	366-376	395-420	453-462	467-476
174_6						
206_16						
267_1						
322_1						
415_2	539-555					
214_3						
587_3	217-226	278-287	318-327	332-342	351-360	377-386
685_1						
54_3	316-325	329-345	355-372	387-396	416-425	438-448
54_4						
54_5						
54_6	396-407	427-436	514-531	541-550	569-578	612-622
328_1						

Table 4

ORF	Antigenic Regions (cont)					
	Region 18	Region 19	Region 20	Region 21	Region 22	Region 23
46_1						
63_4	485-500	513-525				
174_6						
206_16						
267_1						
322_1						
415_2						
214_3						
587_3	396-405	426-442	459-470	485-494	505-514	531-562
685_1						
54_3	455-462	472-491	517-536			
54_4						
54_5						
54_6	639-648	673-681	703-715	723-732	749-760	772-788
328_1						

Table 4

ORF	Antigenic Regions (cont)					
	Region 24	Region 25	Region 26	Region 27	Region 28	Region 29
46_1						
63_4						
174_6						
206_16						
267_1						
322_1						
415_2						
214_3						
587_3	567-578	584-601	607-840	844-854	858-870	877-886
685_1						
54_3						
54_4						
54_5						
54_6	793-802	811-826	834-848	866-876	893-903	907-918
328_1						

Table 4

ORF	Antigenic Regions (cont)		
	Region 30	Region 31	
46_1			
63_4			
174_6			
206_16			
267_1			
322_1			
415_2			
214_3			
587_3	889-911	927-936	
685_1			
54_3			
54_4			
54_5			
54_6	925-944	951-997	
328_1			

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: Human Genome Sciences, Inc.
(B) STREET: 9410 Key West Avenue
(C) CITY: Rockville
(D) STATE: Maryland
(E) COUNTRY: US
(F) POSTAL CODE: 20850

(ii) TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

(iii) NUMBER OF SEQUENCES: 5255

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
(B) COMPUTER: HP Vectra 486/33
(C) OPERATING SYSTEM: MSDOS version 6.2
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/009,861
(B) FILING DATE: 05-JAN-1996

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5895 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TCCATTATGA AGTCACAAGT ACTATAAGCT GCGATGTTAC CAATGTTTTT TAAAATCCCA 60

GTAATAAAAT CAAAAAATAA GTTAAATAAT GTATTCATTT TAAGTCCTCC TTAATAAAGa 120

aaataGGTAA TAATGTAATA GCTTCTATTA TGATGCCTAA TTGAATGAAT TGGGCAAATG 180

GCTCTTTGAT GATAAGTGTG ATAATGAAAA GGGTTAAACT AACAATAATC GCATAATATT 240

TTTTTCGTTT AATAAGTCGC ACAGGAATGG GCTTCTTTTT AGTTGCTGCA GGAGCATATA 300

CTGAGATTAC ACCTAAAGAA ATAACTGTTA AAATAATCAT AATTAAAAAG TTAATATGAA 360

AATTTACTAT TACTAAAGGT AAAAGTATAA ATAGTATAAT ACTTTCTACA TAACACCAAA 420

AAGAAGAAGG TGCATGTGCa CCATGTGCAT GtCTTCTTAT TAAATAAAAT GTTAAATTCG 480

TAATTAACGT AAACAGAAAA ATGTTTAAAA TATAGGCAAT AGTATACATA ACAATTAATT 540

TACCTATATT TTTAGCTAAG ACCTGCATCC CTAATCGTAC TTGCAAAAAT TGAATATGAT 600

CTAAGTTATT TCTCTTTTGA AGATACGTGG CAAACTGGTC AATTTTATTA TCAAAATAAT 660

TCAATTTTAC ACCACTCTCC TCACTGTCAT TATACGATTT AGTACAATCT TTTATCATTA 720

TATTGCCTAA CTGTAGGAAA TAAATACTTA ACTGTTAAAT GTAATTTGTA TTTAATATTT 780

TAACATAAAA AAATTTACAG TTAAGAATAA AAAACGACTA GTTAAGAAAA ATTGGAAAAT 840

AAATGCTTTT AGCATGTTTT AATATAACTA GATCACAGAG ATGTGATGGA AAATAGTTGA 900

TGAGTTGTTT AATTTTAAGA ATTTTTATCT TAATTAAGGA AGGAGTGATT TCAATGGCAC 960

AAGATATCAT TTCAACAATC GGTGACTTAG TAAAATGGAT TATCGACACA GTGAACAAAT 1020

TCACTAAAAA ATAAGATGAA TAATTAATTA CTTTCATTGT AAATTTGTTA TCTTCGTATA 1080

GTACTAAAAG TATGAGTTAT TAAGCCATCC CAACTTAATA ACCATGTAAA ATTAGCAAGT 1140

GAGTAACATT TGCTAGTAGA GTTAGTTTCC TTGGACTCAG TGCTATGTAT TTTTCTTAAT 1200

TATCATTACA GATAATTATT TCTAGCATGT AAGCTATCGT AAACAACATC GATTTATCAT 1260

TATTTGATAA ATAAAATTTT TTTCATAATT AATAACATCC CCAAAAATAG ATTGAAAAAA 1320

TAACTGTAAA ACATTCCCTT AATAATAAGT ATGGTCGTGA GCCCCTCCCA AGCTCGCGGC 1380

CTTTTTTGTA ATGAAGAAGG GATGAGTTAA TCATCATTAT GAGACCCGCC GTTAAAATAT 1440

TCATTTGCAA AGGGCGAAAT GGGTTCTTAC TGAGTTATCT ATTATAAAAA AATAAACATA 1560

GACTTATGAA AAATCTCTCA TAAATCTATG TTTAGTCATG aCATGTGTTA AATATTATTT 1620

CGGGCGCTTC TTATTTATAC AAATCTAATT TAATACTTTT AAATACAGGT ATATTTTCgC 1680

GTTGCTGTTC TACTTCATTT AAGTTTAAAT CTACAGTCAA AATATCTGCG GATTCATTTA 1740

ATTCTCCAAC TAAATCTCCA TTTGGGTTTA TAACTATCGA ATGACCAGCA TATTCTGTGT 1800

TACCATCGAA TCCAGTGCTA TTAGTTCCAA TGACAAACAT ATTATTTTCA ATTGCACGTG 1860

CCTTTAGTAA TGAATGCCAA TGTTGAAGAC GTGACATAGG CCATTGCGCC ACATAAAATG 1920

CAATTTTAGC ACCACTACGA GCAGGATATC TTAATAATTC TGGAAAACGT AAATCATAAC 1980

AGATAAGTTG GGTCACATAA GTACCGTCAG ACAATTGAAA GGGTTCAGCT ACGTATTCGC 2040

CAGCGGTTAA AAATTCATGC TCTCTTAACA TAGGAACTAA ATGAACTTTG TCGTATTCaT 2100

TAATCAGCTG GCCACTTTTA TTCACACTAA AAGCTGTATT AAATATTTGA TTGTTTCTAA 2160

TGTTAGAAAC TGACCCAGCT ACGATATCGA CTTTATATTT TTCAGCTAAA TGTTTAATAA 2220

ATGAAAAACT TTGTCCTAGA TTATTATCTG CTTTTTCATT TAAATGCTCT AAATCATAGC 2280

CATTATTCCA CATTTCAGGT AAAACGACTA CATCTACTTC AGCATTCATA TTTTTTTCGA 2340

ACCATTGCGT TATTTGAGTT TCATTTTTAG AACTATCTCC AAAAACAATC GGTAATTGAT 2400

AAATTTGGAC TTTCATAACA TCACATCCTT GATAGATCTT ATATATAACT TACTAAAAGT 2460

TATGTTGAAA CGCAAAAAAC GAGCACAAGA CATAAAATCA AAGTCCTAGG CTCTACAAAG 2520

TTATATTGAC AGTAGTTGAT GGGGCCCCAA CATAGAGAAA TTGGAACACC AATTTCTACA 2580

GACAATGCAA GTTGGGGTGG GCTCTAACAT AAAGAAATAC TTTTTCTTTA GAAATTAGTA 2640

TTTCTTATAC ATGAGTTTTA CTCATGTATT CCTATTCTTA AGTGCACATT AGCAGCGGCT 2700

AATGTGTAAG AACTACTACA TAATGAATAA CTAATGATTC TTTATCATTT CTGTCCCATT 2760

CCTAACAATA TATTGATTAT TTTTTTATTA CGAAACGATC TTCCACTGGA TTAAATGTTT 2820

TTTCGCCAGC AGCTTCACGA ATATCACCAA ATGGCATTTG AGCAATAAGT TTCCAACTTT 2880

TAGGAATATT AAATTCATTT GAAGTCATCT CATCAACAAG TGGATTATAG TGTTGTAATG 2940

AAGCACCTAT GCCTTTAGTA GCTAATGCAG TCCAAATTGC AAATTGATGC ATGGCATTTG 3000

TTTGAGTTGA CCATATTGCA AAATTATCAT AGTAGTTTGG CATTTGTTCT TGTAAACCAC 3060

TTACAACATC TTGATCTTCA TAAAACAAAA TTGTACCGTA TGAATGTTTG AAGTTATCAA 3120

TTTTTTGTTC AGTTGGCTCG AAATCACGAT TCTCTCCCAT GACTTCTTTT AAAATTGCTT 3180

TTGTGTTATC CCAAAATTTA TTATTGTTGT CATTTAACAA GAGAACAATT CTAGTTGATT 3240

CATCGCTAAT TGATATCGAA TCTTTCAAAT TATATATTGA ACGTCTTTCT TCCATTGCAT 3360

TGTCAAAAGT CATTGCTTTT TTATCTTTTT TAAATAAGCC CATAATTATT GCTCCTTCTT 3420

TAGTAAAGAA TACTTAATAG ACTAAGTATA AAATTTATAC TCGTACTTGT AAAGCAATAT 3480

TTACGAAAAT TTCAAGAATA TTAATATTCA TTTTCAAATT CCAAATATAA ATGCATTTTC 3540

AACGCATATT TATTATACTT AGATTAATAC TTACATGAAA AAGGGAGGTG TCTCGTGAAA 3600

TGTCATATCA TTGGTTTAAG AAAATGTTAC TTTCAACAAG TATTTTAATT TTAAGTAGTA 3660

GTAGTTTAGG GCTTGCAACG CACACAGTTG AAGCAAAGGA TAACTTAAAT GGAGAAAAAC 3720

CAACTACTAA TTTGAATCAT AATATAACTT CACCATCAGT AAATAGTGAA ATGAATAATA 3780

ATGAGACTGG GACACCTCAC GAATCAAATC AAACGGGTAA TGAAGGAACA GGTTCGAATA 3840

GTCGTGATGC TAATCCTGAT TCGAATAATG TGAAGCCAGA CTCAAACAAC CAAAACCCAA 3900

GTACAGATTC AAAACCAGAC CCAAATAACC AAAACTCAAG TCCGAATCCT AAACCAGATC 3960

CAGATAACCC GAAACCAAAA CCGGATCCAA AACCAGACCC AGATAAACCA AAGCCAAATC 4020

CGGATCCAAA ACCAGATCCA GATAACCCGA AACCAAATCC AGATCCAAAA CCAGACCCAG 4080

ATAAACCAAA GCCAAATCCG GATCCAAAAC CAGATCCAGA TAAACCAAAG CCAAATCCGA 4140

ATCCAAAACC AGACCCTAAT AAGCCAAATC CTAACCCGTC ACCAGATCCC GATCAACCTG 4200

GGGATTCCAA TCATTCTGGT GGCTCGAAAA ATGGGGGGAC ATGGAACCCA AATGCTTCAG 4260

ATGGATCTAA TCAAGGTCAA TGGCAACCAA ATGGGAATCA AGGAAACTCA CAAAATCCTA 4320

CTGGTAATGA TTTTGTATCC CAACGATTTT TAGCCTTGGC AAATGGGGCT TACAAGTATA 4380

ATCCGTATAT TTTAAATCAA ATTAATAAGT TGGGCAAAGA TTATGGAGAA GTTACTGATG 4440

AAGACATTTA TAATATTATT CGAAAACAAa ATTTCAGCGG AAATGCATAT TTAAATGGAT 4500

TACAACAGCA ATCGAATTAC TTTAGATTCC aATATTTCAA TCCATTGAAA TCAGAAAGGT 4560

ACTATCGTAA TTTAGATGAA CAAGTACTCG CATTAATTAC TGGTGAAATT GGATCAATGC 4620

CAGATTTGAA AAAGCCCGAA GATAAGCCGG ATTCAAAACA ACGCTCATTT GAACCGCATG 4680

AAAAAGACGA TTTTACAGTA GTTAAAAAAC AAGAAGATAA TAAGAAAAGT GCGTCAACTG 4740

CATATAGTAA AAGTTGGCTA GCAATTGTAT GTTCTATGAT GGTGGTATTT TCAATCATGC 4800

TATTCTTATT TGTAAAGCGA AATAAAAAGA AAAATAAAAA CGAATCACAG CGACGATAAT 4860

CCGTGTGTGA TTCGTTTTTT TTATTATGGA ATAAAAATGT GATATATAAA ATTCGCTTGT 4920

TCCGTGGCTT TTTTCAAAGC CTCAGGATTA AGTAATTGGA ATATAACGAC AAATCCGTTT 4980

TGTAACATAT GGATAATAAT TGGAACAGCA AGCCGTTTTG TCCAAACATA TGCTAATGAA 5040

AATATTAATG AACTTACTGT TGTAGCAATA ATAAATGCCA CGATACGATT ACCTTTAATC 5160

GCATTAAATA ATTCTCCAAA GATTACTTTT CTGAATACAT ATTCTTCTAA TAAAGGACCA 5220

ATAATAGATA CAAAGAAGAT AAATATAGGT ATTTTTCGAG CAATAATAAT TAGCTTTTCT 5280

GTATTAGGAC TTACTTGTTG TCCACCATAA ATTTGCGTTA ATACAATGCT CACTACCATT 5340

TGATAAATCA TTACCAATGC AAATCCAAGC AATGCCCATG GAATGATATA TTTTTTAGGT 5400

TCTTTAACTT CTAATTCTAA TTTTGTTGGA TTTTTAATTT TTAAATTAAT TAAAATAATC 5460

GTCGTGGCGG CGATTAAAAA TAGAACAAGT TGTATGTAAA TGACTGCTTT AGTCAGTTCT 5520

ATGCCACTAT ATTGTACAAA TGGTAATTTT TTTACAATGA GAAGCGGTAA AAATTGAGAC 5580

AATATATAAA TAATAACAGT TAGCAATGAT GCCCATAATC tTGTCATAAT TTTCCTCCAA 5640

ATATTTGTTT ATAATTTATT TTATCGTAAA TAACTTGAAG TTACAAAACT TAATTAAAAG 5700

GTTATGACTT GAAATTTTGA CCAAATTTGA TTATTATAAA TGTATGTTAG CACTCTTTAA 5760

TGTTAAGTGC TAAACTTTAG GTTTTTTAAG GAGGAACAAT CATGCTAAAA CCAATTGGAA 5820

ATCGTGTGAT TATTGAGAAA AAAGAACAAG AACAAACAAC TAAAAGTGGn ATTGTTTAAC 5880

TGATAGTGCT AAAGA 5895

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6796 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TTTGAAAAAA CAAGGTACGA TTGGTTTAAT AACATATATG AGAACCGATT CTACACGTAT 60

TTCaGATACT GCCAAAGTTG AAGCAAAACA GTATATAACT GATAAATACG GTGAATCTTA 120

CACTTCTAAA CGTAAAGCAT CAGGGAAACA AGGTGACCaA GATGCCCATG AGGCTATTAG 180

ACCTTCAAGT ACTATGCGTA CGCCAGATGA TATGAAGTCA TTTTTGACGA AAGACCAATA 240

CCGATTATAC AAATTAATTT GGGAACGATT TGTTGCTAGT CAAATGGCTC CAGCAATACT 300

TGATACAGTC TCATTAGACA TAACACAAGG TGACATTAAA TTTAGAGCGA ATGGTCAAAC 360

AATCAAGTTT AAAGGATTTA TGACACTTTA TGTAGAAACT AAAGATGATA GTGATAGCGA 420

AAAGGAAAAT AAACTGCCTA AATTAGAGCA AGGTGATAAA GTCACAGCAA CTCAAATTGA 480

ACCAGCTCAA CACTATACAC AACCACCTCC AAGATATACT GAGGCGAGAT TAGTAAAAAC 540

AAAGCGTAAC TATGTCAAAT TAGAAAGTAA GCGTTTTGTT CCTACTGAGT TGGGAGAAAT 660

AGTTCATGAA CAAGTGAAAG AATACTTCCC AGAGATTATT GATGTGGAAT TCACAGTGAA 720

TATGGAAACG TTACTTGATA AGATTGCAGA AGGCGACATT ACATGGAGGA AAGTAATCGA 780

CGGTTTCTTT AGTAGCTTTA AACAAGATGT TGAACGTGCT GAAGAAGAGA TGGAAAAGAT 840

TGAAATCAAA GATGAGCCAG CCGGTGAAGA CTGTGAAATT TGTGGTTCTC CTATGGTTAT 900

AAAAATGGGA CGCTATGGTA AGTTCATGGC TTGCTCAAAC TTCCCGGATT GTCGTAATAC 960

AAAAGCGATA GTTAAGTCTA TTGGTGTTAA ATGTCCAAAA TGTAATGaTG GTGACGTCGT 1020

AGAAAGAAAA TCTAAAAAGA ATCGTGTCTT TTATGGATGT TCGAAATATC CTGAATGCGA 1080

CTTTATCTCT TGGGATAAGC CGATTGGAAG AGATTGTCCA AAATGTAACC AATATCTTGT 1140

TGAAAATAAA AAAGGCAAGA CAACACAAGT AATATGTTCA AATTGCGATT ATAAAGAGGC 1200

AGCGCAGAAA TAATATTTTT ATTTCCTAGA TACATTTTAA GATTGTTAAA TAGAATCATT 1260

AGTGAATCTT ATTTTAAAGA TAGTAAAGGA TTAATCTAAA TAAGTGCGGA TAATATAAAC 1320

ATAACAACAT AATTAAmAGA CATAAATGAC aATAAAAGGA GTATAGAAAT GACTCAAACT 1380

GTAAATGTAA TAGGTGCTGG TCTTGCCGGT TCAGAAGCGG CATATCAATT AGCTGAAAGA 1440

GGAATTAAAG TTAATCTAAT AGAGATGAGA CCTGTTAAAC AAACACCAGC GCACCATACT 1500

GATAAATTTG CGGAACTTGT ATGTTCCAAT TCATTACGCG GAAATGCTTT AACTAATGGT 1560

GTGGGTGTTT TAAAAGAAGA AATGAGAAGA TTGAATTCTA TAATTATTGA AGCGGCTGAT 1620

AAGGCACGAG TTCCAGCTGG TGGTGCATTA GCAGTTGATA GACACGATTT TTCAGGTTAT 1680

ATTACTGAAA CACTTAAAAA TCATGAAAAT ATCACAGTTA TTAATGAAGA AATTAATGCC 1740

ATTCCAGATG GATACACAAT TATCGCAACA GGACCACTTA CTACAGAAAC CCTTGCGCAA 1800

GAAATAGTGG ACATTACTGG TAAAGATCAA CTTTATTTCT ATGATGCGGC TGCTCCAATT 1860

ATTGAAAAAG AATCTATTGA TATGGATAAA GTTTACTTAA AGTCCCGTTA TGATAAAGGT 1920

GAAGCTGCAT ATTTAAACTG TCCTATGACT GAGGATGAAT TTAATCGCTT TTATGATGCA 1980

GTATTAGAAG CTGAAGTTGC GCCTGTAAAT TCATTTGAAA AAGAAAAATA TTTCGAGGGT 2040

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AAACCAGTAG GATTAGAAGA TCCAAAGACT GGGAAACGTC CTTATGCGGT GGTTCAATTA 2160

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AGATATGGTG TGATGCATAG AAATACCTTC ATTAATTCAC CGGACGTATT AAACGAGAAA 2340

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GGCAAGGGTG AGGTAGTATT TCCGAGAGAA ACAATGATTG GAAGTATGGC TTACTATATT 2520

TCTCATGCTA AAAACAATAA GAATTTCCAA CCTATGAATG CTAACTTCGG GTTATTACCA 2580

TCTTTAGAAA CTAGAATTAA AGATAAAAAA GAACGCTATG AAGCACAAGC TAATAGAGCT 2640

TTGGATTACT TAGAAAATTT CAAAAAAACT TTATAAAATA GTTAGAAAGA CTAGATATGC 2700

TATTCATTCT TAAGTCATCA ACGAGTAAGT AATGACTTTC TAAATGGAAA ATACTTATCC 2760

TAGTCTTTTT AATTTTGGAA TTGTTACGTA TTTCTGACAA TTTAGAATTC GCATTCAAAA 2820

AATATCTAAA TAAATAACAC GCAATAAGTT GATTGATGTA ACATGTAAGA GAATGTTTTA 2880

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TAGTAATTAA TTTAAAAAAG AGGTATTCTA ATTAACAGGT TTTCCGATTA GTTACAATTA 3000

TTTAATTCTC AAAAGATTTA GAATTGATTA TCAAATTACT GTAAGCCCTT TGCTGTATAT 3060

GCTACAATTC TTATTGATGG AGGGTAAATG TATTGAATCA TATTCAAGAT GCGTTTTTAA 3120

ATACATTGAA AGTTGAACGG AATTTTTCGG AACACACATT GAAATCATAT CAAGATGACT 3180

TAATTCAGTT TAATCAATTT TTAGAACAAG AACATTTAGA GTTGAATACT TTTGAATACA 3240

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CTCGTAAAAT CTCAACGTTA AGAACTTTCT ATGAATATTG GATGACGCTT GATGAGAACA 3360

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TTTACGAAGA AGAAATGGAA GCGTTATTCA AAACTGTAGA AGAGGACACT TCAAAAAATT 3480

TACGGGATCG AGTTATTCTT GAATTGTTGT ATGCTACAGG CATCCGTGTT TCGGAATTAG 3540

TAAATATTAA AAAACAAGAT ATAGATTTTT ACGCGAATGG TGTTACCGTA TTAGGAAAAG 3600

GGAGCAAAGA GCGCTTTGTA CCGTTTGGTG CTTATTGTAG ACAAAGCATC GAAAATTATT 3660

TAGAACATTT CAAACCAATT CAGTCATGCA ATCATGATTT TCTTATTGTA AATATGAAGG 3720

GTGAAGCAAT CACTGAACGC GGTGTACGAT ATGTTTTAAA TGATATTGTT AAACGAACAG 3780

CAGGCGTAAG TGaGATTCAT CCCCACAAGC TCAGACATAC ATTTGCAACG CATTTATTGA 3840

ATCAAGGTGC AGACCTAAGA ACAGTACAAT CGTTATTAGG TCATGTTAAT TTGTCAACAA 3900

CTGGTAAATA TACACACGTA TCTAACCAAC AATTAAGAAA AGTGTATCTA AATGCACATC 3960

CTCGAGCGAA AAAGGAGAAT GAAACATGAG TAATACAACA TTACATGCAA CAACAATTTA 4020

TGCTGTAAGA CATAATGGGA AAGCAGCTAT GGCTGGAGAT GGGCAAGTAA CGCTTGGTCA 4080

ACAAGTCATC ATGAAACAAA CGGCAAGAAA AGTGCGACGT TTATATGAAG GTAAAGTGTT 4140

ATTACAACAG TTTAGTGGTA ACTTAGAAAG AGCTGCTGTT GAATTGGCAC AAGAATGGCG 4260

AGGCGATAAA CAATTACGTC AATTAGAAGC TATGCTAATT GTAATGGATA AAGATGCTAT 4320

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ATCAGGAGGC AACTACGCAT TAAGCGCAGG ACGTGCATTG AAACGCCATG CATCGCATTT 4440

GTCTGCTGAA GAAATGGCAT ATGAGAGCTT GAAAGTAGCG GCTGATATTT GTGTCTTTAC 4500

CAACGATAAT ATTGTTGTCG AAACACTATA ATAATCAGAG CACGATAAAT AATTACGAGC 4560

AATTAATTTT AGTTAAAAGA CGGAGGAATG AAATTAATGG ATACAGCTGG AATAAGATTA 4620

ACTCCAAAAG AAATCGTATC TAAATTAAAT GAATACATCG TTGGACAAAA TGATGCTAAA 4680

CGTAAAGTGG CAATTGCCCT ACGTAATCGA TACAGAAGAA GTTTATTAGA TGAGGAATCA 4740

AAGCAAGAAA TTTCACCTAA AAATATTTTG ATGATTGGAC CAACCGGCGT TGGTAAAACT 4800

GAAATTGCAA GAAGAATGGC CAAAGTTGTC GGCGCGCCAT TTATAAAAGT AGAAGCTACT 4860

AAATTTACTG AGGTAGGTTA TGTAGGACGA GATGTTGAAA GTATGGTTAG AGATCTTGTT 4920

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CAAACGAATA ATCCTTTAGA GTCACTTTTC GGAGGTGCAA TTCCAAATTT CGGACAAAAT 5100

AACGAAGATG AAGAAGAACC ACCTACTGAG GAAATTAAAA CAAAACGTTC TGAAATTAAG 5160

AGACAGCTAG AAGAAGGCAA ACTTGAAAAA GAAAAGGTAA GAATTAAAGT CGAACAAGAT 5220

CCTGGTGCTT TAGGTATGCT AGGTACAAAT CAAAATCAGC AAATGCAAGA GATGATGAAT 5280

CAATTAATGC CTAAAAAGAA AGTTGAGCGA GAAGTTGCTG TTGAGACGGC AAGGAAAATC 5340

TTAGCTGATA GTTATGCGGA TGAACTAATT GATCAAGAAA GCGCTAACCA AGAAGCGCTT 5400

GAATTAGCAG AACAAATGGG TATCATCTTT ATAGATGAAA TCGACAAAGT TGCGACGAAT 5460

AATCATAATA GTGGTCAAGA TGTCTCAAGA CAAGGTGTTC AAAGAGATAT TTTACCTATA 5520

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ATAGGTGCTG GAGCTTTCCA TGTATCTAAG CCGAGTGACT TGATACCAGA ATTGCAAGGT 5640

CGTTTTCCGA TTAGAGTTGA ACTTGATAGT TTATCGGTAG AAGATTTTGT AAGAATTTTG 5700

ACAGAACCAA AATTGTCATT AATTAAACAA TATGAAGCAT TGCTTCAAAC AGAAGAAGTT 5760

ACTGTAAACT TTACCGATGA AGCAATTACT CGCTTAGCTG AGATTGCTTA TCAAGTAAAT 5820

CAAGATACAG ACAACATTGG TGCACGTCGA CTTCATACAA TTTTAGAAAA GATGCTAGAA 5880

GATTTATCAT TCGAAGCACC AAGTATGCCG AATGCAGTTG TAGATATTAC CCCACAATAT 5940

AAATATACAA AAGGAGAAAA ATTCATGAGC TTATTATCTA AAACGAGAGA GTTAAACACG 6060

TTACTTCAAA AACACAAAGG TATTGCGGTT GATTTTAAAG ATGTAGCACA AACGATTAGT 6120

AGCGTAACTG TAACAAATGT ATTTATTGTA TCGCGTCGAG GTAAAATTTT AGGATCGAGT 6180

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AATGTATTAA CAGTATTCCC ACCTGAAAAC AGAGAATTAT TCATAGATAG TCGTACAACT 6360

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GATGATTTTA ATGaAAATGA TTTGGTACTA GGTGAATATG CTGCTACAGT TATTGGTATG 6480

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ACAATGGCAA TTAATTCATT ATCTTATTCT GAAAAAGAAG CGATTGAACA TATCTTTGAA 6600

GAACTTGGCG GTACGGAAGG CCTATTAATC GCATCAAAAG TTGCAGATAG AGTTGGTATT 6660

ACTAGATCTG TAATTGTAAA TGCACTACGT AAATTAGAAA GTGCTGGTGT AATTGAATCA 6720

CGTTCTTTAG GAATGAAAGG TACTTTCATT AAAGTTAAAA AAGAAAAATT CTTAGATGAA 6780

TTAGAAAAAA GTAAAT 6796

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2073 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATCCTAAAAT TnAAAATTAT CACGCCTTTT GaACAGCTTT GTAACCaTCt GGACGATCAT 60

kAAATTCCaA TGTAAATCCT GGTTTAAaGT TGATCTTTAA CCTTATTTAA AyCACCAATT 120

GTACGTATAT TATGTTGTTT AGCAAAATCA CGTTTTACAG CTAAAGCATA CGTATTGTTA 180

TACTTCATTG GTTTTAACAT AGTCATTTGA TATTTCTTTT CAAGACTTTG CTTAGCTTGT 240

TCATAAACTT TTTTCTCTTC TTTTGACTTC AATGGTTCTT TTGTTAATTC ACCTAAAACT 300

GTTCCAGTAA ATTCTAAATA CCCATCTATA TCGTCAGATT TTAAAGCATT AAATAAAAAT 360

GCTGTTTTGC CCATACCATC TTTCACTTCT ACAGTATTTT TGGTCTCTTC TTCTATTAAA 420

ATTTTATACA TATTTGTAAT AATCGATGGC TCGGAGCCAA GCTTTCCAGC TAACGTAATT 480

TTATCACCTT TTTGTGCAAA CATAGGAATA GCGATAGCCA GTATAATAAT CATCACTATA 540

TCAAATATAA TTGCCAATAA GGCTGCTGGA ATTGCACCTA ATAATATCAA CGATGCATTG 660

TTACGGTCTA TACCTAATAA AATTAAATCT CCTAGTCCGC CTGCACCAAT TAATGCTGCT 720

AGTGTTGCTG TACCTATAAT TAATACCATA GCCGTTCTTA CACCAGCCAT TATAACAGGC 780

ATTGCTATCG GAAGTTCGAC TTTAGTTAAA CGTCTAAATG GTTTCATACC TATACCTTTA 840

GCCGCTTCAA TGAGTGATGG ATCAACTTCT TTAATTCCAG TATACGTATT CCTTAAAATT 900

GGTAACAACG CATACACTAC AAGTGCAATA ATTGCTGGCA CACGACCGAT ACCAAATAAA 960

GGAATCATTA AACCTAATAA TGCCAACGAT GGTATGGTTT GAAGAATTGC CGCAATATTC 1020

ATTACGATTT CAGATATCGT TTTAGTCTTC GTTAATAAAA TACCTAATGG TACCGCAATA 1080

GCAGTTGCAA TCAATAATGC GATAAATGAT ATTTGAATAT GTTCTATCAT TGTCGAAAAG 1140

AGTTGCCCCT TACGTTCACT CAATATGTCg AAAAAGTTAG TCATGTTGAG CTACCTCCTT 1200

TTTCTGGGAC AAATATTTGA AGATATCTTT CCTATCAATA ACATATTGAC CTACGCTATC 1260

TTCTTGCATG ACAATGACAC GCTCGCTCTC TGATAAAAGT TGATACAATA CTTCAATTGG 1320

TTGATTGTCA TAAACAATTG GATAAGCGCT CATAGATGTA ACCTCATCGA TTGGTTTCAT 1380

AATATCCAAG TCACGGATAA TTGCGTTCTC TTCAACACAT GGCGCATCAT CTTCTAAATG 1440

ACTACCCATA AATTGTTTAA CAAATTCACT TTGAGGATTA TTTTTAAATC CTTCTGGTGT 1500

GTCAATTTGT TCAATATGCC CTTCATTCAA AAGACAAATC TTATCACCAA GTTTCATCGC 1560

CTCTTGAATA TCATGTGTAA CAAATATGAT TGTCTTCTTA ATTTTAGTTT GTAATTCAAT 1620

TAAATCATCT TGAAGTTTTT CTCGGCTGAT TGGGTCTAAT GCACTAAACG GTTCATCCAT 1680

TAAAATAACT GGTGGATCAG CTGCTAACGC ACGTATAACT CCTACACGTT GTCGTTGCCC 1740

CCCTGACAAT TCATCAGGTT TTCTGTTTTT ATATTTTTCA GGTTCTAATC CAACCATTTC 1800

AAGTAATTCA TCTACTCTTT TATCTATATC TTTTTCTTTC CACTTTTTCA TTTGTGGCAC 1860

TTGTGCAAtA TTTTCTTTGa wTGTCaTATG TGGGAATAAT GCAATCTGCT GcAATACGTA 1920

TCCAATATCC CAACkCATTT CGTATACTGG ATAATCACTT ATTGGTTTAT CTTTAAAATA 1980

AATATAACCT TCACTTAAGT GAATGAGTCG ATTAATCATT TTTAATGTCG TAGTTTTTCC 2040

ACAACCTGAA GGTCCAATTA GCACAAAAAA TTC 2073

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACTATTCTAG CTTCATCAGT TATCATATAT TCTTTGAAAC ACTTGTAAGA AAATATAATG 60

AGTATTTACT ACATAATGAT ATTTCAAATT AGAAAAAAGG AAGTTATGAT TTAATGGCCT 120

TGAGCCTATC ATAACTTCCT TTTATCATTT TATTGTTGTG TTGATGTTTC GATAACGTGG 180

TACATCTTAT CAAACATCAA TTCGAAACCA TGCACCATGG CATCATGATA TTCTTTTTTC 240

TTTTGCTTGT ATTCTAAATT AGTAAATCGT CTTTCTTTTT CAACTAATGA ACGATAATAA 300

AATAGCATTT GGGTGCCACC TGTTTCACGT TCAAAAAATT CTACCTCAAT GACATCTTGC 360

GTTTCACTTA GTCCAGGCAT ACCGATAGTC ATCTTAACGT ATTCATCCAT AACTAAAGAT 420

TCATAAATGC CTTCAATCAC ATTTACTTTG CCATTACGTT GTTGATCTAC AATACGATAT 480

TTACCGCCTT CTTTAACGTC CGCTTCAATC TCTTTATTCG TTCTGGCTGA TGTCATAAAC 540

CATTGTTTCA ACAAATCTTT CTTTGTCCAA GCTTCGTATA CTAACTCTGG AGAAAATTTA 600

TAAAGCTTTT CAATTTCAAC TTCGACATGT TCATTCTCTA CATTAAATTT TGCCACTGTT 660

GTCCACCCAC TTTCGCTCTT ACTTTTATTT TAACGTATTT TTGCTCAGTT CCAAACATAG 720

ATGATCATCA TTTTTAAAAG ATTAGCGTTA TACGGTGAGT ACAACATGAT CTGTTAATAT 780

AACAAGCCAC CTTACTTGGC TACATCGATA TATTGTTAAG CATTAATGTT TCATTTCTTG 840

ACTAGTGTTC TTTTTTAGCT TTGGAAAATT AAATAAAATC GCAATAAGTC CGCATACACC 900

TAATAATATA GGATAAATGC TGTATGGGAA TAACATTAAC GGTGAAATAC CAGCTACACC 960

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ATCAAGAATA CTTGCTGATT TCCTTGAATC TACATCATAT TCATCTGCAA TATTTTTAGC 1080

TAAAGGACCT GACATAATAA TAGAGATGGT GTTGTTTGCC GTGGCAATAT CTGCGACACT 1140

TACCAAACTA GCAATTCCTA ATTCTGCGCC ACGCTTTGAT TTCACTTTAG AGCGAACAAA 1200

TTGCAACAAC CATTCAATAC CACCATTGTG TTGAATAATA CCGACTAAAC CACCAATTAG 1260

CAACGCAATC ATAGCAATAT CTTCCATGCT TATAATACCT TTGGACACTG CATCTAGTAG 1320

CCCCATCCAA CCGAATGAAC CATCTATGAG ACCAATGATT CCGGCTAATA ATGTTCCGCC 1380

AATCAATACG ATAATGACAT TTACACCTAA TAATGCTAAT ACCAATACTA AGATATACGG 1440

TACAACTTTA ATTAGATTAT AATCATAGTt TTTAGCATGA TTTAAAGAAA TGCCATTCGT 1500

TAAGAAATAC AGAATAATAA TCGTTAAAAT AGCACCTGGC AATACAATTT TAAAGTTTAC 1560

TCTGAATTTA TCTTTCATTT TCGTATGTTG TGTTCTAACC GCAGCAATTG TTGTATCTGA 1620

AATCATTGAT AGATTATCGC CGAACATTGC ACCTCCAACA ACTGTAGCCa tTGctAGCGC 1680

TCCTACAGAC GTCCCCATAG ATATAGAAAC AAACATACAA ATCACAAACA ATCCTACAAT 1800

AATTAAATTT TCTGGGATTA ATGATAGTCC TAAATTAACT GTCGACTTTA CGCCACCCAT 1860

TTTTTCAGCT GTATTTGAAA ATGCACCTGC TAAAATAAAA ATCAACATCA TTAAAACAAT 1920

GTTTGAATGG CCTGCACCTT TCGTGAAGAC CTCAACTTTT TTAGCAAATG ATTCTTTTCG 1980

ATTCATTAAT AACGCCACAA TTACCGTTAT CGTAATTGCA ACATTTAATG GCATTGAAGT 2040

AAAATCACCT GTGATAATAC CTACGCCTAA AAACAACGCC ACAAATAATA ACAAGGGGAA 2100

TAATGCCCAA GCATTGCTCT TTTTATGTAC TTCCATCCTT TTTACCTGCT TTCCAATTAA 2160

AAATACCTCT TTCTCACAAA CGATGAAGAA AGAGGTTTTC ATGTGCTTTA CCTGCTTATC 2220

TTCAAACCAT TACGGTTACT GGAATTGGCA CATTCGAGAT GTTGCCGAGG CTTCATAGGG 2280

CCAGTCCCTC CACCTCTCTA GATAAGTGAT GCTTATTTAC GTTTACGTTA CAAGATAATC 2340

CTTAGTACGT CAATCATAAA TTAATCAGGA GTCGTATAAT ATTTTTCATA AACAATCATT 2400

GCTACTGTAA TAATAATCAA AACAATAATG CTAATAACAA GTAAAAGCCA CCATTTAAGC 2460

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AATGTGAATA CTATATATAA TGGTAATTTT TGTTCAGGAA AAACAGTCGC TATTCCAAAA 2880

GCTAATGCTA AAATCAAAAA TAATATAGCT CTAGATACTA TTAATGCCAT AATAACAACC 2940

CCTTTGTTTA ATATCGAGTT TGCAAATTTA CGTTTATCAG CGTTTCTATG ATCAGTACTT 3000

CTACGGGTAG CGTTTCTATG TAATTTACAT CATCTTAACA TATAAATACT TCGCTATTTA 3060

ATTGAAAACA TATCCTATTA TTCTTTGTCC GTTCTGACGT TTAATATCTA GCCTTAGGCA 3120

TTTCACTTGT TAATGAATTT AACTTTCTTC CACTAACCGT CCCTAAACCC AATCCCGCAA 3180

CAGTTTTTAA CTTTTTCGTT GTTGTCCTGA CATCCTCATT AAGAAAGTTT ATTCTGCTTA 3240

AAACTTATAA TCCACACCCT GAGCAAACGC TCCTTATGAC AGAGTATTAA AATAAGCCGA 3300

TAAAGATACA CACCTTTACC GACTATTTAA AATACACTTC ACCAATTCAT TTTAATTTAA 3360

TGGATTGAAG TAACTAAATT AATATTATGT TGTTCAATTA AAAGCTTCAT ACAAACCTAA 3420

TCTATTTGCA CTCCACCGCT AACACCGAAC ACTTGTCCGG TTGTATAACT TGATTCTTCT 3480

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GACCAGAATG GACCAGGCGC TACACAGTTC ACTCTAATTC CTTTTGGTCC TAATTCTTCT 3660

GAAAAACTTT TAGTTAATGA AATAATTGCT GCTTTTGAAG CGGCATAATC ATGAAGAATA 3720

GGACTAGGAT TATAACCTTG TACAGATGAT GTCGTTGTAA TTGACGCACC CGGTTTTAAA 3780

TATTCCAATG CTTTTTGAAC TGTCCAAAAT AGCGGATAGA CATTCGTTTC AAATGTTTCT 3840

GTAAATGCCT CAGTTGTAAA TCCATGAATA TCATCATGAT ACTGTTGATG TCCAGCAACT 3900

AAAGTAACAT TATCTAAGCC ACCTAATTGT TGATATGCTT GTTCAACAAG GTCATAGTTG 3960

AACTGTTCAT CTCTTATATC ACCAGGAATT AACACTGCCT TTTGACCACT TTCTTCAATC 4020

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GCACCTTCTT TAGCATACGC AATTGCTGCT GCACGCCCTA TTGCTGAGTC ACCACCTGTG 4140

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A 13321

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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CCAGTAATCT GCATTATCTT ACCATCATCT TTAGTAATCT TAGCTTTTTG CCAATTTGAA 5640

GTAGAACCAC TTGTGACTAA ACCACCACTA TTCACTGACT GCTTGAAGGC TTCATGTTTC 5700

TCATCCATAT ATCGCTTTTG CTCATCGAAT GTTCTTGAAT ATGCTTGCGC TTTATTTTCC 5760

AAATCAGATA TATGGCTATT AGCAAGTTGC TTTAATTCAT CTATACTTGA AGATTTTGCT 5820

ATTTGAATAT CTGATAGACC TTTTTCTTTA GCTTTTTCAA TCAGACTCGC ATAATCTTCA 5880

CCATTTTTTA TAGCCTCGTC CATTGCTTTC GCACGATCCA TAATAGTTTT TTCTAATTCC 5940

TCAACGTTAA ATGTGATAGT TCTCTCGACA ACTACCACGT CTGAATTACC TAATTCTGCA 6060

ACCGAAACTT GAGCTTGATA ACTTCCATCT CGTTTAATTA CATCATTAGG TAATTGAAAT 6120

TTTAAAATAC CTTTAAATGG ATCTAATATT TCTAGTGGAG CAACTACCAT GACTCCTTTA 6180

CCTCGAATCG CTATTCGTGC kTTGATATTT tCTTCACTCA ATAATAACGG TTGATTATTT 6240

TTAGTGATAT TAAAAAGAAG AACAGAAGAA TCACTCTCTC CTGTTCTAAA AGTTATATCT 6300

AGATTTGAAA TATTTCCATA ATGCGCTGTG TTTTCTAAAT TTATAGCTAC AGATTTCTCT 6360

AAATTACTCA TTAACTTATA ATTCTCCCTT CGTGTAAAGT CCATGGCCCT GAACTTGTTT 6420

TACTATCATA ATTTTTCAAT AGTATCTCAG CAGATGCTGT AACACTATTA CGAACTAGCC 6480

TATGAACAAA GCCACCTGTG TTTGAAGCTT CTACATATAA GTTCCAACCA GCTACCCCTT 6540

TACGTTCAGT TGGAAAATCT GTAAAACGTT TTGTATCATC CGTAGTTAAA TAAAACGACA 6600

TGCCTACTAT GTTAATATCT GACATTTTTG TGATGAATGA AGGTACTCTC TCCCATTTAC 6660

CACTATTTTT AGGCACATAA TTCCAGTCCG AAATGTCTCC AGTTCTTCCA GAAAGCACCC 6720

TTTCAAAAGT CATCATATTC CTTGCATAAC TATTACGCGT CAATATCTGA ATTACATCAC 6780

CGCCAGTTTG TGGTGGCTTA ACTTCCAAGA ACCAACCTGC ATCACGCCAT TCTCTTGGTA 6840

ATGGGAAATC ATCGATTTGA ACTGTATGAT CAGTGTATAA ATAGTAAAGA CCTGGCTCTG 6900

TTAACATCCC AAGATTCTTA AGTTTATCAG GCCTCATTGG TAAAGGTTTA ACTCTACCAC 6960

CTGTGTCACT CaTGATAAAA GGAACGCCTC TTGAGTGAAG TATTTCTAAA ATACCTCTTT 7020

GCCCAATCAT GAAAATACGA TGTGTTCTAT TTCCaTCACC ACCGACAGTA ACACCTAGCA 7080

TCAAAGCTTT TTTACCACTA TCTTTGTCAT AGTATATTTG CAAACCTTtC TgCTTCCGCA 7140

AATTCGCCAG GAAATGAATC tAgTGTTCCA CCATAGTCAG CATTAACCTG ATACGCTTCT 7200

TCTCCTGTTT CTAAATCGAA AGCCGTTAAA TAGTTTCTAT TATTTGGATT ACTGTCTCCT 7260

GTATACCAAT ACAAGTATTT TTCATCAAAA GTCACACCCT GCATTGGTTG GGTTTCGTTT 7320

GTTAGTCTCA TAGGGATACT GATTTTATGC AAAACTTTAT CAATATTTTT ATCAACATCG 7380

TCTAAACTTC TTATCTCTAT ATAAnTCATT GAGTTTTCAA GTTCCCACTG ACTTCTAGGT 7440

CTCTCaATTC TGTATAGAAT TTTATTTTCT TTTTCATTTA TGACAGGGGT GATGTAGGGT 7500

TTTTCTGGGT GTCCTGTAAA TACATCTTGC ATACCATACT TGCCATAGCT AATTTCCACA 7560

TTAGGCGTAT ACTTGAAACG AACTAATGTA TTCTCATTAT TACCATTTAA GATAAAACTA 7620

TAAATCCATA ACTCATcATC AATATATCTA TAACCGTTAT GTGTACCATG ACCCCCACCT 7680

ACAATCAATG AGCTGTCTAT AAATTGACCA TTAGGTCTTA GACGACTTAG CATATAGCCA 7740

ATTACTGCAT TTGTAAgAGG TGCAAGTTCT GTCACAAATA AAAATTCTTG CTTATCAGGT 7860

TCAAAACGAT ACTCGATATC AAGAATTTCT TGTTTGGTCT TATTTAATTC TCTTATAGTT 7920

TCCTCTTTAT TAATTTGAGT TTTGGTTTCC CAATCGTCTA AATGTTCTTT TAATGTGTCA 7980

AAGGTTTCGC CGTTTACATT AACTCGAGCT TGAACAATCT CATTAGCACT GTTATTACGT 8040

GGTGCCACAA CAAGTGCGTT AATTTGACTT TGTAAAGATT TGTTTACTGC TGCTTGCGAT 8100

CTACCATTAT AATAAATTTG CTCAGCGAAG TGTTGAATTG TTTTAGCTyT CTGATGCAAC 8160

TTAAACTCTG TTGTCAAGCC AAGCGCAAAT TGCTCTATTC TTTGTAAGTT TTGTATTTCC 8220

TTAGCTCTAT AATCTCGACC TGCTAAAGCT CCCAAATCCT TTATTAAATA CAAATTTTCC 8280

ATAATGCACC TTCCTTTCTA ATAAAATAGC ACTGTACCAA GTTTCCCACT ATCGTCAACT 8340

GTTATTTTCC ACAATTTACC GTTTGGGGAT TTCTGTACAA TGCTATTTTG AATAATTgcC 8400

TGctTCGCCT ATTTTTAAAT TATCTAATTT ATTTkTATCA TTTACCGAAA TGATACCGTC 8460

TTGAGGCAAT CCATCAATAn CACTACTGCC TGCATAAGGT ATCCCATTTA TAGCTTTCCA 8520

ATGTGTAGCT GGAAAGTACT GTTTATCGT 8549

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AGGCGTGTAG TGACTTACGG nTAGGAAACT ATGTATCCGA ATGATTTATT GAGACCAAAA 60

AGGCATTAAA GTCCATTGAA ATATCnGGTA GCGmGTTGGT ACgTGGACGT GGGGGCCCTA 120

GATGTATGAG TCAACCATTA TTCAGAGAGG ACATTTAACG TAATAAATTA TAGAmACGAG 180

GGTGAAAATA ATGACAGAAA TTCAAAAACC GTATGATTTA AAAGGCAGAT CATTATTAAA 240

AGAAAGTGAT TTTACCAAAG CAGAATTCGA AGGACTTATT GATTTTGCAA TTACATTAAA 300

AGAGTATAAG AAAAACGGTA TTAAGCATCA CTACTTATCT GGAAAAAATA TTGCACTACT 360

ATTCGAAAAG AATTCGACGA GAACGCGTGC TGCGTTTACA GTTGCGTCTA TTGATTTAGG 420

TGCGCATCCA GAATTTTTAG GAAAAAATGA TATTCAATTA GGCAAAAAAG AATCTGTAGA 480

GGATACTGCG AAAGTATTAG GTAGAATGTT CGATGGTATT GAATTCCGTG GTTTTTCACA 540

ACAAGCTGTT GAAGATTTAG CGAAGTTCTC TGGTGTACCG GTGTGGAATG GATTAACAGA 600

TCTAGAAGGA ATAAACTTAA CTTACGTTGG AGATGGACGT AATAATATTG CGCATTCATT 720

AATGGTAGCA GGTGCTATGT TAGGTGTTAA TGTAAGAATT TGTACACCTA AATCATTAAA 780

TCCAAAAGAG GCATATGTTG ATATTGcAAA rGAAAAaGCG AGTCAaTATG GTGGTyCAGT 840

CATGATTACG GATAATATTG CAGArcCAGT TGAAAaTwCm GATGCTATAT ATmCAGATGT 900

TTGGGTATCG ATGGGTGAAG AAAGTGAATT TGAACAcGTA TTAATTTATT AAAAGACTAT 960

CAAGTGAATC AACAGATGTT TGATTTAACA GGTAAAGATT CAACGATATT CTTACATTGT 1020

TTACCAGCAT TCCATGATAC AAATACACTT TATGGACAAG AAATTTATGA AAAATATGGA 1080

TTAGCTGAAA TGGAAGTTAC AGACCAAATC TTTAGAAGTG AACATTCAAA AGTGTTTGAT 1140

CAAGCTGAAA ATAGAATGCA TACAATTAAG GCAGTAATGG CAGCAACATT GGGGAGTTAA 1200

TCACTAAATG GAACGATATG AATATGATGT GTCTGATGAT ATAAGTGTCA TGTACAGACA 1260

CCTCATATTG GTATTAAAGG AGAAATGAAT ATGAACGAAT CAGGAGATAA CAAACTCAGT 1320

AAATCTTCTT TAATTGGACT AGTTATAGGA TCCATGATTG GTGGCGGTGC GTTCAATATA 1380

ATGTCTGATA TGGGCGGTAA AGCCGGTGGA TTAGCCATTA TTATTGGTTG GATTATTACA 1440

GCTATAGGAA TGATTTCATT AGCGTTCGTA TTTCAAAATT TAACCAATGA ACGGCCGGAG 1500

CTAGACGGTG GTATTTATAG TTATGmTCAA GCAGGATTTG GCGATTTTGT AGGATTTATC 1560

AGTGmTTGGG GATATTGGTT CTCAGCGTTT TTAGGCAATG TTGCCTATGC AACACTATTG 1620

ATGTCAGCAG TAGGTAACTT TTTCCCGATT TTTAAAGGAG GCAACACATT ACCAAGTGTT 1680

ATTGTCGCCT CGTTACTACT CTGGGGTGTC CATTTCTTGA TTTTAAAAGG CGTTGAAACA 1740

GCAGCATTTA TCAATAGTAT TGTTACTGTT GCAAAGTTAA TACCGATTTT ACTTGTAATC 1800

ATATGCATGA TAATTGCATT CAATTTTGAC ACTTTTAAAA CAGGCTTTTT CAGTATGACG 1860

TCAGAGGGTG TATTGCCATT TAGTTGGGCG AGCACAATGA GCCaaGTtAA AAGTACGrTG 1920

CTAGTGACAG TTTGGGTGTT TATCGGTATC GAAGGTGCAG TAATTTTTTC TAGTAGAGCT 1980

nAAAATGAGA AAGATGTAGG TAGTGCCACG GTTATAGGAC TTATATCAGT TTTAATTATC 2040

TATyTCTTAT TAACTGTATT AGCTCAAGGC GTGATTTTGC AAAATCATAT TTCGCAATTA 2100

GATTCGCCAA GTATGGCACA GGTGCTTGCA ACTATTGTAG GTGGTTGGGG ATCTACACTT 2160

GTAAATATTG GTTTAATTAT TTCGGTACTA GGTGCATGGT TAGGATGGAC ACTGCTTGCT 2220

GGTGAATTAC CTTTCATTGT TGCAAAAGAT GGATTATTTC CAAAATGGTT TGCTAAAGAA 2280

AATAAAAATG GAGCACCTGT AAATGCACTG CTTATTACCA ATATATTAGT ACAATTATTT 2340

TTAATAAGTA TGCTATTTAC ACAGAGTGCG TATCAATTTG CATTTTCACT AGCATCAAGT 2400

CGACAGCAAG CAACTACTAA ACAATGGACG ATTGGTATCA TAGCCTCAAT TTATGCTATA 2520

TGGCTTATAT ATGCAGCAGG TATCAATTAC TTATTATTGA CGATGTTACT TTATATTCCA 2580

GCTCTTCTTG TTTATACaAT CGkTCmAAAG rATwATCAGa CACGTTTGAT TAAATCAGrC 2640

TATATTCtTT TTATGATTAT tATCGTACTT GCAGTTATCG GGTTAATTAA GTTATTGATG 2700

GGAACGATAA ATGTTTTTTA AAAGGAGCGA CAAAAATATG AAAGAGAAAA TTGTCATTGC 2760

ATTAGGCGGT AATGCGATAC AGACAACAGA AGCAACAGCT GAAGCACAAC AAACAGCTAT 2820

TAGATGTGCG ATGCAAAACC TTAAACCTTT ATTTGATTCA CCAGCGCGTA TTGTCATTTC 2880

ACATGGTAAT GGTCCACAAA TTGGAAGTTT ATTAATCCAA CAAGCTAAAT CGAACAGTGA 2940

CACAACGCCG GCAATGCCAT TGGATACTTG TGGTGCAATG TCACAGGGTA TGATAGGCTA 3000

TTGGTTGGAA ACTGAAATCA ATCGCATTTT AACTGAAATG AATAGTGATA GAACTGTAGG 3060

CACAATCGTT ACACGTGTGG AAGTAGATAA AGATGATCCA CGATTTGATa ACCCAACTAA 3120

AcCAaTTGGT CCTTTTTATA CGAAAGAAGA AGTTGAAGAA TTACAAAAAG AACAGCCAGA 3180

CTCAGTCTTT aAAGAAGATG CAGGACGTGG TTATAGAAAA GTAGTTGcGT CACCACTACC 3240

TCaATCTATA CTAGAACACC AGTTAATTCG AACTTTAGCA GACGGTAAAA ATATTGTCAT 3300

TGCATGCGGT GGTGGCGGTA TTCCAGTTAT AAAAAAAGAA AATACCTATG AAGGTGTTGA 3360

AGCGGTTATA GATAAAGATT TTGCTAGTGA GAAATTAGCA ACGCTGATTG AAGCAGATAC 3420

CTTAATGATT CTTACGAATG TAGAAAATGT ATTTATTAAC TTTAATGAAC CTAATCAACA 3480

ACAAATCGAT GATATTGATG TAGCAACACT GAAAAAAtAC GCGGCACAAG GTAAGTTTGT 3540

GGAAGGATCG tGTTGCCAAA AATAGAAGCT GCGtACgtTT GTTGAaAGtG GGGaAACCAA 3600

A 3601

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CGACACTATT AAATGAATTA GAGCACAATC TAACAAATCA AATTCATTTT TCAAAAGATG 60

AACGACTCAC ACATATCGCT TTAAAGTTAT TCGAAACAAC CGATCCTGTT TCAACAAAGC 120

AACTTGCGCA AGATGTTAAT GTTTCGCGTC GGACAATTGC AGATGATATT AAAATGATTC 180

TTATTGGTGA GGAAGATCAT TATCGTAAAG CGTATGCACA CTTTATACAT CAATATATGA 300

AACAAGCTGC ACCTTTTATA GAGGCGGATA TCTTTAATTC AGAATCAATC GCATTGGTTC 360

GCCGTGCCAT TATTAAGACA TTAAATAGTG AAAATTATCA TTTAGTTCAG TCGGCTATCG 420

ATGGCTTAAT CTATCATATA CTCATTGCCA TTCAGCGTTT AAATGAAAAT TTTTCGTTCG 480

ATATACCTAT CAATGAAATT GATAAATGGC GACATACTAA TCAGTATGCn ATTGCTTCAA 540

AAATGATAGA AAACTTAGAA CGCAGTGTAA TGT 573

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TTGATATTTA TAACGTTATA TTTTAATAGT TCACCTGGAT TATTAAATAA ATAGTCCGCC 60

AAATTTTCTT TTTCTTTATC AATCTGaTkG TAATTAACaC TTTCGaCTTC TGTAGGAATT 120

CTAATGTCAA CAGAAGCATT GATATAAGCT TGATGTTGCA TGCAATCACA CTCCTAATCC 180

TTCATmTmAA ACGGAGAAGT AAACCCGTCA CTATTCAAAT TCAATCCTTT TGCCCAATCA 240

ACAGGCTTAT TCATGATAGT TTCGATTTCC TTAAGTCCAT TTGAACCTCT AGGTATTTCT 300

ACAATTACTT CATCATGGAC ATGGCCAACT ATTTTAAAAC CTAATGCTTC AAGCCTTGCT 360

ATAGAAATCG CAAGTAAATC CCTTGCAGTT GCTTGAACAA TATTCTCGAC TAACTTCCCA 420

CCATACGTTT TTAACTTTGA CCATTTACGG TTAAGATCTA ACCCCATAAA TTCAACAACT 480

TGACTACCCC AACTATTTTC ACCAACTAAA GCTTTTGGAT AAGCTAAAGC TCTTCCACTA 540

GGCAGTTCAA TCATTAGAAA ACCTTTTTTC ATATAAAATC TAAGTCCATG TGTATGATGC 600

GTCTTTCGGG ATTTTACAGT ATTAATTGCA GCCTCTTGGC AAGCCTTCCA AAAATTAACT 660

ATGTTAGGAT TTGCGTTACG CCAACTATCA ACTAAACCTT GTAACTCGTT TTCTTCAATG 720

CCCATTTCCA ATGCACCCAT TGCTTTTAAA GCTCCAGCGC CACCTTGATA GCCTAAAGCT 780

AATTCGGACA CTTTTCCTTT TTGTCTGAGA GGGTCGCCTT TAGTTATGCT TTCTACCGGT 840

ACATTAAACA TTTGAGAAGC CGATGCTTCA TATATCTTTC CGTGTGTGTT GAATACATCT 900

AAACGCCATT GTTCTTTTGC ATACCATGCT ATGACTCTTG CCTCTATTGC AGAAAAATCA 960

CTTACTGCTA GTTCATTACC TTCTTCAGCA GTAAATGTCG TCCTAACTAA TTGACTTAAT 1020

AGATCTCTTG CTATTTCTAA TTCAGTATCT GAAATATAAT GCTTTGTTAA ATTCTGAAGT 1140

TGTACACCTC TACCTGCCCA TCTTCCAGTA CCGGCACCGT AAAATTGAAA CAGACCTCTT 1200

ACCCGTTCAT CACTGCACAT C 1221

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1090 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTTTGTTTGG TATGAGGTAG CAATGACGAC GTGTCATTGG TGGAGATTGT AAAAATACAT 60

AATAAAAAGA AGCGGCAATG TATACCGCTC CTTTTTTATA CTACATACCG ATTTTCAACC 120

ATCTCTTTCT ACTTAGTAAT AAGACAATAG TATTAACTAT AAATAGAAGA ACGAAGAATG 180

ATACTATATT TATAATTTCA GTAGGACACA TAAATGTTGA CTCGTTATTC AATATTTTTT 240

CTACGGCACG ATACATCGTA TTGCTCGCCT CAAATGGAGC AACGATACCA AATATATTTT 300

TATTAATGGC AACTAAGATG ACTGAACCAA TCCAATATAC AATGCTGATA CCTAAGCTGA 360

TTAAAATGTT AGGTGAAACC ATACTAATCG TTCCAACAAC TAAGATATAT TGTAAGATAA 420

CGAGTGAAAA TAAGATTATT AATAGTAAGT AATGTGAGAA ATCCGAATAT ATAATTGAAA 480

TAATAGTGAT ACTTAGAATT ATGAACACTA AACATTCAAA AAATAACACT GCTACCTTTT 540

TATAGAAGAA GGTAAAGATA TTATCGCCAA TCAATTTATA AAACAGGATA TTTTTATTCG 600

AATACTCTTT ATTAATAAAA TATGCAATAA CAAATGAAAA TAGTAAGAAC CCTAATTGCG 660

TTGCAACAGT ATATGAACTG AAGAAAAACT GGCTATAGCT TAAACTTTTA ACTTTGTCTA 720

TACCTATTGG TAAAAAATAC CCAAGTAAGA AAAGGAATGT GAATAGCACA ACAAGCGTGT 780

AAATAATTTT ATTGGAAATA CTTTTTTTAA ATTCTAATTT CAAAGTGGAC ACCTCAATTA 840

TAAATTAATG TAATCATTTA TGACTTCTTC TTTTGATTGG TACTCTTCTA TTTGAAGGTC 900

TTTAAAAATA AAGTATTTAC CCGGCAAAGC ACTTAAATCG GATAAATTaT GTGTAATATT 960

GATAATAGTT TTAGTTTGAT GGCTTTGAAT AAAATCATTT AAAAATTCAT AAATTTCATT 1020

AACTGTTTTC TTGTCTAAAG CGTTTGTAAC TTCATCTAAT ATGATTAAAT CATGATCTTC 1080

CAATAAGAAA 1090

(2) INFORMATION FOR SEQ ID NO: 10:

(A) LENGTH: 904 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TTAGGACTAT TTTATCATAT TCATTTAAAT TACGGCTAAA AATTTTAAAA ACGGGGATTA 60

ATATATGGAA TTAAGCTATG AAAGTTAATT GATACTTGCA TTTTACGCTG ATTTATATAA 120

GAATAACTAT TGTATAGTTT TAAAAACGAA CGTACGTTTG CAGGAGGCGA AATCATTGGC 180

AATGAATAAA CAAAATAATT ATTCAGATGA TTCAATACAG GTTTTAGAGG GGTTAGAAGC 240

AGTTCGTAAA AGACCTGGTA TGTATATTGG ATCAACTGAT AAACGGGGAT TACATCATCT 300

AGTATATGAA ATTGTCGATA ACTCCGTCGA TGAAGTATTG AATGGTTACG GTAACGAAAT 360

AGATGTAACA ATTAATAAAG ATGGTAGTAT TTCTATAGAA GATAATGGAC GTGGTATGCC 420

AACAGGTATA CATAAATCAG GTAAACCGAC AGTCGAAGTT ATCTTTACTG TTTTACATGC 480

AGGAGGTAAA TTTGGACAAG GCGGCTATAA AACTTCAGGT GGTCTTCACG GTGTTGGTGC 540

TTCAGTTGTA AATGCATTGA GTGAATGGCT TGAAGTTGAA ATCCATCGAG ATGGTAATAT 600

ATATCATCAA AGTTTTAAAA ACGGTGGTTC GCCATCTTCT GGTTTAGTGA AAAAAGGTAA 660

AACTAAGAAA ACAGGTACCA AAGTAACATT TAAACCTGAT GACACAATTT TTAAAGCATC 720

TACATCATTT AATTTTGATG TTTTAAGTGA ACGACTACAA GAGTCTGCGT TCTTATTGAA 780

AAATTTAAAA ATAACGCTTA ATGATTTACG CnwGGgTAAA GAGCGTCAAG AGCATTACCA 840

TTATGAAGAA GGGAtCaAAG rGTTgTTAGT atGTCCAaTG ArGGAAAAGA AGTTTTGCCT 900

GACG 904

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GATTTCTAAA TCAAGATCTG TTTTACGATA ACCATTCAAA CCTTGACGTT CATCTTCTTC 60

AGGTTGATTT TGTTGCTGTG TGTCTTTGTT GTCAGAAGTC GCTACTGTTT TTTTATTATC 120

TGTTTCTTTA GTCATAACAA ACGCCTCCGT TATAAAACGC TATATTTAAT GATATGTGAT 180

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TTAATAAGAC GATTCAGCAA GTTTTAAAGT ATTATTTGAC TATGTTGGAT TAGGCATCTA   300
GTCCTATAAT ATCACTGACA TTGTCAAAAT GATGATCTTT TAAGTAACGT GCGATGCCTT   360
TGTTCATTTT CTTAGTTAAA CCTGGGCCTT CAATAACAAG TGATGAATAA ATTTGAATAA   420
GTGACGCACC GTGACGCATC ATTTTGATTG CATCTTCAGT ACTGAATACG CCGCCTGTAC   480
CTATAATTAA AAATTCACCA TTTGTTTGCT GATAAgCATa CTTAATCAAT TTTAAATTAC   540
GTTCAAATAA TGGACGACCA CTCAAACCGC CTTCTTCGAC TTTATTAGCA GAAGTTAAAC   600
CATCTCGTTG TCGCGTTGTG TTTGCTAAGA TGATACCGTC AAATGTCTCA GTAATCGCTG   660
GTAATAGTGC TTTTAAGCCA TCGAAATCCA TATCAGACGT TAGTTTTAAA TAAATTGGCA   720
CTGTTACATC ATGTTGTTTT TTAAATGCTG TTAAAGCTTG GCATAACATT GAAAATTCAT   780
CTTTATCATG GAAGTTTTGA AGATTTTCAG TATTTGGAGA ACTGATGTTG ACTGTGAAAA   840
ATGAAACGTC GTGTTTAAAC GTATCAATAA CCTTTATATA ATCTTGATAA CGCGCTTCAT   900
AAGGTGTCAT TTTATTCACA CCAACATTGA TACCAACAGG TACTTGATAA GCATTTTTAC   960
GCAAATGACT TAGTGCTTTG TTCATACCAA TATTATTGAA GCCCATTCGA TTTATCAAGG  1020
CGTCATCTTC TAATAATCTA AACATGCGTG GTTGAGGGTT ACCCGGTTGA GGTTTAGGTG  1080
TGATACCACC TAATTCTAAA GCACCGAATC CAAGGTGTTC CAATGCTTTT GGTACTTCGC  1140
AAGATTTGTC GAAACCAGCT GCTAAgCCAA TTGGATTGTC GTACGTATTA CCTTGTATCG  1200
TTTGTGATAA CGTTGGATTC TTATAAGTAA ATAGTTTATC GACGACTGGG AATAAAACCG  1260
GaAACTTTTG TaACGTTTTT AATGCATCGA TAGTTAGTCC GTGTGCTTTT TCGGGTTCGA  1320
TTTTGAATAA GAAAGGTTTA ATTAATTTGT ACATGAGTAT GCTCCTATTT CATTATATTT  1380
GAGGCTTACT ATCCTCAACT TAATATATGT GAAATATATT CTTTTAATAG ACTAGCATTT  1440
CCATACATAA TTTCCTAGTT AAAACTAAAA AGTTTTGAAA ATTGACGCAA gTTTGAATAA  1500
CGTTTTTAAG ATTAAATCAT CCTAATTAGG CAATATTATA GTATAAAGTA AGTAGATTGG  1560
AAGGTGTTTG TATGAATGAA CAATGGTTAG AGCATTTACC TTTAAAAGAT ATTAAAGAGA  1620
TTTCACCAGT GAGTGGTGGT GATGTAAACG AAGCATATCG AGTCGAAACA GATACGGATA  1680
CATTTTTCTT ACTTGTCCAA CGTGGACGTA AAGAATCATT TTATGCTGCA GAAATTGCAG  1740
GTTTAAATGA ATTTGAACGT GCAGGTATCA CGGCACCTAG AGTAATTGCA AGTGGCGAGG  1800
TTAACGGTGA TGCGTATTTA GTGATGACGT ATTTAGAAGA AGGGGCTTCA GGGAGTCAAC  1860
GCCAATTAGG GCAACTCGTA GCTCAATTAC ACAGTCAGCA ACAAGAAGAA GGCAAATTTG  1920
GCTTCTCATT ACCTTATGAA GGTGGCGATA TTTCTTTTGA TAATCATTGG CAAGACGATT  1980
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GGCTATGGGA TGCCAACGAT ATCAAAGTAT ATGACAAAGT GCGACGTCAA ATTGTGGCGG 2100

AATTAGAAAA GCATCAAAGT AAACCGTCTT TATTACATGG TGACCTATGG GGTGGTAATT 2160

ATATGTTCTT ACAAGATGGT CGTCCGGCGT TATTTGATCC AGCGCCATTA TATGGTGACA 2220

GAGAATTCGA TATCGGTATT ACAACGGTAT TTGGTGGTTT TACGAGCGAA TTTTATGATG 2280

CGTATAATAA ACATTATCCA CTCGCAAAAG GTGCATCCTA TAGACTTGAA TTTTATCGTT 2340

TATATTTATT GATGGTCCAT TTATTGAAAT TTGGTGAGAT GTACCGTGAT AGTGTTGCGC 2400

ATTCTATGGA TAAGATTTTA CAAGATACAA CAAGTTAGTT AAGACGTTAG ATTGAGATAA 2460

ATAGATAATA TGCACAGATA TTTTTACAAT GAGAAGCGAT ACAGCTGCCT CAATAAAAAT 2520

ATTTGTGCGT TTTTATTGTT GGAAAATAAA ATTTTAATCG CTATTGTTAA TTTCTGTAAT 2580

GTAAAACAAG GTTGAGTTAC AATAAAAGTG ATTTTATAAC TTTTTGTTCA ATAAAATTCT 2640

AGGAATGATA CATATTTATT GATACAATAA TTTTGAATAT AATCATAAAA CAATATTTAA 2700

GTATAATTGA ATGTTTGAAT ATCATATATT GATACAGTTT CTAATAATTT TAAAATAATT 2760

TAAATGGAGA GAGGTGTAAA TGATGAGTAC AGTTCAAAGT GATATTTTTA AGACCAATAG 2820

TGCATCATCA TCTATTAAAA GCGCTGTTGA AACATGTAAT AATGTGTCGA AACCGGATAA 2880

AGATGAAAGT ACAACAGTAA GTGGAAATAA TAATGCTCAT AGTGTGATAG ATGATTTGAT 2940

GAGTAAGAAT CAATCTGTTG CTGAAGCAAT ACGAACTGCG AGCGATAATA TACAAAAAGT 3000

TGGTGAGGCT TTTGACCAAA CTGACGTAAT GATTGGTAAT GAAATTGGTA AAAATTAAAA 3060

CGTGGTGAAA TGATGTCGAA TAAACTGGAT GAAATCAATA AAATAATCAC AGCGAAACAT 3120

GAGCAAATGG ATGACTTATA TGATGAAAAG CGAGAGGTTA AAGCATTGAT AGATGAAAGT 3180

GATGCGCTTA ATCATTCGAT AGATCAATTA TATCAACATT TAGGTGAGCG TTATTATAGT 3240

AGCAATATGG CTAGTCGTAT GGAACAGTTC CGCGATGAAT TTCATTTTGC GAAACGACGT 3300

TCAACGGAAG CGTTATACGA GCAGCAACAG CAAATTCAAC ATGGCATTCG TAAAGTGGAA 3360

GAAGAGATGA TTGACTTGGA AATGCGAAGG AATGTTGAAA TTGAGACGGT GACAAAGGAG 3420

GAAAATAAAT GGAAACAATA GGAAGCATTA TTTATTTAAA AGAAGGTTCG CAAAAGTTAA 3480

TGATTATTAA TAGAGGmCCA aTTGTAGAAA TTGAAAATCA AAAGTATATG TTTGACTATT 3540

CTGCATGTAA ATATCCGATT GGTGTTGTAG AAGATGAAAT TTATTATTTT AACGAGGAAA 3600

ATATAGATTC AGTTATTTTT AAAGGTTATT CTGATCAAGA TGAGGTTAGA TTTCAAGAGT 3660

TGTTTGAAAA TATGAAACAA AATTTGGATA GTGAAATACA ACGTGGAGAA GTTACACAAC 3720

AATAAAGAAA TACTTTTTCT TTATTGGGGT GGGACGACGA AATAAATTTT GTAAAAATAT 3780

ATGTCATTCA TAATCATTTG AACTAAACGT AGCAGCCTTA AATTTTAAAA AAAGACACAT 3900

ACCAACTTCC GAAATGTAGA TGAATTCTCT ACAATAACGG AAGTTTTTCT TTTAATATTG 3960

AAATTTCTCA AGGATAGGTC TATACTTTAT AAATCGTAAT TATTACGATT TATAATCAAA 4020

AACAATAACT TGAAATAGAT CATTGAGGGA GTGTTAATAT GCAACATCAT AAAGTGGCTA 4080

TTATcGGTGC CGGTGCTGCA GGTATAGGTA TGGCCATTAC CTTAAAAGAT TTCGGTATAA 4140

CAGATGTCAT TATTTTAGAA AAAGGAACAG TAGGACATTC ATTTAAACAT TGGCCGAAAT 4200

CGACCCGTAC GATCACGCCA TCATTTACGT CTAATGGATT TGGCATGCCT GATATGAATG 4260

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CATATGCTGA ATATTTACAA GTGGTTGCCA ACCATTACGA GCTGAATATC TTTGAAAATA 4380

CAGTTGTCAC AAATATATCT GTAGATGATG CATATTATAC GATTGCAACG ACAACAGAGA 4440

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GCATCGAAAT GAATGTACAT TATACAGTTA AAGATATTGA TTTTAACAAT GGACAGTATC 4800

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AGAAGGGTTT GGATGTAATG CAGCAGCTAT TTCACAAGCA GCACACCAAT GCCATACCTG 5820

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TGCGACATTA TCTATTTTTA GTGTAGCTGG AAAGTCATGG CTATTTATGC CGTACTTAAT 5940

ATTAGTACTT TTAGGTGGCA TCTTACATAA AGGATATGGT TGAAAAAGAA TGATCAACAA 6000

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GTAATGCTGA TTATTTAAAA AAAATGAACT ATAACTGAAT ATAGAGTCAT GTCAGTCAAT 6540

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GAAAGGGTTT ATGACATTTG AAGACACCGC ACATACGTAT CTCATTCAAT TTACACAAGG 7380

CGGAAAGGGT ATTTCAAAAG AAGACTATCA ATGTTTGGAA CAGTAGTGTT TTCAGTGGAA 7500

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GAGAACAATC AATTAACCCC ACATATTTAA TAATACATCA GCAAAGCCTT CAGGTTTTTG 7680

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TTTATCGCTG TATTTTGTGA AATCATCCAA AGTAATATCT GAATGCGTAT ATTGTCTAAT 7860

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TAACTCGCTT TCTCCATAAT CACGACGATC AACGGCTACA ACAGTAAAAT GGTCTTTTAA 8340

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CTTGATTATT CATAAATTGG ATACGTTCAT CATGATGTGA TAATTCGTCG GCATTTGTAA 9360

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TAATACTTTT CATTTACTTC GCCTCCATAT TGTATTGCAT GTTTATTGCA TCTATTGCAG 9540

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TGAATGATTG GCTTGATTCC TTCAGAAACG TGTTTGGAAT TATTACTAAA ATCACCAACT 9720

AAATCAGTAT TTGTAGCGCC TGGATCAGCA GCATTGATTT GCATGTTAGG TAATCCTTTA 9780

GCGTATTGTA GCGTTAGCAT TGTTACTGCC GATTTAGACG AACAATAAGC TAATGAATTC 9840

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CGTACGATAC CGAATACATT CGTTTGATAT ACTTCTTCAA CGTCACGAGG TGTCAATTTG 10020

GAAGGTGCTG AAAATTGACC AGATATACCT GCATTGTTAA TGAGGATATC AAGACGGCCT 10080

TCTTTTTCAG CAATCATGTT ATAAGCATTT TTGACTGAGT AGTCACTTGT AACATCTAAT 10140

TGTACATAAT GAACACCTAA TTTTTGTGAT GCTTGTTGTC CTCTTACATC ATTCCGAGAA 10200

CCTATATAAA CTTTGTAACC CAATGCTTTA AGTGCCTCTG CACTTGCATA GCCTAACCCT 10260

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GTTTAATAAA TAATTTCTGT ACGCTTCAAT TGAAATATGG CGATGCTCTA TTTGGAAGGC 10380

AAATACACTA GTTGATAATG ATTGCAACAG CATATCTGTT TTGAATTCGT GTAAGTGTCG 10440

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CATAAATCGC TTTTATCTTT GAAATGTCGA TACAATGTCC CCATACCGAT ACCTAGTTCT 10740

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GTATTAGCTA TGACAGCGCC ACTAGGCATT TTTAGTCATC AATTACAACG ATTTATTCAT 11160

TTAGTATGGG ATGTCAGAGA TGTAATAAAC GACAATATTA AAGGAAATGG ACAAACACCA 11220

GAACCATATA CGTATTTAAA AGGTGAAAAA GAGGACTATT GGTTTTTAAG A 11271

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CAACCCGTTC AGAACAAAAT AAAAACCGTA CAATTTTATC ATCTTAATGA TTATTGTACG 60

GAAAAACTTT TTTACATCAT ATCTGCATGT GCATAATCGA TATCGGTAAA TTTATTATAT 120

TGTTTCATAA AATGTAACTT AACTGTGCCT GTTGGACCGT TACGTTGCTT AGCAATGATA 180

ATTTCAATTT CACCGTTTTC ATCATTCGTT TGTGGCTCGA AACCACCATC ATCGTCATCA 240

TCTTCATCGC CGCCACGGTT ATAGTAATCA TCACGGTATA AGAATGCAAC GATATCGGCA 300

TCTTGCTCAA TCGAACCAGA TTCACGAATA TCACTCATCA TTGGACGTTT ATCTTGTCGT 360

TGTTCAACAC CACGAGATAA CTGACTTAAT GCGATAACTG GACATTTTAA TTCACGGGCT 420

AATGCTTTTA ATGTACGAGA GATTTCAGAA ACTTCCTGTT GTCTGTTATC GGACGCACGT 480

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TGCTTTAATC GACGACATTT AGAACGTAAA TCATTAATTC GAATACCCGG TGTATCATCA 600

ATAAAAATCT TCGTACGTGA TAATTTACCT ACCGCTATAG TAAAACGACT CCAATCTTCC 660

TCAGTCATAG TACCCGTTCT TAAGCGGTTT GAGTCAACAT TTCCAGAACT ACAAATCATA 720

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GGCATTTGAT TTTGCTCATA CATTCTATCC ATGAATGGTT ACACCTCTTA TTTCAATCCA 1500

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ACTGAACCGA GTGAACGCGC AGATATACCA ATCAGATTAT CTTCACGTCT CGCAACAACA 2160

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AGAAGTCTTT ATACTTATCA TTCGAGTAAC TCGTTGGTTT TAGCACCGTG CTATAAAGTC 6240

GGTTGCTGAA GTATCACAGG G 6261

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATGCGATTAA CTCTGGAAAT ATCTTTTCCA TATTTACGTn TTAAATTATT CAGCAAATTC 60

ATACGAGaTT CATACTCGTT yAACACTTGT TCGTCGAATT CTGTATTAGC CATTTCATCA 120

TATAACTCAT GTTTTGCATC TTCTAAAATG TAGTAAAATT GATCAATATC TTCTTTTAAT 180

TTGTCATATT TGTTTGGAAC TATATCGTTT ATTGTTAACA AATGGTTGCT TAGTTCATAT 240

AAACGATCAG TGATAGCATT TTCATCCGTT AATGTCATAT ATGCGTTATT AAGCGCTAAG 300

CTTAATTTTT CAGAGTTTTG AATGCGTTTA ATATCTATTT CAAGTTGCTC TATTTCGCCT 360

TCTTTTAGAT GTGCTTCAGA CAATTCTTCT AATTGGAATT TCATTAAATC TAAACGCTGT 420

AGCAATGCTT GGTCTGCTGA TTCTAAATCT TCTAACTCTT GCTTTTTGGC TTTATAATTT 480

TGAAAAGTTT GGTGATATTT ATCCAACAAA TCTTGATAAC GTGATTCTGC GTAATTATCC 540

AATAATGTTA AATGGTATTT TTGTTTCAAC AAAGACTGCG TTTCATGTTG GCCATGAATA 600

TCTAATAATT CTTGCATAAC TTTTCGTAAA TCTTGTAAAG TAACTGTTTG ATTATTAATT 660

TTACAAAGAC TTTTACCAGA GCTGAAAATT TCCCGTTTAA CTAATAAAAA ATCTTCATCT 720

ACATCAATAT CCATATTTTT CAATATATGT ATAGCATCTT TACTCTCGTC AATATCAAAT 780

ATACCTTCGA TGACAGCCTT TTTTTCACCA TGTCTTACAA AATCAGATGA AGCTCTCATT 840

CCAATTAATT GTCCAATTGC ATCTATAATA ATTGACTTAC CTGAACCCGT TTCACCACTT 900

AAAACAGTTA AACCATCAGA AAATTGAATT TCTAATTCTT CAATAATAGC AAATTGCTTG 960

ATTGATAAGG TTTGTAACAT AAACTCATCG CATCCTTATA ACAAATTGAA AATTCTTGAC 1020

TTGATTTCAT CACTTGCCTC TTTGCTTCGA CAAATAATTA AACAAGTATC ATCACCACAA 1080

ATTGTGCCTA GTACTTCTTC CCAATTGATT TGGTCTAATA TAGCTCCAAT AGATTGTGCA 1140

TTACeAGGTA TGTTTTTAGA ACAAGTAAAT TATCAGTACC ATCTATATTA ACAAAGGAAT 1200

CCATTAAATA ACGTCCCAAT TT 1222

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1021 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TTTGTTATTA TTACnTnAAA TAATTGCATT ACTTTTTACT GATGGTACAA CTTTCCATCC 60

TTCTTTTGGC ACGACATAAT TGTCTTTATC TTGAACTAAA TATCCGCCAG ATACTGAAAC 180

AAACTCTTCT TCGTTACTGT CTATAGTCAT ATCAATTTCT AATAATCTTA CATTCTTCTT 240

TTGTTTTAAA ATATCTAATG CTTCATCTGT AAATTTTGGT GCAATAATGA CTTCCAAAAA 300

GATACTATGC AATTGCTCTG CTAACTCAGG TGTTACAGCT CGGTTTAATG CAACAATTCC 360

ACCAAATATT GATTGACTAT CCGCTTCATA CGCATGTTGA AATGCTTGTT CTATCGTGTC 420

ACCGATACCA ACACCACATG GATTCATGTG TTTAACCGCA ACTGTAGCAG GTGTATCAAA 480

CTTTTTAACT AAAGCTAGTG TAGCATCTGC ATCTTTAATA TTGTTATAGC TTAATTGTTT 540

CCCATGTAAT TGTTTAGCGC CTGCAATCGT GTGCTTAGCA TTCGAAGTTC TCACAAAATA 600

CGCTGATTGT TGTGGATTTT CTCCATATCT TAAAGTTTCT TTATCCCCTT TAAAGAAACG 660

TACAATCGCT TCATCATATT CTGCAGTATG CTCAAAAACT TTAATCATTA ATGATTGTCT 720

ATATGACTCA TCTAACGAAT CGTTTCTTAA TCGCGTCAAT ACTTCTTGAT AATCTGCCGG 780

ATGTACAATT GTTGTTACAT GTTTATAGTT TTTAGCTGCA GCACGTAACA TTGTTGGACC 840

ACCAATATCA ATATTTTCAA TTGCTTCGTC CATCGTCACA TCAGGGTTTG CAACAGTTTG 900

TTGGAATGGA TATAAATTAA CTACTACCAT ATCAATTAAA TCTATATGTT GTTCTGATAA 960

TTCATTTAAA TGCTGCGGTT TATTTCGATC AGCTAAAATG CCACCATGAA CAGCCGGATG 1020

T 1021

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3759 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TCATTCACTC CTAAATTGTT ATTACACTAT TACACaTAGC TAATCATCAA TGTGAAATCA 60

CCTTCAAAGA CACTATCCAA ATCTTCAGAA GTCAAAATAA AGTTTGTACC AGTAGTCAGT 120

TTGAAAATTT CACCATCGAC AATCATTTGC CCTTCGCCTT CCAACACTGT AACTAAACAG 180

AACTCTCTAG GCTTCATATA ATTTAACGTG CCAGAAATTT CCCATTTAAC CAATGTAAAG 240

AAATCATTCG ATACAATGTG TGTACACTTA TGGTTTTCAA TAATTTCGCT TTCAGGCAAA 300

ATATTAGGTA ATGGTGCATT GTACTGAATA ACGTCTAAAG CTTTTTCAAT ATTTAACGGT 360

CTATCATTAT ATTGATTATC TTGACGATTG AAATCATAAA GTCTATATGT AATGTCTGAC 420

ATAAAAtAGa ATTCyCCAGG kTTTACtTTA AtatATCyAA gTAtCGaCtC tATCGTTCCG 540

TGTTGAACAT GATTCGCAAC TTCTTCTCTA GACTCTGCTA ATGTCCCtAT AACTATTTCT 600

GCATCTTCTT CTGCATCTAT AATATACCAA CATTCAGATT TGCCATATTG CCCgTTTTCA 660

TGCTCATAAG CATAAGAATT ATCAGGGTGC ACATGAATAG AAAGTGATTC TCTTGCATCC 720

ACTATTTTAG TTAGAAGCGG AAAATCTTTG CTTGGGAAAT CACCAAACAA TTCACGATGT 780

TCTGACCAAA TACGGTCTAA TGTTTGACCT TGATATGGTC CATTAATAAT CTCGCTCGTA 840

CCATTTGGAT GTGCTGACAC ACACCAACAT TCCCCCAGTT GTATCATTGT CTAATTGATA 900

TCCAAACTCA CTTAGACGTT GACCGCCCCA TAATTTTGTT TTTAAAATTG GTTGTAAAAA 960

TAATGGCATT GTTGCACCTC CATTGTGATT AAGTAAGCAA TAGAACTCTG ATGTTGTTGT 1020

TCCATTATAT TTTGATTTTG TTCTCATTTA CATCGTATTA TTAACTTCCA CATTTCAAAT 1080

TAACTATTAG TGATTGTACC ATATTTACTA ACATTGCAGT ACTGCCAATT AAAAGnGCTT 1140

CACTTAAATT TACAGTACTT TAACATTTTC AAAAATTTAT AGCATAGAGA TTATATCTCT 1200

CTTACATTTG TACATATTTC CCTTTAAATT TACTCGCCCA TTATACCAAT TAATAaACAA 1260

CTTTAATAGT TGTGCCATAC ATTGTTCAAA TTCTTTGTAA AACGCATAGA CAATACGTAC 1320

TTATTCATAC TTATAATTCA TCATTTTCAA AAAATAACGA GTTACGAAAA AGTAACCCGC 1380

TTCAAATCAT ATTTACTATC CTTATTAATC CGTTTCATTT TCAAATTGAG TTAAAGCATC 1440

TTTAATGTCC TGATCACCAC TAATAATTTG AAACTCTTGG TGATTAAAAT GATTGGATGT 1500

GACAATTTCT TTTAATACTG TCGCAACATC TTCTCTAGGA ATTTCACCTT TACCATCAAA 1560

ATATTGTGCA GCTTCTATCT TTCCAGATCC TGCTGCATTT GTAAGTGCCC CTGGATGTAA 1620

AATTGTATAA TTCAAACCTG nAACGTCTTA AATAGTCATC AGCGTAATGT TTAGCTATTG 1680

TATATGGCTT TAAATCACCG CTATCATCAA AAGCCTGACG TCTCGAATCA TATGTTGAAA 1740

CCATGACATA GTGTTTAATA TTGGCCTCTT TACTCGCAAT CATTGATTTA ACAGCACCAT 1800

CTAAATCGAC AATAATTGTT TTATCTGCAC CCGTGTTCCC TCCAGAACCT ACTGAAAAGA 1860

TAACTTTATC GAATGGTTTA AACGTCTCAG TTAAAGTCTC TATTGAATCA TTTTCAACAT 1920

CAACAAGAAT TGCTTTCATA CCTTGTGATT TTAACGCATT AAGTTGATCT GATTGCCTAA 1980

CACCAGCAGT AAATGGTACA TTTTCTTTTG CTAATTGTTG CACTAGTAAC GAACCTACAC 2040

CGCCATTAGC ACCTATAACC AAAATATTCA TTTACAACAC TCTCCTATkT ATTATTCTCT 2100

ATGCCATACC ACTTTATGAG ATATGTAAAA CTTGTTACAA CTATAAAAAT CAATTGACAT 2160

ACTACTGGGA ACGTATTAAA TTAATATATG AACAAATATT CATATGAAAG GATTGTCATA 2220

tCaAGGCATT AGcGATTACA ATCGAATACG TATCaTGGAA TTGTTATCaG TCAGCGAAgC 2340

AAGTGTTGGT CACATTtCAC ATCAATTGAA TTTATCTCAA TCAAATGTCT CGCACCAATT 2400

AAAATTACTT AAAAGTGTGC ATCTTGTGAA AGCAAAACGA CAAGGCCAAT CAATGATTTA 2460

TTCATTAGAT GACATCCACG TAGCAACTAT GTTAAAGCAA GCCATACATC ACGCGAATCA 2520

TCCTAAAGAA AGTGGGTTAT AATATGTCTC ATTCACATCA TCATCATGAC CATATGCATA 2580

GTCATGTAAC TACAAATAAT AAGAAAGTAT TGTTTATATC GTTTTTAATA ATCGGTCTAT 2640

ATATGTTTAT CGAAATCATC GGCGGTCTCC TTGCTAACAG CTTGGCATTA CTATCTGACG 2700

GTATCCATAT GTTTAGCGAC ACATTCTCAT TAGGTGTTGC ACTTGTCGCA TTTATTTATG 2760

CTGAAAAGAA TGCCACAACT ACAAAAACAT TTGGTTATAA ACGTTTCGAA GTACTCGCAG 2820

CGTTATTTAA CGGTGTAACG CTTTTTGTAA TAAGTATTTT GATTGTTTTT GAAGCGATTA 2880

AACGTTTCTT TGTTCCTTCT GAAGTTCAAT CAAAAGAAAT GTTAATCATT AGTATTATCG 2940

GTTTAATTGT CAATATCGTT GTTGCATTCT TTATGTTTAA AGGCGGCGAC ACTTCACACA 3000

ATTTAAATAT GCGTGGTGCT TTTCTACATG TTATCGGAGA CTTATTAGGT TCAGTTGGCG 3060

CCATTACTGC AGCTAkTTTA ATTTGGGCAT TTGGATGGAC AATCGCCGAT CCTATCGCAA 3120

GTATTTTAGT TTCCGTTATT ATTTTAAAAA GTGCTTGGGG TATCACAAAA TCTTCAATTA 3180

ACATTTTAAT GGaAGGCACA CCAAGTGATG TTGATATAGA TGAAGTTATA ACTACTATTA 3240

AAAAGGATTC ACGAATACAA AGTGTGCATG ATTGCCATGT TTGGACAATT TCAAATGATA 3300

TGAATGCATT GAGTTGTCAT GTTGTTGTAG ACCATACATT GACAATGAAA GAATGTGAAT 3360

TATTATTAGA AAaCATTGAG CATGATTTAT TACATTTAAA TATTCACCAT ATGACTATTC 3420

AATTAGAAAC GCCTAATCAC AAACATGATG AATCGATTAT ATGTTCAGGA ACACATAGTC 3480

ATTCACATAA CCATCATGCT CATCATCACG CGCATGTACA TTAATAATTT TAACCTACTG 3540

CCATTGCATC GATTAAACTT TTCAATGGCA GTAGGTTTTT TATGTCTTTA TGGCGACTTG 3600

TTTGGTCTTT GATGATGCAA TGTTTATTAA CAAATTTTCA ACTATTATTT CTTACATTAG 3660

TCATATTTTT GACAATTTAC TATTATAATT CTCTAACTTT AGTCACTTTA ATTAATTTTT 3720

ATTAGATATT AATATGAAAA TAACGTGTTT TTTGTTATT 3759

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13086 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TAATTATCGC GCATAACAAA ACATTAGCAG GACAATTATA TAGTGAGTTT AAAGAATTTT 60

TTCCTGAAAA CAGGGTGGAA TACTTTGTAA GTtACTATGA TTATTATCAn CCAGAGGCAT 120

ACGTACCGTC TACTGACACT TTTATTGAAA nAGATGCCTC AATCAnTGAT GAAATTGATC 180

AACTACGACA TTCTGCTACA AGTGCATTAT TTGAACGCGA TGATGTAATT ATTATTGCTA 240

GTGTAAGTTG TATATATGGT TTAGGTAATC CTGAAGAATA TAAAGATTTA GTAGTAAGTG 300

TTCGAGTTGG TATGGAAATG GATAGAAGTG AATTACTTAG AAAACTTGTc AGATGTGCAA 360

TATACACGAA ATGACATCgA TTTcCAACGA GGAACGTTTC GAGTGCGTGG TGATGTAGTG 420

GAAATATTCC CAGCCTCTAA AGAAGAACTT TGTATAAGGG TTGAGTTTTT CGGCGATGAG 480

ATTGACCGTA TCCGAGAAGT TAACTACCTA ACAGGTGAAG TGTTGAAAGA AAGAGAACAT 540

TTTGCGATAT TCCCAGCTTC TCACTTCGTA ACACGTGAAG AAAAGTTGAA AGTTGCGATT 600

GAACGTATTG AAAAAGAATT GGAAGAACGA TTGAAAGAAT TACGAGATGA GAATAAATTA 660

CTAGAAGCGC AAAGGTTAGA ACAGCGTACC AACTATGATT TAGAAATGAT GCGAGAGATG 720

GGATTCTGTT CAGGAATTGA AAACTATTCC GTACATTTAA CTTTGCGACC ACTGGGTTCG 780

ACACCATATA CTTTATTGGA TTACTTTGGC GATGATTGGT TAGTAATGAT TGATGAATCA 840

CATGTGACAT TACCGCAAGT TCGAGGCATG TATAACGGAG ACAGAGCGCG TAAACAAGTT 900

TTGGTGGATC ATGGGTTTAG ATTACCGAGT GCATTAGATA ACCGTCCACT TAAATTTGAA 960

GAATTTGAAG mAAAGACAAA ACAACTTGTG TATGTATCTG CAACGCCTGG ACCATACGAA 1020

ATTGAACATA CGGATAAGAT GGTTGAACAA ATTATTCGTC CTACTGGTTT ACTGGATCCT 1080

AAGATTGAGG TTAGACCTAC TGAAAATCAA ATTGACGATT TATTAAGTGA AATTCAAACA 1140

AGAGTgAGCG TAATGAACGC GTACTTGTTA CAACGCTCAC TAAAAAGATG AGTGAAGATT 1200

aACCACATAC ATGAAAGAaG CGGGTATTAA aGTtAATTAT CTGCATTCAG AAATCAAGAC 1260

ATTAGAACGA ATTGAAATAA TTAGAGACTT ACGAATGGGT ACATATGATG TTATCGTAGG 1320

TATTAATTTA TTAAGAGAGG GTATTGATAT ACCAGAAGTT TCTCTAGTTG TCATATTAGA 1380

TGCAGATAAA GAAGGGTTTT TACGTTCTAA CCGCTCATTA ATTCAAaCAA TAGGTAGAgC 1440

TGCGCGTAAC GATAAaGGTG AAGTCATTAT GTATGCCGAT AAAATGACTG ATTCGATGAA 1500

GTATGCAATT GATGAGACAC AACGTCGTCG AGAAATACAG ATGAAACATA ATGAAAAACA 1560

TGGTATTACA CCTAAAACAA TTAATAAAAA AATACATGAT TTAATTAGTG CTACTGTTGA 1620

AAATGACGAA AATAATGACA AAGCACAAAC TGTGATACCT AAGAAGATGA CGAAAAAAGA 1680

TTTCGAGAAA GCTACAGAAT TAAGAGATAT GTTATTTGAA TTAAAAGCAG AAGGGTGACA 1800

AGTAAATGAA AGAACCATCC ATAGTAGTAA AAGGTGCTCG TGCGCATAAC TTGAAAGATA 1860

TTGATATCGA ACTACCTAAA AaTAAATTAA TTGTTATGAC AGGTTTATCT GGGTCAGGTA 1920

AATCGTCATT AGCATTCGAT ACTATATATG CTGAAGGACA ACGACGTTAT GTTGAATCAT 1980

TAAGTGCCTA TGCGCGTCAA TTTTTAGGCC AAATGGACAA ACCAGATGTT GATACAATTG 2040

AAGGATTATC GCCAGCAATT TCAATAGATC AAAAAACAAC AAGTAAAAAT CCAAGATCAA 2100

CTGTAGCAAC AGTAACAGAA ATATATGATT ATATACGTTT GTTATATGCA CGTGTTGGTA 2160

AACCTTACTG TCCAAATCAC AATATAGAAA TTGAATCGCA AACAGTACAA CAAATGGTTG 2220

ACCGCATTAT GGAATTAGAG GCACGTACAA AGATTCAATT ATTAGCACCT GTCATCGCTC 2280

ATCGTAAAGG TAGTCATGAA AAGCTAATCG AAGATATTGG TAAAAAAGGT TATGTACGTT 2340

TAAGAATCGA TGGCGAAATT GTTGATGTAA ATGATGTACC TACTTTAGAT AAGAACAAGA 2400

ATCATACAAT AGAAGTTGTT GTAGACCGAT TAGTTGTTAA AGATGGAATT GAAACACGAC 2460

TAGCTGACTC TATAGAAACT GCCTTAGAGC TTTCAGAAGG ACAATTAACA GTCGATGTCA 2520

TTGACGGGGA AGACCTTAAG TTTTCAGAAA GCCATGCTTG TCCTATATGT GGATTTTCAA 2580

TCGGAGAGTT AGAACCAAGA ATGTTTAGCT TTAACAGTCC TTTTGGTGCT TGTCCGACAT 2640

GTGATGGCTT AGGCCAAAAG TTAACAGTCG ATGTAGACTT GGTTGTTCCC GACAAAGATA 2700

AGACGCTAAA CGAAGGTGCA ATAGAACCTT GGATACCGAC GAGTTCTGAT TTTTATCCAA 2760

CATTGTTAAA ACGTGTTTGT GAAGTTTATA AAATCAATAT GGATAAACCT TTTAAAAAGT 2820

TAACAGAACG TCAACGTGAT ATTTTATTGT ATGGTTCTGG TGACAAAGAA ATTGAATTTA 2880

CATTTACACA ACGTCAAGGT GGTACTAGAA AACGAACAAT GGTTTTCGAG GGTGTAGTTC 2940

CTAATATAAG TAGACGATTC CATGAATCTC CTTCAGAATA TACACGTGAA ATGATGAGTA 3000

AATATATGAC TGAACTACCT TGCGAAACTT GTCATGGAAA GCGATTGAGT CGTGAAGCkT 3060

TATCTGTTTA TGTAGGTGGT TTAAATATTG GTGAAGTAGT CGAATATTCA ATCAGTCAAG 3120

CGCTGAACTA TTATAAAAAC ATTGATTTGT CAGAACAAGA TCAAGCGATT GCAAATCAAA 3180

TATTGAAAGA AATTATTTCC CGACTCACTT TTTTAAATAA TGTGGGACTT GAATATTTAA 3240

CGTTAAACAG AGCTTCAGGT ACACTTTCAG GTGGTGAAGC ACAACGTATT CGATTAGCAA 3300

CGCAAATTGG GTCGCGTTTG ACTGGTGTCT TATATGTATT AGATGAGCCA TCAATTGGAC 3360

TGCATCAAAG AGATAATGAT CGATTAATTA ATACACTTAA AGAAATGAGA GATTTAGGAA 3420

ATACTTTAAT TGTAGTTGAA CACGATGATG ATACAATGCG TGCGGCTGAT TACTTAGTGG 3480

AGGTAATGAA AGATAAAAAA TCATTAACAG GACAATACTT GAGTGGTAAG AAACGTATTG 3600

AAGTACCTGA ATATCGCAGA CCGGCTTCAG ATCGTAAAAT TTCTATACGT GGAGCTAGAA 3660

GCAACAATCT TAAAGGGGTT GATGTGGACA TACCACTATC AATCATGACG GTTGTTACAG 3720

GTGTATCAGG TTCTGGTAAA AGCTCATTAG TAAATGAAGT ATTATACAAA TCATTAGCTC 3780

AAAAAATTAA TAAATCTAAA GTAAAGCCAG GATTGTACGA TAAGATTGAA GGTATTGATC 3840

AACTTGATAA AATTATTGAT ATTGATCAAT CACCAATAGG TAGAACGCCA CGCTCTAATC 3900

CAGCAACATA TACTGGTGTG TTTGATGATA TACGTGATGT GTTTGCGCAA ACAAATGAAG 3960

CTAAAATTCG AGGATATCAA AAAGGGCGTT TTAGTTTTAA TGTAAAAGGT GGACGCTGTG 4020

AAgcTTGTAA AGGTGACGGT ATTATTAAAA TTGAAATGCA TTTTTTACCT GATGTTTATG 4080

TTCCTTGTGA AGTGTGTGAT GGTAAACGAT ATAATCGTGA GACACTAGAG GTTACTTACA 4140

AAGGTAAAAA TATTGCTGAC ATTTTAGAAA TGACTGTTGA AGAAGCAACA CAATTTTTTG 4200

AAAATATTCC TAAGATTAAG CGCAAGTTAC AAACACTAGT TGATGTTGGT CTTGGATACG 4260

TCACATTAGG TCAACAAGCT ACAACGTTAT CAGGTGGTGA GGCTCAACGT GTGAaACTTG 4320

CATCTGAACT TCATAAACGT TCAACTGGTA AATCTATTTA TATCCTAGAT GAACCGACAA 4380

CAGGGTTACA TGTTGACGAT ATTAGTAGAT TATTAAAAGT ATTAAACCGA TTAGTTGAAA 4440

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TTATAGACTT AGGTCCTGAA GGTGGTAGTG GCGGTGGTAC TATTGTTGCG ACTGGCACAC 4560

CCGAAGATAT TGCTCAGACA AAGTCATCAT ATACAGGAAA GTATTTAAAA GAAGTACTTG 4620

AACGAGATAA ACAAAATACT GAAGATAAAT AAGATTAAAA GAAGTGAAGG ATGTTATAAA 4680

TTTATCCTTC GCTTCTTTTT ATTAATTTAG TAATGAATAG TAGAAAGAAA AGATGCGTAA 4740

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CACAGCTATT GTGTACTTAA AAATAGGaat GCaTgAGTGC AACTCATGCA TAAGaAATAC 4920

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CTTAGGTCAT TGATTTTTGG CTCGGACTTT TATGGCGATA TGAACCATGT AAATTAAGCA 5160

AGCAATAAAT TAATGATTGA TATTGACTTG TAAAATAATA ACAATAATGA ACAATTAATA 5220

TTTATTTTAG CTTTTCAATG TAGATTGGTG TTATATTTTT GATATGATAA GAAGAGATGT 5280

ACATTAAAGT TAGATTTAAT CGCTGGTGAA GAAGGACTAT CGAAGCCAAT TAAAAATGCT 5400

GATATATCAA GACCGGGCTT AGAGATGGCA GGTTATTTTT CACATTATGC GTCAGATAGA 5460

ATACAACTAT TAGGAACAAC GGAACTATCG TTTTACAATT TATTACCAGA TAAGGATCGC 5520

GCAGGTCGTA TGCGTAAACT ATGCAGACCA GAAACGCCTG CAATTATTGT GACACGTGGA 5580

TTGCAGCCAC CAGAAGAATT AGTTGAAGCT GCAAAAGAAT TAAATACCCC ACTTATAGTT 5640

GCTAAAGATG CGACTACAAG TTTAATGAGT CGCTTAACAA CGTTTTTAGA GCATGCACTT 5700

GCAAAGACGA CATCTTTACA TGGTGTTTTA GTAGATGTTT ACGGTGTTGG TGTACTAATT 5760

ACCGGTGATT CAGGAATAGG TAAAAGTGAG ACTGCGTTGG AATTAGTTAA ACGTGGGCAT 5820

AGATTAGTAG CAGATGATAA TGTAGAAATA CGTCAAATTA ATAAAGATGA ACTAATAGGG 5880

AAACCACCAA AGTTAATAGA ACATCTATTA GAAATACGTG GACTAGGTAT TATCAATGTT 5940

ATGACTTTAT TTGGCGCGGG TTCAATATTA ACTGAAAAAC GAATTAGATT AAATATTAAT 6000

TTGGAAAACT GGAACAAGCA AAAGTTATAT GACCGCGTAG GTCTTAATGA AGAGACGCTA 6060

AGTATTTTAG ATACTGAAAT CACTAAAAAA ACAATACCTG TAAGACCTGG TAGAAATGTT 6120

GCGGTAATTA TTGAGGTCGC TGCAATGAAC TATCGATTAA ATATCATGGG CATTAACACG 6180

GCCGAAGAAT TTAGTGAAAG ATTAAATGAA GAAATTATCA AGAACAGTCA TAAGAGTGAG 6240

GAGTAGGTTG AATGGGTATT GTATTTAACT ATATAGATCC TGTGGCATTT AACTTAGGAC 6300

CACTGAGTGT ACGATGGTAT GGAATTATCA TTGCTGTCGG AATATTACTT GGTTACTTTG 6360

TTgCACAACG TGCACTAGTT AAAGCAGGAT TACATAAAGA TACTTTAGTA GATATTATTT 6420

TTTATAGTGC ACTATTTGGA TTTATCGCGG CACGAATCTA TTTTGTGATT TTCCAATGGC 6480

CATATTACGC GGAAAATCCA AGTGAAATTA TTAAAATATG GCATGGTGGA ATAGCAATAC 6540

ATGGTGGTTT AATAGGTGGC TTTATTGCTG GTGTTATTGT ATGTAAAGTG AAAAATTTAA 6600

ACCCATTTCA AATTGGTGAT ATCGTTGCGC CAAGTATAAT TTTAGCGCAA GGAATTGGAC 6660

GCTGGGGTAA CTTTATGAAT CACGAGGCAC ATGGTGGATC GGTGTCACGC GCTTTTTTAG 6720

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TTGCACAATT AGTATCAATT CTTTTAATTT TAATAAGTAT AAGTTTAATT GTATATAGAA 7020

GGATTAAGTA TAATCCACCG TTGTATAGCA AAGTTGGGGC GCTTCCATGG CCAACAAAAA 7080

TTATGGCGTG TATACCGTCT TGTTAAATTT TCGAAAGTTT TTAAGAATGT AATTATCATT 7200

GAATTTTCGA AATTTATTCC AAGTATGGTA CTGAAAAGAC ATATATATAA ACAACTTTTA 7260

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CCAGAACTGA TTACGATTGG TAGTAACAGT GTTATTGGTT ACAATGTAAC AATTTTGACG 7380

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ATTGGTGCAA ATGCTACCAT TTTACCCGGT ATAACGATTG GTGACAATGT AAAAGTTGCA 7500

GCTGGTACGG TTGTTTCAAA AGATATACCG GATAATGGAT TTGCATATGG CAACCCTATG 7560

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ATATAAACGA GCTGCTGAAT ACTTTGAAAA AGTGTTAGAA TTGTCACCTG ATGATCTGGA 7740

AATTCAAATT GATTATGCAC AATGTCTAGT GCAACTTGGT ATTGCTAAAA AAGCAGAACA 7800

TTTATTTTAT GACAATATTA TTTATAATAG GCATCTAGAA GATAGCTTTT ATGAATTGAG 7860

TCAGCTCAAC ATTGAAGTTA ACGAACCAAA CAAGGCATTC TTGTTTGGTA TTAATTATGT 7920

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TCAAAGTGAA GAACAAATTG AACTTGAAGC TCAATTGTTT GTAGTTCAAA TACTATTCCA 8040

ATATCTTTTT TCTCAAGGTC GATTAAAAGA TGCAAAGAAT TATGTCTTAC ATCAACCACA 8100

AGAAGTTCAA GATCATCGTG TAGTACGTAA TTTATTGGCA ATGTGTTATT TATATCTCGG 8160

TGAATATGAT ACgGCTAAAG CATTGTACGA aGCACtATTA CAAGAGGATA GTACaGATAT 8220

ATATGCATTA TGCCATTATA CTTTGCTACT TTATAACACT AAGGAAAATG AACAATATCA 8280

AAAATATTTA AAAATATTAA ACAAAGTTGT ACCTATGAAT GACGATGAAA GTTTTAAATT 8340

AGGTATTGTA TTAAGTTATT TAAAGCAGTA TCGTGCATCA CAACAATTGT TGTACCCTTT 8400

ATATAAAAAA GGGAAATTTT TATCAATTCA AATGTACAAT GCTTTAGCAT ATAATTATTA 8460

TTATTTAGGT GAAGAAGACG AAAGTCATTA CTACTGGGAT AAATTGAAGC AAATTTCTAA 8520

AGTGGAAATT GGACATGCGC CTTGGGTAAT TGAAAATAGC AAAGAAGTTT TTGACCAACA 8580

TATTTTGCCA TTACTTCAAA GTGATGACAG TCATTATCGT TTATATGGTA TTTTTTTATT 8640

GGATCAATTA AATGGTAAAG AAATTGTGAT GACGGAAAGT ATTTGGCAGG TTTTGGAAAA 8700

TCTAAATAAT TATGAGAAAT TGTATTTAAC GTATTTAGTT CAAGGTTTAA CGCTCAATAA 8760

ATTAGACTTC ATTCATCGCG GCTTATTAAC GCTTTACCAT AATGAATTAT TTGTAAGTGA 8820

AAATGATGTA ATGGTTGCAT GGATTAATCA AGGTGAACTC ATAATTGCTG AAAAAGTAGA 8880

TCGAAACGTT ACAAAGAAGC AAATTACAAC ATGGTTAGGC ATAACACAAT ATAAACTGAA 9000

CAAAATGATT GAATTTCTCT TGAGCATATA GATTTATGAA AAGTTAGATT TATTATATAA 9060

TGCGCATAAT GATTAATAAT GAGGAGGCGT TAATAAAATG ACTGAAATAG ATTTTGATAT 9120

AGCAATTATC GGTGCAGGTC CAGCTGGTAT GACTGCTGCA GTATACGCAT CACGTGCTAA 9180

TTTAAAAACA GTTATGATTG AAAGAGGTAT TCCAGGCGGT CAAATGGCTA ATACAGAAGA 9240

AGTAGAGAAC TTCCCTGGTT TCGAAATGAT TACAGGTCCA GATTTATCTA CAAAAATGTT 9300

TGAACACGCT AAAAAGTTTG GTGCAGTTTA TCAATATGGA GATATTAAAT CTGTAGAAGA 9360

TAAAGGCGAA TATAAAGTGA TTAACTTTGG TAATAAAGAA TTAACAGCGA AAGCGGTTAT 9420

TATTGCTACA GGTGCAGAAT ACAAGAAAAT TGGTGTTCCG GGTGAACAAG AACTTGGTGG 9480

ACGCGGTGTA AGTTATTGTG CAGTATGTGA TGGTGCATTC TTTAAAAATA AACGCCTATT 9540

CGTTATCGGT GGTGGTGATT CAGCAGTAGA AGAGGGAACA TTCTTAACTA AATTTGCTGA 9600

CAAAGTAACA ATCGTTCACC GTCGTGATGA GTTACGTGCA CAGCGTATTT TACAAGATAG 9660

AGCATTCAAA AATGATAAAA TCGACTTTAT TTGGAGTCAT ACTTTGAAAT CAATTAATGA 9720

AAAAGACGGC AAAGTGGGTT CTGTGACATT AACGTCTACA AAAGATGGTT CAGAAGAAAC 9780

ACACGAGGCT GATGGTGTAT TCATCTATAT TGGTATGAAA CCATTAACAG CGCCATTTAA 9840

AGACTTAGGT ATTACAAATG ATGTTGGTTA TATTGTAACA AAAGATGATA TGACAACATC 9900

AGTACCAGGT ATTTTTGCAG CAGGAGATGT TCGCGACAAA GGTTTACGCC AAATTGTCAC 9960

TGCTACTGGC GATGGTAGTA TTGCAGCGCA AAGTGCAGCG GAATATATTG AACATTTAAA 10020

CGATCAAGCT TAATTCGAAG TCGAATTAAG ATGTTGAGCT GTAAATTATT TGGATATTTA 10080

TTTTAATAGT GTCATCACAG CGTTAAAATA ATGTCTTACT TTTAAATTAA AGCAAATTAT 10140

ATAGAAAACT AGAACTTAGT ACGTATCATT TGTGCGTTTC AATGAGTTCT AGTTTTTTTA 10200

TATGTTATAT TAAACTTATA ACTTTATGGG AGTGGGACAG AAATGATAAA GAGCCACTAA 10260

TGATTTATTA TGTAGTGGTT CTTAAACATT AGCCACAGCT AATGTGTACT TAAAAATAGG 10320

AATACATGAG TAAAACTCAT GCATAAGAAA TACTAATTTC TATAGAAAAA GTATTACTTT 10380

ATCGTTGTCC CACCCCAACT TGCACATTAT TGTAAGCTGA CTTTCCGCCA GCTTCTGTGT 10440

TGGGGCCCCG CCAACTTGCA CATTATTGTA AGCTGACTTT TCGTCAgCTT CTGTGTTGGG 10500

GCCCCGCCAA CTTGCACATT ATTGTAAGCT GACTTTTCGT CAGCTTCTGT GTTGGGGCCC 10560

CGCCAACTTG CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTATGTTG GGGCCCACAC 10620

CCCAACTCGC ATTGCCTGTA GAATTTCTTT TCGAAATTCT CTGTGTTGGG GCCCACACCC 10680

ACTCGCATTG CCTGTAGAAT TTCTTTTCGA AATTCTCTGT GTTGGGGCCC CTGACTAGAG 10800

TTGAAAAAAG CTTGTTGCAA GCGCATTTTC ATTCAGTCAA CTACTAGCAA TATAATATTA 10860

TAGACCCTAG GACATTGATT TATGTCCCAA GCTCCTTTTA AATGATGTAT ATTTTTAGAA 10920

ATTTAATCTA GACATAGTTG GAAATAAATA TAAAACATCG TTGCTTAATT TTGTCATAGA 10980

ACATTTAAAT TAACATCATG AAATTCGTTT TGGCGGTGAA AAAATAATGG ATAATAATGA 11040

AAAAGAAAAA AGTAAAAGTG AACTATTAGT TGTAACAGGT TTATCTGGCG CAGGTAAATC 11100

TTTGGTTATT CAATGTTTAG AAGACATGGG ATATTTTTGT GTAGATAATC TACCACCAGT 11160

GTTATTGCCT AAATTTGTAG AGTTGATGGA ACAAGGAAAT CCATCCTTAA GAAAAGTGGC 11220

AATTGCAATT GATTTAAGAG GTAAGGAACT ATTTAATTCA TTAGTTGCAG TAGTGGATAA 11280

AGTCAAAAGT GAAAGTGACG TCATCATTGA TGTTATGTTT TTAGAAGCAA GTACTGAAAA 11340

ATTAATTTCA AGATATAAGG AAACGCGTCG TGCACATCCT TTGATGGAAC AAGGTAAAAG 11400

ATCGTTAATC AATGCAATTA ATGATGAGCG AGAGCATTTG TCTCAAATTA GAAGTATAGC 11460

TAATTTTGTT ATAGATACTA CAAAGTTATC ACCTAAAGAA TTAAAAGAAC GCATTCGTCG 11520

ATACTATGAA GATGAAGAGT TTGAAACTTT TACAATTAAT GTCACAAGTT TCGGTTTTAA 11580

ACATGGGATT CAGATGGATG CAGATTTAGT ATTTGATGTA CGATTTTTAC CAAATCCATA 11640

TTATGTAGTA GATTTAAGAC CTTTAACAGG ATTAGATAAA GACGTTTATA ATTATGTTAT 11700

GAAATGGAAA GAGACGGAGA TTTTCTTTGA AAAATTAACT GATTTGTTAG ATTTTATGAT 11760

ACCCGGGTAT AAAAAAGAAG GGAAATCTCA ATTAGTAATT GCCATCGGTT GTACGGGTGG 11820

ACAACATCGA TCTGTAGCAT TAGCAGAACG ACTAGGTAAT TATCTAAATG AAGTATTTGA 11880

ATATAATGTT TATGTGCATC ATAGGGACGC ACATATTGAA AGTGGCGAGA AAAAATGAGA 11940

CAAATAAAAG TTGTACTTAT CGGTGGTGGC ACTGGCTTAT CAGTTATGGC TAGGGGATTA 12000

AGAGAATTCC CAATTGATAT TACGGCGATT GTAACAGTTG CTGATAATGG TGGGAGTACA 12060

GGGAAAATCa GAGATGAAAT GGATATACCA GCACCAGGAG ACATCAGAAA TGTGATTGCA 12120

GCTTTAAGTG ATTCTGAGTC AGTTTTAAGC CAACTTTTTC AGTATCGCTT TGAAGAAAAT 12180

CAAATTAGCG GTCACTCATT AGGTAATTTA TTAATCGCAG GTATGACTAA TATTACGAAT 12240

GATTTCGGAC ATGCCATTAA AGCATTAAGT AAAATTTTAA ATATTAAAGG TAGAGTCATT 12300

CCATCTACAA ATACAAGTGT GCAATTAAAT GCTGTTATGG AAGATGGAGA AATTGTTTTT 12360

GGAGAAACAA ATATTCCTAA AAAACATAAA AAAATTGATC GTGTGTTTTT AGAACCTAAC 12420

GATGTGCAAC CAATGGAAGA AGCAATCGAT GCTTTAAGGG AAGCAGATTT AATCGTTCTT 12480

GCGTTAATTC ATTCTGATGC GCCTAAGCTA TATGTTTCTA ATGTGATGAC GCAACCTGGG 12600

GAAACAGATG GTTATAGCGT GAAAGATyAT ATCGATGCGA TTCATAGACA AGCTGGACAA 12660

CCGTTTATTG ATTATGTCAT TTGTAGTACA CAAACTTTCA ATGCTCAAGT TTTGAAAAAA 12720

TATGAAGAAA AACATTCTAA ACCAGTTGAA GTTAATAAGG CTGAACTTGA AAAAGAAAGC 12780

ATAAATGTAA AAACATCTTC AAATTTAGTT GAAATTTCTG AAAATCATTT AGTAAGACAT 12840

AATACTAAAG TGTTATCGAC AATGATTTAT GACATAGCTT TAGAATTAAT TAGTACTATT 12900

CCTTTCGTAC CAAGTGATAA ACGTnAATAA TATAGAACGT AATCATATTA TGATATGATA 12960

ATAGAGCTGT GAAAAAAATG AAnATAGACA GTGGTTCTAA GGTGAATCAT GTTTTAAATA 13020

AGAAAGGAAT GACTGTACGA TGAGCTTTGC ATCAGAAATG AAAAATGAAT TAACTAGAAT 13080

AGACGT 13086

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CATTAGTCAT GAAAATAGCC GACAACTTCA TCTGTGAAAT CACCGGCCTT TTATTTTAGC 60

TAACTTTATT TCTGATTTTA CGATTTTAAT TGATCATACA GAGAAAGTGA TCTTTTTACA 120

ATTTCTAAAA ACTCATGATC TATATTGGAC ATTTGATGAA AATAAGACAA AATGTTTTCT 180

GTTAGCTTCT CTTGTTTTGG GAATGAATCA TCTTCTTTAA TCCAAATCGC TAATTCGCCT 240

AATGGTGTTT TATCATCTTT AAATGTTTGT ATATATTCGT AAAAGCTCAT AGTATTCCTT 300

CTCTCAATTT ACTTATATAA ATCCTACCAC GAAAGCTTTC AAGAAAACAC AATTAAATGT 360

CTATTTAGTG AACTTTTTAA GGTTGTGCAC TCTTTTAATG TCTGCCAATT AGGTCAATTA 420

ATCATCACAA TGTACAATTA ACTCTATTTT CAGTTCATAT ACTCACACAC CGTTTTTGAA 480

CAACACATTA ACTTCTCATT TAGATAAAAC GCAAAAAAGC CTGGCACCAA TACAATAGAT 540

GCCAGACTAA GAGTCTACTA TATAAATTTA TTTAGCGTAT GGTTTTACTT CGATTGCACC 600

TTCATTTTCA TCATGAACAC CATGCTTATA ATAATCAATA TATTGTGGCT CTAAAGGCTT 660

TCTGCCACGT ATAATGTCTG CTGCTTTTTC AGCTAACATT AAAACAGGTG CGTGTATATT 720

GCCATTTGTC GTACGTGGCA TAGCTGATGC ATCAACTACA CGTAAATTTT CCATACCGTG 780

ACTACAAGAT GGGTGTAATG CTGTTTCACC ATCTCTACGA ACCCAATCAA GAATTTCTTC 900

GTCTGTTTGC ACTTCTGGTC CTGGTGAAAT TTCTCCACCA TTGAATGGAT CCATTGCTTT 960

TTGAGATAAG ATATTTCTTG CTACACGAAT TGCTTCTACC CATTCTTTTT TATCTTCTTC 1020

TGTTGATAAA TAATTAAAGC GGATACTTGG TTTTTCGAAT GGATCTTTAG ATTTGATTTT 1080

CAAGCTACCA CGAGAGTTTG AATACATTGG TCCTACGTGA ACTTGATAAC CATGTGCGAC 1140

CGCTGCCTTT TGACCATCAT ATCTTACAGC TATTGGTAAG AAATGGAACA TTAAGTTAGG 1200

ATAAtCAACT TCGTTATTTG AACGTACAAA TCCGCCACCT TCAAAATGGT TAGATGCTGC 1260

TGCACCTGTA CGTGTGAAAA TCCATTGTAA ACCAATAAAT GGcATGCGCT TGAtATCTAA 1320

GCTTGGCtGt AATGATACAG GTTCCTTACA 1350

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TAATGCTATT GGCAACACCA TATATGAAAn CTCCAAACGA TCCTAAACCG ACTATAGATT 60

CACCAAATTT nACAATCCAT GAATAAAGTA GTGGCCATAA GAATAACAAT ATGACAACTA 120

AAAATGTACA GTAAAATGCA GTCATAATTG GAACTAGACG TTTACCACTA AAAAATGATA 180

ATGCTAATGG TAATTCTGTT TCACTAAACT TATTGTATGC ATAAGCTGCT ATTAAACCTA 240

TTACAATACC AACAAAGACA TTGCCATTAT TCATCTTTTC AAAAGCTGAA TTTATTTCCG 300

ArGCTTTCAT TCCTAATAAA GGCGCTAATT TCATTGGTGA TAATACAACT GTAACTAAAA 360

AATATCCTAA CGTrGCTGCA rGCGsGACTG CACCATCATT TTTCTTTGCC ATTCCTATAG 420

CTACACCAAT TGCAAATAAA ATACCTAATT GCTCTAAAAT CGTAGTACCT ACCGTAGTAA 480

AGAACATTGC GATTTTCGGC GTCGCATGAA GTGCATTTAA CGTATTACCA ATTCCGGCAA 540

TAATTGCTGC AGCCGGTAAA ATGGCAACTG GTAACATTAA CGAACGCCCT AAATTTTGGA 600

AAAATTTATA CATTGAATGT CATCCTTCTT AAAATAATGT AGAAATATAA AGATTACTAA 660

TGTAACTAGA ATAACTACTT CGATACTCCG TTATAGTCAC CTAGGCTTAC TAACCAGCTA 720

TATTTCTACC TCAAGTTATT TTATAAACTT TTTACAATTT CATGCAATTC TTGTTGTAAC 780

TTTGCTGTTC GTGTTTCAAT CTCTTTTGTA ATATAATCGA TACGCTCGTT TCGTTTTAAA 840

AAAGACCGTG AATCTTAGTA GGACCAACAT AAGCAACAGG TAATATTGGT GACTTACTTA 960

ACATTGCAAT TGTTGAAGCA CCaCGTTTCA AAGGTGCACC TTCTTGCGAT GTGCGAGAAC 1020

CTGTTGGGAA GATACCAACT GTCTTATTAT CTTTCAACAA ATTGATTGGG CGTTTTAAAG 1080

TACTAGGTCC TGGATTTTCA CGATCTACAG GAAATGCATT TAAAGACGTT AAAAATTTAC 1140

CAATCCATTT ATTTTTGAAT AATTCTTTTT TAGCCATATA ATGAATTTGA TTAGGATATA 1200

ATGCCATACC TAGCATAATG ACTTCGTTAT AACTTTCATG CGTACAAGTT ACGACATATT 1260

TACTATCCTT AGGAATATTA TCTTTACCGA TTACGTATAA TGATTTTGAC ATTTTAACTA 1320

AAATGAAATT CAAAATCTTA CTAATCACTG AATACATTGT GCCACCTACT TAACTT 1376

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TTGTCATACC AATATTTTGT AAAATATGGA ACACAAGTAA AGTGACGAAA CCAACGATAA 60

AGATTTTGTT AAATTGATCT TCAATTTTCG CAGCTAATCT TATTAGATGG AAGATTAAAA 120

ATAAAAATAT TAAGATCAAT ATGACAGAAC CGATAAAGCC AAGTTCCTCT CCAATCACTG 180

AAAAGATAAA GTCAGTATGA TTTTCAGGTA TATAAACTTC ACCGTGATTG TATCCTTTAC 240

CTAGTAACTG TCCAGAACCG ATAGCTTTAA GTGATTCAGT TAAATGaTAG CCATCACCAC 300

TACTATATGT ATAGGGGTCA AGCCATGAAT TGATTCGTCC CATTTGATAC AGTTGGaCAC 360

CTAATAAATT TTCAATTAAT GCGGGTGCAT ATAGaATACC TAAAATGACT GTCATTGCAC 420

CAACaATACC TGTAATAAAG ATAGGTGCTA AGATACGCCA TGTTATACCA CTTACTAACA 480

TCACACCTGC AATAATAGCA GCTAATACTA ATGTAGTTCC TAGGTCATTT TGCAGTAATA 540

TTAAAATACT TGGTACTAAC GAGACACCAA TAATTTTGAA AAATAATAAC AAATCACTTT 600

GGAATGATTT ATTGAATGTG AATTGATTAT GTCTAGAAAC GACACGCGCT AATGCTAAAA 660

TTAAAATAAT TTTCATGAAT TCAGATGGCT GAATACTGAT AGGGCCAAAC GTGTACCAAC 720

TTTTGGCACC ATTGATAATA GGTGTAATAG GTGACTCAGG AATAACGAGC AAGCCTATTA 780

ATAATAGACA GATTAAGAAA TACAATAAAT ATGTATAATG TTTAATCTTT TTAGGTGAAA 840

TAAACATGAT GATACCTGCA AAAATTGCAC CTAAAATGTA ATAAAAAATT TGTCTGATAC 900

TTGCTAAAAC AGCTATAGTG GCTACTAATA CCCAGTCTAC TTTGCGAAnC aATGCTTATC 1020

CGGCTGTTGA CGAGATGAAT AATTCATTGC AAACTCCTTT TATACTCACT AATGTTTATA 1080

TCAATTTTAC ATGACTTTTT AAAAATTAGC TAGAATATCA CAGTGATATC AGCTATAGAT 1140

TTCAATTTGA ATTAGGAATA AAATAGAAGG GAATATTGTT CTGATTATAA ATGAATCAAC 1200

ATAGATACAG ACACATAAGT CCTCGTTTTT AAAATGCAAA ATAGCATTAA AATGTGATAC 1260

TATTAAGATT CAAAGATGCG AATAAATCAA TTAACAATAG GACyAAATCA ATATTAATTT 1320

ATATTAAGGT AGCAAACCCT GATATATCAT TGGAGGAAAA CGAAATGACA AAAGAAAATA 1380

TTTGTATCGT TTTTGGAGGG AAAAGTGCAG AACACGAAGT ATCGATTCTG ACAGCACAAA 1440

ATGTATTAAA TGCAATAGAT AAAGACAAAT ATCATGTTGA TATCATTTAT ATTACCAATG 1500

ATGGTGATTG GAGAAAGCAA AATAATATTA CAGCTGAAAT TAAATCTACT GATGAGCTTC 1560

ATTTAGAAAA TGGAGAGGCG CTTGAGATTT CACAGCTATT GAAAGAAAGT AGTTCAGGAC 1620

AACCATACGA TGCAGTATTC CCATTATTAC ATGGTCCTAA TGGTGAAGAT GGCACGATTC 1680

AAGGGCTTTT TGAAGTTTTG GATGTACCAT ATGTAGGAAA TGGTGTATTG TCAGCTGCAA 1740

GTTCTATGGA CAAACTTGTA ATGAAACAAT TATTTGAACA TCGAGGGTTA CCACAGTTAC 1800

CTTATATTAG TTTCTTACGT TCTGAATATG AAAAATATGA ACATAACATT TTAAAATTAG 1860

TAAATGATAA ATTAAATTAC CCAGTCTTTG TTAAACCTGC TAACTTAGGG TCAAGTGTAG 1920

GTATCAGTAA ATGTAATAAT GAAGCGGAAC TTAAAGAAGG TATTAAAGAA GCATTCCAAT 1980

TTGACCGTAA GCTTGTTATA GAACAAGGCG TTAACGCACG TGAAATTGAA GTAGCAGTTT 2040

TAGGAAATGA CTATCCTGAA GCGACATGGC CAGGTGAAGT CGTAAAAGAT GTCGCGTTTT 2100

ACGATTACAA ATCAAAATAT AAAGATGGTA AGGTTCAATT ACAAATTCCA GCTGACTTAG 2160

ACGAAGATGT TCAATTAACG CTTAGAAATA TGGCATTAGA GGCATTCAAA GCGACAGATT 2220

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AAACAAATGC AATGCCTGGA TTTACGGCTT TCAGTATGTA TCCAAAGTTA TGGGAAAATA 2340

TGGGCTTATC TTATCCAGAA TTGATTACAA AACTTATCGA GCTTGCTAAA GAACGTCACC 2400

AGGATAAACA GAAAAATAAA TACAAAATTG ACTAACTGAG GTTGTTATTA TGATTAATGT 2460

TACATTAAAG CAAATTCAAT CATGGATTCC TTGTGAAATT GAAGATCAAT TTTTAAATCA 2520

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TGGGGCTGCT TTTTATCAAA GAGGGACACC TATAGATGAA AATGTAAGCG GGCCTATTAT 2700

AAACCCTAAA GTAATTGCCG TCACAGGGTC TAATGGTAAA ACAACGACTA AAGATATGAT 2820

TGAAAGTGTA TTGCATACCG AATTTAAAGT TAAGAAAACG CAAGGTAATT ACAATAATGA 2880

AATTGGTTTA CCTTTAACTA TTTTGGAATT AGATAATGAT ACTGAAATAT CAATATTGGA 2940

GATGGGGATG TCAGGTTTCC ATGAAATTGA ATTTCTGTCA AACCTCGCTC AACCAGATAT 3000

TGCAGTTATA ACTAATATTG GTGAGTCACA TATGCAAGAT TTAGGTTCGC GCGAGGGGAT 3060

TGCTAAAGCT AAATCTGAAA TTACAATAGG TCTAAAAGAT AATGGTACGT TTATATATGA 3120

TGGCGATGAA CCATTATTGA AACCACATGT TAAAGAAGTT GAAAATGCAA AATGTATTAG 3180

TATTGGTGTT GCTACTGATA ATGCATTAGT TTGTTCTGTT GATGATAGAG ATACTACAGG 3240

TATTTCATTT ACGATTAATA ATAAAGAACA TTACGATCTG CCAATATTAG GAAAGCATAA 3300

TATGAAAAAT GCGACGATTG CCATTGCGGT TGGTCATGAA TTAGGTTTGA CATATAACAC 3360

AATCTATCAA AATTTAAAAA ATGTCAGCTT AACTGGTATG CGTATGGAAC AACATACATT 3420

AGAAAATGAT ATTACTGTGA TAAATGATGC CTATAATGCA AGTCCTACAA GTATGAGAGC 3480

AGCTATTGAT ACACTGAGTA CTTTGACAGG GCGTCGCATT CTAATTTTAG GAGATGTTTT 3540

AGAATTAGGT GAAAATAGCA AAGAAATGCA TATCGGTGTA GGTAATTATT TAGAAGAAAA 3600

GCATATAGAT GTGTTGTATA CGTTTGGTAA TGAAGCGAAG TATATTTATG ATTCGGGCCA 3660

GCAACATGTC GAAAAAGCAC AACACTTCAA TTCTAAAGAC GATATGATAG AAGTTTTAAT 3720

AAACGATTTA AAAGCGCATG ACCGTGTATT AGTTAAAGGA TCACGTGGTA TGAAATTAGA 3780

AGAAGTGGTA AATGCTTTAA TTTCATAGAG ATTAGTCGAG GGACCTTTTA CTTATAAAAA 3840

TGATTTGAAT TAATACTAAA AGATTACAAA GAAGAGGTGG TTTTGTGTGT AAATACAAAA 3900

TTGCCTTTTT CTTTTTATGT TAAATCTATA AATTTGAAAC TAAATCAAGG TTAATTCTAT 3960

GTACACACTT TATATAGGAA GTAGTTTGAA TGTTTATATA ATGTTTTACA AAAAGATGTA 4020

GTATTATAAT GTCTAATTTC ACATGTGTTT CAGTAAAATT TGTTGTGGAA TGTTAACGAT 4080

ATACGTATTT TATAAAAaAT TTTTTATAAT GATTATTCGA ATGATGCGTA ACGCTTACAT 4140

CTTATCTAAT GCTAGCTTTT TGACAAAAAT ATGACAATCA ATTAATGTGA TTCTAATAAA 4200

TATTCGCAAA TTGCTTTATT GCGATTAAAT TTTTTTGGTG GTACTATATA GAAGTTGATG 4260

AAATATTAAT GAACTTATAT GCAAAAGTAT ATTGAGAAAT AAACAGGTAA AAAGGAGAAT 4320

TATTTTGCAA AATTTTAAAG AACTAGGGAT TTCGGATAAT ACGGTTCAGT CACTTGAATC 4380

AATGGGATTT AAAGAGCCGA CACCTATCCA AAAAGACAGT ATCCCTTATG CGTTACAAGG 4440

AATTGATATC CTTGGGCAAG CTCAAACCGG TACAGGTAAA ACAGGAGCAT TCGGTATTCC 4500

AGAATTGGCA ATGCAGGTAG CTGAACAATT AAGAGAATTT AGCCGTGGAC AAGGTGTCCA 4620

AGTTGTTACT GTATTCGGTG GTATGCCTAT CGAACGCCAA ATTAAAGCCT TGAAAAAAGG 4680

CCCACAAATC GTAGTCGGAA CACCTGGGCG TGTTATCGAC CATTTAAATC GTCGCACATT 4740

AAAAACGGAC GGAATTCATA CTTTGATTTT AGATGAAGCT GATGAAATGA TGAATATGGG 4800

ATTCATCGAT GATATGAGAT TTATTATGGA TAAAATTCCA GCAGTACAAC GTCAAACAAT 4860

GTTGTTCTCA GCTACAATGC CTAAAGCAAT CCAAGCTTTA GTACAACAAT TTATGAAATC 4920

ACCAAAAATC ATTAAGACAA TGAATAATGA AATGTCTGAT CCACAAATCG AAGAATTCTA 4980

TACAATTGTT AAAGAATTAG AGAAATTTGA TACATTTACA AATTTCCTAG ATGTTCATCA 5040

ACCTGAATTA GCAATCGTAT TCGGACGTAC AAAACGTCGT GTTGATGAAT TAACAAGTGC 5100

TTTGATTTCT AAAGGATATA AAGCTGAAGG TTTACATGGT GATATTACAC AAGCGAAACg 5160

TTtAGAAGTA TTanAGAAAT TTAAAAATGA CCAAATTAAT ATTTTAGTCG CTACTGATGT 5220

AGCAGCaAGA GGACTAGATA TTTCTGGTGT GAGTCATGTT TATAACTTTG ATATACCTCA 5280

AGATACTGAA AGCTATACAC ACCGTATTGG TCGTACGGGT CGTGCTGGTA AAGAAGGTAT 5340

CGCTGTAACG TTTGTTAATC CAATCGAAAT GGATTATATC AGACAAATTG AAGATGCAAA 5400

CGGTAGAAAA ATGAGTGCAy TcGTCCACCA CATCGTAAAG AAGTACTTCA AGCACGTGAA 5460

GATGACATCA AAGAAAAAGT TGAAAACTGG ATGTCTAAAG AGTCAGAATC ACGCTTGAAA 5520

CGCATTTCTA CAGAGTTGTT AAATGAATAT AACGATGTTG ATTTAGTTGC TGCACTTTTA 5580

CAAGAGTTAG TAGAAGCAAA CGATGAAGTT GAAGTTCAAT TAACTTTTGA AAAACCATTA 5640

TCTCGCAAAG GCCGTAACGG TAAACCAAGT GGTTCTCGTA ACAGAAATAG TAAGCGTGGT 5700

AATCCTAAAT TTGACAGTAA GAGTAAACGT TCAAAAGGAT ACTCAAGTAA GAAGAAAAGT 5760

ACAAAAAAAT TCGACCGTAA AGAGAAGAGC AGCGGTGGAA GCAGACCTAT GAAAGGTCGC 5820

ACATTTGCTG ACCATCAAAA ATAATTTATA GATTAAGAGC TTAAAGATGT AATGTCTTGA 5880

GCTCTTTTTT GTTTTCAATA ATTGATTCTC TGTAGATATC aAAGTaCTAA CGTTTTAAAG 5940

GTTAAATATT TAATTGGATT GAGATCTGTA TGCGGTTATA TCaTTCTGTG TAAATATGGT 6000

TCTCCACCAA ATGTGGTGAG TATATAATTT AAAGAACTAT TTTTAAATTA AGAATAATCG 6060

AACATAAATA AACTTTATGA AATTTCAGTA TCATGTTCTT ATAAAAAACA ATAGGGCTTT 6120

TTGctGACGC TAGTGCGCGA TAAATAATAA GTTGAATATA AAAAAGATCA CTGCCAATCA 6180

TTCGTTTAAT GGCAGCGATC TTTTTTATTT AATTATTTCT CTTTCCACTG CAACATTTGA 6240

TAACCAATGC GTGGATGTGT TTTAATAATA TCTTTTGCGT CCTCATGACA TTGTGAAAGT 6300

CCATATATTC GTTTTAATAT CATCTCATAA GTGAGTACTT TTCCTTTATG ATTTGACAAT 6420

AGTTCTAACA AGCTAAATTC ATTTGGCGTC AAATGTACCT CCTGATTATT AATAACAACA 6480

GATTTGGAGC CAAAGTCGAT GCTTAGCAAA CCGTTAGTAA ATACAATGTT AGTTTCTTGA 6540

TGTGACTTAG CGATTCTCTC GATGACTCGT ATTCGTGCCC GAAGCTCATC AACATTAAAA 6600

GGTTTAGTCA TATAGTCATT CGCACCGTTA TCTAAAGCTT GAATAATTGT TTGTTCTTCT 6660

TGTCTTGCAC TTATTACAAT GATAGGAATG TCAGTATGTT GCCTGATTTC TGAAATCAAA 6720

CATAATCCAT CTTTATCTGG TAAACCTAAA TCTAATAAAA TGACATCTGG TTTATCAATT 6780

TGAATTTTAA AGTGTGCTTG TGTGGCATTG TCGGCTGTAG TTACATTGTA ATAATCTAAA 6840

GTTAATGCAA CATCAAGTAA ATGTGTGATT GCGTGATCAT CTTCAATTAT CAATATTTTA 6900

GATTGCATTA TACGTCTCCT TCGTTAAAGT CTGTATATAT ATTGAAATAG AATATACTGC 6960

CGTGTGGTTG GTTCGGTTTA TATTGTAAGT TTGATTGATG TTTGTGTAGG ATAGTCTGTA 7020

CTAAATATAA GCCTAGTCCC ATGCTTTCTT TTTGGTTATC TTTAAAATAT TTATTTGATC 7080

CTGTGTAAAA AGGCTCGAAT ATCTTTTGTt GTTCTTCTAA ACTAATTCCA GGTCCTTCGT 7140

CTATAACGGC AAATTCGATT TGTTCATAGC TAGCATAACG AATAGATAAA TTGATTTTGG 7200

TGTCAGTAGA AGTGTGTTTA ACTGCATTTT CAATCAAATT GAAtAAAgCT TGTAAAATCA 7260

ACTTACTGTC AATGTGTATA AACtGTAAAT TTACTGAGGA TGATACAGTT ATACGCTTTT 7320

TTAAATGGCG ACGTTCTAAA ATACATATCG ATTTCTTATA CTA 7363

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTAACAATCG ATAACCACAA TACTTCTATT GTAATTGTTT AACGATTTCn CGATTAAAAT 60

CATCTAAATC GTCTGGTACT CGACTTGTTA CAATATTGTT GTCTACAcTa CTGACTCATC 120

AACTACATGT GCGCCTGCAT TTGATAAATC TTTGCGTACA TTTAATACTG CTGTTAACGT 180

ACGACCTTTT AAATCGTCTG TATCTATTAG TATTTGTGGC CCATGACAAA TGGCAAATGT 240

TGGTACATCA TTTTTAGTAA AGTATTTAGC AAATGTGCCA TATCGACCTT CTGTATCTCC 300

ACGTAAATGA TCTGGTGAAA ATCCTCCAGG AATTAATAAT GCATCATAAT CTTCTGGTTT 360

ATTTGCAGTA TCTCCAATCA CTACAGTATT AAAGCCTGCA TTCTCTAATG CCTCTTTAGG 480

GCTTGAATAT TCTATATCTT CAAATTCGTT TGCTAGAATA ATTGCTACTT TTTTAGTCAT 540

TGAAAATCAC CTTTCTATAT ATCATTGATA TAATTACTAT AGACAAGTAA ATCAGTGATT 600

AAACATACAA GATATAAAAA ATATTAAGCG ACTGTCGCGA TATCTAACCC TAACACATCT 660

TATGTGGCAT TTACTTAGAT ACTAATTTAA CCTTTTCTTC AAGCTGATCT AACAATCCAA 720

TCCATTCATC TATATCTTCA ACACGTACTT CATCAGGATT TACATGATCG ATATCCTCAA 780

TAAACTTATT TAAACGCGCT TTTATCTGTT CGATTGTTTG CTGTTCATTC ATAAAAAGTT 840

AACTCCTTTT ATTTTGTTTT CTTTTTCATT ATTATCCTAA CAGAAATTGC GTTAAAGCGA 900

TATAATCTTA GCTATATTTA TGACATTCAA ATTATTTTGA CTTTTAAAAA TCCCCTTTTC 960

AATTAACTAA AATTAAGAGA TAATTTGTTA CGAGTGATAA TACGAaGkGG TaTCATACCG 1020

ATATGAACCA AATAGAAAGA AGGAAGTTTA AGACGATGAA TAGCGTCAAA TTGAAGCAAC 1080

CTGTTAGCAT TTACAATGAT CCATGGGAAG TGAAATTTAT ATACATTTAA ATTTCATGAG 1140

ACAATAAACG TTGATTTAAT GCGTTTTTTT GCCTTTTTTA TTTTCCTTAT TTTTTCTGTT 1200

TTACAACAAA ATGGTATCAA AAATGGTATC ATTTGTAGTT ATTTTAGCTT CACATATTAA 1260

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TCTCAGTTCA TGTTGTGGTG ACACTTTAAA CGGTCTGTGC CAGTAGCGAC CGAGTCATTT 1560

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CAGTTGTATT TAAAGTTAAG TTATCTACTT CGCGCTTTCC TTGCCTTAAT TGTGAAATTA 1680

CATATTGCGC TACGCCAGTT TGTTTGTGAA TTTGGTAACC TGTTATATCA CTTTTGATCA 1740

ATTCAATTAT TTTTAATTTA TAATCACTCA TATTATCTAC GTCCATTCTT TTTATCTAAA 1800

CAATAAAAAT GTGTCTTTCT CCCGATAAAT AATAACAATG GTAGGCTTAA TAAAAACAAT 1860

ATTAAATACA TTTGTTCTGT CATAATTGAA AACCTCCAAA TAATATTATA TTATATAAGT 1920

GTAAGGAGGA GCCATCAGGC TCCAAGCATA ATGTTAATCT TTGTTGTTTG GCTTTCGGTC 1980

TAGGTAGCCG AGATGCCaTT CTCTAAGTTG TTTTAACACT TCTGGAATTA TCAGTACTGC 2040

CAATACTTGA TGTTCTAGAA GTGTTTTTAT TATGTCTAGC ATGAGGCTTT TCACCTCCTT 2100

ACACATAATT TGTAAGTCAT CAACTAACCT ACAAATATAA TTATACTAAA CAAATGTTTA 2160

GTTATCTACA TTTAAATCTT GAGAGAAATG TTAAAAAGTT CTAGTAAAAT AATAGCACAT 2280

TTTATCTTTA AATGTAAATA GAAAGCAGGT ATGTAACGCA CCTGCTTAAA TAGaCATGAC 2340

TATGTCATTC TAACTGATTT CTCCCCATAA GTCACCTAAT ATCTGATTAG GTGGGGCAGA 2400

ACCATTCCAT GTTCTAATAG GCAAGTAATA ACGTTGCCCC TCCCATGTAT ATCCTACCCA 2460

AACATGACCA TCTTGTAACA TCACTTCTGT ATAATCACAA TACCCACCAG GTTGGAACTG 2520

ATAACCCACT GGACAAGATA AGAATGGCCC CACTTTTCTT ACTGTGATTG GTTGATTGCC 2580

GTTTGTGAAT CTAGCACTTT CTTCCATGTA GTAAGTACCA TATTTATTAC GTTTCCATGC 2640

ACTTGCAACT GGTTTAACTG TATTACTTGA AGCGCTTGAC TCATTAGAGA CAGTGGCAAC 2700

CGGTATTTTA CCATCCATGT ACGCCCTAAT CTGCTTGATA AAGTAGTCTT TAAGTTGCAA 2760

CCGCTTGTCT TCTGGCAATA GACCGCGAGT TACTGGGTCA AAACCAGTGT GTAAAACCGA 2820

ACTTCTATGA GGGCATGATG TTGAAGTAAA TTCATTGTGC AATCTGATTG TATTTCTGTT 2880

TGCTGGTAAT CCCCATTTTT TCAACAATCT AGCGCATTCT TGGAAAGTTG CCTGTTCATT 2940

TTTTAAGAAT GTCGCGTTAT CTGCGCCCAT TGATTGACAT ACTTCAATAC CGTAATAATA 3000

TTTATTACCT ATTTGATTAG CGGTATGCCA ACCTACTTGT GATTCATCTA AGGCTTGCCA 3060

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ATTTACTAAT CCGTTACGAT ATGCTTCAGC AGTCGCCCCT TTGCTCCCTG CGTCGTTGTG 3180

TATAACTATA CCTTTAGGGT TACTACCACG CTTAGGTAGG TCATAACCTT TAACCACATC 3240

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TTGTGTAGGA GATTGAACTG ATCGTGGCGC TGTCTCACTT TTAAAATTCG GACGGATAAA 3360

CCACATAGGG AAATCATAAG CATGTTGTCG TCTTGTAACT TTTTCCCAAC CCCAGCCGGG 3420

TTGTTCGATT CCGTCAGTCC AGCCACCGCC TAGCCAATTC TGCTCATATA CAATGATGTA 3480

ATCTAAAGTT GCTTCAATTA CCCATGCAAC GTGACCATAT CCAGCACCGT AGTTGCTACC 3540

GAATACCACC ATGTCGCCAG GTTGTGCTAA GAAGTCCGGT GTATTTTGGT ATACAGTAGC 3600

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TCCAAACAAA ACTTTCCAAC CAGCATTGGC ATAATCAAAG CATTGAAATC CATACCATAA 3720

GTCCACATTG AATTGTTTTC CCTCAGAAGT TTTCAACCAC TCTATAAACT CATTTTTAGT 3780

TAATTTTGCT TGCATTGTCG CCACCTCCAT GATGATACTC ATTCACATCA AAGCCAACAT 3840

CGTTAGAGGC GTCTGTGAAA GGTTGTGATG TATCATATTC TTTTGGTGcT TTCGCGCTTA 3900

ATTCCGGCGT TAAACTACTG TCTTGTGATG ATTTCCACGT AACTTGTTGT TCTTCTTTTT 3960

TTGGGTCAGT AATAACGCCA ATACCTGTAA GTAACGTGAG GATAGCGCCT ATAATTGCGC 4080

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AGTTAATATC CATTTGTTTG CTCCTTTTAT CCAAAATAAA AAAACGACTA AAAATTAGTC 4260

GTTTAAAATT ATTCAATGGT CAATGTCGGA GATCCTGAAT AAACATCACT TATAGTGACG 4320

TACAACATCC CTGAAGGATT ACTAAAGTTG ATATTTTTAC TTGCAACTCC GCTATTGACT 4380

CCTGATATTC CTAAATCACT TGACCCTAAA TTAGTTTGCG AAATCCTCAT TATACCGCTA 4440

CGTACATTTT CTATTGTCAC CTGATAACTT TTATTGGGTT CAACTCCATT TATTGTCCAT 4500

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GTTTAGTAAA AGCTTGAGAT GACAAAACAT ACCGCTCGTC ATGATTATGA TTTTTTGGAG 4860

CATATAAATC ATTTAGTGTT TGTTTGAATT CCTCAAAATC TTCTGTATTA ACTTTTGAGC 4920

CAATCTGTTG CAATACACTT TCTGAAATAG AGTTGTTTTG TATTGCTTCT GCTAATTCTC 4980

TTAATGTGTT CATAGATTCA GGCGCGCTAT CAACTAGTTC AGCAATTTTT GTATCCGTAT 5040

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AGATACCTTT TAAGCCGATT TGTTTATATA ACTTAGCGAT TGTACTTGCT TGATGTTGGC 5940

ACCACTCTAT AGCAGTAGCG TATTGGTGGG TAGCTGGATT CTTAGGATTC CATCTAATTC 6000

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GTTTTTATTA TCTACCATAA CTTTTATTCT AGATTTTGTT ACTGTTGGCT TAGTTATAGA 6660

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CGCACTATAA TCTTCACATA CGTCTATAAC TATATAATCA GGTTCATTAG GAACTTCAAA 6960

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GTTTCTAATC ATTATTCCTT TAGGTTTTTC GAGTCGTCGA TTACCTTCTA CTATAAAGTG 7140

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TTTAGGTGCC GGTGTAGTTT TGTCTGGATG ATATGGTGGT CTAACAAAAT ATTTAACCCC 7320

TCCACCTGGT CCATCATGAT AAGAGTGTTT AATTTTATAA GGTGGACTTC CTGTTGCGTT 7380

ATTTGTATAC CAGTTTTGAT CTACGCCATA CCAATAGTCT TTTGTGCATG GTCCCACTAC 7440

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ACTCTTAACT GTTATTTACA TTTACCAAAC CAGAAGCACG CCCAGAAGCT ATATCCTAAA 7860

ATCCCTTTAA GCATGGTAAT CACCTCCTTT AAATACCAAA AACAGTTCTT AGTAAAGCTA 7920

TGACAATCGT ACTGAAGATA GTCCCTATCA AACCTAGAAT CCACATTTTT ATGTCTCTAA 7980

TATTCTTGGC ATTCTTTTCT TTATTCTTTT CATCTTCTAC CTTGTCGCGC TTTAATTCTT 8040

CAAAATTTCT ATCTAATTTG TCATAAATCT TTTCTTGCGC TCTAAGACTA TCTTCTATTC 8100

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CATCTACATC TAAACTATTG CGTAAACCGC CAGTATTAAC GAATCCGATA ACTTCGTTTT 8760

TATCGTTTAC TGTGATTTTC ATTATTTCCA CCCCATAATT TTAGTTATAG TAACTTTGTT 8820

GGCATTCGCT CCAGAACCTG ATGTTTTACC TAAATCAAAG TACACATCGT TATCTATTCT 8880

TAAAGTAGTG CTACTTGTTT TGGATAGTAA GCACTCATAA ATACCGCCAC CGTTGCCGTC 8940

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GTTTTGCTTG ATTTCGATTT GTTGAATGCC TTTTGTCGCA CTATCATTCA CTTTTGCTAT 10080

TAACGTTTGT GTATCAGCCA TATTTTGCTT TAATTGGTTA AAATCTTTAC CGACAGCTTC 10140

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TAAATCATTT TCAATATTGA AGCTAAATTG ACGTTCAACA ACAACATTAT TACTCCCGTT 10260

TTGTGTAAAG AATGCCTGAG CATGCACCTT GCCTGAATGT TTTAAAAATT CATTCGGTAT 10320

CACATACTGC AAACGCCCAT TAATTGCGTC TACTATCGTT AATTCGTCTG AAATATAAGC 10380

GCCTCTATCT ACGTTATAAT CATCGGTTTT TAAnACGATA GATGTTTTAA CATGTTCAGA 10440

ACTTATAGAT AAGGGTCTGT TATnCTTAGT 10470

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3647 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

ATCAGATCTT GAGAATCGAG TTATTAAGTC TATCGAAGAC TTAACTAAAA TCCAACCATT 60

CATGCCTACA CAAGATTTTG ATTTTAAAAC TAAAGAAATT CAATCAAACA TTTCTGAAGA 120

AAGATTTATC GAAATGATTC AGTATTTCAA AGAGAAAATA ACAGAAGGGG ATATGTTCCA 180

AGTTGTGCCA TCAAGAATTT ACAAATATGC GcATCATGCT AGTCAGCATT TAAATCAACT 240

TTCGTTTCAA CTGTATCAAA ATTTAAAACG ACAAAACCCA AGTCCATATA TGTATTATCT 300

TCAAATTGTA ACAACTAATC CTATTGCAGG TACGATTCAA CGTGGTGAGA CGACACAAAT 420

AGATAATGAG AATATGAAAC AACTACTTAA TGATCCAAAA GAATGCAGCG AACATCGTAT 480

GCTAGTTGAT TTAGGACGTA ATGATATTCA TAGAGTAAGT AAAATCGGTA CCTCAAAAAT 540

TACTAAATTA ATGGTTATTG AAAAATATGA ACATGTTATG CATATCGTAA GTGAAGTCAC 600

AGGTAAAATA AATCAAAATT TATCGCCAAT GACAGTTATT GCGAATTTAT TACCAACAGG 660

TACCGTTTCA GGTGCACCAA AATTACGTGC AATTGAAAGA ATATATGAAC AATATCCACA 720

TAAACGGGGC GTTTATAGTG GTGGTGTTGG ATACATAAAT TGTAATCATA ACTTAGATTT 780

TGCATTAGCA ATTCGAACGA TGATGATAGA TGAGCAGTAT ATCAACGTAG AAGCTGGTTG 840

TGGCGTTGTA TATGATTCTA TTCCTGAAAA AGAACTGAAT GAAACGAAAT TGAAAGCTAA 900

AAGCTTATTG GAGGTGAGCC CATGATCTTA GTTGTAGATA ATTATGATTC CTTTACATAT 960

AACCTAGTGG ATATTGTTGC TCAACATACT GACGTCATTG TTCAATACCC TGATGATGAT 1020

AATGTGCTGA ATCAATCGGT GGACGCTGTT ATTATATCTC CTGGTCCAGG GCATCCATTA 1080

GACGATCAAC AGTTAATGAA AATCATATCA ACCTATCAAC ACAAACCCAT TTTAGGTATT 1140

TGTTTAGGGG CTCAGGCACT GACTTGTTAC TACGGTGGAG AAGTCATTAA AGGCGACAAG 1200

GTTATGCACG GCAAAGTTGA TACACTAAAG GTTATATCGC ATCATCAACA TCTGTTATAT 1260

CAAGATATAC CAGAACAGTT TTCAATTATG AGATATCATT CATTAATAAG TAACCCTGAC 1320

AATTTTCCAG AAGAATTGAA AATTACTGGA CGTACCAAAG ATTGTATACA GTCATTCGAG 1380

CATAAAGAAA GACCGCATTA TGGTATTCAG TACCATCCTG AATCATTTGC TACAGACTAT 1440

GGTGTCAAAA TAATTACAAA TTTCATTAAT CTAGTGAAGG AAGGATGAAA ACCATGACAT 1500

TACTAACAAG AATAAAAACT GAAACTATAT TACTTGAAAG CGACATTAAA GAGCTAATCG 1560

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CGGAGCGAGA AATCCAACAA CAAGAATTAA CATATATTGT ACGTAGCTTA ATTAATACAA 1680

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AGTCAAATAG TTTCAACATT TCAACGACTG TTGCTTTTGT TGTAGCAAGT GCTGGcGTAA 1800

AAGTTATAAA ACATGGtAAT AAAAGTATTA CCTCaAATTC aGGTAGTACG GATTTGtTAA 1860

ATCAAATGAA CATACAAaCA ACAACTGTTG ATGATACACC TAACCAATTA AATGAnAAAG 1920

ACCTTGTATT CATTGGTGCA aCTGAATCAT ATCCAATCAT GAAGTATATG CAACCAGTTA 1980

GAAAAATGAT TGGAAAGCCT ACAATATTAA ACCTTGTGGG TCCATTAATT AATCCATATC 2040

ACTTAACGTA TCAAATGGTA GGCGTCTTTG ATCCTACAAA GTTAAAGTTA GTTGCTAAAA 2100

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ATTACACATT AAATGCGACT GATTATGGTT TGAAACATGC GCCGAATAGT GATTTTAAAG 2280

GCGGTTCACC TGAAGAAAAT TTAGCAATCT CCCTTAATAT CTTGAATGGT AAAGATCAGT 2340

CAAGTCGACG TGATGTTGTC TTACTAAATG CGGGTTTAAG CCTTTATGTT GCAGAGAAAr 2400

TGGATACCAT CGCAGAAGGC ATAGAACTTG CAACTACATT GATTGATAAT GGTGAAGCAT 2460

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GGTGCATCTA TGATTTTATT GATCGTTAAC ATCTTATCTG ATAAACAATT GAAAGATTTA 2940

TATAACTACG CTATATCGCA AAATCTAGAA GTGTTAGTTG AAGTACATGA TCGCCATGAA 3000

TTAGAACGTG CCTATAAGGT TAATGCTAAA TTGATTGGTG TAAATAACAG GGACTTAAAA 3060

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ACGTATTAAG CAATACGTCA ATTAACACAA TACAGTTACA CgGCACAGAA TCTATTGATT 3540

TTATACAGGA AATTAAAAAG AAATATTCAA GCATTAAAAT CACTAAAGCT TTAGCTGCaG 3600

ATGgAAAACm TwATCCCAAA caTtAAtnAA tnTTAgGGGG TCCGTGG 3647

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5966 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CcAcCTTGAC CACCTTTACG TGGAATCTTT TCmCCTkGAG CAACaTCGaT AATaTATATT 60

GAAAgTCAAC AAGTTCTGGA CTAAATGTTG CTGCTAAGTT ATCGCCACCA GATTCTATGA 120

AAATTAGTTC TATATCGTCA TGACGTTCTA ATAATTCGTC TATTGCTGCA AAGTTCATAG 180

ATGCATCTTC ACGAATCGCA GTATGAGGAC ATCCACCAGT TTCAACACCA ATGATACGAC 240

TTTCAGGTAG AACTCCTGAA TTTACTAATA TCTTTTCGTC TTCTTTTGTA TATATATCAT 300

TTGTAATAAC GCCGATACTC ATTTCTTTTG AAAGACGTTT TACAACTTTT TCAATTAATT 360

GTGTTTTACC TGCACCTACA GGACCACCAA TACCAATTTT AATCGGATTT GCCACAATTA 420

TAACCTCCTA TGATATGAAA tTCTAACATT GaCGTTCTCA TGCGCCATTT GATTTAGTTC 480

TAAACCAGGC GCTGTCATGC CAAAATCTGC TTCTTTTAAT TCGAAAATCT GCTTTCTTGT 540

TCCTTCTATA TAAGGAATCA TGTGAGTAAC TATCTTTTGA CCAGCAGTTT GTCCAAGTGG 600

AATAGCACGA ACAGCATTTT GAGTTAAACT TGAAACATTT TGATATAAAT AGTAATCAAT 660

AATCGTTTCA ATATCTACAC CTAAATGATG GCCTAGCATA GTAAAACAAA TAGCTGGATT 720

TnACTTTGCT TTCTTATCTT GCATTTGTTG ATGATACCAA GCAATCCATG GGCTATtATA 780

AAGTTCTAAA GCCAATTTAA CCATGCGAGT CCCCATTTGT kTTGCACCAA CACGTGTTTC 840

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AAAGATCTTC TGAATTAACA TCCACAATAA TCATATTATG GTCATCTGCG TATAAAATAT 1380

CTCCATATTG TAAGTCAATA GGTTGTTTTA AACGAATGCC TATTTCAGTG CCATGGTCTG 1440

TAACGACTCT TTGAATACGT TTAACAAGAT CTGAATTTTC AAGGTATACT TTTTCGACGT 1500

GCTTTTGTTT TTCTGAATTT GACAAATTGG CAATATTGCC TTGGATTTCT TCAACAATCA 1560

TTCTATGTTC CTCCTAGAAT AAGAAGTATC TTTGAGTTAA TGGTAACTCA GTTGCTGCAT 1620

TACTTGTAAT TTTTTCTCCA TCTACATATA CTTCATATGT TTGTGGATCA ACGTCTAATT 1680

GACGCACCAT GCGTTTTAAA TTTAATGCAC GATTGATACC ATTTTCATAA GCAGTTTTAG 1800

ACACGAATGT CATTGACGTA CTTGTAAGGT TTCCGCCGTA TTGACCATAC ATTTTACGGT 1860

ACTTCATCGG TTCAGATGTA GGTATAGAAC CATTTGCATC GCCATTTACG GCAGAGTTAA 1920

TTAATCCGCC CTTTACAACT AATTCAGGTT TAACCCCAAA GAAAATTGGG TCCCATAAGA 1980

CAATGTCAGC TAGTTTGCCC GGCTCGATAG ATCCTACATA TTCAGAAATA CCATGTGTAA 2040

TTGCTGGGTT AATTGTATAT TTAGCGATAT AACGTTTGAT GCGATTATTA TCATTATGTT 2100

CAAAATCACC ATCTAAAGGA CCACGTTGTT CTTTCATGCG ATGTGCTACT TGCCATGTTC 2160

GTGTAATTAC TTCACCTACA CGGCCCATTG CTTGTGAATC GGAACTAATC ATACTGAATA 2220

CACCCATATC TTGCAGAACA TCTTCTGCTG CAATCGTTTC TTTACGAATA CGTGAATCTG 2280

CGAATGCGAT ATCTTCAGGA ATAGCCGCAT TTAAATGGTG AGTAATCATT ACCATATCTA 2340

AATGTTCATC TACAGTATTA TGTGTATAAG GCAAAGTTGG ATTTGTAGAT GAAGGTAAAA 2400

TATTTGAAAA TGCAGCGGAT TTAATTAAAT CAGGCGCATG ACCGCCACCA GCACCTTCAG 2460

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TCCTTTTTTA TTCACGTTTT CAGCACCGTT ATCTCCGAAT ACACCTGCAT ATTCATCATT 3360

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ACCAAAAAAT TTACGTTTGC CAGCATATTC AACTAATTGA ACTTCTTTTT TATCCCCAGG 3480

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TAATCATGTG TTCGACACCA TCCATGACAT CTTCTTTGTT TAGAATTTGT CTACCATAAC 3840

TCATTAACTC TGCAACGGTC TTACCATCGC GTGCACCTTC TAATAATTCA TCGCTGATTA 3900

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CCGCCGCCAC TACAATCATT AATTTGTCTT GCTCTCGTTG TGTAAAATGC AAATTAAAAC 4020

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AATTTGTAGA TACATCGTTA AAGTTAATGC CTCAAAACAT TGAAACGGTT AATTTTAGCA 4740

ACAATGATAG AATaCATTTC ATTCAGTCAT TATTTGAAGG ATTCAGTCAA GTATTTATCG 4800

AAGCGAGTGT AATTGGTGGC GTATGTATTT TAATCGGCAT ATTGATAGCA TCAAGAAAAG 4860

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TATTAACAGT AGTGGTGCAA CTAGGTACAA CAACATTGCT TGAACCGTTT GGCTTACCTG 5100

CATTAACATT GCCATTTATT ATCGTGACAT GGATTTTATT ATTTGCTGGT ATTAAACATG 5160

ACAAAGTAGA TGCTTGATAG TTAAATCAAA CCTAATATTG TTTGAATATC ACCTTAAACT 5220

ATACAGCGAA TTGTATAGTT TAAGGTGTAT TTTTATGGAT AAAATTAAGT GCATACTTAA 5280

GTGTTAAACT AGGAATAAAT AATTTATATT GTGTGTTGTG TGGGGTGACT AATATGAATG 5400

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AAGTAATTAG AGATACATTT AAGGCTAAAG CTGAATATAA TGATCAACAT AGCCAATTTC 5520

CATATAAAAA TATTGAATGG TTAATTAAAG AAGGTTATGG AAAATTAACG TTACCAAAAG 5580

CATATGGTGG TGAAGGTGCG ACCATAGAAG ACATGGTTAT TTTGCAATCA TTTTTAGGCG 5640

AACTTGATGG TGCCACAGCA TTATCTATTG GTTGGCATGT GAGTGTCGTA GGACAAATTT 5700

ATGAACAGAA ATTATGGTCT CAAGATATGT TGGAGCAATT TGCTGTTGAA ATTAATAATG 5760

GTGCATTAGT TAATAGAGCA GTTAGTGAAG CTGAAATGGG TAGTCCAACA AGAGGGGGAA 5820

GACCAAGTAC ACATGCTGTT AAAGCTGATG ATGGGTATAT TTTAAATGGT GTGAAGACAT 5880

ATACATCAAT GAGTAAAGCA CTAACACATA TTATTGTTGC TGCTTATATA GAAGAATTAG 5940

AAAGTGTTGG TTTTTTCTTA GTAGAC 5966

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CTGTGTCATC GCGAAATAGT TAGGGTCATT CATTAATCCT TTTGAACGTA TTTCATCAAA 60

ATATAACAAT TTCATTAGTA AAGGGGACTT GTTCAAACCA GCTATAATAC AAAATAGACC 120

TATAGTCACA CTGCTTATAA TATAAGAGGT AACGATCACT TTTTTGCTAT TACCTAACTT 180

AAAGATGATC ATCCCTAAAT AGAAATAAAT GACTACAAAT GCATATTTAA CTGTAGATGC 240

AAGAACTTCC TTAACCGTAA TAAATATCAA ATCATCAAAA AATaGCaAAC AArGCGTAAT 300

AATCATACGA TATGTATACA AAATAATGAm AAACTGTmAA AAATGATTTG CCTTTAATAA 360

ATGGTTAGCG AAAAACAGTA AATAAACTAA TATTAGTAAT GTGATAAAGT CAGCTATAGA 420

AACATTCACA CCGGCAATAA CCGAAGATTG CTGAATAAAA ACCGCTAAAC CGATAAGTAA 480

CAATGTTAGT AATTTACTAT TGTGTTGATT TTCCATTATA AACGTCTTCC ACTTCTTTAA 540

TCATTTTCTC CTCAGTAAAA CATTCTAAAT AACGTTTTCT AGATTGATTA CTCATTTTGA 600

TGTAATCACT GTCTATTAAA TATTTTTCCA GGACTTTAGC AATAGTTTCG GGTTGGTTGT 660

TCATCATACA TATACCATTA TCAGCTACTA ATTCTGAAAT ACCGCCAACA TGACTGGCTA 720

TTATTAAAAT AAACGTATCG TATTGTGATA ATAAATGACT CGCATTAATG ACATTGCCCA 840

AAAATGTGAC ATCATTTTCT AACCCAGCTT GTACAACTTG TTGCTGACAA TCATTTAATG 900

TAGGTCCATC GCCTATAAAT GTAAAATGCG CATGATTACT GTTATGTAAT TTCAATATCT 960

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CAATACCATT ATGTATTGTG GTTAATTTCA ATCGATTAAA TCGATATTTT AACGCTAACT 1200

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CAGTAAAAAC TATACGTGTG TCTTTCGATT TCGAAATGAa CTtCGCAATT CGTCcGACCG 1380

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CACCACCATT GTCTGCTTTA GTAATACAAT ATATAATTTT CAACTGTTAC AAACCCCTTT 1680

AATGCTATAC TTTCAATTTC TTAACATGGC TATCTCATCA GATGAATAGT ATTTATAGCC 1740

ATGCAAATCA ATGATGGCAC ATATTTCTTA ATGCCATTTG ATACTGTCTC AAGGGATTCC 1800

TCGTTATACT GTAACAATTG GTCACAATCT TTAAAATATA ACTTTTATTT GAACTTATTA 1860

AGTAAATTAA GACTACCTTG AGCCTTCCCC TGTAATAACA ACCATCAATG TTCTAATTGA 1920

TATATATAGT TCCATCATTA AACTACCTTT ATGTATATAT TTCATGTCAT ATTTCAGTTT 1980

TTGTTGCGGT GTTAAGTCAT ATCCACCTTG AATTTGCGCA AGTCCTGTTA ACCCTGGTGT 2040

AACAAGACAT CTTTGCTCGA AACCTATCAC TTCTGAACTA AATAATTCTA CAAATTCCGG 2100

ACGTTCCGGG CGTGGTCCAA TAAAACTCAT TTCCCCTTTA ACAACATTAA TTAGTTGTGG 2160

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TTCTAGTTTG TCTAATTTTC TTTGATAGGC ATAACCCTTA TTATTATGGA CAGCTTCAAT 2520

AATTAAAGTA ATCCTTTAAA CCTGTTTCTA CTGTATATTT AGGAACAAAT CCTAATGCCT 2640

TTAAGTTAGA AATATCTGCA TAAGAATGCT TAATATCTCC TTTTCGTGCT TCTTTAAATT 2700

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CAAAAAATGT AAATGGCTTG TTATGCTCAA ATGAATCGAA CATCTTTGAA ATCACACCTG 2940

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TTGGTATGTT ATATAACGAA CAATAATTTA ATGTCGTCCG TTCGCCGTAA TATTTATCTA 3060

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CACCATAAAC AGCTGCTGAC GAAGCAAAGA TAAAACGTTT TATATGATTA TTATATTTTT 3180

TAATGATTTC TAACAATCTT AATGTTGCTA CGACGTTTAT TTCTTGAGAT AAGATAGGTT 3240

TCTCAACCGA CTCAGCAACA CTAACTAATG CTGCTAAATG AATAACATAA TCAAATTGAT 3300

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CATCATAATC TTGTTGTAAA TCATCTACTA AATGCGACCC AATAAAACCA GCCCCACCAG 3480

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CAAAGCAATC TGACTTGTAA ATTGTTCCCA ACCCCATGCT TCAGGTTTAC CTGCTTCTTC 4020

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ATTCACAGTA ATACCTTCAG ACGCTAAATC TTGTGCGGCT ACTTGTGTTA AACCTCGCAC 4140

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AAATAGATAT GGCTGAAACA AACCAGAGTA TTGCAGATAC AAAGTTGCAT AATACTAAAG 5160

CGATAATAGC CAATACAATT AATATGACAC CTTTTGAAAT CCTTTCTTTA AATAAGTCAG 5220

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TATACTTTAC CTTAATATAC CTTATTTTAT TTAATTTTTA TATGCAAAAT ACAAAAATGG 6000

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TCGCTATCAA TACGCTAAAT CATCATATTT CCCTCAACAT CACAGTAAAA CTATTGCTCC 6120

TTCCAATTGC GCAGTTGTTC AACATCATCA TCTTGTTTAA GTAATGCCAG TGGTACTTGA 6240

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AAATAAATGT TTGTACACCT TGTGCCTGCC ATTTTGCAAT ATCTTCATCT TCACGTGGTA 8220

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TGTGTCTTTT CAGCAGTAAA ACGATACTCT GAATCATGTC CTTCTATTGT AAAATGACCG 10500

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ATGTCCTAAG TGATTTACTA CAACGTAATA TTTAAGACGA TGCCATGCTT CATCATGTGC 10920

ATATACAACA GGGCTTGATG CTGCCACAAC ATTTGGCACA AGCTGTTTTT CAGTAGCAAT 10980

CGTTCTAGAT AGACAAATGC CTTCAAGATC TCTGACAAAG CATACGTCGG GTATGCCATC 11040

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TAAACCACTT TGCTCAATCA CTTGTGATAA CTTAGACATC GGTGAATCAG GCATCGTTTC 11220

AAATAATGAC GCCAATACAT GAATATCTTT ATCAGCATGG TAATTCGGTA TCCCTTCACG 11280

AACAATCATG GCACTATTTG TTAATAAATC CATTTCAGGT TCAACTGTTT GCCCTAATGG 11340

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GCCAAGGTCT TTTATTAAAC CTTGTTCACT ATATTGCATA TACTGTGGAT GCTGTCGCAA 11640

CACATTGATT TGATAAGGAT GTGTTGGTAA TAAAATAAAA TCTTTGGGTA TCTCTGATAT 11700

ATCTATGTCT GCTAATTGAT ACAACACTTT CTCAACCTGA TCTTCTTTAC CTTCTACATA 11760

GCGCGTGAGC AGAACATCTT GATGCACAGC TAAATAATGC AATTGGAATG ATGTATGACA 11820

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CGTTAAAGTT TCGAGCTCTG ATAATTGTAT AGACCATTGA TGATTTTGAG GTGGTACTTG 12240

ATATAAATTT TCTTCTCTAA AATATTCATT TAAAATGCGT TCGATAGCCG CATACGCTGC 12300

ATGTTGTATT AATTCTTTAT TTTGCACTTT TTTGTTTCAA CTCCCATAAT TTCATTAATG 12360

TGTGATCGTT GATTTGATTA GTGATGGTTG AACAAATTAA AAATAAACTA CTTACTGCAA 12420

ATACTACGCC CATAACGATA AACGTAGTAG CTGGTGTAGT ATAACTTGTA ATGGCAGCGC 12480

cACTaAGACT GCCAATAATT TGACCAACAA CTAACATACT GTTCGTCGTT CCAACAAATG 12540

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CATATGATTT ATCATTAAAG CGTCCCCATA AAGGCGCGCT TAATATCGAA GCCGTCCAAA 12780

ATGCGGACTG TAAAAATCCA ATCACACTAC GGTCATCTAT CGCTGTATGA TTCACTGATG 12840

AAGCAAGTGG TGATAATGCA GTTAGCATGC CATACATAGC AAAGTTTGCT AAAACGCCAA 12900

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CTTTATTAAT ATTTGGTGTT TGTGATTTTG GCATATGTGT CGTTTCAATC AATTTTAATG 13020

CACCGAAAAT ACAGACAATA AAAGTAATAA CGGCAATACT CATCAGTAAC GCACTAAAAC 13080

CTAATATCGA AGCTGTAACA CCGCCAATTA ATGGCCCCAC AAGAGACCCT GCGCTGACTG 13140

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ACTGCTGTAT GATTCTGCAA TGTTCAGACA CCTCGCATTC TTAATATAGG TTCAATGTTG 15360

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ATGCACCCTT TTGTAACCAA TCATATTCAA TGTATGGTTG ATCCGTTACG GTACATGTAA 15720

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CCGGACGCTG TTGTTGCCAT CTATCAACAA AGCGTGCACA TGCTTCAGAG AATTGATCGT 15840

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CACCACCGAT ATGACTTGGC ATTGCAATAA TTCGATCTGC GATGTGTCCA TTTTCAGGAT 16200

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CTTCTGTTAA TGCGTCCACA TAAACTTGTG AATGATTACC TCCCGCTTGT TCAATATCTG 16320

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AATGACTGAC CCTTTCGCAT CAACAGCAAC AATTTGTGCG TTTGGATGCA CTTCTTTTAT 16740

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AACACACGTG AGTTTTAATC CCTTGATTTT AGCTATCATT GCCAACGCAA TGCCTAAATT 17100

ACCAGAAGTA CTTTCAATTA AATGTGTATT CTCAGTGATT AAACCATGTT TAATACCATG 17160

TTCAATGATG TACTTGGCAG GTCGATCTTT CATGCTGCCT CCAGGATTCA TATACTCTAA 17220

CTTTGCAAAC ACTTCATGTT TCGGAAATAG TTGATGAAGT TGAACCATAG GTGTTTGCCC 17280

TACAGAATCT AACAATGAAT CGTGCACATG 17310

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5423 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

ATACTAGTAA GCGCATCGGT TATTGACATC GAATTCAACT TTAACAGTTT TCATGTTCGG 60

TGATGTTTCa ATAGAATGTG TGTGTTGTAC TTGCGCATTT ATATTTCCAC CTAAATTACT 120

TAAGTTTCCT GTAATACTAG AAATGTCAGG TGCGTTTAAT GTAGGTTGAA ATGCATCAAC 180

TACTTTATCT GCAACATTAG AAACATTACG GATAACTTTA CTTGAATGAT TATCTATACC 240

TTTAACGAAA CCTAACATTG AATACATACC AACATCCATG AATTCACGTG AAGGTGAGTG 300

AATACCTAGC GCTCTTTTGG CTGCATTTAA AGCACCTTTT GCTACACTAG CTGCTTTTTC 360

AGCTAAGTCT CTAGCCATAT TACCAATACC TCTCATCAAA CCACGGATCA TATCAGCACC 420

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ACTAACTTTG TTTACAACAT TAACGAATCC TTGAACAACT CTATTAACAA rGTTAATTAG 540

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TGCTGTAGCT GGATGCGCCT CAAACAAGTT AGCTATCCAA CCAGTTATTG CAACTGCAAC 1680

GCGTAATACT GCACTAGCTA TAGGAGCCAT TGCTGTTGCG AATGCArmTA ATCCTCTTGC 1740

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AAGCACGCTT TGAGACGCTT CTTCCATTCC TCTTGAAATA CCACTAAAAA ACGGTTGTAA 2280

GCTCTGCATT GCAGTTTTAA CAGTATTTAA ACCATTTGCA AGAGTTGTGA AGATAGCGGA 2340

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TATTTTGTGG TTCGTATTCA TCACGTTCGC TACTAAATCT TATATCTTTA CCTTCGTTAA 3540

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CTTTAGGTTT ATTTTCTGTC CCAACATTTT TAGTAGCTGC AGCATCACGA ATAGCAAACG 3660

CAAGTTTGTA ACGTTCGAAT TCTTGGGTTA GCATTTCATA CTCTTTCGCA TACATTCGAT 3720

AGTTATATTC TGTTAATGTC ATTTGCTCAA TAACGTTCAA ATCTGTAATA CCAAGTGTTG 3780

ACATACAAGT TATAACGATT CTGTCGTAAG TTATTAGGcT TCCGCTGGTT TTTCTTCCGT 3840

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CGGTGGTGAA TCTACTTTAG GTTGTGGAAT TGCTGTTAAA TCTTCGCCAG TTAATGCATC 4320

TGCTTTTGTA GTGTCGTGGA ATCTGTATcC AGTCGCCTTA AGTTTCTTTG TTACAGCCTC 4380

AGGTAGTGTT GCAAATCCAC GTTGGAAACG ACCATTCACT CCATATTCAT ATTCATATTC 4440

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ACTATTTTTC ATATTTGCCA TTCAATATTC CTCCGTTTTT TAAAATGTTT TGTAAGATAT 4860

CGTTACTGAT GTGTGTAGCA ATTCTTGATT GGTAGTATCA TCAACTAACT GTGTGATGTT 4920

AGTATCTTCT TCTTCAAAGT CATAATCGTT TGTTTTAACG CTAGGTGTTA AATCATCAAT 4980

ACATCTTTTA ACAAGTCCGT CATGATGTCC TAAATCATCG CTTACACTCC AAATATCAAT 5040

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AAACCACTAT AAGCTGCGTG CGATGTGATA GTGTATTGCA AATCGCCAGT TTTTTTATAT 5400

CTGATATTGC GTGATaAATT ACC 5423

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AAACGCAGAT GTTCAATTAG AACCAGTCTA TCGTATTAAG GAAGGTATTA AACAAAAGCA 60

AATACGAGAC CAAATTAGAC AAGCGTTAAA TGATGTGACA ATTCATGAAT GGTTAACTGA 120

TGAACTAAGA GAAAAATATA AATTAGAGAC CTTGGACTTT ACTTTGAACA CATTACATCA 180

TCCTAAAAGT AAAGAGGATT TATTACGTGC TCGTAGAACC TATGCATTTA CTGAACTGTT 240

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TGAAATTGAT TATGACATAG ACCAAGTTAA ATCATTTATT GATCGTTTAC CTTTTGAACT 360

AACTGAAGCA CAGAAATCCA GTGTTAATGA AATTTTTAGA GATTTAAAAG CACCAATACG 420

TATGCATCGA TTACTTCAAG GTGATGTAGG TTCAGGAAAA ACAGTAGTTG CTGCAATTTG 480

TATGTATGCG TTAAAAACTG CTGGTTATCA ATCAGCATTG ATGGTACCAA CTGAAATTTT 540

AGCAGAGCAA CATGCTGAAA GTTTAATGGC TTTATTTGGA GATTCTATGA ACGTTGCATT 600

TACGATTGAT TGTTTAATTG GAACCCATGC TTTGATTCAA GATGATGTGA TTTTCCATAA 720

TGTTGGTTTA GTAATTACAG ATGAACAACA TCGATTTGGT GTGAATCAAC GCCAGCTTTT 780

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TCGTAAACCT ATCATTACTA CTTGGGCAAA GCATGAGCAA TACGATAAAG TTTTGATGCA 960

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ACATACCAGA ATTAAGGAAG CGTATTAAAT TAGTTGCTGA AAAGAATTAT GACCAAATAA 2040

GTTCTATTGA AGAACAAGAA TTTATTGGTG ATTTGATTCA AGTCAATCCa AATGTTAAAG 2100

CGCAATCAAT TTTAGATATT ACATCGGATT CTGTTTTTCA TAAAACTGGA ATTGCGCGTG 2160

GTCATGTGCT GTTTGCTCAG GCAAATTCGT TATGTGTTGC GCTAATTAAG CAACCAACAG 2220

TTTTAACTCA TGAGAGTAGC ATTCAATTTA TTGAAAAAGT AAAATTAAAT GATACGGTAA 2280

GAGCAGAAGC ACGAGTTGTA AATCAAACTG CAAAACATTA TTACGTCGAA GTAAAGTCAT 2340

ATGTTAAACA TACATTAGTT TTCAAAGGAA ATTTTAAAAT GTTTTATGAT AAGCGAGGAT 2400

TTAGAAGCCG TACAAAAGGC TGTTGAAGAC TTTAAAGATC TAGAAATTAT ACTTTTCGGT 2520

GACGAAAAAA AGTATAATCT GAACCATGAA CGAATCGAAT TTAGACATTG TTCTGAAAAG 2580

ATTGAAATGG AAGATGAGCC TGTTAGAGCG ATTAAACGTA AAAAAGATAG CTCAATGGTA 2640

AAAATGGCTG AAGCTGTGAA ATCTGGTGAA GCAGATGGAT GTGTGTCAGC AGGTAATACT 2700

GGTGCTTTAA TGTCAGCTGG TTTATTCATT GTTGGACGTA TTAAAGGTGT AGCTAGACCG 2760

GCTTTAGTAG TAACATTGCC AACGATTGAT GGAAAAGGTT TTGTCTTTTT AGACGTTGGT 2820

GCAAATGCTG ATGCTAAACC TGAACACTTA TTACAGTATG CGCAACTAGG GGATATTTAT 2880

GCTCAAAAAA TTAGAGGTAT TGATAATCCG AAAATCTCAT TATTAAATAT AGGAACCGAG 2940

CCAGCTAAAG GTAATAGTTT AACGAAAAAA TCATATGAGT TATTAAATCA TGATCATTCA 3000

TTGAATTTTG TTGGGAATAT TGAAGCGAAG ACATTAATGG ATGGCGATAC AGATGTTGTA 3060

GTTACCGATG GCTATACTGG GAACATGGTC CTTAAAAATT TAGAAGGTAC TGCAAAATCA 3120

ATCGGTAAAA TGTTAAAAGA TACGATTATG AGTAGTACTA AAAATAAATT AGCAGGTGCA 3180

ATATTGAAGA AAGATTTAGC TGAATTCGCT AAAAAGATGG ATTACTCAGA ATACGGTGGT 3240

TCCGTATTAT TAGGATTGGA AGGTACTGTA GTTAAAGCAC ACGGTAGTTC AAATGCTAAA 3300

GCTTTTTATT CTGCAATTAG ACAAGCGAAA ATCGCAGGAG AACAAAATAT TGTACAAACA 3360

ATGAAAGAGA CTGTAGGTGA AtCAAATGaG TaAAACAGCA ATTATTTTTC CGGGACAAGG 3420

TGCCCAAAAA GTTGGTATGG CGCAAGATTT GTTTAACAAC AATGATCAAG CAACTGAAAT 3480

TTTAACTTCA GCAGCGAACA CATTAGACTT TGATATTTTA GAGACAATGT TTACTGATGA 3540

AGAAGGTAAA TTGGGTGAAA CTGAAAACAC ACAACCAGCT TTaTTGaCGC aTAGTTCGGC 3600

ATTATTAGCA GCGCTAAAAA ATTTGAATCC TGATTTTACT ATGGGGCATA GTTTAGGTGA 3660

ATATTCAAGT TTAGTTGCAG CTGACGTATT ATCATTTGAA GATGCAGTTA AAATTGTTAG 3720

AAAACGTGGT CAATTAATGG CGCAAGCATT TCCTACTGGT GTAGGAAGCA TGGCTGCAGT 3780

ATTGGGATTA GATTTTGATA AAGTCGATGA AATTTGTAAG TCATTATCAT CTGATGACAA 3840

AATAATTGAA CCAGCAAACA TTAATTGCCC AGGTCAAATT GTTGTTTCAG GTCACAAAGC 3900

TTTAATTGAT GAGCTAGTAG AAAAAGGTAA ATCATTAGGT GCAAAACGTG TCATGCCTTT 3960

AGCAGTATCT GGACCATTCC ATTCATCGCT AATGAAAGTG ATTGAAGAAG ATTTTTCAAG 4020

TTACATTAAT CAATTTGAAT GGCGTGATGC TAAGTTTCCT GTAGTTCAAA ATGTAAATGC 4080

GCAAGGTGAA ACTGACAAAG AAGTAATTAA ATCTAATATG GTCAAGCAAT TATATTCACC 4140

AGTACAATTC ATTAACTCAA CAGAATGGCT AATAGACCAA GGTGTTGATC ATTTTATTGA 4200

AACATCAATT CAAACTTTAG AAGATGTGAA AGGATGGAAT GAAAATGACT AAGAGTGCTT 4320

TAGTAACAGG TGCATCAAGA GGAATTGGAC GTAGTATTGC GTTACAATTA GCAGAAGAAG 4380

GATATAATGT AGCAGTAAAC TATGCAGGCA GCAAAGAGAA AGCTGAAGcA GTAGTCGAAG 4440

AAATCAAAGC TAAAGGTGTT GACAGTTTTG CGATTCAAGC AAATGTTGCC GATGCTGATG 4500

AAGTTAAAGC AATGATTAAA GAAGTAGTTA GCCAATTTGG TTCTTTAGAT GTTTTAGTAA 4560

ATAATGCAGG TATTACTCGC GATAATTTAT TAATGCGTAT GAAAGAACAA GAGTGGGATG 4620

ATGTTATTGA CACAAACTTA AAAGGTGTAT TTAACTGTAT CCAAAAAGCA ACACCACAAA 4680

TGTTAAGACA ACGTAGTGGT GCTATCATCA ATTTATCAAG TGTTGTTGGA GCAGTAGGTA 4740

ATCCGGGACA AGCAAACTAT GTTGCAACAA AAGCAGGTGT TATTGGTTTA ACTAAATCTG 4800

CGGCGCGTGA ATTAGCATCT CGTGGTATCA CTGTAAATGC AGTTGCACCT GGTTTTATTG 4860

TTTCTGATAT GACAGATGCT TTAAGTGATG AGCTTAAAGA ACAAATGTTG ACTCAAATTC 4920

CGTTAGCACG TTTTGGTCAA GACACAGATA TTGCTAATAC AGTAGCGTTC TTAGCATCAG 4980

ACAAAGCAAA ATATATTACA GGTCAAACAA TCCATGTAAA TGGTGGAATG TACATGTAAT 5040

ATATTTGAGC TAAAGCTCAT TGACGCAGTG GTTGACTGGT CATCCAATGG AGAATTGTCT 5100

GACCTAGTCA ACTTTGCGGG GGAAATTCTA AGCAACCTAG ATAAGGTTCC AGAATTTCTC 5160

CCTAAGAAAC ACTAATCAAT aAATTGwTAA GTGTTTCTAA AATTTCTACT TGTTTTTTAG 5220

AATTTAAAAT GGGAAAATAT AGTAGTCTAT GTATAGGCAT TTTTAAAGGA GGTGAATCGA 5280

CGTGGAAAAT TTCGATAAAG TAAAAGATAT CATCGTTGAC CgTTTAGGTG TAGACGCTGA 5340

TAAAGTAACT GAAGATGCAT CTTTCAAAGA TGATTTAGGC GCTGACTCAC TTGATATCGC 5400

TGAATTAGTA ATGGAATTAG AAGACGAGTT TGGTACTGAA ATTCCTGATG AAGAnGCTGA 5460

AAAAATCAAC ACTGTTGGTG ATGCTGTTAA ATTTATTAAC AGTCTTGAAA AATAATAAAT 5520

CTTACATCTG GGTCGTCAGT ATTGTCGACT CAGTTTTTTT CTTTAATTAT CAATAGTTTT 5580

AACGTAAAAT TAAAGATGAT TCAAGAGCAA CACATAAAGG AGATAAAATA ATGTCTAAAC 5640

AAAAGAAAAG TGAGATAGTT AATCGTTTTA GAAAGCGCTT TGATACTAAA ATGACAGAGT 5700

TAGGCTTTAC TTATCAAAAT ATTGATTTAT ACCAACAAGC ATTTTCGCAT TCGAGTTTTA 5760

TTAATGATTT TAATATGAAT CGTTTAGACC ATAATGAGCG TTTAGAGTTT TTGGGTGATG 5820

CGGTATTAGA ATTGACGGTT TCACGATATT TATTTGATAa ACATCCCAAC TTGCCAGAAG 5880

GGAATTTAAC AAAAATGCGT GCCaCTATTG TATGTGAGCC CtCACTkGTA ATATTTGCGA 5940

ATAAAATTGG ATTGAACGAA ATGATTTTAC TTGGTAAAGG TGAAGAGAAA ACAGGGGGAC 6000

ATCAAGGACT AGATATAGTT TGGAAATTTG CTGAGAAAGT CATTTTCCCA CATGTAGAAC 6120

AAAATGAGTT ATTAGGCGTG GTAGATTTTA AAACACAATT CCAAGAATAT GTGCACCAGC 6180

AAAATAAAGG TGATGTAACC TATAATTTAA TAAAAGAAGA GGGACCGGCA CATCATCGTC 6240

TATTCACTTC A 6251

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4920 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ACCTACTGAA GTTGCTAATT TTTTGGAGCA ACTAAGCACT GAAATTGAAC GTCTTAAAGA 60

AGATAAAAAA CAACTTGAAA AAGTAATCGA AGAGAGaGAT ACTAATATTA AGTCTTATCA 120

AGACGTGgCA TCAATCTGTA AGTGaTGCTT TGATACAAGC TCAAAAAGCT GGTGAAGAAA 180

CTAAGCAAGC TGCAGAGAAA CAAGCTGAAG CGATTATAGC TAAGGCAGAA GCGCAAgcTA 240

ATcAAATGGT TGGTGACGCG GTAGAAAAAG CACGCCGTTT AGCATTCCAG ACTGAAGATA 300

TGAAACGTCA ATCAAAAGTA TTTAGATCGC GTTTCCGTAT GTTAGTTGAA GCGCAATTAG 360

ACTTATTAAA AAACGAAGAT TGGGATTACT TGTTGAATTA TGATTTAGAC GCTGAACAAG 420

TGACGCTTGA AAATATTCAT CATTTGCATG AAAATGATTT AAAGCCAGAT GAAGTTGCAG 480

CAAATGCACA AAATAATGCA TCAAATACAC CAGACAATAA TCAACAATCC AATGATTCAG 540

AAACAACTAA GAAGTAAGAA TTAAATAAAG ACAGACGCGT AATATACATT TAACTTTTCA 600

CAGCGAATTA GGTAATGGTG AGAGCCTAGT AAAAGCATGT ATGTTATATC ACTGGCTTTT 660

TAATATTTAA ATAATGTAAT GAGAGAACTC TAAGTTGAGT TAATAAGGGT GGTACCGCGA 720

GCAATCGTCC CTTTTAATTT AACTTAGAGT TTTTTAAATT TTTAAGGAGT GAAAAAAATG 780

GATTACAAAG AAACGTTATT AATGCCTAAA ACAGATTTCC CAATGCGAGG TGGTTTACCA 840

AACAAGGAAC CGCAAATTCA AGAAAAATGG GATGCAGAAG ATCAATACCA TAAAGCGTTA 900

GAAAAAAATA AAGGTAACGA AACATTCATT TTACATGATG GCCCACCATA CGCGAATGGT 960

AACTTACATA TGGGACATGC CTTGAACAAA ATTTTAAAAG ACTTTATTGT ACGTTATAAA 1020

ACTATGCAAG GGTTCTATGC ACCATACGTA CCAGGTTGGG ATACACATGG TTTACCAATT 1080

GAACAAGCAT TAACGAAAAA AGGTGTTGAC CGAAAGAAAA TGTCAACAGC TGAATTCCGT 1140

TTAGGTGTTC GTGGTGACTT TAATGATCCA TATATTACAT TAAAACCTGA ATACGAAGCT 1260

GCACAAATTC GTATTTTTGG AGAAATGGCA GATAAAGGTT TAATTTATAA AGGTAAAAAG 1320

CCAGTTTATT GGTCTCCTTC AAGTGAGTCT TCATTAGCAG AAGCAGAAAT TGAATATCAC 1380

GATAAACGTT CAGCATCAAT TTACGTTGCA TTTGACGTTA AAGATGACAA AGGTGTCGTT 1440

GATGCAGATG CTAAATTTAT TATCTGGACA ACAACGCCAT GGACAATTCC ATCAAATGTT 1500

GCGATTACCG TTCATCCTGA ATTAAAATAT GGTCAATACA ATGTAAATGG cGAAAAATAT 1560

ATTATTGCAG AAGCCTTGTC TGACGCTGTA GCAGAAGCAC TGGaTTGGGA TAAAGCATCA 1620

ATCAAATTAG AAAAAGAATA CACAGGTAAA GAATTAGAGT ATGTTGTAGC ACAACATCCA 1680

TTCTTAGACA GAGAATCGTT AGTGATTAAT GGTGATCATG TTACTACAGA TGCTGGTACA 1740

GgTTGTGTAC ATACAGCACC AGGTCACGGG GAAGATGACT ATATTGTTGG TCAAAAATAT 1800

GAATTGCCAG TAATTAGTCC AATCGATGAT AAAGGTGTAT TTACTGAAGA AGGCGGCCAA 1860

TTTGAAGGGA TGTTCTATGA TAAAGCTAAT AAAGCCGTTA CTGATTTATT AACAGAAAAA 1920

GGTGCACTAT TAAAATTAGA CTTTATTACA CATAGCTATC CACACGACTG GAGAACAAAA 1980

AAACCTGTAA TCTTCCGTGC TACACCACAA TGGTTTGCCT CAATCAGTAA AGTAAGACAA 2040

GATATTTTAG ATGCAATCGA AAATACAAAC TTCAAAGTAA ATTGGGGTAA AACACGTATT 2100

TACAATATGG TTCGTGACCG TGGCGAATGG GTTATTTCTC GTCAACGTGT GTGGGGTGTA 2160

CCGTTACCAG TATTTTATGC TGAAAATGGC GAAATTATCA TGACGAAAGA AACAGTGAAT 2220

CATGTTGCTG ATTTATTTGC AGAACACGGT TCAAATATTT GGTTTGAAAG AGAAGCGAAA 2280

GACTTACTAC CAGAAGGATT TACACATCCA GGCAGCCCTA ACGGTACATT TACTAAAGAA 2340

ACAGACATTA TGGACGTTTG GTTTGATTCT GGTTCATCAC ACCGTGGCGT GTTGGAAACA 2400

AGACCGGAAT TAAGTTTCCC AGCGGATATG TATTTAGAAG GTAGTGACCA ATATCGTGGT 2460

TGGTTCAACT CTTCTATCAC AACTTCAGTT GCTACAAGAG GAGTATCACC TTATAAATTC 2520

TTACTTTCTC ATGGTTTTGT TATGGACGGT GAAGGTAAGA AAATGAGTAA ATCTTTAGGT 2580

AATGTGATTG TACCTGACCA AGTGGTTAAA CAAAAAGGTG CTGATATTGC GAGACTTTGG 2640

GTAAGTAGTA CGGACTATTT AGCTGATGTT AGAATTTCTG ATGAAATTTT AAAACAAACA 2700

TCTGATGTTT ATCGTAAAAT CAGAAATACA TTAAGATTTA TGTTAGGTAA CATTAACGAT 2760

TTCAATCCTG ACACAGATAG CATTCCTGAA TCAGAGTTAT TAGAAGTGGA TCGTTACTTG 2820

CTAAATCGTT TACGTGAATT TACTGCAAGT ACGATTAACA ACTATGAAAA CTTTGACTAC 2880

TTAAATATTT ATCAAGAAGT TCAAAACTTT ATCAATGTTG AGTTAAGTAA TTTCTATTTG 2940

CAAACAGTGT TATATCAAAT TTTAGTTGAT ATGACGAAGT TGTTAGCACC AATCTTAGTG 3060

CATACAGCTG AAGAAGTTTG GTCTCATACA CCACATGTTA AAGAAGAAAG TGTTCACTTA 3120

GCAGACATGC CTAAAGTTGT AGAAGTAGAT CAAGCTTTAT TGGATAAATG GCGTACATTT 3180

ATGAATTTAC GTGATGATGT GAACCGTGCA TTAGAAACTG CTCGTAATGA AAAAGTTATT 3240

GGTAAATCAT TAGAAGCTAA AGTTACGATT GCTAGTAACG ATAAATTTAA TGCATCTGAA 3300

TTCTTAACTT CATTTGATGC ATTACATCAA TTATTTATCG TGTCACAAGT TAAAGTTGTA 3360

GATAAGTTAG ACGATCAGGC AACAGCTTAT GAACATGGTG ATATTGTCAT CGAACATGCA 3420

GATGGTGAAA AATGTGAAAG ATGTTGGAAC TATTCAGAGG ATCTTGGTGC TGTTGATGAA 3480

TTGACGCATC TATGTCCACG ATGCCAACAA GTTGTAAAAT CACTTGTATA ATTGAAATTG 3540

TATAAAGTAC TCATACAGAT GATATAAATT AAAGCTCTCT TCATAATCAT GTTGTAGTTT 3600

TTGTTGACAT GATGAAGAGA GTTTTTTTGT GAATAAAAAA ATGACCAAGT TACCGGTCAT 3660

ATATGTAAAA AATGTGCGAT TTACTAAAAT AAAAATTATT CAGGAATGGT ACAAATTCTC 3720

TGAGGCATAT AAATGCGTTA TAGTTGCTAT TCTCAATTAT GTTCGCGATA ATTTTAAGTA 3780

AAAGTAAGCA CAGATATTGA ATTTGATAGG AGTTAATTGA ATGTATCATA ACAGTAACGC 3840

AAACTTTGTC AATGGTATCA CTTTAAATGT GAGAGATAAG AATGAATTAA AGCCATTTTA 3900

TGAGGACATA TTAGGATTAA ATATTATAAA TGAGACATTA ACATCGATAC AATATGAAGT 3960

AGGTCAAAAT AATCATGTCA TTACACTTGT TGAATTACAA AATGGACGTG AACCTTTAAT 4020

GTCCGAAGCG GGACTGTTTC ATATCGCAAT TAAACTACCT CAAATTAGTG ATTTAGCTAA 4080

TTTACTAATT CATTTAAGCG AATATGATAT TCCAGTTAAC GGAGGTATAC AGCCTGCTTC 4140

GTTATCATTA TTTTTTGAAG ACCCGGAAGG AAACGGTTTT AAATTTTATG TTGATAAAGA 4200

CGAAGCGCAA TGGACGAGGC AAAATAATTT AGTAAAAATT GATATTAGAC CATTAAATGT 4260

ACCGAGATTA GTGAGTCATG CAACAAAATT GTTATGGTTA GGTATTCCAG ATGACGCTAT 4320

TATAGGTGCA TTGCATATTA AGACAATTCA TTTATCAGAG GTAAAAGAGT ACTACCTCGA 4380

TTATTTTGGA TTAGAGCAAT CGGCATATAT GGATGATTAT TCAATATTTT TAGCATCGAA 4440

TGGCTATTAT CAACATTTGG CCATGAATGA TTGGGTATCA GCAACGAAAC GTGTAGAAAA 4500

TTTTGATACG TATGGATTAG CAATTGTTGA CTTTCATTAT CCTGAAACAA CACATTTAAA 4560

TTTACAAGGT CCGGATGGTA TCTATTATCG CTTTAATCAT ATCGAAGTTG AAGATTAGTA 4620

TATACTTTGA ATGGACGAAC CATATAATGA ATCGTTTTTA ATGATCTTTT TATACAAGTT 4680

ATGAAGGAGG CTGGGACATT AAGTTCTTAG GCAATGTAAA AAGCTGATTT CTATTAATTA 4740

TTTTCCTTAT ATTAATTGCC ATTAATACAA AACCTAGCTC TCGTTTAACT TTATTTATTC 4860

CTCGAACTGA CATTCGnGTG AACTCAAAAT nGCCTACTTn CTTAAATTAC CAATATCTAT 4920

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 626 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TGGATTGCCA TTACATGGAC AAGATTTAAC TGAATCAATT ACACCATATG AAGGTGGTAT 60

CGCTTTTGCA AGTAAACCAT TAATTGATGC TGATTTTATT GGTAAATCTG TATTAAAAGA 120

TCAAAAAGAA AATGGTGCAC CAAGAAGAAC AGTGGGATTA GAATTACTTG AAAAAGGAAT 180

TGCAAGAACT GGTTATGAAG TTATGGATTT AGATGGAAAT ATTATTGGAG AAGTAACTTC 240

AGGAACACAG TCTCCATCAT CAGGAAAATC AATTGCACTT GCAATGATAA AAAGAGATGA 300

GTTTGAAATG GGTAGAGAGT TGCTTGTTCA AGTTCGTAAG CGTCAATTAA AAGCGAAAAT 360

TGTTAAGAAA AATCAAATTG ATAAATAATT AAAAAGGGGT GTGCATTGTG AGTCATCGTT 420

ATATACCTTT AACTGAAAAA GACAAGCAAG AAATGTTACA AACAATTGGT GCAAAATCTA 480

TAGGAGAATT ATTCGGTGAT GTACCAAGTG ACATTTTATT AAATAGAGAT TTAAATATTG 540

CTGAAGGCGA ACGGAGAACA ACGTTACTTA GAAGATTnAA TCGCATTGCA AGCAAGAGTA 600

TCACTAGAGG AACGCGTACA TCGTTT 626

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

nGGAAGTGGT GTATATATTT GTAATGAGTG TATTGAATTA TGCTCAGAAA TCGTCGAAGA 60

AGAATTAGCT CAAAACACTT CTGAAGCGAT GACAGAATTA CCTACTCCTA AAGAAATTAT 120

GGATCATTTA AACGAATATG TTATTGGTCA AGAAAAAGCT AAAAAATCTT TAGCTGTAGC 180

TGTTTATAAC CACTATAAGC GTATTCAACA ATTAGGACCA AAAGAAGATG ATGTTGAATT 240

AACCTTAGCC AAGACGTTGA ATGTACCATT TGCAATTGCA GATGCGACAA GTTTAACTGA 360

AGCTGGTTAT GTAGGCGATG ATGTTGAAAA TATCTTGTTG AGATTAATTC AAGCAGCTGA 420

CTTTGACATT GATAAAGCCG AAAAAGGTAT TATTTATGTA GATGAAATTG ATAAAATTGC 480

ACGTAAATCT GAAAACACAT CTATAACACG TGACGTTTCA GGTGAAGGTG TTCAACAAGC 540

ATTGCTTAAA ATCTTAGAAG GTACGACTGC AAGTGTTCCG CCACAAGGTG GACGCAAACA 600

TCCAAACCAA GAAATGATTC AAATTGATAC AACAAATATC TTATTTATTC TTGGTGGTGC 660

CTTTGATGGT ATTGAAGAAG TGATTAAGCG CCGTCTTGGT GAAAAAGTTA TTGGTTTCTC 720

AAGCAATGAA GCTGATAAAT ATGACGAACA AGCATTATTA GCACAAATTC GCCCAGAAGA 780

TTTGCAAGCC TATGGTTTGA TTCCTGAATT TATCGGACGT GTGCCAATTG TAGCTAATTT 840

AGAAACATTA GATGTAACTG CGTTGAAAAA CATCTTAACG CAACCTAAAA ATGCACTTGT 900

GAAACAATAT ACTAAAATGC TGGAATTAGA TGATGTGGAT TTAGAGTTCA CTGAAGAAGC 960

TTTATCAGCA ATTAGTGAAA AAGCAATTGA AAGAAAAACA GGTGCGCGTG GTTTACGTTC 1020

AATCATAGAA GAATCGTTAA TCGATATTAT GTTTGATGTG CCTTCTAACG AAAATGTAAC 1080

GAaGGTAGTT ATTACAGCAC AAACmATTAA TGrAGaACTG AACCAG 1126

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATTGACTTCT TAGCAATnAA TaTGAGTGAA GAACGTACTG TTGAAGTACC AGTTCAATTA 60

GTTGGTGAAG CAGTAGGCGC TAAAGAAGGC GGCGTAGTTG AACAACCATT ATTCAACTTA 120

GAAGTAACTG CTACTCCAGA CAATATTCCA GAAGCAATCG AAGTAGACAT TACTGAATTA 180

AACATTAACG ACAGCTTAAC TGTTGCTGAT GTTAAAGTAA CTGGCGACTT CAAAATCGAA 240

AACGATTCAG CTGAATCAGT AGTAACAGTA GTTGCTCCAA CTGAAGAACC AACTGAAGAA 300

GAAATCGAAG CTATGGAAGG CGAACAACAA ACTGAAGAAC CAGAAGTTGT TGGCGAAAGC 360

AAAGAAGACG AAGAAAAAAC TGAAGAGTAA TTTTAATCTG TTACATTAAA GTTTTTATAC 420

TTTGTTTAAC AAGCACTGTG CTTATTTTAA TATAAGCATG GTGCTTTTTG TGTTATTATA 480

AAGCTTAATT AAACTTTATT ACTTTGTACT AAAGTTTAAT TAATTTTAGT GAGTAAAAGA 540

CTTACTAAGC TAAAGAATAA TGATAATTGA TGGCAATGGC GGAAAATGGA TGTTGTCATT 660

ATAATAATAA ATGAAACAAT TATGTTGGAG GTAAACACGC ATGAAATGTA TTGTAGGTCT 720

AGGTAATATA GGTAAACGTT TTGAACTTAC AAGACATAAT ATCGGCTTTG AAGTCGTTGA 780

TTATATTTTA GAGAAAAATA ATTTTTCATT AGATAAACAA AAGTTTAAAG GTGCATATAC 840

AATTGAACGA ATGAACGGCG ATAAAGTGTT ATTTATCGAA CCAATGACAA TGATGAATTT 900

GTCAGGTGAA GCaGTTGCAC CGATTATGGA TTATTACAAT GTTAATCCAG AAGATTTAAT 960

TGTCTTATAT GATGATTTAG ATTTAGAACA AGGACAAGTT CGCTTAAGAC AAAAAGGAAG 1020

TGCGGGCGGT CACAATGGTA TGAAATCAAT TATTAAAATG CTTGGTACAG ACCAATTTAA 1080

ACGTATTCGT ATTGGTGTGG GAAGACCAAC GAATGGTATG ACGGTACCTG ATTATGTTTT 1140

ACAACGCTTT TCAAATGATG AAATGGTAAC GATGGAAAAA GTTATCGAAC ACGCAGCACG 1200

CGCAATTGAA AAGTTTGTTG AAACATCACG ATTTGACCAT GTTATGAATG AATTTAATGG 1260

TGAAGTGAAA TAATGACAAT ATTGACAACG CTTATAAAAG AAGATAATCA TTTTCAAGAC 1320

CTTAATCAGG TATTTGGACA AGCAAACACA CTAGTAACTG GTCTTTCCCC GTCAGCTAAA 1380

GTGACGATGA TTGCTGAAAA ATATGCACAA AGTAATCAAC AGTTATTATT AATTACCAAT 1440

AATTTATACC AAGCAGATAA ATTAGAAACA GATTTACTTC AATTTATAGA TGCTGAAGAA 1500

TTGTATAAGT ATCCTGTGCA AGATATTATG ACCGAAGAGT TTTCAACACA AAGCCCTCAA 1560

CTGATGAGTG AACGTATTAG AACTTTAACT GCGTTAGCTC AAGGTAAGAA AGGGTTATTT 1620

ATCGTTCCTT TAAATGGTTT GAAAAAGTGG TTAACTCCTG TTGAAATGTG GCAAAATCAC 1680

CAAATGACAT TGCGTGTTGG TGAGGATATC GATGTGGACC AATTTCTTAA CAAATTAGTT 1740

AATATGGGGT ACAAACGGGA ATCCGTGGTA TCGCATATTG GTGAATTCTC ATTGCGAGGA 1800

GGTATTATCG ATATCTTTCC GCTAATTGGG GAACcAATCA GAATTGAGCT ATTTGATACC 1860

GAAATTGATT CTATTCGGGA TTTTGATGTT GAAACGCAGC GTTCCAAAGA TAATGTTGAA 1920

GAAGTCGATA TCACAACTGC AAGTGATTAT ATCATTACTG AAGAAGTGAT CAGCCATCTT 1980

AAAGAAGAGT TAAAAACTGC ATATGAAAAT ACAAGACCCA AAATAGATAA ATCAGTGCGC 2040

AATGATTTGA AAGAAACGTA TGAAAGCTTT AAATTATTCG AAAGTACATA CTTTGATCAT 2100

CAAATACTAC GTCGCTTAGT AGCGTTTATG TATGAAACAC CTTCGACAAT TATTGAGTAT 2160

TTCCAAAAAG ATGCAATCAT TGCAGTTGAT GAATTTAATC GTATTAAAGA AACTGAAGAA 2220

AGTTTAACAG TAGAGTCTGA TTCGTTTATT AGCAATATTA TTGAAAGTGG TAATGGATTT 2280

ATAGGACAAA GTTTTATAAA ATATGATGAT TTTGAAACAT TGATTGAAGG CTATCCTGTC 2340

TCATGTAAAC CTGTCCAACA ATTTTATGGG CAATATGACA TTATGCGTTC TGAATTTCAA 2460

CGATATGTTA ATCAAAACTA TCATATCGTG GTTTTGGTCG AAACCGAAAC TAAAGTTGAA 2520

CGTATGCAAG CGATGTTAAG TGAAAtGCAT ATTCCATCAA TAACAAAATT GCATCGCTCA 2580

ATGTCATCGG GGCAAGCAGT GATTATTGAA GGCAGTTTAT CTGAAGGATT TGAACTACCT 2640

GATATGGGAT TAGTTGTCAT TACTGAGCGT GAgcTTTTTA AATCAAAACA GAAAAAGCAA 2700

CGAAAACGTA CGAAAGCTAT CTCAAATGCT GAAAAAATTA AGTCTTACCA AGATTTAAAT 2760

GTGGGAGATT ATATTGTTCA TGTGCATCAT GGTGTTGGTA GATATTTAGG TGTTGAGACG 2820

CTCGAAGTGG GGCAAACGCA TCGTGATTAT ATTAAATTGC AATATAAAGG TACGGATCAA 2880

CTATTTGTTC CAGTAGATCA AATGGATCAA GTTCAAAAAT ATGTAGCTTC GGAAGATAAG 2940

ACGCCAAAAT TAAATAAACT CGGTGGCAGT GAATGGAAAA AAACAAAAGC TAAAGTTCAA 3000

CAAAGTGTTG AAGATATTGC TGAAGAGTTG ATTGATTTAT ATAAAGAAAG AGAAATGGCA 3060

GAAGGTTATC AATATGGGGA AGACACAGCT GAGCAAACAA CATTTGAATT AGATTTTCCA 3120

TATGAACTTA CGCCTGACCA AGCTAAATCT ATCGATGAAA TTAAAGATGA CATGCAAAAA 3180

TCGCGTCCAA TGGATCGCTT GCTATGTGGT GATGTTGGTT ATGGTAAAAC TGAAGTTGCA 3240

GTGAGAGCAG CATTCAAAGC TGTAATGGAA GGAAAGCAGG TTGCATTTTT AGTTCCTACA 3300

ACTATTTTAG CTCAGCAACA TTATGAGACG TTAATTGAGC GTATGCAAGA TTTTCCTGTT 3360

GAAATTCAAT TAATGAGTCG TTTTAGAACG CCTAAAGAGA TAAAACAAAC TAAGGAAGGA 3420

CTTAAAACTG GATTTGTTGA CATAGTTGTT GGTACACACA AATTACTTAG TAAAGATATA 3480

CAGTATAAAG ATTTAGGGCT GTTGATTGTA GATGAAGAAC AACGATTTGG TGTACGCCAT 3540

AAAGAGCGTA TTAAAACATT AAAACATAAT GTAGATGTAC TAACATTGAC TGCAACCCCA 3600

ATAGCTAGAA CATTGCATAT GAGTATGCTA GGTGTGCGGG ATTTGTCAGT GATTGAAACG 3660

CCGCCAGAAA ATCGTTTCCC AGTTCAAACA TATGTATTAG AACAGAACAT GAGTTTTATC 3720

AAAGAAGCTT TAGAAAGAGA ACTATCCCGT GATGGCCAAG TGTTTTATCT TTATAATAAA 3780

GTGCAATCCA TTTATGaAAA ACGAGAACAA CTCCAGATGT TAATGCCAGA TGCTAACATT 3840

GCAGTTGCTC ATGGACAAAT GACAGAGCGC GATTTAGAAG AAACGATGTT AAGTTTTATC 3900

AATAATgAAT ATGATATTTT AGTAACGACG ACGATTATTG AAACAGGTGT CGATGTCCCA 3960

AATGCAAATA CTTTGATCAT TGAAGATGCA GATCGCTTTG GATTGAGTCA GTTGTATCAA 4020

TTAAGAGGTC GTGTTGGTCG TTCAAGTCGT ATTGGTTATG CATACTTCTT ACATCCAGCA 4080

AATAAGGTAC TAACTGAGAC TGCAGAAGAT CGATTACAAG CGATTAAAGA ATTTACGGAG 4140

TTAGGTAAAC AACAGCACGG CTTTATTGAT ACAGTTGGAT TTGATTTGTA CAGTCAAATG 4260

TTAGAAGAAG CTGTAAATGA AAAACGTGGT ATTAAGGAAC CAGAATCTGA GGTGCCAGAA 4320

GTCGAAGTTG ATTTAAACTT GGATGCATAT TTGCCAACAG AATATATTGC AAATGAACAA 4380

GCTAAAATTG AA 4392

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TTTCTTTTGA ATCTATATCG AGGTGGTTGG TAGGTTCATC TAAAATAAGT ACATTGTCAC 60

GTTGCAACAT AAGTAGTGCT AGTTGTAAAC GTGCTTTTTC ACCACCAGAT AAATCATTAA 120

TTATCTTTTT AACATCGTCT TGTACAAATA AGAAACGTCC AAGAACTGCT CGAATATCTT 180

TTTCATTCAT TAACGGATAT TGATCCCACA CATAATCTAA AATCGTTTTA CTAGATTTAA 240

ATTCTGCTTG CTTTTGATCA TAATAACCAA TTTGTAAATT TGCGCCGAAA GTAATATCGC 300

CATTAAGCGC TTTTTGTTGA TTAGCAATAG TTTTAATTAA GGTCGATTTT CCAATACCAT 360

TTGGCCCAAT GATTGCTATA TGATCGCCTT TAGAGACCTC TATACTCATA GGTTTGGTAA 420

TTGCAGTTTG ATAACCGATT TCTAAATTTT TTACATGCAT GACGTCATTA CCTGTATTCC 480

GGTCAAAGCC AAATTGAATA TTTGCACTTT TGGCATCTAA CATTGGTTTA TCAATGCGTT 540

CCATTTTTTC TAAAATCTTA CGTCTACTTT TTGCCATTCC ACTTGTTGAA GCACGGGTAA 600

TATTTTTCTC AACAAAAGTT TCTAATCGTT TTATTTCTGC TTGTTGACTT TCATATTCTT 660

GCATTCGTTT TTGATAATAT AAATCCCGTT GCTGTATAAA TTCCTCGTAA TTACCAACAT 720

AGCGTTTGA 729

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13856 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TGATGTTTCG ATACATTTGT TGCACCTTGT GGATATACTT TAAAGGTTGT GTCGTATGTT 120

TCCTTACTAT CTTTAGCTTC AGATTCCTGT GATTCAACCG TTTTATATTT TTCAAGTGCA 180

TGTCCTTCAA TATCAACTCG TGGAATAATG CGATTCAACC ATGCTGGTAA ATACCACGAA 240

CCTTTtCCAA ACAATTTCGt TAATGCAGGA ATTAACATCA TtCTGACTAC GAAGGCATCA 300

AAGAGTACAC CAAACGCTAA TGCCATACCC ATTGATTTAA TCATGACATC TTCTTGGAAT 360

ACAAACGCAA AGAAGACACT AAACATAATT AATGCAGCTG CTACAATAAC AGGACCGCTT 420

TCTTTCAATC CTACTTTGAT AGAATAATCA TTATCCCCTG TTTTACTATm yyCTTCATGr 480

ATTCGCGACA TAAGGAAGAC TTCATAATCC ATCGCTAATC CAAATAAGAT ACCTATAGTA 540

ATAACCGGTA AAAATGCTAG CATTGGTCCT GTCGTTTCAA TACCAAACAG ACCTTTCATA 600

AAACCATCTT GCATTACTAA TGTTGTAAAT CCTAATGTTG CCATTAATGA CAAGACGAAT 660

CCTAAAACTG CTTTTAATGG TATTAGAATT GAACGGAAGA CAATCATTAA TAAGAAAAAT 720

GCTAATACAA CAATGACTGA GGCAAATAAA GGTATCGCCT CATTTAACTT TTTAGACATA 780

TCAATATTAA TGACACTTTG TCCCGAAATC TCCGTTTTGA ACCCATATTT ATCTTGTGCA 840

TCTTTATGAT AATCTCGTAA ATCATGCACT AAATCATTTG TACTCTCTGC ATTAGGCCCT 900

TGCTTAGGTA TCACGACCAT CAAAGCGTAA TCATTATCTT TACTCATTTG TGGTGGCGTA 960

ACGATATCTA CATTTTTCTT ATCTTTAATA TCTTTATATA CAGACTGTAA ATCTTGTTGT 1020

AATCCTTGTG GATCATCCTT TTTATCTTTC ACATTTATCA ACATCGGTAT TTGGCCATTA 1080

AATCCTTCAC CAAATTTATC CGAGATAATA TCGTAAGCTT TTTTCTGTGT AGAATCTGCT 1140

GGTTTAACAC CGTCATCTGG AATACCAAGT CGCATATGAC TAACTGGTAT TGCAGCTGCT 1200

ACTAATATGA TTAAACCTAG TAATACTGCC GCAAGTGCAT TTCCTGTAAT AAATTTAGAC 1260

CATGGCGTAT CAATATCTTT TTTGAATTTA GACTGTAATT TATTCACTTT AATGCGTTtA 1320

TGGAAAATGC TTATTAATGC AGGTAATAAA GTTAAAGCGC TAAGTACTGC AAAAACAACA 1380

CTAATTGCCG AAGCAAATCC CATTACCGCT AAGAAGTCAA TGCCTACTAA TGATAAACCA 1440

CATACTGCAA TTACAACTGT TACACCAGCA AAAACAACTG CACTACCTGC TGTTCCTATT 1500

GCAAGACCAA TGCCTTTAAT GTAATCTGTT TCAGTTTTCA TAACTTGTCG ATATCTGAAT 1560

AAAATAAATA ATGCATAATC GATACCAACT GCTAGTCCAA TCATTACGGC TAATGTCAGT 1620

GTGACATTTG GTATATCGAA TGCATAAGTT AACAAACTGA TAATACCTAC ACCAGAGGCT 1680

AGACCAATCA ATGCACTTAT AATTGGTAAT CCTGCAGCAA TGACTGAACC GAATGTGATT 1740

AACAGTACAA CAAATGCAAC AATAATACCA ACTAGTTCAG AATTACCGCC TACTTCTGTA 1800

AAATGACTTT TAACATTATC TCTAGAGCCA TCTTTTAAAG ATGTTTGACT AACGTCATAT 1920

GTGATATCTG CAAATGCAGT TGTTTTATCT TTACTAATTT GCTTATTTTC ATAAGGATCT 1980

GATATTTTAT CAATGTGCTT GTCATCTTTT TTAATATCAT CTAACGTTTT CTTAATATCT 2040

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TGTGCCTTTT CACTATCTTG ATTAAAATGT TTTTCAATCT TTTTATTCGT ATCTAACGAC 2160

TCTAATCCTG TCATTTTAAT ATCATTGTCA AATTTCGGTG CATTTGTAGC AAGTGGTATC 2220

AATATTGCAG CTACAATCAC TATCCATGCA ATGACCGCGG ACCATTTATG TTTTGCGATG 2280

AATGTCCCCA TCTTATATAA AAATTTTGCC AAAGTATATT GCCTCCTTTT AAAATCAACG 2340

TTATAGTTTA AATATACAGT GTAGATTATT GTTCGATTAT AGTATCTATC CCCGACCTCT 2400

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TGTTAGAACA GCAATTATTC CAAACGATTA CTGTCAATCA AATTTGCGAC AACGCACTCG 2580

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TCAATCAATT GACTAAAGAC TACTTTGCTA GAGATATCAG TGACCGTCTT AATCATCCAT 2700

TCCAAACGAT GAGTGATACG ATTAATAATA AAGAGGATTT GAGAGAAATC GCAGAATTCC 2760

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ACGATATCAA AAATAATAGA GACCGTATCG ATATTGACAG CGACATCCCA GATAATCTCA 2880

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TTGATTGGCC TGGCGAAGAT ATTGATAACA TTTTCCATAG ATTAATCAAT ATTAAGATTA 3000

AATAGTAGAT GAGAAACTCA TGAGCGTTAC CAACATTCAT AATAAAAACG ATAGTGkACA 3060

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TTTAAAGTTA TAAATAAAAA GAGCCAACCG CAATGGATGG CCCTTGTTCA TTATGAAGCA 3360

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TGTTTTAGCG TCCGTACCTG ACATTTTGAA ACCACCAAAT GGATGGTATC CAACAACTGC 3480

TGAAGTACAG CCTCTGTTAA GGTATAAATT GCCTACATCA AATTCGTTTA CCGCTTTAAT 3540

CCAATGCTCG CGATTATTTG TAATCACTGC ACCAGTTAAA CCGTAATCTG TATCATTTGC 3600

TTCTTCTTGC ATGATTCTAT CTTTAGATTT AAGTCCTGAA ATGATTGTTG GTTCTACAAA 3720

GTAACCTTTT GAATCATCAG TGCCGCCACC TTGTTCTAAT TTACCTTCTT CTTTACCAAT 3780

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ATTGTCTACA GTATTGCCCA ACGTTAATTC TTTTGTTAAT TTGATTGATT TCTCTAATAC 3900

TTCGTCATAA ACGTCTTTAT GCACAATTGC ACGTGAACAT GCTGAACATT TTTGACCAGA 3960

AAAACCAAAT GCTGACGTTA CAATAGCTTC TGCTGCCATA TCTGTATCAA TATTTTCATC 4020

AACTACAATG GCATCTTTAC CACCCATTTC AGCGATAACA CGTTTCAAGA AGTTTTGACC 4080

TTCTTGAACA ACGGCACTAC GTTCATAAAT TCTAGTACCT GTCGCACGTG ATCCTGTAAA 4140

TGTAACGAAA TGCGTATCTT TATGATCAAC TAAGTAATCA CCAATTTCTT TCGGATCACC 4200

AGGAACAAAG TTAACTACGC CTTTTGGTAA TCCTGCTTCT TCTAAAATTT CCATTAATTT 4260

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CTTACCTTGA GCCAAGTCCA TCATTGAACG TGCATAGTAT TCAATAAAAT CAATACCTTC 4500

AGCTGCATCA CCAACTGCTT CATCCCATGG CTTACCTGCT TCATAAACCA TAATTGCTGC 4560

AATTTCCGCT TTTCGACGAC GAATAATTGC CGAAACACGT AACATAAGCT CTGCACGATC 4620

ATTTGCTGAC CATGTTTTCC AAGATTTATA AGCTTCGTTT GCTGCTTTAA ACGCATCTTC 4680

AACATCTTGT TTTGTTGCCT TTGATGCATT TGCAATCACT TGTGATGTGT CTGCAGGATT 4740

GATTGATTTA ATTTTGTCAT CTTTGAAAAT CTTCTCTCCA TTAATCACTA ATGGTATGTC 4800

TTGACCTAAT TCTTTTTCCA CGTCTTTCAA TGCTTTCTTA AACATATCCA CATTTTCTTG 4860

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CCAAGTATTA CTGCCAATAT GAATGGGTCC GGCTTTTTCA AAACCTTCAT TTCTATGATG 5340

GAAATTAAGT GGATGTGTCG CTGTGTAGAA TCCACAATTA GGTCCTATAA AAACATTATC 5400

TCCTAGTTTA ACGTTCCAAC CATAATCTGT ATCAAAAGGA ATCGAAATAC TTACATTGTC 5520

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AATCTATTAA CGTACAATGT GAGTAAGAGA AATATAAAGG AGTATGATAG CGATGAGAAT 5940

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TTACGAAATG ACAAACGACA CGAGTCGTcA GTTGTCAGAC AACAAAGATG ATGATAAAGT 6060

CATCCATCTT AATAATTTTA AAAATTTACA TGCGAAAGAA TTTAACCCAT CTGATTTCTT 6120

TTAAGTCACC TAAGAATTGC AAATCCAGAA GTCATTTAAG TTTTACCTTT CATTCATACA 6180

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GTTCAAAATG CAACGGTCAA TTTAACAACA GAGCAAGCTA AAGTTGACTA TTATCCTGAA 6720

GAAACAGATG CTGATAAACT TGTCACTCGC ATTCAAAAAT TAGGTTATGA CGCGTCTATT 6780

AAAGATAACA ATAAAGATCA AACGTCACGC AAAGCTGAAG CGCTACAACA TAAATTGATT 6840

AAGCTTATCA TATCAGCAGT ATTATCTTTA CCACTATTAA TGTTAATGTT TGTACATCTT 6900

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CCTGTACAAT TTATTATTGG ATGGCAATTT TATGTAGGTG CTTATAAAAA CTTAAGAAAT 7020

GGTGGCGCCA ATATGGATGT ACTTGTTGCT GTTGGTACAA GTGCAGCATA TTTTTACAGT 7080

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TTAAAAGATG GTAATGAAGT GATGATTCCT CTAAATGAAG TACATGTTGG AGATACACTT 7320

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CCAACTTCTA TTATGGTAGG TACTGGTCGC GCTGCTGaAA ATGGTATTTT ATTTAAAGGT 7800

GGCGAGTTTG TTGAACGCAC ACATCAAATT GATACCATCG TTTTAGATAA GACGGGTACC 7860

ATTACAAATG GTCGTCCAGT CGTGACAGAT TATCATGGTG ACAATCAAAC GCTACAACTA 7920

CTTGCTACTG CTGAAAAAGA TTCTGAACAC CCATTGGCAG AAGCCATTGT CAATTATGCA 7980

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AATGATATTA GCTTGCCTAA GCATATTTCT GATGATTTAA CACATTATGA ACGAGATGGT 8160

AAAACTGCTA TGCTCATTGC TGTTAATTAT TCATTAACTG GTATCATCGC AGTGGCAGAT 8220

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GCCATGTTAA CTGGCGATAA TAAAAACACT GCTCAAGCCA TTGCAAAACA AGTAGGCATA 8340

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ACCATTCGTA ATATTCGTCA AAATCTATTT TGGGCATTCG GCTATAATAT TGCCGGTATC 8640

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GGTACATGTA ATGTCACGAT ATCAGCACCT TCAACCGCTT CCTCAATCGT ATCTTTGTAA 9780

TCGACATACG TTGCAATTTT AGCATTAGGA AACGGtCGTA TGCGACCACA TCACTTTGAT 9840

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CACTCATGAT TTTAATTTTT GTCATTTTAA CATCACCCTT AACTTTATTA TTCATATAAA 10380

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TCTTTCGTAG CTGTCGATCC AGTTGGATTA TTTGGATACG TTAAATAAAT GAGTTTTGTT 11040

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ATTACTGCAA TCTTCATTAT TCAACCACCT ATATTCTATG ATATTTACTA TTTATTTCAT 13500

GAAACAACTT TGCCTTTTTC CTCTTATCCA CAAAAACACG TTCATGTAAT GTATAGTTAG 13560

CCTGTCTCAC TTCGTCCAGT ATTTCAATAT ATATACGTGC TGCTAATTCT ATGATTGGTT 13620

GTGCTTCAAT ACTAAATACT TTGATTTGAT CCATAACATC TTGAAAATCT TTTTCTGCGA 13680

TAGCTGCATA ATATTCCCAT AAGTCAATAT AATGATTATT AACACCATTT TGGTACACTT 13740

CAGCAATATC AACTTCATAT TGCTTTAATC GTTGCTTACT AAAATATATC CGTTCATTGT 13800

CAAAATCTTC ACCGACATCT CTTAATATAT TAAnGGGATC CTCTAGAGTC GACCTG 13856

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10088 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ATATATAAAT ATAGATTAAG TATATAGATT AATCAACTTT TTTGGAAGAG CAAATCACGC 60

AATCAACAAA TAATATAAGA AGTTTTTGCG ATAGTTTTAA AATAGCTGTA ATAGAATACT 120

AAATGTGACA AACTTAGAAC TAATATCAAG TGTTGATGTT TTGAATATAA AAATGCTAAT 180

ATAATTGGTT AATATATGAG TAATTAGAAA ATAGACAAAG GATGACGATT TATGTATATC 300

AATATGAAAG ATTATGGGTT AACAGGCATA AACAAAACTA AAGATACTCG AGCAATACAA 360

CGTGCGTTAA ATCGTGGAAG ATGTAAACCA ACGACAGTTT ATATACCGAA AGGGACGTAT 420

GATATTTGCA AACCATTAAC GATATATGGC AATACAACAC TTTTGTTAGA TAATGAAACT 480

ATTTTACGCC GATGTCATTC TGGTCCTTTA TTAAAAAATG GTCGTCGCTT TGGTTTTTaT 540

CGTGGTTATA ATGGACACAG TCATATTCAT ATTAAAGGCG GCAAGTTTGA TATGAATGGT 600

GTATCGTATC CTTATAACAA TACAGCTATG TGCATTGGGC ATGCTGAAGA TATTCAATTA 660

ATAGGTGTGA CCATTAAGAA TGTAGTGAGT GGTCATGCAA TTGATGCTTG TGGGATTAAC 720

GGACTCTATA TTAAAAGCTG TTCATTTGAA GGATTCATAG ACTATAGTGG CGAACcTTTT 780

ATTCTGAAGC AATACAATTA GACATTCAAG TACCTGGTGC TTTTCCAAAA TTCGGAACgA 840

CAGATGGTAC GATAACGAAA AATGTCATTA TCGAAGATTG TTATTTTGGA CCTTCAGAAT 900

TGCCCGAAAT GGGAAGTTGG AATCGTGCTA TTGGCTCACA TGCAAGTAGA CATAATCGAT 960

ACTATGAGAA TATTCATATT AGAAATAATA TATTTGAAGA TATACAAGGT TATGCATTAA 1020

CTCCCTTGaA GTATAAAGAT GCTTTCATTA TTAATAATAA GTTTATTAAC TGTGaGGGTG 1080

GCATTAGATA TTTAGGAGTT AGAGATGGTA AAAATGCAGC AGATGTGaTG ACAGGaAAAG 1140

ACTTAGGTTC CCAAGCAGGC ATAAATATGA ATATAATTGG AAATGAATTT AAAGGATCAA 1200

TGTCTAAAGA TGCGATACAT GTACGTAATT ATAATAATGT TAAACATAAA GATGTATTAA 1260

TCGTTGGGAA TACATTCAAT AATTCGACTC AATCAATTCA TTTAGAAGAT ATTGATACAG 1320

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TTATCTTTTT GTTTTTAGGT GGATTTATTT TGGCAATTGC AATGGAAAGA TGGAATTTAC 1980

TTGGATTCAT GGTGGCAACA GGATTCTTAT CTATGTTTGT ATCGAACACT GCAGCTGTAA 2100

TGATTATGAT TCCGATTGGT TTAGCAATTA TTAAGGAAGC ACATGATTTA CAAGAAGCCA 2160

ATACGAATCA AACAAGTATT CAAAAGTTTG AAAAATCTCT AGTTTTAGCA ATTGGCTATG 2220

CAGGTACGAT TGGTGGCTTG GGTACATTAA TCGGAACCCC GCCATTAATT ATTTTAAAAG 2280

GACAATACAT GCAACATTTT GGACATGAAA TTAGTTTTGC TAAATGGATG ATTGTAGGGA 2340

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AACATCGCCG TATCATTGAC TGGGAAGTTG CAAAAGAGCT CCCTTGGGGT GTATTAATTT 2700

TATTTGGTGG CGGTTTAGCA TTAGCGAAAG GTATTTCTGA AAGTGGTTTA GCAAAATGGT 2760

TAGGCGAACA GTTGAAATCA TTAAATGGTG TTAGTCCGAT TCTTATTGTA ATTGTCATAA 2820

CAATCTTTGT CTTATTTTTA ACTGAAGTGA CATCTAATAC TGCAACTGCA ACGATGATTT 2880

TACCGATTTT AGCAACGTTG TCTGTTGCTG TTGGAGTGCA TCCATTACTA CTTATGGCAC 2940

CTGCAGCTAT GGCGGCTAAC TGTGCATACA TGTTACCAGT AGGGACACCA CCGAATGCAA 3000

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TAAGAACAAT ACAAACAAAA GAAAGTCAAC CAAGGATGGA TTCCTATTTT AATCCTTGGT 3300

TGACTCTTTA TTTTATTTAA ATTGTAGAAC CTAGAAAATA AAGTTTAATT AAAAGCACCA 3360

ATCATTTCTA CTTTGAAATC TAAGGTTTCT AAAATAGCAA TGACTTTCTT TATATCGGTT 3420

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CGAGACTCAA TCCAGGATAA ATTAATATTA AACAAAGCAA ATGTATTAAG CACACTTGCT 3540

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ATCTTTATTA AATGAATTAT TTTTAAGTGT ATCAAATTCA AACGCATCTG CAACTTTTTC 4500

TAGTAAATTG TAACGGTAAT CATCAATAAA GTTACGTACG CCAATTTCAG TTACCATATA 4560

CCAACCGTTA AAGGGTGCAG TTGGATATAC AATGCCACCG ATTTTTAAGT CCATATTGGA 4620

AATGATAGGG ACTGCATACC ATTTTAAGTT CAATTTTCTT AATTTTGGAT AATGATTATG 4680

TTCAATAGGT ACTTCTTTAA TTAATGAAGT AGGATATTCG TAAAATTTAA CTGACTCATT 4740

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ATAGCGAATT AATTGATTGT TGAAAATTTT AGGTCCATCC TTTGGAGCAT ATATAGTAAT 4920

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GAACGATGCT TCGTCAGTAA CATCTCTTGC ATCAATGACA TTTAACGAAT CCCAAAATAA 5040

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TTCTGTATGT GTATATGTCC CAGTTTCTTT TATTTCTAGT TCAATGTCAT GTAAACGTTT 5160

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TTATATCAAA TAAATATGGC TGAAAGTTAT TGGAATGATA ATATTCATGA AAAAATGGCT 5520

GTATTTGATT TGTATTTTAG AAAAATGCCA TTTAATAGTG GCTATGCTGT TTTTAATGGT 5580

TTAAAGTCTA TTGGCTACAA GGATGATTTC TTATCATATT TAAAAGATTT AAAATTCACA 5700

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GTTACGACGC CAGGTAAGAA AAATGTATAT CGCATTATAA ACAAGAAAAC AGGTAAGGCA 6540

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CATCATAATA TTTATGAAAA TGGTAAATTA GTATATCAAA TGCCAACAGA AGATGAATCA 6720

CGTGAATATT TAGCACTAGG ATTACAATCT ATTTGGGATG AAAATAAGCG TTTCCTGAAT 6780

CCACAAGAAT ATCCAGTCGA TTTAAGCAAG GCATGTTGGG ATAATAAACA TAAACGTATT 6840

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TAAACGACAA GGTCGTCAAT TATTAGCGTA TCTTGGTGCG CCAAAGGAAT TATATGAAAA 7500

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ACCTCGAAAC ATACATGGTG GATTCTGGAC TAAAGGCATT CGTCGTAGAA AGCTTAAAGA 8520

TTATGAACCA GAAGAACTGG AAaGTGTAGT AGAaCATGAA aTTCmAAGTA AaTGAGAaTG 8580

AAmCAATtGC TGATTGTTTG TCACGAATGA AAtGCAAGGG TATATGCCGG TAAAACGTAT 8640

TGAAAAAACCC GTGTTTCAAG AGCAAAAAGA TGGCACGGTT GAAGTATCAC ATCAAGAAAT 8700

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CAATAACAAT TGAGCTATTA TTTTTATTAT ATAATGTGAG TTGTTTGTGT TCTGTATTTA 9180

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TCCATATAAT TATAACCTCT TGTCCATTAT CTAATTTAGC GTTCCCAACA ACTGCCATGG 9540

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GACGTGGTGT TTTTAGTACT AGTTTAGCTT TATGATTTTG AGTACCACAT AGTAACCTTT 10080

TGAGTTGT 10088

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7563 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CGGAAACGnA CCCnATGCGT ATGCTTGACG TGCCAAAATT AAATACGAAG TTCATAGCTT 60

TGAGGTACCA GAAGAACATT TATCTGGTCA AGAAGTCGCA GnACTCATAC AAGCAAATGT 120

TAAAACAGTA TTTAAAACGC TTGTTCTAGA AAATACAAAA CATGAACATT TTGTATTTGT 180

TATCCCAGTA AGTGAAACTT TAGATATGAA AAAGGCAGCT GCTTTGGTTG GAGAGAAGAA 240

ATTGCAGCTT ATGCCTTTAG ATAATTTGAA AAATGTAACG GGATACATTC GTGGTGGGTG 300

TTCGCCTGTT GGTATGAAAA CATTGTTTCC AACAGTCGTT GACAAATCGT GTGAAAATTA 360

TAGTCATATC AGTGTGAGTG GTGGGCTTCG AACAATGCAA ATCACAATAG CTGTTGAGGA 420

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TGCCACACTC CTTTTTGATT GAATTAGCAT TTTACGATCA TAAACAGTCA TTATAATTGA 600

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GGTTAAATCA TTTGTTATTA GATGGATTAA ACAATTTATC AGGTTCTAAT ATTGTATTAT 3840

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TTGCACTTCT AGTTGGCACA TTAGTTTCAG CATTAATTTA CGGTTTAATC AAACCAAAGT 4320

TAACTGAAAC AGAAATCGAA GCTTCAAAAT CAATGGACGA GTAGTTTTAA TGATGTAAAA 4380

TGATTGTTAG CAAAGAGCTT CATATTAAGT TGTATGTTCA ATGAATATAT GTTAGTTTTA 4440

TATATCGTGT TAACGGTAGC TTATACAAAG CTGTAAAAAC ACTTTCTATT AATTCAGTTT 4500

TTATGAATTG ATATGAAAGT GTTTTTATTT TTAGATAAAT GAATGAAGAA ATAGACACCA 4560

CAAATGTATA GACTTTTTTA ATATTTTGCA AAAAGTTATG CCAAACGAAG CAGATATAGT 4620

AAAATATGAG TGTCTTAAAG TGAAAATTTA TAAATAAAGA AGGGTTTATA CGTGTCAGAA 4680

TTAATTATAT ATAACGGCAA AGTTTATACT GAAGATGGCA AAATCGATAA TGGTTACATT 4740

CATGTGAAAG ATGGACAGAT TGTTGCAATT GGAGAAGTGG ATGATAAAGC AGCAATTGAT 4800

AATGATACGA CAAATAAAAT TCAAGTGATT GATGCTAAAG GTCATCATGT ATTACCAGGT 4860

TTTATTGATA TACATATTCA TGGTGGTTAT GGTCAAGATG CAATGGATGG GTCATACGAT 4920

GGCTTAAAAT ATCTATCCGA AAATTTGTTG TCTGAAGGGA CGACATCATA CTTGGCCACT 4980

ACAATGACGC AATCGACTGA TAAAATAGAT AATGCACTTA CAAATATTGC TAAATATGAA 5040

GCGGAgCAAG ATGTTCACAA TGCAGCGGAA ATTGTAGGTA TACATTTAGA AGGACCATTT 5100

ATATCTGAAA ATAAAGTTGG TGCTCAACAT CCGCAATACG TTGTACGCCC ATTTATCGAT 5160

AAAATTAAAC ATTTTCAAGA GACTGCTAAC GGATTAATAA AGATTATGAC GTTTGCACCT 5220

GAAATTGAAG GTGCAAAAGA AGCGCTTGAA ACGTATAAAG ATGACATTAT TTTTTCAATT 5280

GGTCATACAG TAGCAACATA CGAAGAAGCA GTTGAAGCTG TTGAGCGAGG AGCTAAACAT 5340

GTCACGCATT TATATAATGC AGCGACGCCA TTCCAACATA GAGAACCAGG TGTTTTTGGA 5400

GCAGCATGGT TGAATGATGC TCTACATACC GAAATGATTG TTGATGGCAC TCATTCTCAT 5460

CCGGCATCGG TTGCAATTGC TTACCGTATG AAAGGTAATG AACGTTTTTA TTTAATTACC 5520

GATGCAATGC GTGCAAAAGG TATGCCTGAA GGAGAATATG ATTTGGGTGG ACAAAAAGTA 5580

ACTGTTCAAT CGCAACAAGC ACGTCTTGCA AATGGTGCGC TTGCTGGTAG TATTTTAAAA 5640

ATGAATCATG GGTTACGTAA CTTAATATCA TTTACAGGTG ATACATTAGA TCATTTATGG 5700

CGAGTAACAA GTTTAAATCA AGCCATTGCA TTAGGTATCG ATGATAGAAA AGGTAGTATT 5760

AAAGTAAATA AGGATGCAGA TCTTGTTATT CTAGATGATG ATATGAATGT AAAATCTACA 5820

ATAAAACAAG GCAAGGTTCA CACATTTAGC TAATAAATAA TCATAATTAA ATGTATGCAA 5880

TTTTCTGGGG GTGTCTAAAT GGGAAGGCGA TAACATGTAG TTGTAATTTA AGTCATAGTG 6000

ATAAATTTGA ATGCGTGTTA CCCATGAGTG ACACATATAA CATGGAGGTG AATCCCTAGA 6060

AATAGGGAAT TAATTGGAAA CTTCGACCAT AATTAGTTTG ATTATATTTA TTCTATTAAT 6120

TGCATTAACC ACTGTATTTG TTGGTTCAGA ATTTGCATTA GTAAAAATTA GAGCAACAAG 6180

AATTGAACAG CTAGCAGATG AAGGAAATAA ACCTGCTAAA ATAGTAAAAA AGATGATTGC 6240

TAATCTAGAT TATTATCTTT CTGCTTGTCA GTTAGGTATA ACAGTAACAT CTTTAGGGTT 6300

AGGTTGGCTT GGTGAACCAA CGTTTGAAAA GCTATTACAC CCAATATTTG AAGCAATCAA 6360

TTTACCAACT GCATTAACGA CGACGATTTC GTTTGCAGTG TCATTTATAA TCGTTACGTA 6420

TTTGCATGTA GTACTTGGTG AATTAGCGCC TAAATCTATA GCTATTCAAC ATACTGAAAA 6480

GCTTGCTTTA GTATATGCAA GACCATTGTT CTATTTCGGT AACATTATGA AACCATTGAT 6540

TTGGCTGATG AATGGTTCTG CACGTGTTAT TATTAGAATG TTTGGTGTAA ATCCTGATGC 6600

CCAAACTGAT GCAATGTCAG AAGAAGAAAT CAAAATTATT ATTAACAATA GTTATAATGG 6660

TGGAGAAATC AACCAAACTG AATTGGCATA TATGCAAAAT ATCTTTTCAT TCGATGAAAG 6720

ACATGCAAAA GATATAATGG TACCTAGAAC TCAAATGATT ACACTAAATG AACCTTTTAA 6780

TGTAGACGAA TTACTAGAAA CAATAAAAGA ACATCAATTT ACGCGTTATC CAATTACTGA 6840

TGATGGTGAT AAAGACCACA TTAAAGGATT TATTAACGTC AAAGAATTTT TAACTGAATA 6900

CGCTTCTGGA AAAACGATTA AAATAGCAAA CTATATaCAT GAGTTGCCAA TGATTTCAGA 6960

GACAACACGT ATCAGTGATG CATTAATTAG AATGCAACGT GAACATGTAC ATATGAGTCT 7020

TATTATAGAT GAATATGGTG GAACGGCAGG TATTTTAACG ATGGAAGATA TTTTAGAAGA 7080

AATCGTTGGA GAAATTCGTG ATGAATTTGA TGATGATGAA GTGAATGATA TCGTTAAAAT 7140

TGATAATAAG ACATTCCAAG TAAATGGCAG AGTACTATTG GATGATTTAA CTGAAGAGTT 7200

CGGTATAGAA TTTGATGACT CTGAGGATAT TGATACGATA GGTGGATGGT TACAATCTCG 7260

TAATACCAAT TTACAAAAAG ATGATTACGT GGATACAACT TATGATCGCT GGGTTGTTTC 7320

AGAAATCGAT AACCACCAAA TTATTTGGGT GATATTAAAC TATGAATTTA ATGAAGCGAG 7380

ACCTACTATC GGACAGTCTG ATGAAGATGA AAAATCAGAA TAGATATTAA TATATAAACC 7440

AACTAAGAAT GATTTAATTC ATTTTTGGTT GGTTATTTTT TTGACTAAAA TTAAnGAAAA 7500

GTGAAAATAG TATTGGAACT CAATATCTTT AATGATTTAA TGAATAAnTT TTATTGAAAG 7560

CGA 7563

(2) INFORMATION FOR SEQ ID NO: 34:

(A) LENGTH: 3492 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TTATATCAAC TTCATGGCGG AACCATTGAT GACCCATTAG ACGAAACAAT AAGCGCATTT 60

sATGAATTGA AACAAGAAGG AATTATACGT GCTTACGGTA TTTCTTCTAT TCGCCCAAAT 120

GTAATTGATT ATTATTTAAA ACATAGTCAA ATCGAAACGA TAATGTCTCA ATTCAATTTG 180

ATTGATAATC GTCCAGAATC ATTATTAGAT GCAATTCACA ACAATGATGT TAAAGTATTG 240

GCAAGAGGAC CTGTGTCTAA AGGATTATTA ACTTCAAACA GTGTTAATGT GCTCGACAAT 300

AAATTTAAAG ATGGTATTTT TGATTATTCT CATGATGAAT TGGGTGAAAC AATAGCCTCT 360

ATTAAAGAAA TTGAAAGTAA TTTATCTGCA TTGACATTTA GTTATTTAAC ATCACATGAC 420

GTGCTTGGTT CCATCATTGT AGGTGCAAGT AGCGTCGACC AATTAAAAGA AAATATTGAA 480

AACTATCATA CTAAAGTTAG TTTAGATCAG ATTAAAACAG CAAGAGCTCG TGTAAAGGAT 540

TTGGAATATA CCAATCATTT AGTGTAGAAG TCATTTTCAG TAATAAAAAC AGCAGCATGA 600

GGCGTTTCAT TATAAAAATG CCTTACTGCT GTTGTTTATG TACAATTCGC TATAATTTAT 660

GATTATGATT ACTCACTTAT GATAGAAATT AAAGCGTTGT CCTCACGCAT CAGTATTTAG 720

TAATTTCGCC TTGCGGCATT GCCTTAAGCA AACTTCTGCC ACTTCATCTC TTAATAATTT 780

TATTAAAACA TCTTTCTATA TTTCACTTCG CATGTTGATT CATCATTATT AGTTATTATT 840

TGTACACCCA GCACATTTCC TTGCAACACA AGTAGTTTGA ATTTTTCACA AGTATAATAT 900

AATGTACCGT CTGAAATTTG GTCTACAGAA ATATCGCCTA AAATATCCAG CACTGTAAAT 960

TCTTCAAATA CTGATAGTTG TTCCGCATAT CGTACACAAA GTCTTACCAC ACTCTCCGAT 1020

TGACAGTTCA TTGCCATCCC ACCTATTTAT GCTTTATTTT TAAATAATTT AGGGAAACAT 1080

CGTTCAAAAA ATCTAGGCGC AATTTGATAC ATTTTCAACG CATGaTGCAT CCATTTAGGC 1140

CGATTAATTT CCAATTGTTT TGTTTTAATG CCATAAATGA TATCTTCTGC AAGCTGATTA 1200

GCATCAAGCA TAATTTCCCC CATCTTTTTA gCATACTTCA TTGATGGGTC GGCTTTTTGA 1260

TGAAAAGGTG TATCAATCGG GCCAACATTA ACTGTCATGA TATGTAAGTT TGGTGACTCT 1320

AGTCTTAAAG CATTCATTAA TGCATAAAAC CCTGCTTTCG ATGCCCCATA ATGTGCAGCA 1380

TTTGCTTGTG TGGAAAATGC AGCTTGACTT GAAATACCTA CAATATGTGC GTTAGATGTT 1440

AAATATGGTC TCAACACAGT ATATAAAACA TTAAAACTAA TTAAATTAAG CTGATACGTT 1500

TAAATGAATC CATCGAATGA TGTATTGTCT TCAAATTGCA GTGCCTGTAT CGACTTCAAA 1620

TCATTTAAGT CACAAGGAAT AACATTTATA GTTTTCCCCA ATTCCTGTTC AAAGATTCTA 1680

GTTGCTTTAT CAACATCACG CACCAACAAC GTTACATGCA CTTTATTTTC TAGTAACTTT 1740

CGGACAATCG ATAAACCTAA ACCACTCGTA CCACCAGTCA CTATAAAATG TTGTCCTTTC 1800

ATCAATTAAC CTTCCTTTTC AATTATATAG AATGCAATTT ATCAACTTTA CATAATTGAG 1860

ACAAGTTGAT TATCTTTCCT AATATATATA CAATAATAAG AAAATATAAC ATACAAATCA 1920

AAAACTAAAG GGATGTGaCG TTAATGrAAC TCGTATTTTA TGGAGCTGGT AATATGGCAC 1980

AAGCTATATT TACAGGrATT ATTAACTCmA GCAACTTAGA TGCCAATGAT ATATATTTAA 2040

CAAATAAATC TAATGAACAA GCTTTAAAAG CATTCGCTGA AAAACTAGGT GTTAACTATA 2100

GTTATGAtGA TGCGACATTA TTAAAAGATG CAGAyTATGT ATTTTTAGGT ACCAAACCAC 2160

ATGACTTTGA TGCTCTAGCA ACACGCATCA AACCACATAT TACAAAAGwC AATTGCTTCA 2220

TTTCAATTAT GGCAGGTATT CCGATTGATT ATATTAAACA ACAATTAGAA TGCCAAAATC 2280

CaGTTGCTAG AATTATGCCA AACACAAATG CGCAAGTTGG ACACTCTGTT ACTGGCATTA 2340

GTTTTTCAAA CAACTTTGAC CCTAAATCTA AAGATGAAAT TAACGATTTA GTTAAAGCAT 2400

TTGGTTCTGT AATTGAAGTA TCAGAAGATC ATTTACATCA AGTAACAGCT ATCACCGGAA 2460

GCGGCCCAGC ATTTTTATAT CATGTATTCG AGCAATATGT TAAAGCTGGT aCsAAACTTG 2520

GTCTAGAAAA AGAACAAGTT GAAGAATCTA TACGCAACCT TATTATAGGT ACAAGTAAGA 2580

TGATTGAACG TTCAGAtTTG AGCATGGCTC AATTAAGAAA AAATATTACC TCTAAAGGTG 2640

GTACGACACA AGCTGGCCTT GATACATTGT CACAATATGA TTTAGTATCT ATTTTCGAAG 2700

ATTGTCTAAA CGCTGCCGTC GACCGTAGTA TTGAACTTTC TAATATAGAA GACCAATAAA 2760

AACAAACCCG CCAACACATG TATGCATCAT CGCAAGCACT GTGTTTGACG GGTTATTTTT 2820

ATAATTTATT GTTATTTGGC AAGCATTGTT TATTACTTTG TCATTAGATT TTAAAACTAT 2880

CAAAATCTTT TACAAAATTA AAATTAGGTG TATCTTCATT TTGTATCAAT GTTTGATAAA 2940

TTTCATTTAT ATCTTCTGTA TTATAGCGAT TGCTCAAATG TGTAATCAAC GTACGTTTAA 3000

CATTGGCTTC TTTTATCAAT GCAAATACGT CTTCAATATG GCTATGATGA TAATTGTTGG 3060

CTAAATGCTT TTCACCATCT ATATAGGTCG CTTCATGTAC CATCACATCA GCATCTCTAG 3120

AAATCACACG TTCATTAGAA CATGGTTTTG TATCACCAAA AATTGCTACA ACTGGACCCT 3180

GTTTGGACTC ACCTCTAAAA TCTTTTGATT GATAAACTTG ACCATTATGT TCAAATGTAT 3240

CATGAGATTT TACTTCTTGA TATTTAGGAC CTGGTTCAAG ACCAATGTTT TTTAACGCTT 3300

CATGATTAAG TAAATGCGCC TCTACAGTAA AACCATCCAT GATGATATGT CAGATGATCA 3420

TCGATTTCAA TATATGtAAT TGGATAGTTT AAATGTGACT CTGATAAATT CATAGACATT 3480

TCCACATATG CT 3492

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1973 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATCTAGCGGT ACAAGCGTCT TGGAGGCTAG TATGTTGAAC ATTGTAAACC CTGAAGATCA 60

CTTCGTTGTC ATTGTTTCAG GTGCCTTTGG TAACCGATTT AAACAAATTG CACAAACTTA 120

TTACAAAAAT GTGCATATTT ATGACGTAAC ATGGGGAGAA GCTGTAGATG TCAAAGATTT 180

CATCAATTTC CTTTCAACTT TAAATGTTGA AGTTAAAGCA GTATTTAGTC AATATTGCGA 240

AACATCTACG ACAGTGCTAC ACCCTATTCA CGAGTTAGGA AATGCCATTA ATCAATTTAA 300

TAGTAATATT TATTTTGTAG TTGACGGCGT AAGTtGCATT GGTGCTGTTG ATGTTGACAT 360

TAACAAAGAT AAAATTGATG TACTTGTTTC TGGTAGTCAA AAAGCAATTA TGTTACCTCC 420

AGGATTAGCT TTTGTAGCTT ATAGCCACCG TGCAAAAGAA CATTTCAAAG AAGTAACTAC 480

GCCAAAATTT TATCTAGACT TAAATAAATA CATTTCGTCA CAAGCTGACA ATTCTACACC 540

GTTCACACCA AATGTGTCTT TATTTAGAGG TGTAAATGCA TACGTTGAAA CCGTAAAAGC 600

AGAAGGTTTC AATCACGTAA TAGCACGACA CTATGCAATT AGAAATGCAT TAAGAAGCGC 660

CTTAAAAGCA TTAGATTTAA CTTTATTAGT CAATGATAAA GATGCATCTC CAACGGTTAC 720

AGCATTCAAA CCTAATACAA ATGATGAAGT GAAAATAATC mAAGATGAAC TTAAAAATnG 780

CTTTAAAATA ACAATTGCnG GTGGTCAAGG CCATCTTAAA GGTCAAATTT TnAGAATTGG 840

TCATATGGGG AAAATTAGTC CTTTCGATAT TTTATCGGTA GTATCTGCTT TAGAAATTAT 900

TTTAACTGAA CACCGTAAAG TTAACTATAT CGGTAAAGGT ATATCAAAAT ATATGGAGGT 960

TATTCATGAA GCAATTTAAT GTACTCGTTG CAGATCCCAT ATCAAAAGAT GGTATCAAAG 1020

CATTATTAGA TCACGAACAA TTCAATGTAG ATATTCAAAC TGGCTTGTCC GAAGAAGCAT 1080

TAATCAAAAT TATACCTTCA TACCATGCTT TAATCGTTCG TAGTCAAACT ACGGTTACTG 1140

AAAATATCAT AAATGCTGCT GATTCTTTAA AAGTAATCGC ACGCGCCGGT GTTGGTGTAG 1200

GTAATACGAT TTCAGCTACT GAACATACAC TGGCAATGTT ATTATCAATG GCACGAAATA 1320

TTCCGCAAGC ACACCAATCA CTTACAAATA AAGAATGGAA TCGAAATGCA TTTAAAGGTA 1380

CTGAGCTTTA TCATAAAACA TTAGGTGTCA TTGGTGCTGG TAGAATTGGT TTAGGTGTTG 1440

CTAAACGTGC GCAAAGTTTC GGAATGAAAA TACTAGCTTT TGACCCTTAC TTAACGGATG 1500

AAAAAGCAAA ATCTTTAAGC ATTACGAAGG CAACAGTTGA TGAGATTGCC CAACATTCTG 1560

ATTTCGTTAC ATTACATACA CCACTAACAC CTAAAACAAA AGGCTTAATT AATGCTGTCT 1620

TTTTTGCCAA AGCAAAACCT AGTTTGCAAA TAATCAATGT GGCACGTGGT GGTATTATTG 1680

ATGAAAAGGC GCTAATAAAA GCATTAGACG AAGGACAAAT TAGTCGGGCA GCTATCGATG 1740

TGTTTGAACA TGAACCTGCA ACTGACTCGC CTCTTGTTGC ACATGATAAA ATTATTGTTA 1800

CACCTCATTT GGGTGCTTCA ACAGTCGAAG CTCAAGAAAA AGTGGCAATT TCTGTTTCAA 1860

ATGAAATCAT CGAAATTTTA ATTGATGGTA CTGTAACGCA TGCAgTGAAT GCACCTAAAA 1920

TGGACTTAAG CAATATAGAT GATACTGTAA AATCATTCAT CAATTTAAGC CAA 1973

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GGTGTTTCAG ATGTCACTGG TTGATTTTTA ATTGTAGACG GGTATTTTGG GCTTTCGCCA 60

TATTTATTTG CCGGCTTACT GTCAAAGCAT AGGAATACTA TCATAACAAT TGTTAGGCCT 120

AAATAAACAA AATAAAGAAG TACTAACAAA ATATTAAGAC CCATCGGCAT TAATGTAAAA 180

TCACTGTCAT AATAACTATC GATAATCTGT AATACTATAT AAAATATAAT ACTGAATACT 240

GTCATAATCA TTGGAAATAA CATTGTTCTT GATATATCGT GAAATCTTCG AACGCACAAC 300

GCTAAATTTG GAATAAACGT TGCCAAACTA TAGACAAAAG TATACACAGA TGTAAGGATA 360

ATCATCAATA TACTCATAAC TATTAATGTT TCGTTATCCG CCGCTATAGA AATAAAGAAT 420

AGAAATAGGT TTATTATTAG CACACACACA GCTGGAACCA TAAGTATCAA ATGCCATAGT 480

GCCATATACC AATATTCACT ACGTCTTGAT CTCCCCTTAA AATTTACATA ATTTTTCCAA 540

AATAAAACGA ATGATTTCAT AAAACCTACT TGAGGTAATT GTTCCATTGT AATCTCCCTT 600

TCGTTAATCA TATTTATATT TTTAATTATT GTTACCGTTA TAATTTACAA GATTCATTAT 660

GTAAAATGAA AACCCGCTAC AAGTACACAT CTATATGGAG ACTCATTTGA AAGTCAACGC 780

TTCGTTAACT ATACTAAAAA TATGTCATAC TGCAATGTTC ACGTTTAAAA GAGTCTCAAT 840

CTATGCAAAT AAAATATTCC ATAACAAAGT ATATACTTTA CATTTTTATA ATTCTTAACA 900

ATACTATTTT ATCAAACATT TACCACAATA AAAATATCTT TTTCATTTTT ATTTAAATTA 960

ATCATATAAT TGCGAGGAGA ATATTATGGA TTTCGTTAAT AATGATACAA GACAAATTGC 1020

TAAAAACTTA TTAGGTGTCA AAGTGATTTA TCAGGATACC ACTCAAACGT ATACAGGCTA 1080

CATCGTGGAA ACGGAAGCTT ACTTAGGTTT GAATGATCGT GCGGCTCATG GCTATGGCGG 1140

TAAAATAACA CCTAAAGTCA CGTCATTATA TAAACGTGGT GGTACAATTT ATGCACATGT 1200

CATGCATACG CATTTACTCA TTAATTTTGT AACAAAATCT GAAGGTATAC CTGAAGGCGT 1260

ACTTATCCGC GCAATTGAAC CAGAAGAAGG TTTATCCGCT ATGTTCCGTA ACAGAGGTAA 1320

GAAAGGCTAC GAGGTAACGA ATGGCCCAGG AAAATGGACT AAGGCATTTA ACATTCCACG 1380

GGCTATCGAT GGCGCTACGT TAAATGACTG TAGATTGTCT ATTGATACTA AGAATCGTAA 1440

ATATCCTAAA GATATTATTG CTAGTCCACG AATCGGTATT CCAAATAAAG GTGATTGGAC 1500

ACATAAATCT TTACGTTACA CAGTGAAAGG TAATCCATTT GTGTCTCGCA TGCGTAAATC 1560

AGATTGTATG TTTCCCGAAG ATACTTGGAA ATAAATGCCA TCTTTCATTG ATTACTATCA 1620

TGAAAATGAA ATCTATCTCC TTATAAGTCA ATCAATCGTG CCGTCAACAT GCGGATGGGT 1680

TGATTGTTTT TCTTTGTATC CATCATATTT TTTGATTCAT CTCCTCTTAT TGAACTTGTT 1740

CTTAATTATA AAATATAACA ATAGAATTAT TTATAATTAT TAAATTTAGA TGCATTAATA 1800

TTATTGATAT TATTTTCAAA AACTAGAAAT ATTGATTTGT TGCATGTATA ATGTTAAAAG 1860

CGCCCTTTTA TAACGCTTAC ATATAAAAGC TTATTTAGGG AGAGGGATAT TCAACAAGGG 1920

GGATTTGAAA ATGATAGAAC TTAATGCAAT TACAACATTA TGTTTAGCTT GTATCCTTTA 1980

TTTACTTGGT AAGGCTATCG TTAATCACGT TAATTTTTTA AAACGTATTT GTATACCAGC 2040

ACCAGTGATT GGCGGCTTAA TCTTTGCTAT TTTAGTTGCG GCTTTGGATT CATTTGGCAT 2100

GGTTAAGATT AAATTAGATG CTTCATTCAT TCAAGATTTC TTCATGTTAG CATTCTTTAC 2160

GACAATCGGT CTTGGTGCAT CATTGAAATT ATTTAAATTA GGTGGCAAAG TCTTGCTATT 2220

ATACTTTATG TTTTGTGCTA TCATTTCAGT CATTCAAAAC ATAGTTGGTG TATCACTAGC 2280

AAAAGTATTA AATATTAAAC CTTTGTTAGG ATTAACAGCA GGTTCCATGT CTATGGAAGG 2340

CGGTCATGGT AATGCTGCTG CTTATGGTAA GACAATTCAA GATTTAGGTA TTGATTCGGC 2400

ACTGACAGCG GCTCTTGCAG CTGCAACTTT AGGTCTTGTA TTTGGAGGGC TTATCGGTGG 2460

ATTTAAAGAT TATAGCCAAG TAGCATATAA CGAACATTTA CATAGTAAAT TTAATGCCAC 2580

TGAAGTATTC TTCATTCAAT TTACAATCGT TGTATTCTGT ATGGCAGTTG GAAGTTATTT 2640

CAGTCATTTG TTTACAGCTC AAACAGGGAT TAATGTTCCA ATTTACGTTG GCTCATTATT 2700

TGTAGCTGTT ATTGTCCGAA ATATCTCTGA AAGTTTTAAT TTTAATATTG TAGATTTAAA 2760

AATTACTAAT CAAATTGGCG ATGTCGCATT AGGTATTTTC TTATCTCTTG CGCTAATGAG 2820

CATTCAATTA ATCGAAATTT ATAAACTTGC TATACCTCTT ATTATTATCG TTTTAGTTCA 2880

AGTTGTCGTT ATGATTTTAT TTGCTGTTTT AATTTTATTT AGAGGTTTAG GAAAAGATTA 2940

TGATGCTGCA GTAATGGTAG GTGGTTTTAT CGGTCATGGG CTTGGTGCAc GCCAAATGCC 3000

ATGGCAAATT TAGATGTTAT TACTAAAAAA TATGGAAACT CACCTAAAGC ATATTTAGTT 3060

GTACCTATTG TTGGTGCATT CTTAATCGAT TTAATTGGTG TTATAGTCAT TATGGGATTC 3120

ATACAATGGT TTAGTTAAAC ACCAAACTCA TAAATAAAAG AGGAGGCCTT CGCCTCcTcT 3180

TTTATTTATC CTCGATGTAT ATTCAAGTTA CGTTGTTCTA TCCATGACAA TATTTCCGGA 3240

CTAAATACGA TTTGTTTTTG TGTTAAGTCG TCAATATTTT TAGCATCTAA CATCGTCATT 3300

ATTGATTTCA TGTGTTCAAT AAATGATTCT ACATAAGCTA CTGTATGTGC AATGCCATTA 3360

TTTTCAACTT GATTTAAAAA CGGACGTGAC ATACCAGTTG CCTTTGCACC AAGTGCTAAA 3420

CTTTTAATTG CATCGAGTGG TGTACGTAAA CCACCACTCG CGAAAACTGA AATTTCGCTT 3480

TGATAAGCCG TTGTTTCAAG TAATGACTCA ACTGTAGACT GTCCCCATGA TGATAAGTAA 3540

TCCATATCTT TATTTGCACG ACGTTCATTT TCAATATCTA CAAAGTTAGT ACCACCTTTG 3600

CCACTAACAT CGACATACTT GACGCCTATT TGTTGTAAGT CATGCATTAA TTCTTTGCTC 3660

ATACCAAATC CAACTTCTTT TATAATGACT GGAACAGACA CTCGTGATAC AATCGACGCT 3720

ATATTATCTA ACCAAGTCAC AAATTCACGA TTCCCTTCAG GCATAACTAA TTCTTGAGGA 3780

GAATTAACAT GGATTTGTAA CGCTTGTGCC TCAAGTAATT CAACTGCTTC CAAAGCCTTT 3840

TCTACTGGTA CGTCCGCACC AACATTGCTA AAAATCATGC CTTCAGGATT CATTTTTCGC 3900

GCAATCGTAA ACGTCTCAGC CATGCGTGGA TTTCTCAATG CCGCATGTGT TGATCCAACT 3960

GCCATCGCTA AGCCAGTTTC TCTTGCAACT ACAGCTAGCT TTTCATTGAT GTTTTTCGTC 4020

CACTCGCTAC CACCCGTCAT TGCATTAATA TAAACCGGAT ATGCCATCGT TAAGTCAGGC 4080

GTCTGTGATG TCAAATCGAT ATCATTTACA TTAATTGATG GGATAGAATG ATGCACAAAA 4140

CGCATCTTAT CAAAATCTGA ATGCATTGCG TCAGATTGGG CCATTGCTAT TTCAACATGT 4200

TCATTTTTTC TCTGTTCTCT TTGAAAATCA CTCATGATTA AACCTACCTT TTCGTCATTT 4260

ATTACAGCTA AGCAAATATA ATATCCATAA TGTAAATGTA ATGCCGGCAT ATTTACAAAG 4380

TTCATACCAT AAATCCCAGC TATGAATGTT AACGGTGAAA ATATAACTGA TACTAATGTC 4440

AGTACTTGCA TAATACTATT CATTCTAAAT GACGTGTATG ACTCAAAATT TTCTCGTATT 4500

TCGTTTGTCA TTTCTTGAGC AGTACGAATG ATATTACGTT GCTTAATCAA GTGGTCATCG 4560

ATATGTTGAA TGTATAGCGA ATGTTTATTA TCTATAATCA AATCACCATT TTGTTTCATT 4620

GTATCAATTA GCTCTTGCAT AGGAAACAGT ACACGTTTTA CTTTAATCAA ATCCGAACGT 4680

AACTTAAAGA CACTATCCAT GACCATTTTA TTAAAGCGAT CATCTACATG GCGGTCTTCA 4740

AAATGATAAA CACTATCTTC AAGTGCATAT ACAAAGTTGA AATATTTATC AACCATCATA 4800

TCTAAAATTA ATATGACGAC ATCTGCACAA TCTAATTCTG CATCTAATGT ATTCATATAC 4860

TTATAGACTA CTTTATTTAA TGATTCCAAC GTTTGATGAT GATATGTTAC TAATACATTG 4920

TCTTGTATAA AAATATTTAG TGCTATTGGT GAATAGTTTG ACCCCATAAT ACTATGGAAT 4980

ACTAAGTATT GATAATCTTT ATAAGATTTA TATTTAGCTC GTGGCATACC GTTAATTGCA 5040

TCATCCACTT CTAAATCATT AAAATTAAAA TGTGCTTTAA ACCATTCATT TTCTTGTTCA 5100

TTCGGTTCAT CAAAATCATA CCAAACAATA GTCGCATCTT TTGGTATCTC TTTGATATCA 5160

TCAACTACTT TAAACGGTTC ATATGTAGTT TGATACCGTA TCTTTAAAGC CATCGATACT 5220

CCCCCTAAAT AACGAATTCT CTATTATTTT ATCATGAATT AAATAACGTG TATGTCTTAA 5280

TTTATTTTAG TATGATAGTC ACTAAGGAGA TGGTTATTAT CAAACAACTT TTTACACATA 5340

CTCAAACCGT AACATCTGAA TTCATTGACC ATAACAATCA TATGCATGAT GCAAATTATA 5400

ATATCATTTT TAGTGACGTC GTGAATCGTT TTAATTACAG CCACGGTCTT TCTTTAAAAG 5460

AACGCGAAAA TTTAGCATAT ACGCTATTTA CACTAGAAGA ACATACGACA TACCTCTCAG 5520

AATTGTCTCT TGGCGATGTA TTTACTGTTA CTTTATATAT TTATGATTAC GATTATAAGC 5580

GGTTGCATTT ATTTTTAACA TTAACTAAAG AAGATGGTAC ACTAGCATCA ACAAATGAAG 5640

TAATGATGAT GGGAATTAAT CAGCACACAC GTCGTTCTGA TGCTTTTCCT GAATCATTTT 5700

CAACACAAAT AGCACACTAT TATAAAAATC AATCAACTAT CACTTGGCCT GAACAATTAG 5760

GACATAAAAT AGCAATTCCA CACAAAGGAG CATTAAAATG ACAGATGCAT TACAACAAAA 5820

GATTCATATC GAATTACTAG ATTTATTAGA TGATGTTAAG TTTGAATTAA CAGAATTAAA 5880

TGCACAAAAA GGGTTATACA TTAACGGACC AGCAAATCAG CTACTTAAGC GTGGCGTGCA 5940

TATGGCTTAT GTTCAAGGAC AAAAGCAAGC CATCGATAAT ATTATGACTA TTGTGGAACA 6000

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TGGCAATTTG TTTAATAGCT TTATGTGATT GTCTAATTGG ATAAATTGGA AAATCATGTA 6420

CCATCTTAGG ATAATCATAA AACTCAATGT ATTGATGATG TTGCAACATC ATTTGTTCAA 6480

ATAGCTTCAT ATCAGGATGT GTCATTTCAC GTCCACCACC AAACATATAA ACTGGTGGCA 6540

ATCCTTCTAT TGTGCCATTA ATTGGCGATA TGCGCTTATC TGTTAATGGT AGGCCATTCG 6600

CCCATTTTTT CATAATCTCA TTGACACCAA ACTGACTTAG aACCGCATCT TGTTCGATTA 6660

AGGCGTCCGA AATATCTTTA TTAGATAGTG TTGCATCTAA AATTGGTGAG ATTAAATACA 6720

ATTTATTCGG TAATGGCTGT TGATTAkCTA AAAGAGATTG TACAAAGGAT AATGCCAGTG 6780

CACCACCTGA ACCATCACCC ATGACTACGA CATTTTGATG TCCTACTTCA GATACTAATT 6840

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TGGATAGATA GGCAGTACAA CCTCATATAA TGtACTTAAA GTGATTTTAT CCCAACAATC 6960

TCCAATGGAA CGGTGATGGT TGTAGTGCAT TGAATCCACC GTGAATATAT AAAATTTTCT 7020

TATCAATTTG ATGTCTGAAA TTAAAGCGAA AGACTTGCAT ATCATCTAAT GACAATTTTT 7080

CTAAATTTGC TTTAACATTT AATGTTGAAG GCTGCTTATG TTTTTTTCTA TTTTCAATTT 7140

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TCAACAACCG AATATTCATC GTGGTAAGCG ATATGGTAAG AAAAAACGTT CATTGGTAAG 7560

CATGATTATT CAAATCATTG TTGTwATATT AACCACCATC GCTGGAATAC AGCATGGTGG 7620

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9834 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GTCATtACCG amTTTCtTAG AaTCATTTAA AGATGATAAA TATACAAACG TTGGTAATTT 60

AAAAGAAGTG AATTTTGATA AAATTGCTGC GACGAAACCC GAAGTAATCT TTATCTCTGG 120

ACGTACAGCT AATCAAAAGA ATTTAGATGA ATTCAAAAAA GCTGCACCTA AAGCGAAAAT 180

TGTTTATGTT GGTGCAGATG AAAAGAACTT AATTGGTTCA ATGAAACAAA ACACTGAAAA 240

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CAAAATTGCT TCAATGAAAG ATAAAACGAA AAACTTCAAT AAAACTGTTA TGTATTTACT 360

AGTTAACGAA GGTGAATTAT CAACATTTGG ACCTAAAGGT CGTTTTGGTG GATTAGTTTA 420

CGATACATTA GGATTCAATG CAGTTGATAA AAAAGTAAGT AATAGCAATC ATGGACAAAA 480

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TCAAGCGATA AGTGGTAAAT CAACTGCGAA ACAAGCATTA AATAATCCTG TATTAAAAAA 600

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AGCTGGATCA ACTACAACTA CAATTAAACA AATTGAGGAA CTTGATAAAG TTGTAAAATA 720

ATTTTAAAAG AGGGGAACAA TGGTTAAAGG TCTTAATCAT TGCTCCCCTC TTTTCTTTAA 780

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TTGGATGTTC ACCAATAATG CGAACTTCAC GATTTAATTC AATGCCAAAT TTTTCTTTGA 1440

CGGTCTTTTG TACATAATGA ATAAGGTTTT CATAATCTGT AGCAGTTCCA TTGTCTACAT 1500

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CAAATTCAAG GCCAGTAAGT GCGTAATCAC GAGCAACACG TGAGACATCA ATAATTGCAG 1980

CGCCGCTACC GGCTATTATC GCATCATCAG ATACTTCGAT ATGATCTAGT GATAATAAAC 2040

TAATTACAAT ACCGCGAATA CCACCTTCAC GGATAATAAT ATTTGAGCCA TTTCCTAAAT 2100

ATGTAACAGG AATCTCATTT TGaTAGGCAT ATTTAACAAC TGCTTGTACT TCTTCATTTT 2160

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CAAATGTTTG GGTATTCATT TGAATGATAT GTAGACGCAC CTGTTGTTTT AGTTCATGAA 2640

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CTAAAATATC TAAAATTGGC TCTGTTGAAT ATTTAAAATG aTGctACCGC CAATATGTTT 2820

TGTATATTTT ACTGGGCTGT CTAAGAGGTT GAATAATAAT GATTCAATTT CAGTGTATTG 2880

TGATTGAAAA CAATTAGTTA AATCACTATT AATGAATGGT TGAACATTTG AATACATGAT 2940

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CAATGAAAGT TAAGAAATTA AAAAAAGAAT ATATGACGCT TGCAAATGAG AAGAAGGATG 3420

CGATATATCA ATTAAAAAAA TTCATAGGTT TATGTAATCA ATCTATCAAG TATAACGAAG 3480

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TTGAAAAAAA GCTTGAAAAA TTAGAAGAAA AATAACTATA ATCATTTTTC AAAGTTAAAA 3960

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AACTATATGT ATAAAAATGT CACGCAGATG CTATTTAAAT GTGATAAATA TTTTTAGAGG 4080

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GCAGTCTTGA ATGGACTGTA TCAAGCTGAA ATATTAACCA GTCATGCATT AGTAGACCAA 5640

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TGAACTAGTA TATAATCGTT GGTTTTTAGT GATTTTCAGC GATATCTTCT ACAATTCCAA 6180

TGATTACTTG TACTGCTTTT TCCaTAACAT CAATGGATGC aTATTCATAT GGGCCGTGGA 6240

AGTTACCGCA ACCTGTAAAG ATGTTTGGAG TTGGTAACCC CATAAATGAC AATTGTGAAC 6300

CATCTGTACC ACCGCGAATA GGTTCAGTGT TTGCTGGAAT ATCTAATTTG GCAAAGACAC 6360

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GATCCGATAT ATCAACTTTA ACTGGATAAT TTTCAAAATG GGCATTGATA TCGTCACGTA 6480

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CATCCATAGT ATAAGCAAAA TCAGCATTGA AGCGGTCAAC ATCAAATTTA TGTGGACCAC 6840

GACCGATTTC TTCGTCTGGT GTAAATCCAA TGCGAATGGT ACCATGTTTA ATTTCTGGAT 6900

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CTAGTAACGA TGTACCATCA GTTACCATTA ATGTATGACC AACTAAACTG TTAAGTTCTG 7020

GAAATACTTT AGGATCTAAG ACACGTTTAG TATTGCCTAG TTTGTATGGC TTACCATCAT 7080

GCGCCAAAAA TCCAACTGTT GGGACGTCGA CATCGATGTT ACTTTCTAAT GTAGCAAATA 7200

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ACCCCTTAAA CTCTATTATT CATGTTGTAA GATTTTTTAT ATGTCTTACC TTTGATTTTA 7440

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AAAGCAATCG CACCTGAAAT CAGTGTAcTT CTAAAAATGT ATTTACAGCA CTTGTATAAT 7560

CATTTGATAC TAAAAAACGA GTCGCTTGAT AAGCTGCACC ACCAGGTACT AATGGTATAA 7620

TGCCTGGCAC TATGAATATA ATTACCGGTC GTTTATATCT GCGACTCATA GTATGACTCA 7680

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TAAAGGAACG AATGTTAAGT GAATTAAATA ATCTTCACGA TAAGGGATAG GGTAGACAGA 9780

TAATAATAAT GATACGATTG TCATTAAAAC AGTGACATAA GCCTTAGAAA AAAC 9834

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

TCTCAATCAG ATGAAAAATT GCATATCGTA GGTTTTACAG AAAGTGCAAA ATATAATGCG 60

TCATCAGTCA TTTTCACGAA TGACGCTACC ATTGCCAAGA TCAATCCTAG ATTGACTGGA 120

GATAAAATTA ATGCAGTTGT TGTACGTGAT ACAAATTGGA AAGACAAAAA ATTAAACCAA 180

GAGCTTGAAG CGGTAAGTAT TAATGACTTT ATTGAAAATT TACCAGGTTA TAAACCACAG 240

AACTTAACAT TAAACTTTAT GATTTCATTC TTATTTGTCA TTTCAGCTAC AGTTATAGGC 300

ATTTTCCTAT ATGTCATGAC ATTACAAAAG ACGAGTTTAT TTGGCATATT AAAAGCTCAA 360

GGATTTACGA ATGGCTATTT GGCGAATGTG GTAATTTCGC AGACGGTCAT ATTAGCACTA 420

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GTTATGTCTA ATGAAGACTA TCAGCAACTT ATGTCACAAT TAGGTCTAAC TTCATTGCTT 1020

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GTATTGAACC TTTATCACAA GCAGATATTG TATCAGCCAA TCCAATTCCA ATCTATATTA 2280

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TTGGTTCAAT TGTATTTAAA AAATATCCAA TTGTTACTAA GCAAGACATG ATTAATCGAG   2520
GTGCAGTAGA CGCATAGCAT CATCATATTG AATAGTAAAA ACAAATAAAA CATAGTAACG   2580
TGATTCAGTC GATGTAACAG TCGATAATGA GTCACGTTTT TTTATAGAAA AATACAAGAC   2640
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TCAAGTACCT TTTACACGAT GGAATGAACT TACTTTTTAC GAAATTATGC GTATTTTATA   2760
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AGACTATGCC TTAATAGATG AAGGTAAGGA TGCACAAAAG GCATTGCAAG ATTCAGTGAC 18240

ACTTGCAAAA TTAGCAGATC GACTTGGCTT TAAGCGAATT TGGTTTACGG AACATCATAA 18300

TGTACCAGCG TTTGCGTGTA GTAGTCCAGA ACTTTTGATG ATGCATACAT TGGCGCAGAC 18360

AAATCACATA CGAGTTGGCT CTGGTGGTGT GATGCTGCCG CACTATCGAC CTTATAAAAT 18420

TGCTGAGCAT TTTAGAATGA TGGCAGCGTT ATATCCAAAT CGTATTGATT TAGGTATTGG 18480

TAGTTACGAT GAATCGATTT CGTTATTACG TGATTATCTT ACAATAAAGG ATAAACCAAG 18600

TGCGCATACG TTAGGTGTCC AACCACACAT TGATCATTTT CCAGAAATGT GGTTATTAAG 18660

TAGTAGCGCA ACATCTGCCA AAATAGCTGC CGAACTAGGT ATAGGGCTTT CTGTTGGAAC 18720

ATTTTTGCTA CCAGATATAA ATGCGATACA TACAGCGAAG GATAACATTG ATATTTACAA 18780

AAAACATTTC CAAGCATCAA CGATTAAAAT GGACGCAAAG GTGATGGCAT CTGTATTTGT 18840

CATTGTAGCT GATAACGAAG CGGAAGTAGC AGCATTACAA CATGCCTTAG ATGTTTGGTT 18900

ATTAGGTAAA TTACAATTTG CAGAATTTGA AGATTTTCCT TCAGTAGACA CAGCACAAAA 18960

GTATAAGCTT AATGATCGAG ACAAAGAGAT GATTCAAGCA CATCAAGCAC GCATCATTGC 19020

AGGTACACAA GAAAAGGTTA AAGCACAATT AGATGATTTC ATTGCTACGT TTGAAGTTGA 19080

TGAGGTGTTA GTAGCACCGC TTATTCCAGG TATTGAACAG CGTTGTAAAA CATTAAAATT 19140

ACTCGCGGAA ATTTATTTGT AGCATTTTAA ATAGAAGAGA AAGGATGAAG ATAAGATGAA 19200

AAAGTTAGCC AATTATTTAT GGGTAGAAAA AGTAGGAGAT TTGTATGTGT TTAGTATGAC 19260

ACCTGAATTG CAAGATGATA TTGGGACAGT AGGTTATGTT GAATTCGTAA GTCCAGATGA 19320

AGTTAAAGTG GATGATGAAA TTGTGAGTAT CGAAGCATCG AAAACGGTCA TTGATGTGCA 19380

AACGCCATTG TCAGGAACGA TTATTGAGCG AAATACAAAA GCGGAAGAAG AACCGACAAT 19440

TTTAAACTCT GAAAAACCAG AAGAAAATTG GTTGTTCAAA TTGGATGATG TCGATAAAGA 19500

AGCATTCCTA GCATTACCGG AGGCTTAAAT GGAAACGTTA AAATCAAATA AAGCGAGACT 19560

TGAATATTTA ATCAATGATA TGCATCGAGA GAGAAATGAC AATGACGTAT TGGTAATGCC 19620

ATCTTCATTT GAAGATTTGT GGGAATTATA TCGAGGCTTA GCAAATGTCA GACCGGCATT 19680

ACCTGTAAGT GATGAATATT TAGCTGTACA AGATGCTATG TTAAGTGATT TGAATCGTCA 19740

ACATGTTACG GATTTGAAGG ATTTGAAGCC GATAAAAGGT GACAATATCT TTGTTTGGCA 19800

AGGTGATATC ACGACGTTAA AAATCGATGC TATTGTTAAT GCTGCAAATA GTCGTTTTCT 19860

AGGATGTATG CAAGCTAATC ATGACTGCAT TGATAATATT ATTCATACAA AAGCGGGTGT 19920

TCAAGTTCGA CTTGATTGTG CAGAGATCAT TCGACAACAA GGGCGCAATG AAGGTGTAGG 19980

TAAAGCCAAA ATAACACGTG GATATAATTT GCCAGCAAAG TATATAATTC ATACGGTTGG 20040

TCCGCAAATA CGTCGATTGC CTGTTTCAAA GATGAATCAG GACTTGTTAG CTAAATGTTA 20100

TCTTAGCTGT CTTAAATTGG CTGATCAACA TAGTTTAAAT CATGTCGCTT TTTGCTGTAT 20160

ATCTACAGGT GTATTTGCTT TTCCTCAAGA TGAAGCAGCA GAAATTGCTG TTCGAACAGT 20220

AGAAAGCTAT CTCAAAGAAA CAAATTCAAC ATTGAAAGTC GTGTTCAATG TATTTACAGA 20280

CAATGTCTCT GTTAATGGAT GACAAGACAA AGCAGGCTGA AGTATTGCGT ACTGCGATTG 20400

ATGAAGCAGA TGCGATAGTG ATTGGAATTG GTGCAGGCAT GTCTGCATCT GACGGATTTA 20460

CATATGTAGG AGAGCGTTTT ACGGAAAATT TCCCAGATTT TATTGAAAAA TATCGCTTCT 20520

TTGATATGTT GCAAGCGAGT TTACATCCTT ATGGCAGTTG GCAAGAGTAT TGGGCATTTG 20580

AGAGTCGTTT TATTACATTA AACTATTTAG ATCAACCTGT AGGTCAGTCT TACCTCGCTT 20640

TAAAATCCTT GGTGGAAGGT AAACAGTACC ACATTATAAC TACGAATGCA GATAATGCTT 20700

TCGATGTAGC TGATTATGAT ATGACTCATG TATTTCATAT ACAAGGGGAG TATATACTGC 20760

AACAGTGTAG cTCAGCATTG TCATGCTCAA ACGTATCGCA ATGATGATTT AATTCGTAAA 20820

ATGGTTGTTG CGCAACAAGA TATGCTTATA CCTTGGGAGA TGATTCCAAG ATGTCCAAAA 20880

TGTGATGCCC CAATGGAAGT GAATAAACGT AAAGCGGAAG TTGGGATGGT TGAAGATGCT 20940

GAATTTCATG CGCAACTACA TCGTTATAAT GCTTTTCTAG AGCAACATCA AGATGATAAA 21000

GTGTTGTATT TGGAAATTGG AATTGGTTAT ACTACACCAC AATTTGTGAA GCATCCTTTT 21060

CAGCGTATGA CACGTAAAAA TGAAAATGCC CTTTATATGA CGATGAATAA AAAGGCATAT 21120

CGCATTCCGA ATTCAATTCA AGAACGTACC ATACATTTAA CTGAGGATAT CTCAACATTG 21180

ATTACAGCAG CACTCCGGAA CGACAGCACA ACGAAAAATA ACAACATTGG AGAGACAGAA 21240

GATGTACTTA ATAGAACCGA TTAGAAATGG AGAATATATT ACTGATGGTG CGATTGCACT 21300

CGCTATGCAA GTTTATGTTA ACCAGCATAT CTTTTTAGAT GAAGATATTT TATTCCCTTA 21360

TTATTGTGAT CCAAAAGTGG AAATTGGACG TTTTCAAAAT ACTGCTATAG AAGTGAATCA 21420

AGATTATATA GATAAACACA GTATTCAAGT AGTTCGCCGA GATACTGGTG GTGGCGCTGT 21480

GTATGTTGAT AAAGGTGCCG TTAATATGTG TTGTATTTTA GAACAAGACA CTTCAATTTA 21540

TGGTGATTTT CAACGATTTT ATCAACCAGC TATAAAGGCG TTGCATACAT TAGGTGCAAC 21600

AGATGTGGTA CAAAGCGGTA GAAATGATTT AACATTGAAT GGTAAAAAAG TGTCAGGCGC 21660

CGCAATGACA TTAATGAATA ATCGTATTTA TGGCGGTTAT TCGCTATTAC TTGATGTTAA 21720

TTATGAAGCA ATGGATAAAG TGTTAAAGCC TAATCGCAAA AAGATTGCAT CGAAAGGGAT 21780

TAAATCTGTG CGCGCACGTG TTGGTCATCT TAGAGAAGCA CTGGATGAAA AGTATCGTGA 21840

TATAACCATT GAAGAATTTA AAAATTTAAT GGTGACGCAG ATTTTGGGAA TCGATGACAT 21900

TAAAGAGGCG AAACGATATG AATTAACGGA TGCAGATTGG GAAGCGATTG ATGAATTAGC 21960

TGATAAAAAG TATAAAAATT GGGATTGGAA TTATGGCAAG TCACCCAAAT ATGAATACAA 22020

TCGAAGTGAA AGATTATCTT CAGGTACGGT AGACATAACA ATTTCTGTTG AACAAAATCG 22080

AGAAGCATTA CAAGGAACAA AAATGACAAG AGAAGATTTA ACGCATCAGT TAAAGCAATT 22200

AGACATCGTT TATTATTTTG GCAATGTTAC GGTAGAAGCA TTAGTGGATA TGATTTTAAG 22260

TTAATATTGT TATTTTATGT ATGCTGAATC ATTGGAAGTG TTTGCTTGCT CTTGAAAAGG 22320

TGACAATAGT GTTTGGTGAA GGTTGAACAT ATGAGTGGAA ATTATTGCCT TTAACTATTC 22380

AAAGTATGAT ATATATATGG TTTTTGTTTC TAAATGATTG GGTATTTGAA AATAGATGAG 22440

TTTAATATTT TAAGGAATAT AATGATGTTT ACTTTTATAA TTCATATAGA ATATTAAGCA 22500

ATATAAGTCT GTTGATATAT ACAAAATATA ATGACTGCTA TAATGAGTAA TCAATAGACA 22560

CAAAGAGGAG ATTATGTGAT GAATAATAAA GTATTAGTAA CCGGTGGTAC AGGGTTTGTT 22620

GGCATGCGAA TTATTTCACG ATTATTAGAA CAAGGTTATG ACGTACAAAC GACGATACGT 22680

GATTTAAGTA AAGCTGATAA AGTAATTAAA ACAATGCAAG ACAATGGCAT TTCCACAGAG 22740

CGATTAATGT TTGTCGAAGC GGATTTATCA CAAGATGAAC ATTGGGATGA AGCAATGAAA 22800

GATTGCAAGT ATGTCTTGAG TGTAGCATCT CCGGTGTTTT TCGGTAAAAC AGACGATGCA 22860

GAAGTGATGG CGAaCTGcAA TTGAAGGTAT ACAACGTATT TTAAGAGCTG CAGAACATGC 22920

GGGTGTTAAA CGTGTGGTAA TGACTGCAAA CTTTGGTGCA GTTGGTTTTA GTAATAAAGA 22980

TAAAAATTCA ATCACAAATG AAAGTCATTG GACAAATGAA GATGAACCAG GCTTATCAGT 23040

ATATGAAAAA TCAAAATTGT TAGCTGAAAA GGCAGCGTGG GATTTTGTTG AGAATGAAAA 23100

TACAACAGTA GAATTTGCCA CAATCAATCC AGTTGCAATT TTTGGGCCAT CATTAGATGC 23160

ACACGTTTCA GGAAGCTTTC ATTTATTAGA AAATTTATTG AATGGTTCAA TGAAACGTGT 23220

ACCGCAAATT CCGTTAAATG TTGTTGATGT GAGAGACGTA GCTGAACTGC ACATTTTGGC 23280

AATGACAAAT GAACAAGCTA ATGGCAAGCG ATTTATTGCG ACGGCTGATG GACmAATTwA 23340

tTTGTTGGGA ATTGcCAAAt TAATTAAAGA AAAGGGCCTG GAAATAGCTC CAAAAGTTCC 23400

TACTAAAAAA TTACCCAGCT TTATTTTGAG CnAnGnGCC 23439

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CCCTTTGAGA GTATATCATC TAGTCAAATT ATGCCTGTCA TTAGAGCGAC TAGCTTTGAT 60

TATTATGCAG TCGATTTAGG GAAATCATAT CGTCTAATTG ACGAAAGCAT GTTAGAGGAT 180

TTGAAGTTAA CTGAACAACA AATAAGAGAA ATGTCTCTGT TTAATGTTAG AAAATTGTCA 240

AATTCATATA CGACTGATGA AGTAAAAGGT AATATTTTTT ATTTTATTAA CTCAAATGAC 300

GGGTATGATG CAAGTAGGAT ACTAAATACT GCATTTTTAA ATGAAATTGA GGCACAATGT 360

CAAGGCGAAA TGCTCGTAGC AGTGCCACAC CAAGATGTGT TAATTATTGC AGATATACGC 420

AATAAAACAG GATATGATGT GATGGCACAT TTAACAATGG AATTTTTCAC TAAAGGTCTA 480

GTTCCAATTA CATCATTATC CTTTGGATAT AAACAGGGTC ATCTTGAACC GATATTTATT 540

TTAGGTAAAA ATAATAAACA AAAAAGAGAT CCAAACGTGA TTCAGCGTTT AGAAGCAAAT 600

CGTCGTAAAT TTAATAAAGA TAAATAGAAA TAATTGGATA AGGAGTTTTG TCATAATGAA 660

TTTATTTTAC AATCCTAAAT ATGTAGGAGA TGTCGCATTT TTACAAATTG AACCAGTTGA 720

AGGTGAATTA AACTACAATA AAAAAGGTAA TGTTGTTGAA ATTACtAATG AAGGTAATGT 780

TGTAGGTTAT AATATTTTTG AAATTTCAAA AGATATAACA ATTGAAGAAA AAGGTCATAT 840

TAAATTAACT GATGAACTTG TAAATGTATT CCAAAAGCGT ATTTCAGAAG CTGGTTTTGA 900

TTATAAATTA AATGCTGATC TATCACCGAA ATTTGTAGTT GGCTACGTTG AAACTAAAGA 960

CAAACATCCT GATGCAGATA AATTAAGTGT ACTAAATGTA AACGTTGGAA ATGACACATT 1020

ACAAATTGTA TGTGGCGCGC CTAACGTTGA AGCTGGACAG AAAGTTGTTG TTGCTAAAGT 1080

AGGTGCAGTG ATGCCTAGCG GTATGGTAAT TAAAGATGCT GAATTACGTG GTGTTGCCTC 1140

AAGCGGTATG ATTTGTTCAA TGAAAGAATT GAATTTACCT AATGCACCTG AAGAAAAAGG 1200

TATTATGGTA TTAAATGACA GCTATGAAAT TGGACAAGCA TTtTTTGAAT AATTAAGGAA 1260

GGTAGTGAAA ATATGAGCTG GTTTGATAAA TTATTCGGCG AAGATAATGA TTCAAATGAT 1320

GACTTGATTC ATAGAAAGAA AAAAAGACGT CAAGAATCAC AAAATATAGA TrACGATCAT 1380

GACTCATTAC TGCCTCAAAA TAATGATATT TATAGTCGTC CGAGGGGAAA ATTCCGTTTT 1440

CCTATGAGCG TAGCTTATGA AAATGAAAAT GTTGAACAAT CTGCAGATAC TATTTCAGAT 1500

GAAAAAGAAC AATACCATCG AGACTATCGC AAACAAAGCC ACGATTCTCG TTCACAAAAA 1560

CGACATCGCC GTAGAAGAAA TCAAACAACT GAAGAACAAA ATTATAGTGA ACAACGTGGG 1620

AATTCTAAAA TATCACAGCA AAGTATAAAA TATAAAGATC ATTCACATTA CCATACGAAT 1680

AAGCCAGGTA CATATGTTTC TGCAATTAAT GGTATTGAGA AGGAAACGCA CAAGCCAAAA 1740

ACACATAATA TGTATTCTAA TAATACAAAT CATCGTGCTA AAGATTCAAC TCCAGATTAT 1800

CACAAAGAAA GTTTCAAGAC TTCAGAGGTA CCGTCAGCTA TTTTTGGCAC AATGAAACCT 1860

AAACAAAAAT ATGATAAATA TGTAGCTAAG ACGCAAACGT CTCAAAATAA ACAATTAGAA 1980

CAAGAAAAAC AAAATGATAG TGTTGTCAAA CAAGGAACTG CATCTAAATC ATCTGATGAA 2040

AATGTATCAT CAACAACAAA ATCAATGCCT AATTATTCAA AAGTTGATAA TACTATCAAA 2100

ATTGAAAATA TTTATGCTTC ACAAATTGTT GAAGAAATTA GACGTGAACG AGAACGTAAA 2160

GTGCTTCAAA AGCGTCGATT TAAAAAAGCG TTGCAACAAA AGCGTGAAGA ACATAAAAAC 2220

GAAGAGCAAG ATGCAATACA ACGTGCAATT GATGAAATGT ATGCTAAACA AGcGGAACgC 2280

TATGTTGGTG ATAGTTCATT AAATGATGAT AGTGACTTAA CAGATAATAG TACAGATGCT 2340

AGTCAGCTTC ATACAAATGG CATAGAGAAT GAAACTGTAT CAAATGATGA AAATAAACAA 2400

GCGTCAATAC AAAATGAAGA CACTAATGAC ACTCATGTAG ATGAAAGTCC ATACAATTAT 2460

GAGGAAGTTA GTTTGAaTCA AGTATCGACA ACAAAACAAT TGTCAGATGA TGAAGTTACG 2520

GTTTCGAATG TAACGTCTCA ACATCAATCA GCACTACAAC ATAACGTTGA AGTAAATGAT 2580

AAAGATGAAC TAAAAAATCA ATCCAGATTA ATTGCTGATT CAGAAGAAGA TGGAGCAACG 2640

aATAAAGAAG AATATTCAGk AAGTCAAATC GATGATGCAG AATTTTATGA ATTAAATGAT 2700

ACAGAAGTAG ATGAGGATAC TACTTCAAAT ATCGAAGATA ATACCAATAG AAACGCGTCT 2760

GAAATGCATG TAGACGCTCC TAAAACGCAA GAGTACGCAG TAACTGAATC TCAAGTAAAT 2820

AATATCGATA AAACGGTTGA TAATGAAATT GAATTAGCAC CGCGTCATAA AAAAGATGAC 2880

CAAACAAACT TAAGTGTCAA CTCATTGAAA ACGAATGATG TGAATGATAA TCATGTTGTG 2940

GAAGATTCAA GCATGAATGA AATAGAAAAG AATAACGCAG AAATTACAGA AAATGTGCAA 3000

AACGAAGCAG CTGAAAGTGA ACAAAATGTC GAAGAGAAAA CTATTGAAAA CGTAAATCCA 3060

AAGAAACAGA CTGAAAAGGT TTCAACTTTA AGTAAAAGAC CATTTAATGT TGTCATGACG 3120

CCATCTGATA AAAAGCGTAT GATGGATCGT AAAAAGCATT CAAAAGTCAA TGTGCCTGAA 3180

TTAAAGCCTG TACAAAGTAA GCAAGCTGTG AGTGAAAGAA TGCCTGCGAG TCAAGCCACA 3240

CCATCATCAA GATCTGATTC ACAAGAGTCA AATACAAATG CATATAAAAC AAATAATATG 3300

ACATCAAACA ATGTTGaGAA CAATCAACTT ATTGGTCATG CAGAAACAGA AAATGATTAT 3360

CAAAATGCAC AACAATATTC AGAGCAGAAA CCTTCTGTTG aTTCAACTCA AACGGAAATA 3420

TTTGAAGAAA GTCAAGATGA TAATCAATTG GAAAATGAGC AAGTTGATCA ATCAACTTCG 3480

TCTTCAGTTT CAGAAGTAAG CGACATAACT GAAGAAAGCG AAGAAACAAC ACATCCAAAC 3540

AATACTAGTG GACAACAAGA TAATGATGAT CAACAAAAAG ATTTACAGTC ATCATTTTCA 3600

AATAAAAATG AAGATACAGC TAATGAAAAT AGACCTCGGA CGAACCAACA AGATGTTGCA 3660

CCAAGTGTTT CATTACTAGA AGAACCACAA GTTATTGAGT CGGACGAGGA CTGGATTACA 3780

GATAAAAAGA AAGAACTGAA TGACGCATTA TTTTACTTTA ATGTACCTGC AGAAGTACAA 3840

GATGTAACTG AAGGTCCAAG TGTTACAAGA TTTGAATTAT CAGTTGAAAA AGGTGTTAAA 3900

GTTTCAAGAA TTACGGCATT ACAAGATGAC ATTAAAATGG CATTGGCAGC GAAAGATATT 3960

CGTATAGAAG CGCCTATTCC AGGAACTAGT CGTGTTGGTA TTGAAGTTCC GAACCAAAAT 4020

CCAACGACAG TCAACTTACG TTCTATTATT GAATCTCCaA GTTTTAAAAA TGCTGAATCT 4080

AAATTAACAG TTGCGATGGG GTATAGAATT AATAATGAAC CATTACTTAT GGATATTGCT 4140

AAAACGCCAC ACGCACTAAT TGCAGGTGCA ACTGGATCAG GGAAATCAGT TTGTATCAAT 4200

AGTATTTTGA TGTCTTTACT ATATAAAAAT CATCCTGAGG AATTAAGATT ATTACTTATC 4260

GATCCAAAAA TGGTTGAATT AGCTCCTTAT AATGGTTTGC CACATTTAGT TGCACCGGTA 4320

ATTACAGATG TCAAAGCAGC TACACAGAGT TTAAAATGGG CCGTAGAAGA AATGGAACGA 4380

CGTTATAAGT TATTTGCACA TTACCCATGT ACGTAnTATA ACAGCATTTA ACnAAAAAGC 4440

CCCATATGAT GAAAGAATGn CAAAAATTGT CATTGTAaTT GATGAGTTGG CTGATTTAAT 4500

GATGATGGTC CGCAAGAAGT TG 4522

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 751 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TCAAGTTTAC GGATACGTAT ATATTTTGCA TGACATTTAG TGCAATAATA TTCATAATTT 60

GCCCGTTGTT GATAGCTTTC AATGCTGTTA CAAAATCTAG GCGCTCCAAC CTGTTGGCTC 120

AATCGTTTAA AATCTTGATC TTTATGTTGA TAACCTTTAC CAGCAATATG CAAGTGATAA 180

TGACACAATT CGTGCAGTAT AATTTTTACA ACAGCATCTT CTCCATAATG CTCATATTGT 240

TTTGGATTAA TTTCAATATC ATGGGACTTT AAAAGATAAC GTCCGCCTGT TGTACGTAAC 300

CTTTTATTAA AATATGCACA ATGTCGAAAC GTACGTCCAA ATTTTTCTTC CGAAAGATTC 360

TCAACCATTC GCTGAAGTTT GTCATTATTC ATGTGGATCA ATCATCGTTA ATGATACTTT 420

GTCTTTATTT TTGTCAATAC TGTAAATCCA AACGTCAACG ATATCACCAA CACTGACAAT 480

ATCCATTGGA TTTTTTACGA ACTTCTTAGA AAGTTTCGAA ACATGGACAA GTCCATCTTG 540

TTTCATTCCT TCTTGTAAAT CTTCAATTGA TAGCACATCG GATTTAAGGA TTGGTGTTTC 660

AAACTCGTCC CTTGGATCTC GATTAGGTGC GTTCAAGGAT TTAATAATAT CCTCTAATGT 720

AGGTACACCG ACTTGTAATT CAATCGCCAG T 751

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1076 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TCTCCAGCTT TAACTTGATC TGGCACTTTA ACAATTGTCT GATCCATACA TACGCGACCA 60

ATAACTTCGC ATTGATGACC ATTTACATTT ACAAAGCTAC CTTGCATTAT GCGTAAATGG 120

CCATCTGCAT ATCCAATAgG TAACAATGCT ATTGTAGTTG GGTCAGTAGC TGTATAAGTT 180

GCACCATAAC TTACAGACTC ACCCGCTTGT AGCGTCTTTG TTTGAACTAC ATTAGCAATT 240

AATTGCACAC TTGGTTTAAG GTGTACTTTA ACTTTTTGCT GTACATACTC TGATGGATAA 300

TATCCATAAA GGGAAATTCC TGGTCTTATT GCATTACAGA ATTGGCAATC CATTAATAGA 360

GAGCCTGCTG AGTTCTGACA ATGTATATAT TCAGGTTTAA TTGCTTCATT GACCATATCT 420

TTAAAACGTT GATATTGTTC AGTTGTCATA TCTCCTGGTT CGTCAGCACA GGCAAAGTGT 480

GTAAACACGC CTTCAAATAC AAGTTGCTCA TATTGTTGAA TGATTTCAAT CACTTCTTGA 540

TACGTTTTAG TATCTTTAAT ACCTAAACGT CCCATTCCTG TATCTAATTT AATGTGCAAC 600

CATAACTTTT TCTCTTGCTC ACCAGAAATG TTTTTAATTG CTTCTTTCAA CCACTGTTTA 660

GACGGAACCG TTAAGGCAAC TCGGTGTTGT ATCGCTTTAT CAATATCTTT AGCTGGTAAC 720

ACACCTAAGA CTAAAATTTT AGCAGTAATC CCATGCATTC TAAGTTCTAT CGCTTCATCT 780

AACGTTGCTA CAGCAAAAAA TGTGGCGCCA TTTTCCATTA AATGACGTGC TACTTTAACA 840

CTACCTAGTC CATAGGCATT GGCTTTAACG ACAGCCATCA CTGTTTTATT TGGATGCAAT 900

GTACTGAATA CTTTGAAATT TGATGCAACA GCGTTTAAAT CTACATTCAT ATACGCAGAT 960

CTATAATATT TATCCGACAT ATTACTTCCT CCTGTAATTC CCACACGTTT TAAAACTAGA 1020

TCTTAATTAT CATTGTATAA CAAATTTAAA ATGCTGACTT TTCTAAAACA ACTTGG 1076

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2930 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

TGACCACAAT GCCCAATACA ACCATCCCAT GGTAAAGCCA AGAGATGAGT CAATAAAGCG 60

TGTTGAATAA GAGCTGAATG AACCTGATAC TGGATAAAAT GTTGCCAACT CTCCAATTGA 120

TGACATTAAG AAATATAGCA TGACACCAAT AACAAGATAA GCGAGTATAG CGCCTCCAGG 180

ACCAGCTTGA GAAATGATAT TACCAGTAGC TACAAATAGA CCAGTCCCAA TTGCACCACC 240

TATAGCAATC ATGGAAATGT GTCTTGAGTT AAGACTACGG TTCATTTTAT TATCTTCCAT 300

ATTTAGTCTC CCATCTATTT AAATATACCC ATTATTGTAA GCTTTTTAAG TGTACTATTC 360

AATAACTATT TAGTACTGTA AAGCGAAAAA ATTAAAATTT TCTGATTTTT TAATCATCTT 420

GAGCATGTTT AATTGTAATT TTGATGGGGT TAAATTATAA TATGTATTAA ATTATAATTA 480

TnATAAATTG TGGAGGGaTG ACTATGTCAC AACAAGACAA AAAGTTAACT GGTGTTTTTG 540

GGCATCCAGT ATCAGACCGA GAAAATAGTA TGACAGCAGG GCCTAGGGGA CCTCTTTTAA 600

TGCAAGATAT TTACTTTTTA GAGCAAATGT CTCAATTTGA TAGAGAAGTA ATACCAGAAC 660

GTCGAATGCA TGCCAAAGGT TCTGGTGCAT TTGGGACATT TACTGTAACT AAAGATATAA 720

CAAAATATAC GAATGCTAAA AtATTCTCTG AAATAGGTAA GCAAACCGAA ATGTTTGCCC 780

GTTTCTCTAC TGTAGCAGGA GAACGTGGTG CTGCTGATGC GGAcGTGACA TTCGAGGATT 840

TGCGTTAAAG TTCTACACTG AAGAAGGGAA CTGGGaTTTA GTAGGGAATA ACACACCaGT 900

ATTCTTCTTT AGAGATCCAA AGTTATTTGT TAGTTTAAAT CGTGCGGTGA AACGAGATCC 960

TAGAACAAAT ATGAGAGATG CACAAAATAA CTGGGATTTC TGGaCGGGTt TCCAGAAGCA 1020

TTGCACCAAG TAACGATCTT AATGTCAGAT AGAGGGATTC CTAAAGATTT ACGTCATATG 1080

CATGGGTTCG GTTCTCACAC ATACTCTATG TATAATGATT CTGGTGAACG TGTTTGGGTT 1140

AAATTCCATT TTAGAACGCA ACAAGGTATT GAAAACTTAA CTGATGAAGA AGCTGCTGAA 1200

ATTATAGCTA CAGATCGTGA TTCATCTCAA CGCGATTTAT TCGAAGCCAT TGAAAAAGGT 1260

GATTATCCAA AATGGACAAT GTATATTCAA GTAATGACTG AGGAACAAGC TAAAAACCAT 1320

AAAGATAATC CATTTGATTT AACAAAAGTA TGGTATCACG ATGAGTATCC TCTAATTGAA 1380

GTTGGAGAGT TTGAATTAAA TAGAAATCCA GATAATTACT TTATGGATGT TGAACAAGCT 1440

GCGTTTGCAC CAACTAATAT TATTCCAGGA TTAGATTTTT CTCCAGACAA AATGCTGCAA 1500

GGGCGTTTAT TCTCATATGG CGATGCGCAA AGATATCGAT TAGGAGTTAA TCATTGGCAG 1560

GGTCAAATGC GCGTAGTTGA CAATAACCAA GGTGGAGGAA CACATTATTA TCCAAATAAC 1680

CATGGTAAAT TTGATTCTCA ACCTGAATAT AAAAAGCCAC CATTCCCAAC TGATGGATAC 1740

GGCTATGAAT ATAATCAACG TCAAGATGAT GATAATTATT TTGAACAACC AGGTAAATTG 1800

TTTAGATTAC AATCAGAGGA CGCTAAAGAA AGAATTTTTA CAAATACAGC AAATGCAATG 1860

GAAGGCGTAA CGGATGATGT TAAACGACGT CATATTCGTC ATTGTTACAA AGCTGACCCA 1920

GAATATGGTA AAGGTGTTGC AAAAGCATTA GGTATTGATA TAAATTCTAT TGATCTTGAA 1980

ACTGAAAATG ATGAAACATA CGAAAACTTT GAAAAATAAA TTTGATATGT AGTTTCTATA 2040

TTGCGTAGTT GAGCAGTTTA TGATATCATA ATAAATCGTA AAGATTCCTA ACAAGAGAGG 2100

GTGTTTAACG TGCGCGTAAA CGTAACATTA GCATGCACAG AATGTGGCGA TCGTAACTAT 2160

ATCACTACTA AAAATAAACG TAATAATCCT GAGCGTATTG AAATGAAAAA ATATTGCCCA 2220

AGATTAAACA AATATACGTT ACATCGTGAA ACTAAGTAAT TCTTATCATT CAAATACGAC 2280

GATTTGAAAA TAAAGCGGGC TTACCTATTA TATTGGGGAG CTCGCTTTTT TATGAAATTT 2340

TTGTGAAGAG TGATTAATGG ATTGAGTTTC ATCGGTAGAA CAATATATGA TTATATTAGT 2400

TGTTACTTTA TTAAAaTTTG AGAATATTTA TAGAAGGAAA TAGATTACTG ATTTTATAAA 2460

GTCACTTTGT TAGCGAATGC TTGAAAGAGT ATTTAATATA GTAGAATTTA AAATTTCAAA 2520

GCGGAATTTA ATAAGTACGA AGTAGTTCTG GGTATGTTTT ATAAATGTTC GATAATACAC 2580

TTTAATCTTA AATATGATGG TTTAGAAAAT GATTTAACAA AGAAATGAaA CTTTACTGTT 2640

GAATTATGTG AGGATTGTGT TATTATATAA ATCGTAATAA TTACGATTTG ATAAAAAGTG 2700

AGGTAACTAT ATATGGCTAA GAAATCTAAA ATAGCAAAAG AGAGAAAAAG AGAAGAGTTA 2760

GTAAATAAAT ATTACGAATT ACGTAAAGAG TTAAAAGCAA AAGGTGATTA CGAAGCGTTA 2820

AGAAAATTAC CAAGAGATTC ATCACCTACA CGTTTAACTA GAAGATGTAA AGTAACTGGA 2880

AGACCTAGAG GTGTATTACG TAAATTTGAA ATGTCTCGTA TTGCGTTTAG 2930

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3606 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTTCTTGCCA TGGCTCTCTT TATTTAAAAA TGCTTCCAAC TTGTCCATTT GATTGTTTCT 60

TTATAAAAAA CTAATTTTAC AAATGCTTTT GCGTTCTTAC AAAAAATGCA TTTGACTATT 180

ATTATAATAA GCGTATAATT GTCGCATATT ATTTTTTGTA TTTTTGGCAA TAACGAAGGA 240

GTATTTATGA ATAAAGACAA GCAATTGCAC AACGACAAAA TCAATCTATC CCAATTAGTC 300

TTATTAGGGT TAGGCTCTTT AATAGGATCT GGTTGGCTAT TTGGTGCGTG GGAAGCATCA 360

TCAATAGCTG GACCAGCAGC AATCATATCA TGGGTTCTTG GATTCCTAGT CATTGGAACC 420

ATTGCCTATA ACTACATTGA AATCGGCACA ATGTTTCCTC AATCAGGTGG CATGAGTAAC 480

TATGCCCAGT ATACACATGG CTCATTATTA GGCTTTATTG CTGCTTGGGC GAATTGGGTG 540

TCTTTGGTGA CAATAATACC TATCGAAGCT GTGTCAGCTG TTCAATATAT GAGTTCTTGG 600

CCGTGGCATT GGGCGAAACC AATGAGATAT TTAATGGAAA ATGGCTCTAT TAGCACATAC 660

GGATTGCTAG CTGTATATCT CATCATTGTT ATTTTTTCAT TATTAAACTA TTGGTCCGTA 720

AAACTTTTAA CATCATTTAC GAGTTTAATT TCTGTATTTA AATTAGGCGT ACCCATGTTA 780

ACCATCATCA TGTTGATGCT ATCAGGATTC GACACTTCAA ATTACGGCCA TTCGGCAAGC 840

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GCAATTTTAC TATACATTGA AGCTTTTGTA TCACCATTCG GTACTGGCGT GTCATTTGTC 1200

GCCGTTACAG GTCGAGTTTT ACGAGCAATG GAGAAAAATG GACATATCCC TAAATTTCTT 1260

GGGAAGATGA ATGAAAAATA TCATATCCCA CGTGTAGCAA TCATCTTTAA TGCCATCATT 1320

AGTATGATTA TGGTTACATT ATTTAGAGAT TGGGGTACGC TAGCAGCAGT TATTTCTACT 1380

GCAACTTTAG TAGCCTATTT AACTGGCCCA ACGACAGTGA TTGCATTAAG AAAAATGGGA 1440

CCAACAATGA CTCGTCCATT TAGAGCAAAA ATTTTAAAAG TAATGGCACC ATTATCATTT 1500

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CTGTCATTTA TAGGAAGCAA AGAATTTAAA GGCTTAAATA TGATTCACTA TCCATTTGAC 1740

TTTATCGTTA TTATTATTGT GGCACTTATC TTCTATTACA TCGGTACAAC GAGTTCATTT 1800

GAAAGCGTCT ATTTCCGTCG CGCAACACGA ATCAATACGA AGATGCGTGA GTCACTAAAT 1860

CACACACATT AACCAACCAT TGATTTCAAC ATCTTGGTTG GTTTTTTATT TTGAAAATCG 1980

GTTATAAATA ACTAACATAA CAAGATGATG ATCAGGCTGG GACATAAATC AATGTTCTAT 2040

GCTCTACGAA gTTATATTGG CAGTAGTTGA CTGAACGAAA ATGCGCTTGT AACAAGCTTT 2100

TTTCGATTCT AGTCAGGGGC CCCAACACAG AGAATTTCGA AAAGAAATTC TACAGGCAAT 2160

GCAAGTTGGG GTGGGACGAC GATAAAGAAA TACTTTTTCT ATAGAAATTA GTATytCTTA 2220

TGCATGAGTT TTACTCATGT ATTCATATTT TTAAGTACAC ATTAGCTGTG GCTAATGTAT 2280

AAGAACCACT ACATAATAAA TCATTTGTGG CTCTTTATCA TTTCTGTCCC ACTCCCGTAG 2340

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AGTTCATGAC AATCGCTTTA AACATTCTAC GTTAAAAACA CAATGGTCAG AGCCAATTGA 2640

TGCAACTGAA ATACAACCCA TCCCACCGCA ACCAGACAAC AAATTAGAAG ATTTTTTCTC 2700

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TCAATTTATT GAATCCTTCG GTGGCGACGC TAATAACATT ACTTTAATGG GTCAGTCTGC 3060

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AGTCGTTCTA CTAAGTGGCG CACTACGATT AGACACCCTT GAGAGTGCAC GCAATAAAGC 3180

ACAACATTTC CAAAAAATGA TGCTCGATTA TTTAGATACA GATGATGTTA CATCATTATC 3240

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GCTTGATTTA ATATATGCGC CTATTAAAAC AGATTATATA CAAAATAATT ATCCAACAAC 3360

GAAACCAATT TTTGCATGTT ATACAAAAGA TGAAGGCGAT ATTTATATTA CTAGTGAACA 3420

GAAAAAATTA TCGCCGCAAC GCTTTATCGA CATTATGGAA TTAAATGATA TTCCTTTAAA 3480

ATACGAAGAT GTTCAGACGG CGAAGcAACA ATCTTTAGCG ATTACACATT GTTATTTCaA 3540

ACAGCCGATG aAGCAATTTT TACmACmACT CAATATACmA GATTCCAACC GCACCAACTA 3600

TGGCTT 3606

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAAATTAAAA AAGCAATTGG nACAAGATGC AACAGTGTCA TTGTTTGATG AATTTGATAA 60

AAAATTATAC ACTTACGGCG ATAACTGGGG TCGTGGTGGA GAAGTATTAT ATCAAGCATT 120

TGGTTTGAAA ATGCAACsAG AACAACAAAA GTTAACTGCA AAAGCAGGTT GGGCTGAAGT 180

GAAACAAGAA GAAATTGAAA AATATGCTGG TGATTACATT GTGAGTACAA GTGAAGGTAA 240

ACCTACACCA GGATACGAAT CAACAAACAT GTGGaAGAAT TTGAAAGCTA CTAAAGAAGG 300

ACATATTGTT AAAGTTGATG CTGGTACATA CTGGTACAAC GATCCTTATA CATTAGATTT 360

CATGCGTAAA GATTTAAAAG AmAAATTAAT TAAAGCTGCA AAATAATTCA GCTATATAAG 420

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TATAGCTAGA AAGTTAGATA TTTGTATTTT TTTAAATAAT AAGTGCCGTT GTTATCGTTC 540

AATTTAATTA ATGATAGATT AGTATTATTA TAGCTAAAGT AGTATACCTG AGAAAATAGC 600

TCAATGTATC TCTTTATTAA TAAGTTATAT CATAATTATT TTAGTGCATA CTTTATGGAA 660

GGGATATCAG GGAATGGCTT TCAATTAAAG AAGAGGTTTA AAAGGATTAC AACAGAATGT 720

TATGATTTTG TAGAAAGATA TATAACAACG TTTTATAAAA ACATAATATT GTTAATGGAA 780

AATGAAATGT AAGGGGGATT TCGAGTGACT AAGAAAGTTT ATTTTAACCA CGATGGTGGT 840

GTAGATGATT TAGTATCTCT ATTTTTATTA TTACAAATGG AAAACGTTCA ATTGATAGGG 900

GTCAGTACAA TTGGTGCTGA TTGTTATTTA GAGCCATCTT TGAGCGCATC AGTAAAAATT 960

ATTAATCGTT TTTCAAATGA AGATATTCAA GTTGCGCCAT CATATGAACG AGGAAAAAAT 1020

CCATTTCCTA AAGAATGGCG TATGCATGCC TTTTTTATGG ACGCATTGCC AATTTTAAAT 1080

GAGCCAGTCA AACATGTTGC TTCAAATGTG AGCGACAAAG AAGCCTTTGA AGACATTATT 1140

CAAACTTTAA AGAGACAATC AGAAAAAGTA ACATTATTAT TTACAGGCCC GCTTACAGAT 1200

TTAGCAAAAG CACTACAAAA AGATTCATCT ATCGTTCAGT ATATAGAAAA ATTAGTTTGG 1260

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AGTTATGGAC CAAGTCAAGG TAAGACATTT GAGTGTAAAG ATGGGCGCAA AATTAATGTC 1680

ATAAATCATG TAGATAACAA CGCATTTTTT GATTATATAA CTGCACTTGC TAAAAAAGTA 1740

AATTAACAGC TGTGTAGAAT AATTAAGGTT TTAATTTATA TAGAACAACT TATTGTAAAC 1800

TTTTCATTTC TTAAAGTTTA CAATGGTGCT ATAATAATGG TCATGAAATA CGAAAGGAAG 1860

TAAAAAATGA CAACAAAACA GTTAGTATAT ACAGCTTTAA TGACAGCGAT TATCGCTATT 1920

TTAGGATTGG TACCGGTAAT TCCACTACCA TTTTCTTCAG TACCAATTGT ACTTCAAAAC 1980

ATTGGTATTT TCTTAGCAGG TGCGATTTTA GGACGTAAAT ATGGCACATT AAGTGTTATC 2040

GTCTTTTTAT TATTAGTAGT TGCTGGCTTG CCATTGTTAT CAGGTGGTCG CGGTGGCATC 2100

GGTGTATTCG CAGGTCCTTC AGCAGGGTTT TTACTATTAT ATCCAGTTGT AGCATTCATG 2160

ATTGGGGCGA TTCGAGATAG ATTCATCAAT GAAATTAATT TCTGGATTTT ATTCGTTGGT 2220

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CAAATTATGG GAATAAAATA ATCATATTTA AGATAGTAAA GTAATTGAAT AAGTTGCTTT 2460

GAAATTTATA AAAGTGAAAG GAGTAGGTGT CAATGGCTAG TATAAGTATG TCAGATATAT 2520

ATTGTAACGG CACTATATTT GAAAATGACG ACGAGCAGTT GATTTATTTA ACGCCTTCTT 2580

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TGCCGCGTAA CTCTGACGTT GAAATTGCCA TCGTTGACGA GTCGCATATA GATGCCTATT 2880

TAAAAGTTGC ATATCAGTTT AGTTTGCCAT TTGGAAAAGA CTATGCAGAT GCACATGAAG 2940

AAATGGTAAG GGAACATTAT CAAAAAGATG TGATTAAACG CTTAGTAGCT TATTTAAATA 3000

ATGAACCTAT TGGCGTTGTA GATGTCATTG AAAGTGAAAA TTACATTGAA TTAGATGGAT 3060

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TAAGCTGGTT TCGAGTAGAA ATCAACTTAC TGCTTTTTAA ATTGTTTTGA GCTACTTATA 3360

CTTATAAAAA TAGTGCGTTT AAATTGTTGA TTCATGTAGA ATATCGTTCA TTATGACACA 3420

CTATAATGAA TATGTTATTG TTCAGAATCA ATGATACGTT CTGGATGACT GTATATATTA 3480

AAGCCACCAT TTCGAATAAA TCCAACTGCC GTAATATTTA GGTCATTAGC TAAGGTTACA 3540

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ATTAAAATTT CTGATGAAAT ACGTCCACTA AAAATTAATA CTTTATCTCG GACAGTAATA 3660

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CGATGTACAA AAAATGTCAA ACCATCGCTT ATAGCAGCAT TATGTAAGCC ACCTGTTTCT 3780

TGGTAAATAT GACTTGCACT TTGTAATCGA GTCATCATGT TAATAATTTG CATTGGAGTT 3840

AAAGTGATTT TAGACATAGA TGTTTTAGCG ATAGCAGCAT CATTTTGAAA ATAAAACTCA 3900

CGACTCTTTC CGCAACAAGA TGCAATCATT CGTTTTGTGG AATATTGAAA GCGATCGCCT 3960

AAATCTTTAT TAAGTTCAAC ATGGGCAAAA CCTTTACTAT CATCAATCAG TACAGATTTT 4020

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AGGTTTGTTG GACTGCATAT AACAGTCGCA AATTCTTCAC CATTCACCAT AATTGTAAGT 4140

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TTATTTTAAA GCAATTTGCT TAAAATTTTA ACATATTTGC TTAAGTTTGA AATTTGATTG 4320

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GGGCATCAAT TAATAAATAT CAATCTTATG CAAATTTGAC AATTGTTTGA ATCAATATAT 4440

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AGTAAATTAG CAAAAGAGTG GATGGAATTC TTAAAATCAG ATAAAGCTAA AGAAATACTA 5280

AAAGAATACC ACTTTGCAGC ATAAGGAGTT GTAATCCATG CCTGACTTAA CACCTTTTTG 5340

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AGATAGAAGG CTTTGGGGAA TTGTTTAGAT ATTTGAGTTA TGTTGAAGAT GTTGGCACGC 8160

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TCGCGGTCCT TGCAACATAT GGCTATGCAG AGGTTAAAGT TATTAAGCAA CCGAGTGTCG 9420

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GGATTCAGAC GTCGATCACA TGAAGCATTT TGAAGCGGGG GCAGATCAAA GTATTGTACA 10320

AGGTTTTCAA TATCAGCAAA CTGTAACACG TGTAGATAAT CAAAATCTTA CTCAAATTAT 10380

TGAAAAATCT GTTACAATTG ACACCAATAT CGTATTAGTT GAAGGCTTTA AAAATGCTGA 10440

GAATGTTTGT TATAGCATTA ATGTAAGGGA GCATGAAGAT TTTACAGCAT TTGAGCAATG 10560

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ATGAAGAAGC AAAGAGGGAG GAATAAGAGA GATGAAGGTA CTTTACTTCG CAGAAATTAA 11100

AGATATATTA CAAAAAGCAC AGGAAGATAT TGTGCTTGAA CAAGCATTGA CTGTACAACA 11160

ATTTGAAGAT TTATTGTTTG AACGTTATCC GCAAATCAAT AATAAAAAGT TTCAAGTTGC 11220

TGTAAATGAG GAATTTGTAC AAAAATCGGA TTTCATTCAA CCTAATGATA CTGTTGCATT 11280

AATTCCACCG GTTAGTGGAG GTTAAGGGAG CATGAAAGCA ATAATTCTTG CAGGTGGTCA 11340

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TAGAGTAATT AAGACATTAG AATCAACAAA TATGTTCAAT GAAATTATTA TTAGTACAAA 11460

TGCGCAATTG GCAACGCAAT TTAAATATCC AAATGTTGTT ATAGATGATG AGAATCATAA 11520

TGATAAAGGT CCATTAGCAG GAATTTATAC AATCATGAAG CAACATCCTG AAGAAGAATT 11580

GTTTTTTGTC GTTTCTGTTG ATACACCAAT GATTACTGGT AAAGCTGTAA GCACGTTGTA 11640

TCAGTTTTTA GTTTCTCATC TTATTGAAAA TCATTTAGAT GTCGCAGCTT TTAAAGAAGA 11700

TGGACGTTTT ATTCCAACAA TTGCATTTTA TAGTCCGAAT GCATTAGGCG CTATAACTAA 11760

AGCACTACAT TCTGATAATT ACAGTTTTAA AAATGTATAT CATGAATTAT CAACGGATTA 11820

TTTGGATGTA AGGGATGTAG ATGCGCCCTC ATATTGGTAC AAAAATATAA ATTATCAGCA 11880

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GTAACTTTAG GTGTGATTAT TGCATGCCTA AAGAGGTATT TGGAGATGAT TTCGTATTTT 12060

TACCTAAAAA TGAACTTTTA ACGTTTGATG AAATGGCTAG AATCGCTAAG GTATATGCAG 12120

AATTAGGTGT AAAAAAAATA CGCATTACAG GTGGAGAACC ATTGATGCGA CGGGATTTAG 12180

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TAAATGTTGT TATACAAAAA GGTATTAACG ATGATCAAAT CATACCAATG CTTGAATATT 12480

TTAAAGATAA ACATATAGAG ATTCGATTTA TAGAATTTAT GGATGTTGGT AATGATAATG 12540

GATGGGATTT CAGTAAAGTT GTAACTAAAG ATGAAATGCT TACAATGATA GAGCAGCACT 12600

TTGAAATCGA TCCTGTAGAA CCAAAATATT TTGGGGAAGT AGCAAAATAT TATCGCCATA 12660

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CAGTTGCCAA TCGTCAACGT AAAAAGATAA ACATGAATTA TATTGGTGGT TAATGTGTAG 12960

GGACCACTAC ATATTAAATC ATTAGAGATG TTTTAATATT TCTGTCTTAC TCCCTAAAAT 13020

ACAATATTAT TTATTAAAGT AAAAACGGTC ATATCTATGC CAGATTTAAT AGAAATGATC 13080

GTTTTTAAAG TTTTTACAAG TTGGCGGGGC CCCAACACAG AAGCTGACAG AAAGTCAGCT 13140

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AATCACTACA TAATAAATCT TTAGTGGTTC TTTAACATTG ATGTCACACT CCATGCCATT 13440

GAGTTGTAAT ATATCTTTTT TAGGTATAAA TGTTGTCGAA TAAACAACAA GTTGTCCAAA 13500

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CATTACATTT TGAAATGCTA TGGGATACAA GTAAAATCGA TGTGATTATC CGTAAAaTCT 13860

ATAAAAAAGA GCTTATTTCT AAATTGCGTT CTGAAACGGA TGAAAGACAA GTATTCTATT 13920

TCTATAGTAC TTCTCAAAAG AAATTGTTAG ATAAAATTAC TAAAGAAATA GAAGTGTTAA 13980

GCGTTACAAA CTAAAAACTT aAAAAgcaTG CCAATCTCTA TTCATCATAA TTGCGTCTTG 14040

GTTCATGGCA TTTCTAGTTA CATGACGTCC ATGAATTAAG AAGTAAACAA GCATAGTAAT 14160

GATTGCTAAA GCGGCCATAA AGCCGAAGAT TTCACTATAT GAAAACATAT GAGTAAATAA 14220

CCCAAGGAAT GATGGACCGA AGCCGACACC TGCATCTAGA CCAACGTAAA AAGTAGATGT 14280

CGCGATACCA TATTTAATCG GGGGTGAGAC TTTTATCGCA ATAGATTGCA TTGCAGATGA 14340

TAAATTTCCA TACCCTAAAC CTAGGCAAGC ACCAGCAAGT AATATTAACC AGCTTTGATA 14400

GCTTGAAATT AAGCATACAA ATGAAAGGAA AAGCATGATA AATGCTGGGT AGACAATAAT 14460

ATTTTCATTT TTATCATCCA TCAATCTACC AGCAATAGGT CTAGTAATTA ACGATGCTAT 14520

AGCATAGCAA ATAAAGAAAT AGCTTGCTGC AGTGACTAGG TGTCGCTCTA AAGCAAATGC 14580

TTGTAAATAA GTTAGGATGG ACGCATAGGT AACGCCAATT AAAAGCATAA TTACAGCAAC 14640

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AGTTGTCACA ACTGCAGTTG CGATACCGTT TATGAGACGT ACAAAGATTA AAAAAGCTAA 15000

AGATCCATCA ATAAAATAAA GTAATTGCGT GATAATTAAA GCAATTAAAC CAATAAATAA 15060

TAATCGTTTA GGTCCrATTT sATTTACAAA TTTACCTGTA GCAAATCGA 15109

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9072 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GAGAGTCAAT GGCAAGAAGA ATATAAATAT TTGAGAGCGT TAATCTTTAA TGAAACAGAA 60

TTAGAGGAAG CGTATAAATG GATGCATCCT TGTTACACGT TGAATAATAA AAATGTAGTA 120

CTTATCCATG GCTTCAAAAA TTATGTTGCA CTATTATTTC ATAAAGGTGC CATTTTGGAG 180

GATAAATATC ATACACTCAT TCAACAGACT GAAAAGGTGC AAGCAGCTCG TCAGTTACGA 240

TTTGAAAATT TAACAGAGAT TCAAGCACGT ACCGAAGAAA TTAAATATTA TCTAGCCGAA 300

GCAATTAAAG CTGAAAAAGC TGGTAAAAAA GTTGAAATGA AGAAAACAGA GGAATATGTT 360

AAATTAACGC CAGGCAGACA ACATCAATAT ATATATCATA TTGGACAAGC TAAACGCAgT 480

GgAACAAGAC AAAAGCGTGT TGAAAAGTAT ATTAACCAAA TACTAGAAGG TAAAGGGATG 540

CATGATAAGT AATTAATGAG TAAAGCATAC CGGTTATACA ACAACATACA AGATGACACG 600

AAACAACCAA TGGCTCATGC TGTTGGTTGT TTTTTTAGGT GTGTCTGTCA TGGGCAACAC 660

TTTGACGTTG GAATTCCGTT ACAGGCTTGG GAGTAGAAAA TGTTAGCAAA AGGCAAGGGT 720

GTCTACAATG AATGATGAAG ATATTAAAAT ATAAGGATGA CTTTGTGAGT GGCGGATGGG 780

CGGTTGTCCG TCTGTAACAA TGGATGCGTG TGCATTATTA CAAAAATTCG ACTTTTGTAA 840

TAATATTTCA CATTTTCGAC ACTTTTTTGC TATAAAACAA CCAATTGAGC GATAATAAAT 900

TCGCTTTTAA AAAATATGAG TTATCTATTT AGTTGCCAAA GATAAAATAA TAATGTTTAA 960

TAACATCATA TAGAGTATGT TAGTTTTAAA TGTCGAATAT ACGAATGTGc AAACAAAGTA 1020

ATCGGTAGAA ATTCAACATA CATAGCGCCG TTTACTGTTA AGTATTCACA TTACAGATGA 1080

AAAATATAAA ATTCTACATA ATCAAGACCA TGATGTGTAC TTGTTTAACT TATGACTCTA 1140

TTTGTTTAAC AATTGCGATA ATGGTCTTTT TATTTTATGC GTATCATTCG TCATATTTTT 1200

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GTGGTGCAAT TTGATACGCC AGACAATATT TTAAGACATC CCGCAAATGA TTTTGTACGT 1920

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GTAATGATTA AACCAATCAC GATACAAGCA GAAGCAACAC TGAATGACGC CGTTCATATT 2040

ATGAGACAAA AACGTGTTGA TACTATTTTT GTAGTAGATA GTAATAACCA TTTACTAGGT 2100

TTCTTAGACA TTGAAGATAT AAATCAGGGT ATACGTGGAC ACAAAAGTTT ACGAGACACC 2160

ATTTTAAAAA GAAACGTTAG GAATGTACCT GTCGTAGATG ATCAACAGCG TTTAGTAGGA 2280

CTGATTACGC GTGCCAATGT TGTTGATATT GTATATGACA CGATTTGGGG CGATAGTGAG 2340

GATACAGTGC AAACAGAACA TGTGGGGGAA GACAcTGCGT CCTCAAAAGT GCATGAGCAA 2400

CACACTACTA ATGTCAAAGT ACGTGACATA GGAGATGATA AATCATGATT GAGTTCCTAC 2460

ATGAACATGG TGGACAGTTG ATGTCGAAAA CACTGGAACA TTTCTATATT TCTATAGTGG 2520

CATTATTACT TGCCATCATT GTTGCAGTAC CTATAGGCAT TTTATTATCA AAAACAAAGC 2580

GAACTGCCAA TATTGTATTA ACTGTGGCAG GTGTCTTACA AACTATTCCA ACACTAGCTG 2640

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ACGTTTTTTG ATTCGTATGG TTTTGCGAAT ACGTATGCAT TCATGGTAAC GAAGGAAACC 3540

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GAGTATGGTT TTGACTTTGG TACAGTGAGA CCAATGCAAA TAGGTCTAGT CTACGACGCA 3720

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CTTGCTAGCA ATTGTTGCAT TTTTAGTCAT TTTACTATTA GTTCCTAAAA ATCAAACGAA 6420

TTTGTAAAAC TGAAATGAAA GCAAGTTATT ATGTAGGGAT TTTAAAGGAA ATTTTGTGAA 6480

AGTAAGTTTA TCATACACAC TTAATGTTGC GTATTGACGT TTAATGTTAG GTGTGTTCTT 6540

TTATAGACGA TAAAAGCTGT GTGCATATTA AGCGAATGAT TTTCAAATTG ACGCTAATAT 6600

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TCAAACGCAC GGCTCGAACA AGTCTTTTTT ATTATGTCTT CGTTATCTTT GTATGAAGGA 8880

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TAATTTCTAT TGGTAGCCAA GTCAGTACAA AAGACCAATT ATTGCTACCG AGAATGAGAT 9000

ATGGTAATGC ATATAATATG AGCGCTAAAG CGATACATAT ACATAATGAT AACCAACTCA 9060

ATACAGCAAT CC 9072

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16826 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GTGGAACAGC TGTAACTATA TCATTTCTTT CAACATTTAT TGGGAAAATG TTAGCTACAT 60

TTCTATATCC GATTAATAAT GTAGTACTTT CATATATnTC TGTAAATGAA AGTGACAATA 120

TAAAGAAGCA ATATTTGaAA ACTAATCTAA TTGCTATAGC TGCCCTATGT TTAGTCATGA 180

TTATATGTTA TCCAATTACA ATAATTATTG TCTCTTTACT GTATAACATT GATTCAAGTT 240

TATATTCGAA GTTTATTATT TTAGGTAATA TAGGTGTTTT ATTCAATGCA GTGAGTATTA 300

TGATCCAAAC TTTAAATACA AAACACGCAT CAATAACATT ACAAGCGAAT TATATGACGC 360

TTCACACGAT TACATTTATA TTCATAACTA TTTTAATGAC AATTGCGTTT GGTCTAAATG 420

GATTCTTTTG GACAACGCTG TTCAGCAACA TTATTAAGTA TGTGATTTTA AATATTATAG 480

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TGATTTTATG TCAGTATTTT TATCCGGAAT ATGTATCTTC TGCGACGTTA CCAACTCAAT 600

TGGCGGAAGA TTTAATTGCG AATCACATTA ATGTCGATGT CATGTGTGGA TGGCCATATG 660

AATATAGTAA TCATAAACAG GTTTCTAAAA CCGAGATGCA TCGTGGTATT CGCATTCGAC 720

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GCACTACTGC TGTTGTAAAG ATGGCAGTAG TTTTTTTATG ATTACATCTA AGTATAGTCA 16740

CGGCTATGTT AGGACAATGA TTTAACATTT ACGCACATAT GTGTTCACTT ACGCAATTAT 16800

TGAnAAATnT CATTCATGTG GnAATC 16826

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4012 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

TTCAATGAGA GTAGTGGGCT GATGTTTAGC GATATCGCGT AAGATTAACC ATTGGCCATA 60

ATATATATTG TGTTTTTCTA AAATCGGCTC GGCTAATTTT AAATAGGGGC GATATATTGT 120

TATAAAACTA TTGAAAAATT CTTGTGATAG CATAGTGACA TCTCCTAAGA CAAAATAGTT 180

AGCTTAGCTA mCCTTTTTAC AACAATAGTA ATTATAAAAC GGGAGCAATT AGAAATCAAT 240

ATATAATTAT TAAGAGCAAA AATAATTATA CTTTGTTAAA ATAAGCGTAA TTACATGTAA 300

ATAGGGGGAT ACTAATGATA TTGAAATTTG aTCACATCAT TCATTATATA GATCAGTTAG 360

ATCGGTTTAG TTTTCCAGGA GATGTTATAA AATTACATTC AGGTGGGTAT CATCATAAAT 420

ATGGAACATT CAATAAATTA GGTTATATCA ATGAAAATTA TATTGAGCTA CTAGATGTAG 480

AAAATAATGA AAAGTTGAAA AAGATGGCAA AAACGATAGA mGGCGGAGTC GCTTTTGCTA 540

CTCAAATTGT TCAAGAGAAG TATGAGCAAG GCTTTAAAAA TATTTGTTTG CGTACAAATG 600

ATATAGAGGC AGTTAAAAAT AAACTACAAA GTGAGCAGGT TGAAGTAGTA GGGCCGATTC 660

ATCAGGATGA TGATGAAATT AAGCCACCAT TTTTTATTCA ATGGGAAGAA AGTGATTCCA 780

TGCGTACTAA AAAATTGCAA AAATATTTTC AAAAACAATT TTCAATTGAA ACTGTTATTG 840

TGAAAAGTAA AAACCGATCA CAAACAGTAT CGAATTGGTT GAAATGGTTT GATATGGACA 900

TTGTAGAAGA GAATGACCAT TACACAGATT TGATTTTAAA AAATGATGAT ATTTATTTTA 960

GAATTGAAGA TGGTAAAGTT TCAAAATATC ATTCGGTTAT CATAAAAGAC GCACAAGCAA 1020

CTTCACCATA TTCAATTTTT ATCAGAGGTG CTATTTATCG CTTTGAACCA TTAGTATAAA 1080

TATACGTAAG TGCTATGAGC GAGAATGCCC ATATGAATAA TGACAAGCAC AATGGAAAGA 1140

ATCGTTAATA TATTATTTAA TCGTGATGAC TTAATTAAAA TGAAAAAGAT TGATAATATA 1200

AATGTGAAAA AGATAAGTAT AACCCGTAAA CTAAAGTAAT TCACGGTGAG AGGTTGACTC 1260

AATGTCATAA TGATTGCAAC GATGTTCATA ATTATAAATA GACTTAAAAT AATTGTTCTC 1320

ATATCAAACA CCTCATTGTT AGATTATTGA CATTATAACA GGGGTAATTG TATATGAACA 1380

TTAATGTGGT TGCTTGAGGA AAAATTTATT CATTGAAGTC AAGTTGGTTC ATTTTAGAAA 1440

TGAATATCGT GTTAGATGAT GAAAGTATAT TGAAGTATAG GTAACTAGTT GAAAAGTATT 1500

AATTGTACGA TAACATTAAA TTTAACACGA AACATAGATA TAAAATGATT CACAATTAAA 1560

ATGGGTAAAT TTGAACTTGC TAAACTATTA ATTGGAGCAT GGACATTTCA AAAATAAGAG 1620

TTCAAATCTT ACACAAGCTC TGAATCGACA CTATAAGATA CAAACTGTAT AATTAAAGGT 1680

ATTGTTAAAT AGAAGGAGAT ATCATAAATC ATGGAAAAGA TGCATATCAC TAATCAGGAA 1740

CATGACGCAT TTGTTAAATC CCACCCAAAT GGAGATTTAT TACAATTAAC GAAATGGGCA 1800

GAAACAAAGA AATTAACTGG ATGGTACGCG CGAAGAATCG CTGTAGGTCG TGACGGTGAA 1860

GTTCAGGGTG TTGCGCAGTT ACTTTTTAAA AAAGTACCTA AATTACCTTA TACGCTATGT 1920

TATATTTCGC GTGGTTTTGT TGTTGATTAT AGTAATAAAG AAGCGTTAAA TGCATTGTTA 1980

GACAGTGCAA AAGAAATTGC TAAAGCTGAG AAAGCGTATG CAATTAAAAT CGATCCTGAT 2040

GTTGAAGTTG ATAAAGGTAC AGATGCTTTG CAAAATTTGA AAGCGCTTGG TTTTAAACAT 2100

AAAGGATTTA AAGAAGGTTT ATCAAAAGAC TACATCCAAC CACGTATGAC TATGATTACA 2160

CCAATTGATA AAAATGATGA TGAGTTATTA AATAGTTTTG AACGCCGAAA TCGTTCAAAA 2220

GTGCGCTTGG CTTTAAAGCG AGGTACGACA GTAGAACGAT CTGATAGAGA AGGTTTAAAA 2280

ACATTTGCTG AGTTAATGAA AATCACTGGG GAACGCGATG GCTTCTTAAC GCGTGATATT 2340

AGTTACTTTG AAAATATTTA TGATGCGTTG CATGAAGATG GAGATGCTGA ACTATTTTTA 2400

GTAAAGTTGG ATCCAAAAGA AAATATAGCG AAAGTAAATC AAGAATTGAA TGAACTTCAT 2460

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CAAAATATGA TTAATGATGC GCAAAATAAA ATTGCTAAAA ATGAAGATTT AAAACGAGAC    2580

CTAGAAGCTT TAGAAAAGGA ACATCCTGAA GGTATTTATC TTTCTGGTGC ACTATTAATG    2640

TTTGCTGGCT CAAAATCATA TTACTTATAT GGTGCGTCTT CTAATGAATT TAGAGATTTT    2700

TTACCAAATC ATCATATGCA GTATACGATG ATGAAGTATG CACGTGAACA TGGTGCAACA    2760

ACTTACGATT TCGGTGGTAC AGATAATGAT CCAGATAAAG ACTCAGAACA TTATGGATTA    2820

TGGGCATTTA AAAAAGTGTG GGGAACATAC TTAAGTGAAA AGATTGGTGA ATTTGATTAT    2880

GTATTGAATC AGCCATTGTA CCAATTAATT GAGCAAGTTA AACCGCGTTT AACAAAAGCT    2940

AAAATTAAAA TATCTCGTAA ATTAAAACGA AAATAGATTA ACGACTGAAA TCTGAACGCT    3000

CATAAGACTG TCATTTGCGT TCAGATTTTT TTACACAATA TAGAATGGTT GAGTAAAATA    3060

TTTTTGAATA TAGTGAAAGA GGGGGAAGTA CTGTGATAAA AAAGCTATTA CAATTTTCTT    3120

TAGGGAATAA GTTTGCTATC TTTTTAATGG TTGTTTTAGT TGTCTTGGGC GGTGTATATG    3180

CGAGTGCTAA ATTGAAATTA GAATTACTAC CAAATGTACA AAATCCAGTT ATTTCAGTTA    3240

CAACAACAAT GCCGGGTGCA ACGCCACAAA GTACCCAAGA TGAAATAAGT AGTAAAATTG    3300

ACAATCAAGT AAGATCATTG GCATATGTGA AAAATGTTAA AACGCAATCC ATACAAAATG    3360

CTTCAATTGT AACAGTTGAA TATGAAAATA ATACAGATAT GGATAAAGCA GAAGAACAGC    3420

TTAAAAAAGA AATCGATAAA ATTAAATTTA AAGATGAAGT TGGTCAACCA GAATTAAGAC    3480

GTAATTCGAT GGATGCTTTT CCGGTTTTAG CATATTCATT TTCAAATAAA GAGAATGACT    3540

TGAAAAAAGT AACGAAAGTA CTGAATGAAC AATTAATACC AAAATTGCAA ACGGTAGATG    3600

GTGTGCAAAA TGCGCAATTA AATGGGCAGA CGAACCGTGA AATCACCCTT AAATTTAAGC    3660

AAAATGAACT TGAAAAATAT GGGTTGACTG CTGATGATGT AGAAAACTAT CTAAAAACGG    3720

CAACAAGAAC AACGCCACTT GGATTGTTCC AATTTGGTGA TAAAGATAAT CAATTGTTGT    3780

TGATGGTCAA TATCAATCTG TTGATGCTTT TAAAAACATA AATATTCCAT TAACGTGGCA    3840

GGAGGACCAA GGGCATCTCA TCCCAAAGTG ACCATAAACC AAATTCAGCC ATGTCAGACG    3900

TTATCAGGCA TCACCACAGC AAATTCAAAG CGTCAGCnCC AATATATAGT GGATGCCGCA    3960

nGAACTAGGG GTTTAGCGnT ATCAGTGGTG TGGCGACTCT ATTCTAAACG AT            4012
```

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7778 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CAATATAGGT CGCCGAGTTT CAACTaCATC AACTGGTTCA GTTACATTAG ATAATGCGCT 60

AGGTGTAGGT GGCTATCCTA AAGGACGAAT TATTGAAATT TATGGTCCTG AAAGTTCTGG 120

TAAGACAACA GTAGCGCTTC ACGCTATTGC TGAAGTACAA AGTAATGGCG GGGTGGCAGC 180

ATTTATCGAT GCTGAACATG CTTTAGATCC AGAATATGCT CAAGCATTAG GCGTAGATAT 240

CGATAATTTA TATTTATCGC AACCGGATCA TGGTGAACAA GGTCTTGAAA TCGCCGAAGC 300

ATTTGTTAGA AGTGGTGCAG TTGATATTGT AGTTGTAGAC TCAGTTGCTG CTTTAACACC 360

TAAAGCTGAA ATTGAAGGAG AAATGGGAGA CACTCACGTT GGTTTACAAG CTCGTTTAAT 420

GTCACAAGCG TTACGTAAAC TTTCAGGTGC TATTTCTAAA TCAAATACAA CTGCTATTTT 480

CATCAACCAA ATTCGTGAAA AAGTTGGTGT TATGTTCGGT AATCCAGAGA CTACACCAGG 540

TGGACGTGCA TTAAAATTCT ATAGTTCAGT AAGACTAGAA GTACGTCGTG CAGAACAGCT 600

TAAACAAGGA CAAGAAATTG TAGGTAATAG AACTAAAATT AAAGTCGTTA AAAATAAAGT 660

GGCACCACCA TTTAGAGTAG CTGAAGTTGA TATTATGTAT GGACAAGGTA TTTCTAAAGA 720

GGGTGAACTT ATTGATTTAG GTGTTGAAAA CGACATCGTT GaTAAATCAG GAGCATGGTA 780

TTCTTACAAT GGCGAACGAA TGGGTCAAGG TAAGGAAAAT GTTAAAATGT ACTTGAAAGA 840

AAATCCACAA ATTAAAGAAG AAATTGATCG TAAATTGAGA GAAAAATTAG GTATATCTGA 900

TGGTGATGTT GAAGAAACAG AAGATGCACC AAAGTCATTA TTTGACGAAG AATAGTACAC 960

AAATTTATAT CTATAGTTAA ACTTAGCAAA TATCCTTATA GGATTGATTG AAAGTGATAT 1020

TCATCTCATA AAGCTAGAAT AATATCTAAC TTTATGGGAT ACACTACAAA TCGAGACTAT 1080

AAGGTTTTTT ATTTTATTTA TTATTACATT ATCAATAGTT TTATAATCGA GCTTCAAAAC 1140

TTTAGAAAAT AGTAGAAATA GCATTCAATA TAGTGCAAAA GTGCAAATTG ATAACTTGAC 1200

ACTTATCTCC TATAAACCGT ACAATTAATT TGTATGATTT ATATATAATT TCATAAAGTC 1260

ATATTGAATT TCATATAAAG AGCAAACCCT AGAAAAGGAG GTGTTTGTGT GAATTTATTA 1320

AGCCTCCTAC TCATTTTGCT GGGGATCATT CTAGGAGTTG TTGGAGGGTA TGTTGTTGCC 1380

CGAAATTTGT TGCTTCAAAA GCAATCACAA GCTAGACAAA CTGCCGAAGA TATTGTAAAT 1440

CAAGCACATA AAGAAGCTGA CAATATCAAA AAAGAGAAAT TACTTGAGGC AAAAGAAGAA 1500

AACCAAATCC TAAGAGAACA AACTGAAGCA GAACTACGAG AAAGACGTAG CGAACTTCAA 1560

AGACAAGAAA CCCGACTTCT TCAAAAAGAA GAAAACTTAG AGCGCAAATC TGATCTATTA 1620

GATAAAAAAG ATGAGATTTT AGAGCAAAAA GAATCAAAAA TTGAAGAAAA ACAACAACAA 1680

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CGCATCTCCG GTCTCACTCA AGAAGAAGCT ATTAATGAGC AACTTCAAAG AGTAGAGGAA  1800
GAACTGTCAC AAGATATTGC AGTACTTGTT AAAGAAAAAG AAAAAGAAGC TAAAGAAAAA  1860
GTTGATAAAA CAGCAAAAGA ATTATTAGCT ACAGCAGTAC AAAGATTAGC AGCAGATCAC  1920
ACAAGTGAAT CAACGGTATC AGTAGTTAAC TTACCTAATG ATGAGATGAA AGGTCGAATC  1980
ATTGGACGAG AAGGACGAAA CATCCGCACA CTTGAAACTT TAACTGGCAT TGATTTAATT  2040
ATTGATGACA CACCAGAAGC GGTTATATTA TCTGGTTTTG ATCCAATAAG AAGAGAAATT  2100
GCTAGAACAG CACTTGTTAA CTTAGTATCT GATGGACGTA TTCATCCAGG TAGAATTGAA  2160
GATATGGTCG AAAAAGCTAG AAAAGAAGTA GACGATATTA TTAGAGAAGC AGGTGAACAA  2220
GCTACATTTG AAGTGAACGC ACATAATATG CATCCTGACT TAGTAAAAAT TGTAGGGCGT  2280
TTAAACTATC GTACGAGTTA CGGTCAAAAT GTACTTAAAC ATTCAATTGA AGTTGCGCAT  2340
CTTGCTAGTA TGTTAGCTGC TGAGCTAGGC GAAGATGAGA CATTAGCGAA ACGAGCTGGA  2400
CTTTTACATG ATGTTGGTAA AGCAATTGAT CATGAAGTAG AAGGTAGTCA TGTTGAAATC  2460
GGTGTAGAAT TAGCGAAAAA ATATGGTGAA AATGAAACAG TTATTAATGC AATCCATTCT  2520
CATCATGGTG ATGTTGAACC TACATCTATT ATATCTATCC TTGTTGCTGC TGCAGATGCA  2580
TTGTCTGCGG CTCGTCCAGG TGCAAGAAAA GAAACATTAG AGAATTATAT TCGTCGATTA  2640
GAACGTTTAG AAACGTTATC AGAAAGTTAT GATGGTGTAG AAAAAGCATT TGCGATTCAG  2700
GCAGGTAGAG AAATCCGAGT GATTGTATCT CCTGAAGAAA TTGATGATTT AAAATCTTAT  2760
CGATTGGCTA GAGATATTAA AAATCAGATT GAAGATGAAT TACAATATCC TGGTCATATC  2820
AAGGTGACAG TTGTTCGAGA GACTAGAGCA GTAGAATATG CGAAATAATT TTTGTCTCCC  2880
TCACAAATTA GTGAGGGAGC TTTTTTAAGT TGTAGTCTTA AtCTAGTTAG ACAGCACTTT  2940
ATCGGTAATA ACTATATTAA ACAGTAGTTA TTTGAAAGTA AGACGGACCT TATATTAAAT  3000
AAGAAGTTAT TGCTTTTAAT AAAAATGTTT TAGGCTTCGT AATTACTATA TTTATATTAT  3060
GTAAACCTAT AAAGATGATT GGTTTTCTAT CCAATAAAAA AGAAGAGAAG ATGTAACACA  3120
TCTTCTCTTC yGCAATATTA ATTAGGATTT ATTTCTAAGT TGAGTTATTT TAATTGTAAA  3180
TCTGTTTTCT TTAATTCTTT TATAACTTCT GCAGTATCAT AACAATTTGT TGCAATTGTT  3240
GAATATCTCT CTGCTAAACG ATATGCATTA ATGTAAAGCT TTAAACTTTC TTTAGCTATA  3300
TCCTCTGCAT CTTCGAATTT TGATGGGTTA GACATAACCA CTAATTCTGC AAATTTTTCT  3360
GGATCAATAT TAATAGACAT GTATTTATTT ACAACTCCTA TTTATTTTGA TGTCTTAATA  3420
CTAACATATT GAAGTTTTCA GACAAAGTAA TGTCTCTCTA TAATTGAAGA AAAATAATTC  3480
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GGATGAACAA AACATGAGAA TAATGTTTAT AGGGGATATC GTAGGTAAAA TTGGACGAGA 3600

CGCAATTGAA ACGTACATAC CTCAACTGAA GCAAAAGTAT AAACCAACAG TTACAATTGT 3660

AAATGCTGAA AATGCAGCAC ATGGTAAAGG TTTGACTGAA AAAATATATA AACAATTACT 3720

AAGAAATGGT GTAGATTTCA TGACTATGGG TAATCACACA TATGGTCAAC GTGAAATTTA 3780

TGATTTTATA GATGAAGCAA AACGACTAGT AAGACCAGCG AATTTTCCGG ATGAAGCGCC 3840

GGGAATTGGT ATGAGATTTA TACAAATTAA TGATATTAAA CTTGCAGTTA TTAATCTGCA 3900

AGGAAGAGCG TTTATGCCAG ATATTGATGA TCCTTTTAAA AAGGCAGATC AATTAGTCAA 3960

GGAAGCACAA GAACAAACTC CGTTTATATT TGTTGATTTT CATGCAGAAA CAACTTCTGA 4020

AAAGTATGCA ATGGGATGGC ATTTAGATGG TAGAsTAGCG CTGTTGTTGG AACGCATACA 4080

CACATTCAAA CAGCAGATGA ACGTATTTTA CCAAAGGGGA CAGGGTATAT AACGGATGTT 4140

GGTATGACAG GTTTTTATGA TGGCATTTTA GGAATAAATA AAACAGAGGT AATTGAGCGT 4200

TTTATCACTA GTTTGCCACA AAGACATGTT GTTCCAAATG AAGGTAGAAG TGTATTATCT 4260

GGTGTTGTTA TTGATTTAGA CAAAGAAGGT AAAACAAAGC ACATCGAACG TATATTGATA 4320

AATGATGACC ATCCATTTTC AACATTTTAA AATTACGTAA GTAAACATTC GAATTGGACC 4380

CTATCGTCCA TTAGTATGAA TTTAATATAG TACCACTGTT TACATAGTAA ATCGGTGGTT 4440

CTTTTTGTTA TCATTTAATA TGAAATATAT CCATAGGAGG CATATAACTA TGAAACCACA 4500

ATTATCGTGG AAAGTTGGCG GTCAACAAGG CGAAGGTATT GAATCAACTG GGGAAATCTT 4560

CGCTACGGCT ATGAATAGAA AAGGATATTA TTTATATGGA TATAGACATT TTTCAAGTCG 4620

TATCAAAGGT GGACATACGA ATAATAAAAT TAGAGTTTCT ACGACGCCTG TTCATGCAAT 4680

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TGAAATGAGA GAAGACAGTA TTATTTTArC TGATGCCAAG GCTAAACCTG TGAAaCCAGA 4800

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AGCATTAATG AAAAACATGG TTGCAATAGG TGCTACTAGC GCATTGATGA ATTTGAATAC 4920

AAATACATTT GAAGAACTTA TTACTAATAT GTTTTCTAAA AAAGGTGACA AGGTAGTTGA 4980

AGTCAATATC CAAGCATTAA ACGAAGGTTA TCAATTAATG CAATCTCGCT TACCTGAAAT 5040

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CGATGCCATT GGATTAGGTG CAATTGCTGC AGGTTCACAA TTTATGGCGG CATATCCTAT 5160

TACACCTGCG TCTGAAGTTA TGGAATATAT GATTGCCAAT ATATCTAAAG TAAACGGAGC 5220

GGTTATTCAA ACAGAAGATG AAATTGCTGC TGTAACTATG GCTATTGGTG CAAATTATGG 5280

TGGATTATCT GGTATGACTG AAACGCCATT AGTCATTATT AATACCCAAC GAGGTGGACC 5400

TTCTACTGGA TTACCTACGA AACAAGAACA GTCAGATTTA ATGCAAATGA TTTATGGTAC 5460

ACATGGTGAT ATTCCAAAAA TTGTTGTAGC ACCAACAGAT GCAGAAGATG CATTTTATTT 5520

AACTATGGAA GCATTTAATT TAGCAGAACA ATATCAATGC CCTGTTATAG TTCTAAGTGA 5580

TTTGCAATTA TCTTTAGGTA AACAAACTGT TGAAAAATTA GATTATAATC GTATTGAAAT 5640

TAAACGTGGT GAAATCATTC AATCTGATAT TGAACGTGAA GAAGATGATA AAGGTTATTT 5700

CAAGCGTTAT GCGTtAACAT CCGATGGTGT TTCTCCTAGA CCTATCCCCG GTGTTAAAGG 5760

AGGTATTCAT CATATAACTG GTGTGGAaCa CAATGAAGAA GGTAAACCTA GTGAATCTGC 5820

GTCAAATAGA CAACAACAAA TGGAAAAACG AATGCGTAAA ATTGAGCAGT TACTAATTGA 5880

ATCGCCAGTA GAAGCTAACT TACAACATGA GGATGCAGAT ATTCTTTATA TCGGTTTTAT 5940

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TAATAAAGCG AAGAAAGTCG TTGTAGTGGA GCACAATTAT CAAGGACAAT TGGCTAGTAT 6120

TATAAAAATG AATGTCAATA TTCATGATAA GATTGAAAAT TATACAAAGT ATGATGGGAC 6180

ACCTTTCCTA CCACATGAAA TCGAAGAAAA AGGCAAAATA ATTGCTACTG AAATAAAGGA 6240

GATGGTATAG ATGGCGACAT TTAAAGATTT TAGAAATAAT GTTAAGCCTA ACTGGTGCCC 6300

CGGATGTGGC GATTTCTCAG TACAAGCTGC AATTCAAAAA GCAGCCGCAA ATATAGGGTT 6360

AGAACCTGAA GAAGTAGCTA TCATCACCGG TATAGGATGT TCTGGCCGTC TTTCAGGATA 6420

TATTAATTCT TATGGCGTTC ATTCTATTCA CGGACGTGCA TTACCTTTAG CTCAAGGTGT 6480

AAAAATGGCG AATAAAGATT TAACTGTTAT TGCATCGGGA GGAGATGGTG ATGGTTATGC 6540

TATAGGTATG GGGCATACAA TCCATGCTTT AAGAAGAAAT ATGAACATGA CGTATATAGT 6600

CATGGATAAT CAAATTTATG GTTTGACAAA GGGACAAACA TCGCCGTCAT CAGCAGTAGG 6660

ATTTGTTACT AAAACAACGC CAAAAGGTAA TATAGAAAAA AATGTTGCGC CTTTAGAATT 6720

AGTATTATCA TCTGGTGCCA CATTTGTAGC CCAAGGTTTT TCAAGCGATA TTAAAGGATT 6780

AACAAAACTA ATTGAAGATG cAATTAATCA TGATGGATTT TCATTCGTTA ATGTCTTTTC 6840

ACCATGTGTG ACTTATAATA AAATTAACAC ATACGATTGG TTTaAAGAAC ATTTAACAAG 6900

TGTTGATGAc ATTGAAAATT ATGATTCTAC AGATAAACAA TTAGCGACTA AAACTGTTAT 6960

TGAACATGAA TCTTTAGTAA CTGGTATTGT TTATCaAGAT AAAGAAACAC CATCATATGA 7020

ATCtCAAATT AAAGAGTTAG ATGATmCACC ACTTGCTAAA AGAGATATCa AAATTaCTGA 7080

TGTATTTATA ACAGATCCAT TTATGCTACT CAGTTTTTTA CTATTACAAA AAATAAAGGA 7200

GTTTTTAAAA ATGAAAGACA CATTAATGAG TATACAAATA ATTCCTAAAA CACCAAACAA 7260

TGACAATGTT ATACCTTACG TAGACGAGGC GATTAAAATA ATTGACGAAT CTGGTTTGCA 7320

TTTTAGAGTA GGTCCGTTAG AAACGACAGT ACAAGGAAAT ATGAATGAAT GTTTAATTTT 7380

AATACAATCA TTAAATGAAC GAATGGTGGA ACTTGAATGT CCAAGTATTA TTAGCCAAGT 7440

TAAGTTTTAT CATGTGCCAG ATGGCATCAC TATTGAAACT TTAACTGAAA AATATGATGA 7500

ATAACATTAA AAGTGAAGTA AACTGGATTT GAATTGGCTT GTTAGAGATG ACGTATAACT 7560

TTAACTGTTT TTGCACTTTA TAGTTAAATT TAATATAATT ATTAAATGAT ACGGGCAAAT 7620

AGAAAGGATT TTGTAAAGTG AACGAAGAAC AAAGAAAAGC AAGTTCTGTA GATGTTTTAG 7680

CTGAGAGAGA TAAGAAAGCA GAAAAAGATT ATAGTAAATA TTTTGAACAT GTTTATCAGC 7740

CGCCTAATTT AAAAGCAAGC GCAAAAAAAG AGGTnAAA 7778

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

AGATGAAGTT GTTACgAAAA TTGCGTACGC TGTTTCAGAA CATGTCAAAA TAGAAACAGG 60

TAATCCATTC TTTCAAACAT CACATAGTGG TTGTGCGACG GGCGGATCCT GTAATTGTTC 120

ATTATAAAAA ACATCGAGTC AGAAAAAGGT GGTTATTGAA cCACTAACTA GCATCTGACT 180

CGATGTTTTT ATTTATTCGG GATTGTTTGT TTGAATTGTT GTGCTAAATC TGGTCGATCT 240

GTCACAATCG TGTGTGCACC TTTTTGGTAT AAATCATTCA TCAGATTTAT ACTATTTACG 300

CCATAATAGC CTGGAATGAT ATTCATATCA TTTAACCATT TGATAAAACG AGATGAAGTC 360

AAATCAATGC CTTTAAAATG AGTAGGCATT TGGAACGTTT GTGCTAATGG TTGGTAGTAC 420

CTACCACCTA ATAAATGATA TTTTAAAAAT GCTTCTGTAA CTTCCTGTTG GCTAGCACCA 480

ATTGCGACGG ATCCTTGTGC AATTTTATTA AAACGAACGA TTTGTTCTTT ATAAAAACTT 540

GTCACAAGAA CGCGGTCAAA TGCTTGATTT TCTGCAATTG TATCAAACAT AATTTGTGGT 600

GCGATTGAGC CTTCATAGGA TTCAGGAGCA TCTTTTAAGT CTACGTTTAT ATACATATCA 660

GGATATTGCT TCAGCAACTc ATCGAAGGTT AGTATAGCTG TGTGTGCATG ACCACGATAT 720

AATGTATGGG CACTAACTTT TCCAGAGCCG TTCGTCGTTC TATCAACAGT TGCGTCATGA 840

AAAACGATAA GCTGTTGATC TTTTGTGAGT CTCACATCTG TTTCAAAGCC ATCAACGCCT 900

AATTGTTTAG CATAGTCAAA TGCAAGTTGC GTTTGCTCTG GTCTTAAAGC CATACCACCG 960

CGATGCGCAA ATATATATGG TGCATTGCCT TTGAAAAAAG CAGGGATGGT TTGCTTTTTA 1020

GTAATCACTT TATTTTTATT GATCATTAAT AGACTACTTA AAAATCCAGC ACCGACTAGT 1080

ACCGCATTTA AAATGTTTCT GTTTACnTTT TTCATAAAAA ATTCCTCC 1128

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CAAGCAAACA ATCGTCGATA AAATTGCTAA AATAATAAAA GTAATTCGAA CTTTCATCAT 60

GATCATCCTT TGTTTATAGA GTCAATATAA GTATGGAATA TGTTAGGTAT ATAGTCAAAT 120

GCGTCAACTA ATGGGAATTT TGGCATAGAT AGAGAATTTA AGGCAATTAA AAAGGCATCA 180

AACAGTAATA TGCTGCTTGA TGCCCAAATG ATGACTTTAG CTAAATTGAT TAGTCACTTT 240

TAAAGATAAA GAATTGTCAT GAATTAAAAC TCATGTAATG ATGTGTTACA TTTCGCAATG 300

ATGGCTTTCA GTTATTTATC GATAACATCA CTCTTGATAC CTTTAGATTT TAAGAAATCT 360

TTAATTTTAT CTTGTTGCTT TTTATTAACA TCACCGGCAT ATTTTGTTGG CACGTCGACA 420

ACATTGATTT TATTTTGCGG TTGATAGCTA AGCTTTTCAA TATCTTCATC AACATTGGCG 480

ATTGTACTAT TTAAAGCTTT GAAGTAATTC ATCATTAATT CAACGGGTTT CTTATATTCT 540

TTAGGAATAT TGTTTTCAGT GACAAATTTC TTGAAATGCA AATCGTTTTT AACAGCTAAG 600

TTAGATAAGT GGCTAAGTGT TTCTGCTTGT TTTTCAGTCA CTTTTGTTTG ACTGTCAATT 660

TGTTTATCTA GTTTATGTTG CATAATATAT TTGTTATCAA GTATATCGCT ATTTACAGAC 720

AAATACTTTT CTATAGCTTG CTTCATCTCT GCATCACTAA TATCACTATT TTTCTTATCT 780

GAGTTAAAGA TATCTTTTGT tTCTAATTTT TTAGCGCTTT TAGGTGCATG GATGCCAGTA 840

CTTGTATGAT GATCTTCGTT ATCAGATTGA TCGGACGCGC AACCTGTAAG AATTAATGTC 900

GATGCTAAAA ATGTACTTAG TAGTAATCTC TTTTTCATAA TGTAATATAA CTCCTTAGTT 960

TATCTTTAAT TGAAAAAATA TGTATTCATG TTTAATAGAG TAACATTGAA TTAGTTTGGA 1020

TCTATCAATA ATGCATCATT TTGGACGTTG TTAAGGATAG CTTTATCTAT AAATAACTGC 1140

ATAATTGGTT GTACTAATTT AGACGTAGGT ATCGTACGTA AAAGCATAAT AATTTCGTTC 1200

ACATACTTTT CTTTCTCAAT ATCATTTTTC ATATTGATTT GTTTGCGAGA GGTACATACT 1260

TTAAGCATTA TCGCACATCT CGTTGTATAT ATTAAGTTTA TCATAACATG ATTTTATGTC 1320

GGGATAAAAA AATAACAGCA TCTTAACAAA TGTAAGATAC TGTCAGTGAA ATGAATGAAA 1380

CTTTAGTTTC TGaTAATATA GTCAAAGGCA TTTAATGCTG CATTTGCACC AGCGCCCATT 1440

GAAATGATAA TTTGTTTGTT CTTCTGATCT GTGACATCGC CAGCAGCAAA TATTCCAGGA 1500

ACATTCGTAT TATTGTTACG ATCAATCACA ATTTCACCAC GTTCGTTTAA TTCAACAGCA 1560

TCGTTTAACC ATGATGTGTT TGGAAGTAAA CCAATTTGAA CAAAGATACC ATCTAAGTTA 1620

AGTAGATGTT CTTCGCCGGT GTTCATGTCT TCGTAACGTA TACCTGTAAC ATGGTCTTCT 1680

CCGACAACTT CAGTAGTTTT GGCATTTGTT TTGATATCAA CATTTGATAA AGAACGTAAA 1740

CGATCTTGTA ACACGTTGTC TGCTTTTAAT TCGCTAGCGA ATTCGAATAA TGTAACATGA 1800

TTAACGATAC CAGCAAGGTC AATTGCTGCT TCAACCCCAG AGTTACCGCC ACCGATAACT 1860

GCTACGTCTT TATTTTCAAA TAGAGGTCCG TCACAGTGAG GGCAGAATGC AACACCTTTA 1920

TTAATCAATT GCTCTTCACC TGGAATGTTT AGCTTACGCC AACCTGCACC AGTAGCAATA 1980

ATGACTGTTT TACTTTCTAA GACAGCACCG TTTTCTAACG TAACTTTAAT TGCTTCGTCA 2040

GTCTTTTCGA TATCTGTAGC ACGTATACCT GTCATTGCAT CAATGTCATA TTGATCAATG 2100

TGCGCTGCTA AGTTAGAAGA AAATTCAGAA CCAGTTGTTT CTTTAACAGT AATGAAGTTC 2160

TCAATACCAG CAGTATCATT AACTTGGCCA CCGATACGAT CAGCAACTAT ACCAGTACGT 2220

AAACCTTTAC GTGCTGTGTA AATCGCTGCA CTACCACTAG CAGGACCACC ACCAACGATT 2280

AAGACATCAT AAGGTTCTTT ATTTTCAAAC TCAGATGCAT CTGCCGTACT GCCTAGTTTC 2340

GAAAGAATAT CTTGGATTGT CATACGACCA TTGCCAAATT CTTCGCCATT TAAAAAGACA 2400

GCAGGGACTG CCATGATGTT TTCAGATTCT TCACGGAACA CTGCACCATC AATCATAGAA 2460

TGCGTGATGT TAGGGTTGAT CACACTCATT AAGTTAAGTG CTTGAACGAC ATCAGGACAT 2520

TTTTGACACG TTAAACTAAT GAATGTTTCA AAATGGAATG AACCTTCTAA TTTTTTAATT 2580

TGGTCAATGA TTGACTGTTT TTCTTTAGGT GCACGACCAC TAACCTGTAA AATTGCTAAA 2640

ACAAGTGAGT TAAACTCGTG ACCTAATGGA ATACCTGCAA ATGTTACACC TGTTTCTTCG 2700

CCAGGACGAT TGACTGAGAA ACTTGGTGTA CGTTTTAAAG ATTTTTCAGA AAGAGATAGT 2760

CTAGGTGACA TATCAGTAAT TTCTGTCAAC AAATCTTTAA GTTCTTTGGA TTTATCATCT 2820

TGTTGTTTTA AATCAGCATT AAGCATGGTT GTAATGCCTC CTTAGATTTT ACCTACTAAA 2940

TCTAAACCAG GTTGCAATGT TTTAGCGCCT TCTTCCCATT TAGCTGGGCA TACTTCGCCA 3000

GGGTTTTTAC GAACATATTG AGCTGCTTTG ATTTTGTGAG CTAATGTACT AGCGTCACGG 3060

CCAATTCCGT CAGCGTTAAT TTCAGATGCT TGTACAACAC CGTCTGGGTC GATAATGAAT 3120

GTACCACGTT GAGCTAAACC AGTAGCTTCA TCTAATACAT CAAAATTACG AGTGATTGTT 3180

TGTGATGGGT CACCAATCAT AGTGTAAGTG ATTTTGCTAA TTGCATCTGA ATGGTCATGC 3240

CATGCTTTGT GTACGAAGTG AGTATCAGTT GATACTGAGA ATACATTTAC GCCTAATTTT 3300

TGTAATTCTT CATATTGGTT TTGTAAGTCT TCTAATTCAG TTGGACAAAC GAATGAGAAG 3360

TCAGCAGGAT AGAAGCATAC TACGCTCCAA GAACCTTTTA AATCTTCTTG TGTAACTTCT 3420

TTAAATTGAT CTTTTTTTGG ATCGAAArCT TGCGCTGTAA ATGGTAAGAT TTCTTTGTTA 3480

ATTAATGACA TAAATATCTT CCTCCTAAGA ATTTAAGTAT GAATTAGAAC TATCAATTGA 3540

TTGCGCTTAA TTATAATAAT TCTAATCTCT TAGTTAGCAT TATTACATTT TGATCCAGAA 3600

TAGTCAACTG GATAACTTTG TAAAGTGAAT GATTACTTTT AAAATAAAGA AAGATAATAT 3660

AAAGTGCTTT GATAATGGAT TTTGTAGTTG ATGATTTAAA AGGTTGTGTC TATATTTAAT 3720

ATCTTGATTT TAATGTAAAA AATGTAAAAA AAGAAGATTT GTATTCTCAA CTAAGTCAAC 3780

CTTATTGATA ATGGTATGAG AATATTTGTT CGAGATGGAT GAAGGTAATG AGTGAGAAAC 3840

TGGATTTTTA AAGTATGAGA CAATATTTTA AAAAGTTCAA TTATTAACTT ATAAGCAAAT 3900

AATTGCTATA AAAAAGTTTG GACGTGTACA ATTGCAATAT GAAGATTTTA AATTAATTGT 3960

AAAGTATCGA GGAGTGGGTA ACGTGTCAGA ACATGTATAT AATCTTGTGA AAAAGCATCA 4020

TTCTGTTAGA AAATTTAAGA ATAAACCTTT AAGTGAAGAC GTTGTTAAGA AATTGGTAGA 4080

AGCTGGACAA AGCGCTTCGA CGTCAAGTTT CCTGCAAGCA TACTCAATTA TTGGTATCGA 4140

CGATGAGAAG ATTAAAGAAA ATTTACGAGA AGTTTCTGGA CAACCTTATG TTGTAGAAAA 4200

TGGCTATTTA TTCGTCTTTG TTATTGATTA TTATCGTCAT CATTTAGTTG ATCAACATGC 4260

TGAAACTGAT ATGGAAAATG CATATGGTTC AACGGAAGGT TTGCTAGTAG GTGCAATCGA 4320

TGCAGCATTA GTTGCCGAAA ATATTGCGGT AACTGCTGAA GATATGGGGT ATGGCATTGT 4380

CTTTTTAGGA TCATTAAGAA ATGATGTTGA ACGCGTTCGA GAAATTTTAG ACTTACCTGA 4440

CTATGTCTTC CCGGTATTTG GTATGGCAGT AGGGGAACCc GCAGATGACG AAAATGGTGC 4500

AGCCAAGCCA CGCTTACCAT TTGACCATGT CTTCCATCAT AATAAGTATC ATGCTGATAA 4560

GGAAACACAG TATGCACAAA TGGCAGATTA CGACCAGACA ATCAGCGAGT ACTATGATCA 4620

CAAAGCAAGA TTAGATATGT TAGAACAATT GCAAAAATCA GGCTTAATAC AGCGATAgCA 4740

AGATACCAAA ATAACCCGCC CCCCTCTAGC TTAAAATGAT AAGTATAGCT AGAGGGGGCG 4800

GGTATTTCTT GCAATGAATT AGTGTGAAGT TAATGCAGCA TTATCATTTG AATCGAAAGT 4860

ATCTTTATCC CAATGTTTAG TTAACTTGGC GGTACCTGTA CCAGCTAGCA TTGAATCGTT 4920

CACGTTTAAT GCTGTTCTAC CCATGTCAAT CAATGGTTCA ACGGAGATGA GCACGCCGGc 4980

TAAAGCGACT GGCAAGTTTA ACGTTGACAA CACCAATATG GATGCAAATG TAGCCCCGCC 5040

ACCGACGCCA GCAACGCCGA ATGAACTAAT AATCACGACA GCGATTAACG TTACAATAAA 5100

TTGTAAATCA ATTTCTACAT TAGCGACGGG TGCGACCATA ATTGCAAGCA TGGCAGGGTA 5160

AATGCCTGCA CAACCATTTT GTCCAATCGA CAATCCAAAT GTCGCAGCGA AATTGGCAAT 5220

ACCTTCTGGC ACGCCTAGAC GTCTTGTTTG TGTTTGTACA TTCAATGGTA AGGCACCCGC 5280

GCTTGAGCGT GATGTGAATG CAAAGATTAA TACTTCCAAA GTCTTTTTAA CATAGCGAAT 5340

TGGGCTAATA CCTAACAGGC TTAAAATAAT TAAGTGAATG ATATACATCG TAATTAATGC 5400

AGCGTACGAT GCGATTAAGA ATTTTCCTAA AGTCCAAATG GCGCCAAAGT CACTTGTCGA 5460

TAATGTGTTG GCCATAATTG CTAATACACC GTATGGCGTT AAACGTAAGA CGAACGTCAC 5520

AATCGCCATT ACTAGTGAAT AGATAGCGTC AATCGCACGC TTAAGCAATT CACCATGATC 5580

AGGTTGTTTG CGTnTACGCG TAAATAAGCA AATCCTATAA ACGAAGCAAA TATCACGACA 5640

GCAATCGTGG aAGTTGCACG TTGTCCaGTG AAATCTAAGA ATGGATTTTT AGGCAATAAT 5700

TCCAAAATTT GTTGTGGTAA CGTATGTGCT GTTAAATCTT TCGCTTGTTT AGCAATTTCG 5760

CTTCCACGTG CTTGTTCAGC GTTACCAAGG TTAATTGTTG ATGCATCTAA ACCAAACACC 5820

AAGGCATACA CAACACCAAC AATCGCAGCA ATGGTGACAG TGCCAATTAA AAAGATAAAA 5880

ATGAGACTAC CAATTTTAGC AAACTTTTCT CCGATTTGAA TTTTAGTGAA TGCAGCTACA 5940

ATAGAAATGA AAATTAAAGG CATAACAATC ATTTGCAACA ATGCAACGTA ACCTTGTCCG 6000

ACAATGTTGA ACCAGTCACT TGTTGATGTA ATAACATTCG AATGTGTGCC ATAAATAAGA 6060

TGCAATAACA CACCGAATAC TATACCAATC CCTAAAGCTG TAAACACACG TTTCGCAAAA 6120

GATATATGTT TGCGAGCCAT CATGTGCAAT ATTACGATGA AAATCACCAA TACAATAATA 6180

TTAATCAGTG TAAGAAAAGC ATTCATGAAC GTCACTCCTT AAATTTTTGA ATATAATTCC 6240

GACTAGTATG CT 6252

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6730 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

ATCAAATCnC AAAATATTTA TTAATnAnAA GGGGATTATC CaTGTgAGAA ACAAAGTAAT 60
GCTCTTTTTT TACCTCTTGT GGGTTGAAAA aTGGATCATC AGAGATAGAC TTCTTCTTTT 120
TCGAAGATGA CATTTGATAC TTTAATCTTC TAAAACCATA ACTTGTCGCA TCAAAAATGC 180
CTTCTTGTAC AAGTAAAATC AAAAATATGC TAATAAAAAT AATTAATGAA ACATAAAACA 240
ATATATTTAA ATATGTAATG ATAGTATGGC TATTAAAAAG CCATATAATA AACGTTAATA 300
TTGGCGTTAT TAGTGCCATT CCAAGCCATT TTTTCAACAT TTGATCACTC CCACTTATAG 360
AAAACTCTTA CGCATAGTTT ACATTAAAAT CAGACATTGA GGAATGATTT TTTAATTTCT 420
TCAGCTTTAT TGAAATTCTA AAATCAATCA TTCTTCATTA GTTTAAAGCA AAAAAATATT 480
GATATATAGT AAATATTGTA TATATAATAT TAGTTAAGAT TTCaGAAAAT TTTGAAGGGA 540
ATGGAAATTT AGAAATCGGA ATTTGTTAGA GGAGGGGATT AGATGGGGAA ATATATTTTC 600
AAACGATTTA TTTATATGCT TATTTCTTTA TTTATTATTA TTACAATTAC ATTTTTCTTA 660
ATGAAATTAA TGCCAGGTTC GCCATTTAAC GATGCTAAAT TAAATGCTGA ACAAAAAGAA 720
ATTTTAAATG AAAAATATGG ATTAAATGAT CCTGtAGCTA CGCAgTATTT ACATTATTTA 780
AAAAATGTTG TTACAGGCGA TTTTGGTAAT TCATTCCAGT ATCATAATCA ACCTGTGTGG 840
GATTTGATTA AACCGAGACT ACTACCTTCT TTTGAAATGG GTCTTACAGC AATGTTCaTC 900
GGTGTGATAC TGGGACTTAT TTTAGGTGTT GCAGCAGCTA CTAAACAAAA TTCTTGGGTT 960
GACTATACAA CTACAGTTAT TTCAGTTATT GCAGTATCTG TACCATCTTT TGTACTTGCT 1020
GTACTTTTAC AATATGTATT TGCAGTTAAA TTAAGATGGT TCCCAGTAGC TGGATGGGAA 1080
GGTTTTTCGA CCGCGGTATT ACCGTCACTT GCATTATCTG CAGCTGTTTT AGCAACTGTC 1140
GCCAGATACA TAAGAGCAGA GATGATAGAG GTATTAAGTT CAGACTATAT TTTATTAGCG 1200
AGAGCTAAAG GTAATTCGAC AATGCGTGTA CTTTTTGGAC ATGCACTTAG AAATGCTTTA 1260
ATTCCAATTA TTACAATTAT CGTTCCCATG TTAGCAAGTA TTTTAACAGG CACTTTAACA 1320
ATTGAAAATA TTTTTGGAGT TCCTGGATTA GGGGATCAAT TCGTACGTTC AATTACAACA 1380
AATGATTTCT CAGTAATCAT GGCAATCACA CTATTATTTA GCACACTGTT TATCGTTTCT 1440
ATTTTTATTG TAGATATTTT GTACGGTGTG ATAGATCCAC GAATTCGTGT TCcAAGgAGG 1500
TAAAAAATAA TGGCTGAAAA TAAAAACAAT TTGTCGATTA ACGACGATCA TTCTAATGCA 1560

TGAATCAGGA ACCTGAAATG CAACGAGAAA GCAAAAACTT TTGGCAAGAT GCTTGGGCTC 1680

AGTTAAAACG AAATAAGTTA GCTGTTGTCG GTATGATAGG TTTAATTATC ATTGTAATAT 1740

TTGCTTTTAT CGGTCCAGTT ATAAATAAAC ATGATTATGC TGAACAAAAT GTAGAACATA 1800

GAAATCTTCC GGCAAAAATA CCTGTATTAG ACAAAGTTCC ATTTTTACCT TTTGATGGTA 1860

AAGATGCAGA TGGCAAGGAT GCTTATAAAG CAGCAAATGC TAAAGAAAAT TATTGGTTTG 1920

GTACTGATCA GTTGGGTCGA GATTTATGGA CAAGAACATG GAAAGGTGCT CAAATTTCAT 1980

TGTTTATCGG TGTTGTTGCA GCGATGTTAG ATATTTTTAT TGGTGTTGTA TATGGTGCGA 2040

TTTCTGGATT CTTCGGTGGA CGTGTCGATA CGATTATGCA ACGTATACTT GAAGTCATAG 2100

CATCTATTCC GAATTTAATT GTCGTAATTT TATTTGTATT AATTTTTGAA CCATCCATTT 2160

GGACAATTAT ATTGGCTATG TCTATCACAG GCTGGTTAGG CATGAGCAGA GTTGTACGTG 2220

GAGAATTTTT AAAATTAAAA AATCAAGAGT TTGTCATGGC TTCGAAAACA TTGGGGGCTT 2280

CAAAATTCAA ATTGATATTT AAGCATATTT TACCTAATAC ATTAGGTGCT ATCGTGGTTA 2340

CATCAATGTT TACAGTACCT AGTGCTATTT TCTTCGAAGC ATTTTTAAGT TTCATTGGTA 2400

TAGGTGTACC CGCACCTCAA ACATCGTTAG GGTCATTAGT AAATGATGGG CGCGCAATGT 2460

TATTAATTTA TCCACATGAA TTATTTATAC CAGCAATGAT TTTAAGTTTA TTAATTCTAT 2520

TCTTTTACTT ATTTAGTGAT GGATTACGTG ATGCATTTGA TCCGAAAATG CGTAAATAAA 2580

AAGGGGGCAT AGCATATGAC TGAAAGAATA TTAGAAGTAA ATGATTTGCA TGTTTCCTTT 2640

GATATTACAG CAGGGGAAGT GCAGGCAGTG AGAGGCGTAG ATTTTTATTT GAACAAAGGG 2700

GAAACATTGG CAATTGTTGG TGAATCAGGT TCAGGTAAAT CTGTAACAAC AAAAGCAATT 2760

ACAAAATTAT TCCAAGGGGA CACAGGAAGA ATTAAAAAGG GAGAAATTTT ATTTTTAGGG 2820

GAAGATTTAG CAAAAAAACC TGAAAATGAG TTGATTAAAT TACGTGGCAA AGATATTTCA 2880

ATGATCTTTC AAGATCCAAT GACATCTTTA AACCCAACGA TGCAAATTGG TAAACAAGTC 2940

ATGGAACCAT TAATTAAGCA CAAAAATTAT AGTAAAGCAC AAGCTAAAAA GCGCGCATTG 3000

GAAATACTAA ATCTTGTAGG TTTACCAAAT GCAGAAAAAA GATTTAAAGC ATATCCTCAT 3060

CAATTTTCAG GTGGACAAAG GCAAAGAATT GTTATTGCAA CCGCATTAGC TTGTGAACCT 3120

AAAGTGCTCA TTGCTGATGA ACCAACGACT GCATTAGACG TAACGATGCA GGCACAAATT 3180

TTAGATTTAA TGAAAGAACT ACAACAAAAA ATCGATACAG CAATTATTTT TATAACGCAT 3240

GATTTAGGGG TTGTTGCGAA TATTGCTGAT AGAGTGGCAG TTATGTATGG TGGTCAAATG 3300

GTTGAAACAG GAGATGTTAA CGAAATATTT TATGATCCAA AGCATCCATA TACATGGGGA 3360

GGAGCGCCAC CTGATTTATT ACACCCACCT AAAGGTGATG CATTTGCGAG ACGTAGcAAT 3480

ATGCATTAGA TATTGATTTT AAAGTAGAAC CACCGTGGTT TAAAGTTTCA CCGACACATT 3540

TTGTGAAATC TTGGTTATTA GACGCACGTG CACCAAAAGT TGAACTACCC GAGCTGGTAA 3600

AACAACGTAT GAAACCGATG CCTAATAATT ATGAAAAACC ACTCAAGGTA GAAAGGGTGT 3660

CGTTCAATGA AAAATGATGA AGTGCTATTA TCTATTAAAA ATTTAAAGCA ATATTTTAAC 3720

GCAGGAAAGA AAAACGAAGT GgaGCGATTG AAAATATTTC GTTTGATATA TACAAAGGGG 3780

AAACATTAGG TTTAGTAGGA GAATCGGGGT GTGGTAAATC TACAACTGGT AAATCAATTA 3840

TTAAACTTAA TGATATTACA AGTGGAGAAA TTTTGTATGA GGGTATTGAT ATACAAAAGA 3900

TTCGTAAACG TAAAGATTTG CTTAAATTTA ATAAAAAGAT ACAGATGATT TTTCAAGACC 3960

CATATGCGTC TTTAAATCCT AGGTTAAAAG TAATGGATAT AGTAGCTGAA GGTATTGATA 4020

TCCATCATTT AGCAACTGaT AAGCGTGACC GAAAAAAACG TGTCTATGaT TTACTTGaAA 4080

CTGTTGGATT AAGTAAAGAA CATGCCAATC GCTATCCTCA TGAATTTTCA GGTGGaCAAC 4140

GCCAACGTAT TGGaATTGCC CGTGcATTAG CCGTTGaACC AGAATTCATT ATCGCGGACG 4200

AACCAATATC GGCATTGGAT GTTTCAATCC AAGCTCAAGT AGTTAATTTA TTATTAAAAT 4260

TACAACGTGA AAGAGGGATT ACGTTCCTAT TTATAGCTCA TGATCTATCA ATGGTGAAGT 4320

ATATTTCAGA TCGTATTGCA GTCATGCATT TTGGGAAAAT AGTTGAAATT GGACCGGCAG 4380

AAGAAATTTA TCAAAATCCA TTACACGATT ATACTAAGTC TTTATTATCA GCCATTCCAC 4440

AACCTGATCC TGAATCAGAA CGCAGTCGCA AACGATTTAG TTATATTGAT GATGAAGCAA 4500

ATAATCATTT AAGACAATTA CATGAAATTA GACCGAATCA CTTTGTCTTT AGTACTGAAG 4560

AAGAAGCGGC ACAACTACGA GAAAATAAAT TGGTGACACA AAATTAAGGG GAAGGGGGAA 4620

ATGCAATGAC GAGAAAATTT AGAACACTTA TTTTAATTTT GATTGCTACA ATTGCATTAA 4680

GTGGTTGTGC TAATGACGAT GGTATTTATT CAGATAAAGG TCAAGTATTC AGAAAAATTT 4740

TGTCATCAGA CTTAACATCC CTTGATACAT CATTAATAAC GGATGAAATA TCTTCTGAAG 4800

TGAcTGCGCA AACATTCGAA GGTTTATACA CATTAGGAAA AGGTGACAAA CCGGTGTTAG 4860

GTGTTGCGAA AGCTTTTCCT GAAAAGAGTA AAGATGGTAA AACTTTAAAG GTTAAATTAA 4920

GAAGCGATGC TAAATGGAGC AATGGTGACA AAGTGACTGC ACAAGACTTT GTTTATGCTT 4980

GGAGAAAAAC AGTTGACCCT AAAACAGGTT CTGAATTTGC ATACATTATG GGGGACATTA 5040

AAAATGCGAG TGATATTAGT ACTGGTAAGA AACCTGTAGA GCAATTAGGT ATCAAAGCAT 5100

TAAATGATGA AACATTACAA ATTGAATTAG AAAAGCCGGT TCCATATATT AATCAATTAT 5160

ACGGTACGGC AGCTGATAGA GCGGTATACA ATGGTCCaTT TAAAGTTGAT GATTGGAAAC 5280

AAGAAGATAA AACCTTACTA TCTAAAAATC AGTATTATTG GGATAAAAAG AATGTAAAAT 5340

TAGATAAAGT GAATTATAAA GTTATTAAAG ACTTACAAGC CGGTGCATCA TTGTATGATA 5400

CTGAATCAGT AGATGACGCA TTTATTACTG CAGATCAAGT AAATAAATAT AAAGACAACA 5460

AAGGATTAAA CTTTGTGTTA ACGACTGGGA CATTTTTTGT AAAAATGAAT GAAAAACAAT 5520

ATCCTGATTT TAAAAACAAA AATTTAAGAT TGsTATCGCA CAAGCAATAG ATAAAAAAGG 5580

ATACGTTGAT TCAGTGAAAA ACAATGGCTC AATTCCTTCC GATACACTAA CAGCCAAAGG 5640

AATTGCGAAA GCGCCTAATG GCAAAGATTA TGCGAGTACC ATGAATTCGC CTTTAAAATA 5700

TAATCCTAAA GAAGCAAGAG CACACTGGGA CAAAGCTAAA AAAGAGTTAG GTAAAAATGA 5760

AGTGACATTT TCAATGAACA CAGAAGATAC ACCAGATGCA AAAATATCTG CTGAATATAT 5820

CAAATCGCAA GTTGAGAAAA ATTTACCAGG AGTTACTTTG AAAATTAAGC AATTACCGTT 5880

TAAACAAAGA GTATCACTAG AACTGAGTAA CAATTTTGAA GCATCACTTA GTGGTTGGTC 5940

TGCAGATTAC CCTGATCCTA TGGCTTATTT AGAAACAATG ACCACAGGTA GCGCACAAAA 6000

TAATACAGAC TGGGGTAATA AAGAATATGA TCAATTACTT AAAGTAGCAA GAACCAAATT 6060

GGCACTTCAA CCGAACGAAC GATATGAAAA CTTGAAAAAA GCAGAAGAAA TGTTCCTAGG 6120

AGATGCACCG GTAGCACCAA TTTATCAAAA AGGTGTtGCA CATTTaACAA aTCCTCAAGT 6180

AAAAGGATTA ATTtACCATA AATTTGGTCC AAATAACTCA CTTAAACATG TATATATTGA 6240

TAAATCGATA GATAAAGAAA CAGGTAAGAA GAAAAAATAA TATGCTTTGT AAATTAGGCT 6300

GGAGACATAT CTCCAGTCTT TTTGTGTTGG ATAAAAaCTT TGGGAATAAA AATTTAAAAT 6360

AAGTCGTTTT TTAAATTACT GAAATTGATT AAATGCATAA ATAACTGAAT ATTCTAAAAA 6420

TAAACTTGTA ATAATTTTTT CTATGAGTAA ACTAAAAAGA AAAAATTAGA TTGAAAGTAG 6480

GAGGCATATG TATGGGGAAG CTAATTAAAT ATATTTCAAT ACTTCTTATT GTCGTTTTAG 6540

TGTTGAGTGC TTGCGGAAAA AGCAGTAATA AAGATGAAGG AGTAAAAGAT GCTACTAAAA 6600

CGGAAACCTC AAAACATAAA GGTGGTACCT TAAATGTAGC ATTAACAGCA CCGCCAAGTG 6660

GTGTTTATTC TTCGTTATTA AATAGTACAC ATGCAGATTC TGTAGTTGAG GGATATTTTA 6720

ACGAAAGCTT 6730

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

AATTTTTGTC ATTATTAAAA ACCTCGCTTT TAAAAGATTG AAAAGTAAAT GAGTGAAATT 60

AAAGATTATG CACATTAAAA TCACGCCACA ATTTAATTGT GAAAAATATC ACAAATATAT 120

TATAACACTA AATTTCCCAA AATTCAAAAG TGTGTTTTAT TGCAGAAAAC TTATAACAyG 180

TGCACAAGTT ATAGTGAATT GCAAACGGAT TACTTTAGTC TTTTTAAAAC ATGAAGTATA 240

ATTTGTATAG CAATAAATAT AAAAATGGGA GGCTATGTTC AATGAGCAAT ATGAATCAAA 300

CAATTATGGA TGCATTTCAT TTCAGACATG CGACTAAGCA ATTCGATCCA CAAAAGAAAG 360

TTTCGAAAGA AGATTTTGAA ACAATATTAG AGTCAGGTAG ATTGTCTCCA AGTTCTCTTG 420

GGTTAGAACC TTGGAAGTTT GTCGTGATTC AAGATCAAGC GTTACGTGAT GAATTAAAAG 480

CGCACAGTTG GGGCGCAGCA AAACAATTAG ATACAGCGAG CCATTTTGTG CTAATTTTTG 540

CGCGTAAAAA TGTAACGTCA AGATCACCGT ATGTACAACA TATGTTAAGA GATATTAAAA 600

AATATGAGGC ACAAACGATT CCAGCTGTTG AACAAAAATT CGATGCATTC CAAGCAGATT 660

TCCATATTTC TGATAATGAT CAAGCCTTGT ATGACTGGTC AAGTAAACAA ACGTATATTG 720

CATTAGGCAA TATGATGACG ACAGCCGCAT TGTTAGGTAT TGATTCATGT CCGATGGAAG 780

GTTTTAGTCT GGATACAGTG ACAGACATTT TAGCAAATAA AGGGATCTTA GATACTGAGC 840

AATTTGGTTT ATCAGTGATG GTCGCATTTG GCTACAGACA ACAAGAGCCA CCGAAAAATA 900

AAACACGCCA AGCTTATGAA GATGTTATTG AATGGGTTGG ACCAAAAGAA TAAATAGAAT 960

ACCGTATGTC TAAATATATA AAATTAAAAA GTTAGCAATA AAAAAGCCTG CGATTACATA 1020

AATGAATCGC AGGcTTTTGC GTGAAAAAAT TGTATTAATA AAGTATGGAT GATTATTTTT 1080

CTGGAACAAG GTCAGTATTT GAATGAACTG TGATGTCAAA CCCTTCTGGT GCCGTAAATG 1140

TATGTGTTGA GGCGTCGGGT TGATAAATAT CAACATGTGT TAATCCATAA CTTTGTGAAT 1200

TGTTTTGTCT TGCTTGATTG GATTGCCAAG TATTAGCAGC AATATGATGG TGATAATGAT 1260

TCGTTGACAT AAATAGCGCA CGTGGAAAAT CAGACACATG TTGGAATCCT AATTGTTCAA 1320

TGTAACATTG ATATGCTGCG TCTAAATCAT GTGTTTTTAA ATGTAAGTGT CCAATCATGC 1380

CTTTTGCTGG CATTCCTTGC CAACCTTCAT CAGTACGATG TGTTAATAAG GTTTGGCTAT 1440

CAACTTCTAA AGTATCCATT TTAACTTTGC CATTTTGCCA TTCCCATGAA GATGAAGGTC 1500

TATCGCGATA GACTTCAATA CCATTACCTT CGGGGTCGTT GAAATATAAA GCTTCACTTA 1560

CTAAATGATC ACCAGCGCCG ATGCCCATAT TTTTTTGTGC CACGAAATAT AAGAAGTTAG 1620

aAGTCTGACG GcCGTCTTCT AATAAATGTA ACGTTAGAGT ATGGcCACCA GTCCCAACAG 1740

ATAATACGGT TGTATTATCG TCAGAACTTT TAACGGATAG TCCTAAAATG TTTTTGTAAA 1800

ATGTTGTCAT TAAGTCTAAG TCTCTTACGT TCAGTACAAT GTTTGTCACT TGTGTTGCTG 1860

TTTTATCGTG AAATGCCATT ATGCATCGCC TCTTTTTCTA TTTTTCTATA AGTTAGTATA 1920

AAAAGTATAC CAGAAAAGAA AATGAATTGA TAGCATAAAG TTTGAAATGC AAAATAACTA 1980

GTCGTTTTGC AATTTTAtAT TGATGCGAAC AAAAAAGCGA TGGTACAGTT GCACCATCGC 2040

AAAATTTATT TAACCAAGAT ATACATCTTG ATATGAATCT TCTTTTTCTA ACATATGTTT 2100

GGCAAATGAA CATGAGGCAA TAATTTTCAA ATTATTTTCT CGAGCGTGTT CAACAACTGc 2160

TTTAAGTAGT TTTTTGCCAA CACCTTGACC ACCAAGTTCA TCAGATACGC CTGTATGATC 2220

AATGTTAATT TCATTATTAT CCACAAAACG GTATGTGATT TCAGCTAAAG CATTATTTTC 2280

ATCATCACCA ATATAGAATT TGTTCTCGCC TTGTTTGATT TCAAGGTTAC TCATACATAT 2340

CAACTCCTAT CATGATTGAT TATAGTATTT CCCTATTCTA TTTTAACTTA AACGAAGTCA 2400

AAGGTGCATG ACAGTCATGT GACGACATTG CCACATCTAT GTAGTCGTTT TTATTAAGCA 2460

CAGTTTGAAA TGAAGATGAA AACACGTATC TTGACATTAA ATCTATTCAG CTATATAATT 2520

TATCTCGAAA TCGAAATAAA ATAAAAAAGT TGGTGATCAT ATGGATCGAA CGAAACAATC 2580

TCTCAATGTT TTTGTCGGAA TGAATAGGGC GTTAGACACA TTAGAGCAAA TTACAAAAGA 2640

AGACGTAAAG CGATATGGCT TAAATATTAC TGAATTTGCA GTGCTCGAGT TGCTTTATAA 2700

TAAAGGTCCG CAACCAATTC AACGTATTAG AGACCGCGTA TTAATTGCAA GTAGCAGCAT 2760

TTCATATGTT GTAAGTCAAT TAGAGGACAA AGGTTGGATT ACACGTGAAA AGGATAAAGA 2820

TGATAAACGT GTATATATGG CTTGTTTAAC TGAAAAAGGT CAAAGTCAAA TGGCAGATAT 2880

TTTCCCTAAG CATGCTGAGA CATTAACAAA AGCGTTTGAT GTGTTAACAA AGGATGAATT 2940

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AAGGCGACTA ATATGAGTGC GCTCAGCCAA TACGGTAAGT TGAAACTTTG ATGAATGGTT 5520

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TAAAGTTGTT ATAATACAGT TAACAGGAAT TAGCATAGAT ACACCAATCC CCTCACTACT 6060

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GTTGACTGAT AAGCTTTTGA AAAGCCACCA TCAATGACAA GCATCTTTCC ATCAGCCTTG 6480

AT 6482

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16592 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ATTTAAGGCG ATTGCTTGTG TATTTCTCTC TTTTGTAGGC AAACCTGCAC TCGTTCCAAA 60

AAATGTAACT TCCATATATG CCCCTCCTTT TCTTCAATTC ATTTTATCAT AAAATTTGTA 120

AATTTTTCTA ACTTTAACGT AGACATAACT ATATAAATTT TGATAATTAC GTTATACTTA 240

TCATTAATAA GTATCACATT AAACATGATA CATGAATCGA TATTTCATTT AAGACACTGC 300

ATACAGTCGA GCATATTGTA TGACCTACTG AATGGATTAT CTTATAATAA TAAATCATAT 360

ATCTAATTAA GAATTGAGGT TTTAATCTTG AGTACTAAAA ACAAACACAT CCCATGTTTA 420

ATCACAATCT TTGGTGCACT GCGTGACTTA AGCCATCGTA AGTnGTTTCC ATCAATATTC 480

CATCTCTACC AACAAGACAA TTTAGATGAA CATATTGCCA TcATCgGTAT TGGACGTCGT 540

GACATkwnTA ATGATGATTT CCGTAATCAA GTAAAATCAT CAATTCAAAA GCACGTAAAA 600

GATACAAACA AAATTGACGC GTTTATGGAA CATGTCTTCT ATCATAGACA TGATGTTAGT 660

AATGAAGAAA GCTATCAAGA ATTACTAGAT TTTAGTAATG AATTAGATAG CCAATTTGAA 720

TTAAAAGGTA ATCGACTATT CTATTTAGCA ATGGCACCAC AATTCTTTGG CGTTATTTCT 780

GATTATCTAA AATCTTCTGG TCTTACTGAT ACAAAAGGAT TTAAACGCCT TGTTATCGAA 840

AAACCATTCG GTAGTGATTT AAAATCAGCC GAAGCATTAA ACAATCAAAT TCGTAAATCA 900

TTTAAAGAAG AAGAAATTTA TCGTATTGAC CACTATTTAG GAAAAGACAT GGTTCAAAAT 960

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TTAGCTATGG AAGCACCTAT TAGTTTAAAT AGTGAAGATA TCCGTGCTGA GAAAGTAAAA 1200

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CtAAATGcTA AGaAAAATAC ACAAGGTATC gAAACAGrAC CTGtCCmATT GtCTTACTCm 1620

ATGaGCGcTC aAGaTAAAAT GaATACTGTA GATGCATATG AAAATCTATT ATTTGATTGT 1680

CTTAAAGGTG ATGCCACTAA CTTCACGCAC TGGGAAGAAT TAAaATCAAC ATGGAAATTT 1740

GTTGATGCAA TTCAAGATGA ATGGAATATG GTTGaTCCAG AATTCCCTAA CTATGAATCA 1800

GGTACTAATG GTCCATTAGA AAGTGATTTA CTACTTGCTC GTGATGGTAA CCATTGGTGG 1860

GGACGATATT CAATAATTGA ATTAAAACGC ACATGTTAAA CAAAAATAAA TGAGCGAATG 1920

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TAGAGCCTTT CAATTTGCAA GAATTAAGTG ATTACGTTGG TCTTTCGCCA TACCATCTTG 2220

ATCAATCATT TAAAATGATT GTCGGCTTAT CTCCAGAAGC TTATGCACGC GCGCGTAAAA 2280

TGACACTCGC TGCAAATGAT GTGATTAATG GTGCTACACG ACTTGTAGAT ATCGCTAAAA 2340

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CACCTATTCA AGCCTCTACT AAAAAAGATG AATTACAAAT TCAAGAGCGA TTATATATCA 2460

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CGGATTTTTT AGAAGACTTG CTCATTGATG GTAAAATTAA AGAGTTACGA CGATATAATG 2640

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ATGATGGTCG CTCATCGATG CAACTTGTGG TAAGTGAGAG ATACAAATAA CTTGTATATA 16560

TTCTGCTaTA TCTCGCATTT TCTCTGCCAT TT 16592

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13794 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

CCAATACAAC GTAAAAAGAT TGCTTGTGTT ATTAATGAGT TAGATAAAAT AATTAAAGGA 60

TTTAATAAGG AAAGAGACTA CATAAAATAT CAATGGGCTC CAAAATATAG CAAAGAnTTT 120

TTTATACTTT TTATGAACAT TATGTACTCA AAAGATTTTT TAAAATATCG ATTTAATTTA 180

ACATTTCTTG ATTTATCTAT CTTATATGTA ATATCATCTC GAAAAAATGA GATACTAAAT 240

TTAAAAGATT TGTTTGAAAG TATTAGATTT ATGTATCCTC AAATTGTTAG GTCAGTTAAT 300

AGATTAAATA ATAAAGGTAT GCTAATCAAA GAACGATCCC TTGCAGATGA AAGGATTGTG 360

TTAATCAAAA TAAATAAAAT ACAATATAAC ACTATTAAAA GCATATTCAC AGATACTTCC 420

AAGATTCTCA AACCAAGAAA ATTTTTCTTT TAAATTTAAA CAGATTTACC TCTTGATAAA 480

ATAAATAAGC AATCATACTA CTTCTCAATT TAGTATAAAT AAAAATACAT AATTAACTTT 540

CTTTTGTTTT TATATTATTT CAATACCCTA CTATATATCA CAACACATAA ATTAAGCATG 600

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TCATTTTTTG TGCAcTTTGT TAAATATAGG CCCTGCAATG AGTGTAACTG GaATGGCAAT 9540

AATCATACCA TACAGTAATA CATCTCCAAC ATTTGCCTTT AATTCTTTTG CGATGACTAC 9600

CGGTCCTGGA TGTGGTGGTA AAAAGCCATG TGTCACTGAT AAAGCTGTTA CCATAGGTAG 9660

TCCTAGTTTT AACACTGAAA CATTTGCGCG TTTTGCTACT GTAAATACTA ATGGAATCAG 9720

TAAGACTAAA CCTACTTCAA AGAACAATGC AATACCGACG ATAAATGCTG CAACAAGCAT 9780

TGCCCATTGT ACATGTTTTT GACCAAATTT TTGAATCAAC GTGTCTGCGA TTCGAGTTGC 9840

ACCACCACCA TCAGCAAGCA ATTTCCCAAG TATGGCACCT AAACCGAATA TCAGTGCAAT 9900

GTGGCCGAGC GTACTGCCCA TTCCTTTCTC AATCGTCTCC ATAATTTTAG TCAATGGTAT 9960

ACCTAGCATT AACGCTGTAA TCATCGATGT GATAATTAAT GAAATAAATG TATTTAATTT 10020

AAACCCAATA ATTAATACTA ATAAAATAAC GATACCTAAA ACAACACTGA TTAACGGCCA 10080

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TGTTCATAAT TCTCTGTTAA AGAACGACTT AAATTGATAA AAATGGATAC GATCTCTTGG 10320

TAAACAGTGA CATTTTCTTC AATCGGCGTA TGATTGTTTG TGGCACCGAC CATCGATGAA 10380

ACGATTGAAA AATCTTCAAT GTCACCTACA GCTTTAAGTC CGAGCACGCA GGCACCTAAG 10440

CATGAACTTT CATAACTTTC AGGAACCACT AACTCTGTGT CAAATATATC TGACATCATT 10500

TGACGCCATA CTTCACTTTT CGCAAAACCA CCTGTTGCTT TTATCATCTT AGGTGTTTCA 10560

TTCATTACTT CAATAAGCGC AAGATAGACG GTATACAAAT TGTAAAGAAC ACCTTCTAAT 10620

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ACACATGTGC ACCCATTCTT TCTAATTGGA TGAGTTGATT TTGTTGCAAT AATTTAAATG 12300

CATCTCGAAT TGGCGAACGA CTCACATTAA ATTGCTTTGC CATTTGATTT TCAGTGAGTA 12360

ACGTACCTTC AGCTATGTGA CCATTCACAA TGCCTAAGCG TAATTCTGCC GCGATACCTT 12420

CTCCAGTTGT CATACCTTCC AACCATTTCT CTGGATATCC ATACATCATC AAAGTCACTC 12480

CTTCATTACA CGACATACTT GTATACAAGT ATGTTAATAT AGTTATTATG AGTTTGCAAG 12540

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ATTCGAATCG ACGTGTTGTC GCTGTATGTT TCGCTTTGAT AACTGCCCAC AAAGATGGTG 12780

AGAATATATG CTGGCAGTTA GGACATAAAT AGGCAACCTT TTGTTGGTAA TAAAAAGTAA 12840

CACCAATGCC ATAACCAATC ATAAATGGTA AAGCAATTAA AAACGGCCAT TTATTTTTCA 12900

TCAAAATTGC ACTTATAATG CTAGAATATT GAATTATTCC TATAATACCA GCACTAATCC 12960

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TTTCAGTAAA TCTCGATACT TTTCCGTCTC TGCATTGTTT TTATAACGTA TTTTATGTTC 13680

TAAACTTGCC CACATATCCA TACCTATCGT TCTAATTTGA ATTTCAACAG GCAATACCTC 13740

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1059 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GGATAAGTTC AGGTAAATTC ATTTCTTTTT CAATTTTGAT TTTCATTGTT TCCGCCCTTT 60

TAAAATAAAG TTAGTTGCTT CTGTTCCTCA TATTCCAAAT CACTTTGCTT TATATATGTT 120

TCAAGCTCTT CCGCTGTATC AAATGTCTTT TTCACACCTT GCCAACCTGG CACGATATGA 180

CCGTGAAAGT AATAAGTGCC ATTTACTACA TGGATATGTG CCACTCGTTC GTTATCCTGA 240

TACAGATATC TCTTAGATCC AAAGAATTGA TTTAGGTATT CTTTACGCGC GCTATCTGTC 300

ATGGTCATCA CTCCTTTTAA CAATTAGGCA GACCAAACGA CATGCATTCG TCGTATAGCT 360

CTTCATTACT TATGCTTGCC TTATAGTTTT CAATCACATT GCTAACTTCT TTATGACTCA 420

TTGCTTTAAC TTGTTCGTCT GTATATTTTT CGCAGTCTTC TAATTCCAGT TGCTCCTGTA 480

ATGACATCAC ATATTCAACT TGTCTTTGGG TTGCCATCGT TAACCCTCCC ACAAGTCAAA 540

AGCTCTTTGG ACGTAAAACT TCGCCTTTGC TAAATCCTCA TGACCATTCT TTAACGGTGC 600

TCTAGACATG TATTTGATTG CATTACCTAT TGCGAATGCT AGTTGAGGTG GATACTGTGC 660

CGTAACCTGT TCGATAAAAT CTATAATTTC AATGTCGCCG TATGTGTAGT GCGCTGGTTG 720

CTTAACATTG TCTTGCGCTT CGTTCATATC TACTTTTCTG TTACTGATTA CGCTCATTAT 780

GCTTCACTCC ATTTCTTGAA CATTTGGTTA TAAGTGACAT CGAACCAGTA CGGATCACGT 840

GAATGTTTTT GTGGCGTTCC ATCATAAAGC CATGGTCTTA ATCTTCTCTT TCTTTCCTGT 900

TCATATTCCG CTCTCACATT TCGTTGGTAT CGGTTCAAAA TCGCTTTTTT TCTGATTTTT 960

TCTCTCCCTT TTTCTTCATC TTTnATTtTGA CTCTnCATAT ATTCAACTTC TTCTGTAGAT 1020

nTTGAGTCCT TTCTTCCACA CAATAATTCA nCGCCGCGC 1059

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GAAGTAAAAG AAGAATTAAA TTTAACATTA ACAATGGATG AAATTGAATA TGTCGGGACA 60

ATTGTAGGTC CTGCATATCC ACAACAGGAT ATGTTAACTG AGTTAAATGG ATTTCGCGCA 120

TTAACCAAAA TCGATTGGGA AAACGTAACT ATCAATAATG AAATTACGGA TATACGCTGG 180

ATTGATAAAG ATAATGATGC GTTGATTGCG CCTGCTGTCA AAGTTTGGAT TGAAACTTAT 240

GGTGGTAAAC ATGACAAATA ATGACACCAT CATGTTACGA CATTATGTCC CACAAGATTA 300

TTCGATGTTA GAAGCTTTTC AATTAAGTGA AAGTGATTTG AAGTTTGTTA AAACGCCAGA 360

GGAAAATATT ACAGCTGCAA TGTCTGATAA TGAAAGGTAT CCCATCGTTG TAATGGATGG 420

CAGGCAATGT GTGGCCTTTT TTACATTACA TCGTGGAAAA GGGGTCGCAC CATTTAGCGA 480

TAACCAAGAT GCAGTATTTT TCAGGTCATT TAGTGTTGAT CAACGTTATC GTAATAGAGG 540

AATAGGTAAA GTGGTAATGG AAAAATTGGC GTCATTTATC ACTTCAACAT TTCAGGATAT 600

TAATGAGATT GTGTTAACGG TTAATACTGA CAATCCACAT GCCATGGCAC TTTATCGCCA 660

ACAAGGATAT CAATATATGG GAGATAGTAT GTTCGTCGGA AGACCTGTTC ATATTATGGC 720

GTTAACTATA AAATAAATTA AATTTAAAAG CATCTTTACT CATCGTCGAC CACAACAATT 780

AATGATGAAT AAAGGTGCTT TTTGTTATAG ATCATCGGAC AATTTACTAT AGTAAAAAGC 840

GACCTAGTGA ACAATTGACA TATATCCACA GGTCGCTTAA CTTAAGTTAT ATTGCTAGTT 900

GCGATTAATT GATAGACTCA TCATTTTTGC GCTGTCGAGA TGGTCTTTTT ATTAAAAATG 960

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AAATAAATTC TTGGGCAAAT ATTTTCGAGT TTATAATATG ACCAAATGAA TATTTAAGTT 1080

TGAAAAACCA AATAAATAAA GCAAGTTGGC CACCAAAAAA GGCAAGGTAA ATCGTGTTCG 1140

CAGATGTCGC TAAAATTTCT CTACCAACAC GCATGCCAGA TTGGAATAAT TCGTATTGCG 1200

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ATGACCGAAG TAGACCGATA AATAAATGAG TGTAATCAAC AATATTGTTG TAACGATAgT 1440

GCtGgATAAA TGCaGCTTGT GTTTTAACAT TGTAACTATT GAGTACGAAT AAATTACAAG 1500

CGCCAATAAT AATGCAGAAA AAGAATGTGA CGACATAAAT CGGTACGCCA AAAATAATCA 1560

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TGCACCGGAT AAATATGAGA ATAATAAGAT GTTAGTCATT GTTCCCATAA TATCTTGGCC 1920

GATGTTTCGC CCAGCAAGCG CCCATCTCCT CATTGAAATG TGTGGCGTAC GCTGTAAAAT 1980

TTCATGCATA CCACTAGCAA TTGTAATTGC AACATCCATA ATAGCGCCAA GTGAACCTAT 2040

TAACACTGAG GCTAGGAAGA TATCTTTCGG TGGTAATGAT AAAAAGTTCA TCGTTTCATA 2100

TTTAATGCCT TTACCATCTG TCATATATAT GATTAATTCT GTTAAACCTA TACTCAAAAA 2160

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CTTGTTAGAA ATATGTAATA ATACTTTTTC GTGTGTGCGA AATGCCTCAG AATCTGCTTG 2520

CGATTTGACG TACTGATGAT TAATCGTCGT CGTTTCTCCA GCAAATTGAC CATTTAATAT 2580

TTTGACTTTT AATTGATTTT TATATTTAAT ATCACGATTA TTTTGTGCAT CTTTTGTAGG 2640

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ATTAAATGGC TTTGTAAATA AATTTCTATA TTTCAAAAAC AAAACCCCAA TTCTATGAAT 2820

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GTAAAACGAA AATCATCATT GATAGCATCG AATTACTTAA TGGAATGTAG ACGTTTTAGT 2940

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TGTAATAGCA CATATCGTTC TTTTTAATTC AGTATGATCT AATTTTATAT CTATCCATGA 3060

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AAGTTCCGTG AAACCAATGT CTATATTCCC ATTTAATACG CTATTTATAA TTGTGTCATG 3420

TTCTAATAAG CTCGGTATGA CATGTGTATC ATTTTGTAAA TGAAACGTTT GGATAAGTGG 3480

TAGTAACATG TGGGATACGT CACTCTCATC ATAGCCAATG TAGATACTTT TATTTTTAGT 3540

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GAAGGCGAAG GGTTATCAAT TCTTGGTTAT CGTAATGTAC CAGTTAATAA AGATGCCATT 4380

GCTAAACATG TAGCAGATAC GATGCCAGTC ATTCAACAAG TGTTTATTGA TATTAGGGAC 4440

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TGGTTACGAT CAGACCAAAT TAAAAAACTA TATACAGATT TATCGGATGA TTTATATCAA 4620

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CAAGTTGATG GAAGCAACAA AGTAAGTGCG ATTAAACAAG TTGCTTCTGG GCGTTTTGGT 6720

GTAACTAGTG ATTATTTACA ACATGCCAAA GAAATTCAAA TTAAAGTTGC GCAAGGTGCA 6780

AAGCCTGGTG AAGGTGGTCA ATTACCTGGT ACTAAGGTAT ATCCGTGGAT TGCGAAGACA 6840

AGAGGGTCAA CGCCAGGTAT CGGTCTGATT TCACCACCGC CACATCATGA TATTTATTCA 6900

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GTTGCAACTC AAAACAAAGA TTTACGTGCT TTATATAGAG GTAAAGCACA TCATGTTGTT 7380

AATTTTATGC ATTTTATTGC ACAAGAATTA AGAGAAATTT TAGCATCTTT AGGTTTGAAA 7440

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GAAGTAACGA AGCCATATAT TGCTGAAGGG CGTCGCTATA CAGGTAGCTT TACAGTAAAT 7680

AATGAACAAC GTGATGTAGG GGTTATTACA GGTAGTGAGA TTTCGAAACA ATATGGAGAA 7740

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CAATTGGAAA CTACATTCCT GAATGGAACG ACTTAGTGTA TCATCAAGAT TTTAAAACTG 8760

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AGAAGCATTT GTTGTTAAGC AAATTTTACA ACATTTAGCT ACGAAACATG GAATTAATTT 30240

TCAAGA 30246

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TATTCCCCCA TCGGTTTATT AAATCGTCCA TTTCAATACT GTTTTTCCCC AAGATGTCGA 60

TAAATCCATT TCAAACGCTT GGACGATATC TTGCATCGTA CATACATTAA TTTCATGTCC 120

TTTTAATAAT GCTAACTTTT CAACTATGTC TGGGTACTTA CGATATAAAT CAACAACTTG 180

CTCAAAATCT TTAGAGCCGC TTCGACTACT ACCAATCAAC GTTAATCCTT TTTCAAGTAC 240

TAATCGTGTA TTCACTTCCA CGGGTAATTC ACTTACGCCT AACAAAGCAA TACTGCCTTC 300

TGGTGAAATA TGTTCAACTA TTTGTTGAAG TGCAACTTGA CTTCCTTTAC CTCCAACACA 360

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ACCAAAGCTG GTTTTCAAAG GTATAGATTT ACGTTCAAAT CGTTGTATAG CATGATAACT 600

TACTGACACT AACTCTGTGT ATGAAATCGT ACTCAAATCA ATGTCATTAG GCAGCGGAAC 660

GATACGATCA TGTGCCATCA CAACGTAGTC TTGCATAAAA CCATCATAAC CACTAGATCT 720

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GACATGATTA CCATAAATAT CAACATTATT ATATGTGACG TCGAACTGTC TCGGTGCAAC 1020

GAGTTGATAT ACTTGATTAA TCATCGGCAA TATCACCTTG AATAATGGCA TTTGCTACTT 1080

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TGATTTCAGA ACTTACAATA AAATTTCCTT GGCTTGTTCT TTCAAGTTTT GGATAACCCT 8760

CTTGTTCAAG CCACAAATTG ATTTTTTGAA TGCGATATCC TAGTTGTCTA CGAGACAAAC 8820

CAAATATCGA TTCAAGTTCT TTACCATGAA TAGTAGGATT CAATACAATT TCTCTGAGTA 8880

TCAATCGTCA CACCGATGTA CACACTTTGA ACACATATTT TCAAAATGAG CATGTACATC 9000

ATTGTGATGT TTTAACAACA TTTCAATTAT ATCTATATTT TTTGTGATTT TAATCTTTTA 9060

AAATAAAGCA ATTGAAATTT TTGCATATAT TTTTGTGTTT TGTGTTTTTT TGAAGCATTT 9120

TTAACATACA TATCTCAATC ATTATCAAAT TGTCATGACC ATTGTAACCC AATACAAAAA 9180

CCCTAAGGAC GCTTATATCA GGCGCCTTAG GGTTAACTGT ATCTATTTAA TTAAGTATTA 9240

TTATTCGTAT GTACGTAACT TATGGTCTAT CAAGTTCCAC ACTTCTTCAA CATCAACTGC 9300

TGTAGCAAAA TAAGCATTGG CAGGCTTACC TGTAACATGA TTTAAATCGA CAGCCATAGT 9360

GCCATAAGTT AGTGGACTTT GATGTTCAAT GTCGATATTA ACGGGTACCA TTGTAAACAA 9420

TTCTGGTTGT AACAAATACA AAATTGTACA AGCATCATGT ATTGGACCAC CATCCATATT 9480

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AGGATTATTG ATACTTTCAA AGCGTTCAAT CACGTGATCG TCGGCTAAAA CTTGATGTGT 9600

TACATCTAAA CCAAACACAT TTATAGTAAT CCCACTTTCA AAAACACGCT TCGCTGCTTC 9660

AGCATCTACC CAAATATTGA ATTCTGCTGT AGGCGTCCAA TTTCCAAATG TACCACCACC 9720

CATCAAAGTA ATAGATTCAA TATGCTCAGC GATTCTTGGC TCACGAATCA ATGCCGTTGC 9780

TACATTCGTA AGAGGACCTG TCGCTACAAT TGTTACAGGT GTATCACTCG TCATCACTTT 9840

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TAACGGCCTA TCCGCACCTT TCGCTACTGC TATATCTTGG CGTCCCATAA TATCCAATAC 10020

GTTCAAGGCG TTTGTCGTAT TCTTGTCAAC TGATTGATTA CCTGCGACTG TTGTTACAGC 10080

TAATATCTCT AGTGGACTGT CAATTGCCCC CGCTAAAATT AATGCTATTG CATCATCGTG 10140

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TCAAAAGCTA TATTGAGAAT AATTAGGAGG GATGTTGATG AAATCTTTAT TTGAAAAAGC 10560

ACAGCAGTTC GGCAAGTCCT TTATGTTACC TATCGCAATC TTACCAGCTG CAGGTCTATT 10620

GTTGGGTATC GGTGGTGCAT TAAGTAATCC AAACACCGTT AAAGCATACC CTATTTTAGA 10680

AAATTTACCG GTCATCTTTG CAATTGGTGT CGCAATCGGA TTATCTAGAA GCGATAAAGG 10800

TACTGCAGGT tTAGctGCGC TGCTCGGTTT CTTAATTATG AACGCAACTA TGAATGGCTT 10860

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CAACAGGATT TGTAGCTACC AAGAAAATAC CATCAAATTT TGATGCCATT ACTTCACCAA 13020

CAATTGATTT GAATATTTTC AAGTTTTTAG ATACTAAATC TAAACGTGTT TCTCCAGGTT 13080

TTTGTGCAGC ACCAGCACAG ATGACAACTA GATCCGCATC ATGACAATCA CTGTATTCGC 13140

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AATCAAACGA ACCAAAAACG AGGCATGCAA TCTTCAGCAT TAGCACAAGC TGTAATGGCC 14100

GCAGCGGTTA ATATCGATAA CTTAAGTGTT ATTAAACCAG TCATTATGCC AGTCGCATAT 14160

AAACACTGCG CACTACAAGT TTATGCTGAA CATTATCCAA TTGTGGGGAA AAATTTATTA 14220

AAAGCCATTC AAGACGTGAC AGGATTAGAA GAAAATGACC CTGTCATTCA AGCTTGGGCA 14280

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8779 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GGTATTTTnG GAnGGGTACC TAAAGCAATT CCGGCAAAGG GTnAATCCAG GTACCGAAAT 60
GGACTTCCCG TTATCGATAA TACCGACATA TATTGTGACA AGTAGATTTT ATGGACATTT 120
AGGCTTACTT TTACTTGTGA TAATTGCATG TATGTTTACT GGTATTTAtC CaTCaATACA 180
TATCATTCAA TTATTGATAT ATGTACCGTT TTGTTTTTTC TTAACTGCCt CGGTGACGTT 240
ATTAACATCA ACACTCGGTG TGTTAGTTAG AGATACACAA ATGTTAATGC AAGCAATATT 300
AAGAATATTA TTTTACTTTT CACCAATTTT GTGGCTACCA AAGAACCATG GTATCAGTGG 360
TTTAATTCAT GAAATGATGA AATATAATCC AGTTTACTTT ATTGCTGAAT CATACCGTGC 420
AGCAATTTTA TATCACGAAT GGTATTTCAT GGATCATTGG AAATTAATGT TATACAATTT 480
CGGTATTGTT GCCATTTTCT TTGCAATTGG TGCGTACTTA CACATGAAAT ATAGAGATCA 540
ATTTGCAGAC TTCTTGTAAT ATATTTATAT GACGAAACCC CGCTAACCAT TAATAAATGG 600
AAGTGGGGTT CATTTTTGTT TATAATTTAA GTAAATAACA TATTAAGTTG GTGTATTATG 660
AACGTTTTAA TAAAGAAATT TTATCATTTG GTAGTTCGAA TACTTTCTAA AATGATTACG 720
CCTCAAGTGA TTGATAAACC GCATATCGTA TTTATGATGA CTTTTCCAGA AGATATTAAG 780
CCTATCATCA AAGCATTAAA TAATTCGTCG TATCAGAAAA CTGTTTTAAC AACACCAAAA 840
CAAGCGCCTT ATTTATCTGA ACTTAGCGAC GATGTTGATG TGATAGAAAT GACTAATCGA 900
ACATTGGTAA AACAAATTAA GGCTTTGAAA AGCGCGCAGA TGATTATTAT CGATAATTAT 960
TACCTATTGC TAGGTGGATA TAATAAGACT TCTAATCAAC ACATTGTTCA AACGTGGCAT 1020
GCAAGTGGTG CATTAAAAAA CTTTGGCTTA ACAGATCATC AAGTCGATGT GTCTGACAAG 1080
GCAATGGTTC AGCAGTACCG TAAAGTTTAT CAAGCGACGG ATTTTTACTT AGTGGGTTGT 1140
GAACAAATGT CACAATGTTT TAAACAGTCT TTAGGTGCAA CAGAAGAGCA AATGCTGTAT 1200
TTTGGGCTTC CGAGAATTAA TAAATATTAC ACAGCTGATA GAGCAACGGT TAAGGCAGAG 1260
TTAAAGGATA AATATGGAAT TACAAATAAG TTGGTATTAT ATGTACCAAC ATATAGAGAA 1320
GATAAAGCAG ATAATAGGGC TATTGATAAA GCTTATTTTG AAAAATGTTT ACCAGGATAT 1380

ATCGACACGT CTACATTAAT GCTAATGTCA GATATAATTA TTAGCGACTA TAGTTCGCTG 1500

CCAATAGAAG CTAGCTTGTT AGATATTCCA ACTATATTTT ATGTGTATGA TGAAGGAACA 1560

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GATAAGATGG TGACAAAATG AGGTTTACGA TAATCATACC TACATGTAAT AATGAGGCAA 1800

CAATTCGACA ATTGTTAATA TCTATTGAGA GTAAAGAACA CTATAGAATC CTTTGTATTG 1860

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TGGATATCAA AATGACAGAT CCACATGATA GTGACGCATT TATGGTCATA AAACCAACAT 2040

CAATCGTATT GCCAGGTAAA TTAGATAGGT TAACTGCTGC TTTCAAAAAT AATGATAATA 2100

TTGATATGGT AATAGGGCAG CGAGCTTACA ATTACCATGG TGAATGGAAA TTGAAAAGTG 2160

CTGATGAGTT TATTAAAGAC AATCGAATCG TTACATTAAC GGAACAACCA GATTTGTTAT 2220

CAATGATGTC TTTTGACGGA AAGTTATTCA GTGCTAAATT TGCTGAATTA CAGTGTGaCG 2280

AAACTTTAGC TAACaCATAC AATCACGCAA TACTTGTCAA GGCGATGCAA AAAGCTACGG 2340

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GTAACGATGA AGATTTTAAT AGATATATCA CAGAAATTAT GAAAATAAGA CAACGAGTCA 2460

TGGAAATGTT ACTATTACCT GAACAAAGGC TATTATATAG TGATATGGTT GATCGTATTT 2520

TATTCAATAA TTCATTAAAA TATTATATGA ACGAACACCC AGCAGTAACG CACACGACAA 2580

TTCAACTCGT AAAAGACTAT ATTATGTCTA TGCAGCATTC TGATTATGTA TCGCAAAACA 2640

TGTTTGACAT TATAAATACA GTTGAATTTA TTGGTGAGAA TTGGGATAGA GAAATATACG 2700

AATTGTGGCG ACAAACATTA ATTCAAGTGG GCATTAATAG GCCGACTTAT AAAAAATTCT 2760

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GCTTCGTCGT GCAAGAGAGA TGGGCGATTA TTTAATAGTA GCATTATCAA CAGATGAATT 3000

TAATCAAATT AAACATAAAA AATCTTATTA TGATTATGAA CAACGAAAAA TGATGCTTGa 3060

ATCAATACGC TATGTCGATT TAGTCATTCC AGAAAAGGGC TGGGGACAAA AAGAAGACGA 3120

TGTCGAAAAA TTTGATGTAG ATGTTTTTGT TATGGGACAT GACTGGGAAG GTGAATTCGA 3180

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CTTTATAATG TGCAACTTGT CCGTTTTTAG TATGTTTTAT TTTCTTTTTC TAAATAAACG 3420

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AGTGAATAAT GGATGTTCTT CCCACATACT TTTAGCAACA GTATTTGCCT TTTGAATAAT 3540

TGGCTGATGA ACTTCTACAG TTGGAGGTCC ATAATCTTTA TTAATAAATT CTCTTGGATA 3600

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TGGTAAAACA TCGTAAAGAT CATTTTCAAC ATAATATTTC TTACCATTTA TCCTTTGCTC 3720

ACCTTTAGAC AATATTTTTA CATATTTATA CTGATCAAAT GAGCGTTCCA TTAATGCATT 3780

CCCCATCATA TTACGTTGCT TCTCGCCACC AAGGTTTTTA TAGTCTCCTG CACCCATGAT 3840

AACTTGATTA ATTCTAAATT TACCTCGTTT GGTAGTAATC GTATGGTTGT AATTTGCTGT 3900

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CAATTTGATG AAGGATATGA CACGCTTGTA GGTGAACGAG GATTGAAACT GTCTGGCGGA 6540

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ATGGATAGGC ATAAAAGGTA GTTTCGGTTT AAACCAAATT TTAGGTGTGT TTATGTATCC 8100

ATTTGCGCTA TTACTCGGTT TACCTTATGA TGAAGCGTGG TTGGTAGCAC AACAAATGGC 8160

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GACAGTAAGG ACTAGGTACA GTCATAGTAC TTCGAGCAAA ATTTGTTTTG TTATTATAAA 8700

CAACACAAAG GAGATAACTT CTCTAnTGAA GAAGTTAAAA ACATTATAGC AGACAATGAA 8760

ATGAAAGTAA ATTAAAAAT 8779

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31096 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GTTGCAGTAG TCAAAGAATT AAACAAGGTG AAGGcGTGTA GCTTGCACAC CCGAAAATGT 60

GCGTAAGTTA aCGGATGCAG GACATAAAGT AATTGTTGAA AAAAATGCTG GCATTGGTTC 120

AGGATTTTCT AACGATATGT ATGAAAAAGA AGGCGCTAAG ATCGTAACTC ACGAACAAGC 180

ATGGGAAGCT GATCTTGTTA TCAAAGTAAA AGAACCTCAT GAAAGCGAAT ATCAATATTT 240

CAAAAAGAAT CAAATTATCT GGGGATTTTT ACATCTAGCA TCTTCAAAAG AAATAGTAGA 300

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TCGTAAAGCT GAAGCATTAC AAAGATTGGA TCAATTAACA CATCTAAACA ATGCTCAAAG 30540

ACAATTAGCA ATCCAACAAA TTAATAATGC TGAAACGCTA AATAAAGCAT CTCGAGCAAT 30600

TAATAGAGCA ACTAAATTAG ATAATGCAAT GGGTTCAGTA CAACAATATA TTGACGAACA 30660

GCACCTTGGT GTTATCAGCA GCACAAATTA CATCAATGCA GATGACAATT TGAAAGCAAA 30720

TTATGATAAT GCAATTGCGA ATGCAGCACA TGAGTTAGAT AAAGTGCAAG GTAATGCAAT 30780

TGCaAAAGCT GAAGCAGAGC AATTGAAACA AAATATTATC GATGCTCAAA ATGCATTAAA 30840

TGGAGACCAA AACCTTGCAA ATGCCAAAGA TAAAGCAAAT GCGTTTGTTA ATTCGTTAAA 30900

TGGATTAAAT CAACAGCAAC AAGATCTTGC ACATAAAGCA ATTAACAATG CCGATACTGT 30960

ATCAGATGTA ACAGATATTG TTAATAATCA AATTGACTTA AATGATGCAA TGGAAACATT 31020

GAAACATTTA GTTGACAATG AAATTCCAAA TGCAGAGCAA ACTGTCAATT ACCAAAACGC 31080

TGACGATAAT GCTAAA 31096

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

ATGACAGAAT GGGAGCGAGG ACTTAGAATG TTTCCTAAAT CAGGTTTATT AAATTTTGAG 60

TTAGCGATAG mAAATCGTTC ATTAAATGAT GATGAAAAAG CATTAAAATA TGTGCGTAAA 120

GCATTAAATG CAGACCCTAA AAATACAGAT TATATTAACT TAGAAAAAGA GTTGACTAAA 180

TCAAATGAGT CGAAAAATAA ATAACTTTTA TGATGTACAA CAGTTATTGA AAAGTTACGG 240

ATTTCTAATA TATTTTAAAA ATCCAGAAGA TATGTACGAA ATGATTCAAC AGGAGATTTC 300

TAATCAGAGA AGGAATGAAC AGAAATGACA AAAATTATTT TAGCAGCTGA TGTAGGCGGG 420

ACGACTTGTA AATTAGGTAT TTTCACACCT GAATTAGAAC AATTACATAA ATGGTCTATT 480

CACACTGATA CATCTGATAG TACAGGATAT ACACTTTTGA AAGGAATTTA TGATTCGTTT 540

GTTGAAAAAG TAAATGAAAA TAATTATAAT TTTTCAAATG TACTTGGCGT AGGTATTGGT 600

GTACCAGGTC CTGTTGACTT TGAAAAAGGT ACAGTAAATG GAGCAGTAAA CTTATATTGG 660

CCAGAAAAAG TTAATGTACG TGAGATTTTT GAACAATTCG TTGATTGTCC AGTGTATGTA 720

GATAATGATG CTAACATAGC TGCTTTAGGG GaGAAACACA AAGGTGCTGG TGAAGGTGCC 780

GATGATGTTG TTGCCATCAC ACTTGGTACA GGTCTAGGTG GAGGAATTAT TTCCAAATGG 840

TGAAATCGTA CATGGTCATA ATGGCTCtGG CGCAGAAATA GGTCATTTTA GAgCAGACTT 900

CgATCAACGA TTTaAATGTA ATTGTGGTCG TTCTGGATGT ATTGAAACAG TTGCTTCaGC 960

GACAGGCGTT GTTAACTTAG TTAACTTCtA CTATCCGAAG TTGACGTTTA GATCTTCTAT 1020

ATTAGAATTG ATTAAAGAAA ATAAGGTtAC aGCAAAAGCT GTTTTTGATG CGGCAAAAGC 1080

TGGTGACCAA TTCTGTATTT TCATTACTGA AAAGGTTGCA AACTATATTG GATATTTATG 1140

TAGTATTATT AGTGTTACAA GTAATCCGAA ATATATCGTT CTAGGTGGAG GAATGTCTAC 1200

TGCAGGACCT ATTTTAATTG AAAATATTAA AACAGAATAT CATAATTTAA CATTTGCACC 1260

TGCTCAATTT GAAACTGAAA TTGTACAAGC GAAATTAGGT AATGATGCAG GTATTACAGG 1320

AGCAGCAGGA TTAATCAAGA CCTATGTATT AGATAAAGAG GGGGTAAAAT AATGGCTATT 1380

GTTGATGTGG TTGTTATTCC AGTTGGAACG GAAGGTCCGA GTGTTAGTAA ATATATTGCA 1440

GATATTCAGA AAAAACTTCA AGAATATAAA GCAATGGGTA AAATTGATTT TCAATTAACA 1500

CCAATGAATA CTCTAATTGA AGGTGAATTA AGCGATGTAT TAGAAGTTGT GCAAGTGATA 1560

CATGAATTAC CTTTTGATAA AGGTTTAAGT AGAGTTTGTA CAAATATCCG TATTGATGAC 1620

CGACGAGACA AATCTAGAAA AATGAATGAT AAACTAACAT CAGTACAAAA ACATTTAGAA 1680

AATAGTGGTG AAAACCTATG AGGATTTCAA GCTTAACTTT AGGCTTAGTT GATACTAATA 1740

CGTATTTCAT CGAAAATGAC AAAGCTGTTA TTCTGATTGA CCCTTCAGGT GAAAGTGAAA 1800

AAATTATTAA AAAATTAAAC CAAATAAATA AACCGTTAAA AGCTATTTTA TTAACACATG 1860

CACACTTTGA TCATATCGGA GCAGTCGATG ATATAGTTGA TCGATTCGAT GTCCCGGTTT 1920

ATATGCATGA AGCAGAGTTT GATTTTCTAA AAGATCCCGT TAAAAATGGG GCAGATAAAT 1980

TTAAGCAATA TGGATTACCA ATTATTACAA GTAAGGTAAC TCCTGAAAAG TTAAmCGAAG 2040

GTAGCACAGA AATAGAAGGA TTTAAGTTnT nAyrTGTaCA CACACCTGGA CATTCACCAG 2100

GAATCGGACG TACAGATTTA TATAAAGGTG ATTATGAAAC GCTAGTTGAT TCTATTCAAG 2220

ATAAAATATT TGAATTAGAA GGC 2243

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8009 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TTGGnATCAT tyAcgGTAAA AAGAATAAaG CAAGATTtAT TTCATTAGTA CTAATTTGTG 60

CAATGTTTGC AATTTGTTGG GTTGCATATA TTCAATGGGA GTCTACAATC GCTTCATTTA 120

CACAATCTAT TAATATTTCa ATGGCACAAT ATAGTGTTTT ATGGACAATT AACGGAATAA 180

TGATTTTAGT AGCACAACCA TTAATTAAAC CGATTCTCTA TCTGTTAAAA GGAAACTTAA 240

AGAAGCAAAT GTTTGTCGGC ATCATCATTT TTATGTTGTC GTTCTTTGTC ACGAGTTTTG 300

CCGAAAACTT TACAATATTT GTTGTCGGTA TGATTATTTT AACTTTTGGA GAAATGTTTG 360

TATGGCCAGC AGTTCCAACT ATAGCCAATC AGTTAGCGCC AGATGGTAAG CAAGGACAGT 420

ACCAAGGTTT TGTGAATTCA GCTGCTACAG TAGGAAAAGC ATTTGGTCCA TTTCTTGGTG 480

GTGTATTAGT TGATGCGTTT AATATGCGCA TGATGTTTAT CGGTATGATG CTACTACTTG 540

TATTTGCATT AATATTATTA ATGGTTTTCA AGGAGAATAA TACGCAACCT AAAAAAATAG 600

ATGCATAATG AGTAAATAGA ATTAACGTTA TAGACTTGAA ATAAATGTCG TTATAACATA 660

ATATTAATTT GTATAATTTA ATTTCGTTTG GAGCTTTTCT ACAGAAAGCT AGTGATGCTG 720

AGAGCTAGTG TTAAGGACTA AATGTAAATC GTATTAATTT TAAATTGAAT GAATGACATC 780

TCTTACTATT AAAATGAGTG CACAATTTTT GTGAAATAGG GTGGTAACGC GGCAAATGTC 840

GTCCCTATGT AAATAGAATA GTTAGAGGTG TCTTTTTTAT TGAATAGGAG GAAATGTGTT 900

GAATTACAAC CACAATCAAA TTGAAAAGAA ATGGcAAGAC TATTGGGACG AAAATAAAAC 960

ATTTAAAACA AATGATAACT TAGGTCAAAA GAAATTTTAT GCTTTAGACA TGTTTCCATA 1020

TCCATCAGGT GCTGGTTTAC ATGTTGGACA TCCTGAGGGc TATACAGCAA CAGATATCAT 1080

TTCAAGATAT AAAAGAATGC AAGGATATAA TGTATTACAT CCGATGGGGT GGGATGCATT 1140

CGGATTACCA GCAGAGCAAT ATGCTTTAGA CACTGGCAAC GACCCACGTG AATTTACAAA 1200

GAAAAATATC CAAACTTTTA AACGACAAAT TAAAGAATTA GGGTTCAGTT ATGATTGGGA 1260

GTTATATAAC AAAGGTTTAG CATACGTTGA TGAAGTTGCA GTTAACTGGT GTCCAGCATT 1380

AGGCACTGTT TTATCTAACG AAGAAGTGAT TGATGGTGTC TCTGAACGTG GTGGACATCC 1440

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ATTAGCAGAT TTAGATGATT TAGATTGGCC TGAGTCTTTA AAAGATATGC AGCGCAATTG 1560

GATTGGACGT TCTGAAGGGG CCAAAGTTTC ATTTGATGTA GATAATACGG AAGGAAAAGT 1620

AGAAGTATTT ACGACTAGAC CAGATACAAT CTATGGTGCA TCATTCTTAG TCTTAAGTCC 1680

TGAACATGCA TTAGTTAATT CAATTACAAC AGATGAATAT AAAGAAAAAG TAAAAGCTTA 1740

TCAAACAGAA GCTTCTAAAA AGTCAGATTT AGAACGTACA GATTTAGCAA AAGATAAATC 1800

AGGTGTATTT ACTGGTGCAT ATGCAACTAA TCCTTTATCT GGTGAAAAAG TACAAATTTG 1860

GATTGCTGAT TATGTATTAT CAACATATGG TACTGGAGCA ATTATGGCAG TACCAGCGCA 1920

TGATGACAGA GATTATGAAT TTGCTAAAAA GTTTGATTTG CCAATCATTG AAGTCATCGA 1980

AGGTGGAAAT GTTGAAGAAG CAGCATACAC TGGTGAAGGT AAACATATTA ATTCTGGTGA 2040

ACTTGATGGT TTAGAAAATG AAGCGGCAAT TACTAAAGCT ATTCAATTAT TAGAGCAAAA 2100

AGGTGCTGGC GAAAAGAAAG TTAATTACAA ATTAAGAGAT TGGTTATTCA GTCGTCAGCG 2160

TTATTGGGGC GAACCAATTC CTGTCATTCA TTGGGAAGAT GGAACAATGA CAACTGTTCC 2220

TGAAGAAGAG CTACCATTGT TGTTACCTGA AACAGATGAA ATCAAGCCAT CAGGGACTGG 2280

TGAGTCTCCA CTAGCTAATA TTGATTCATT TGTAAATGTT GTAGATGAAA AAACAGGTAT 2340

GAAAGGACGT CGTGAAACAA ATACAATGCC ACAATGGGCA GGTAGTTGTT GGTATTATTT 2400

ACGTTACATC GATCCTAAAA ATGAAAATAT GTTAGCAGAT CCTGAAAAAT TAAAACATTG 2460

GTTACCTGTT GATTTATATA TCGGTGGAGT AGAACATGCG GTTCTTCACT TATTATATGC 2520

AAGATTTTGG CATAAAGTCC TTTATGATTT GGCTATCGTA CCTACTAAAG AACCTTTCCA 2580

AAAATTATTT AACCAAGGTA TGATTTTAGG AGAAGGTAAT GAGAAGATGA GTAAATCTAA 2640

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TTACGAAATG TTTATGGGAC CTTTAGATGC TGCAATTGCA TGGAGTGAAA AAGGATTAGA 2760

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GAGTTCAAAA ATTGTAACTA CAAATAATAA ATCTTTAGAT AAAGTTTATA ACCAAACTGT 2880

TAAAAAGGTA ACAGAAGACT TTGAAACATT AGGATTTAAT ACTGCTATTA GTCAATTAAT 2940

GGTATTTATT AATGAGTGTT ATAAAGTTGA TGAAGTTTAT AAACCTTACA TTGAAGGCTT 3000

CGTTAAAATG TTAGCACCTA TTGCACCACA TATCGGTGAA GAATTATGGT CAAAATTAGG 3060

TGATGAAGTA GAAATCGTTG TTCAAGTGAA TGGTAAATTG AGAGCTAAAA TTAAAATTGC 3180

TAAAGATACA TCAAAAGAAG AAATGCAAGA AATTGCCTTA TCTAATGACA ATGTTAAAGC 3240

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TGTAGCTAAA TAATGTTTTA AGGAGGACTT TGAAATGAAG TCAATTACTA CAGATGAATT 3360

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AACAGCAATG GGATATATTC CTAATGCAAA GTTAATTCCA ATGGATACCA TTCCGGATAA 3480

TTTAAATTCA TTTAATAAAA ATGAAATATA TTATATTGTA TGTGCTGGTG GAGTTCGAAG 3540

CGCTAAAGTT GTAGAATATT TAGAGGCAAA TGGCATTGAT GCCGTAAATG TCGAAGGCGG 3600

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TTAAAATAAT ATTACATTTG TAATGACACC AAGTAACGTT TCGGTTGCTT GGTGTTTTTT 3720

GGTATGAATT ACTTTCTGTT ACAAAACAAT CTAAAGCGTT CTTGTTATGT TTTATTAAGA 3780

TTTTAATTAC AAAACGGAAA CTAAATTGTA ATAAAATAAA ACTTTATTTT ATAAAATGAT 3840

GATGATAAAA TTGAGTGAAC TTAAAATATT GTACAAAATA ATATAGCTAT AAATATAATA 3900

TAGCTATAAA TATAATATGA GGGAGCGTAT ATTTTTAGCA TAATTCTTAA CAACACAGCA 3960

GAGAACAGAC AACCAGGAGG AAAATGAAAT GAATTTGTTA AAGAAAAATA AATATAGTAT 4020

TAGGAAGTAT AAAGTAGGCA TATTCTCTAC TTTAATCGGA ACAGTTTTAT TACTTTCAAA 4080

CCCAAATGGT GCACAAGCCT TAACTACGGA TAATAATGTA CAAAGCGATA CTAATCAAGC 4140

AACACCTGTA AATTCACAAG ATAAAGATGT TGCTAATAAT AGAGGTTTAG CAAATAGTGC 4200

GCAGAATACA CCTAATCAAT CTGCAACAAC CAATCAAGCA ACGAATCAAG CATTGGTTAA 4260

TCATAATAAT GGTAGTATAG TAAATCAAGC TACGCCAACA TCAGTGCAAT CAAGTACGCC 4320

TTCAGCACAA AACAATAATC ATACAGATGG CAATACAACA GCAACTGAGA CAGTGTCAAA 4380

CGCTAATAAT AATGATGTAG TGTCGAATAA TACCGCATTA AATGTACCAA CTAAAACAAA 4440

TGAAAATGGT TCAGGAGGAC ATCTAACTTT AAAGGAAATT CAAGAAGATG TTCGTCATTC 4500

TTCAAATAAA CCAGAGCTAG TTGCAATTGC TGAACCAGCA TCTAATAGAC CGAAAAAGAG 4560

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TCAAGGCGCA ACAAATGTTA TTATCAAAAA TGCTGATACT AATGATACGA TTGCTGAAAA 5100

GACTGTTGAA GGCGGTCCAA CTTTGCGTTT ATTTAAAGTA CCTGATAATG TGAGAAATCT 5160

CAAAATTCAA TTTGTACCTA AAAATGACGC AATAACAGAT GCGCGTGGCA TTTATCAACT 5220

AAAAGATGGT TACAAATACT ATAGCTTTGT TGACTCTATC GGACTTCATT CTGGGTCACA 5280

TGTTTTTGTT GAAAGACGAA CAATGGATCC AACAGCAACA AATAATAAAG AGTTTACTGT 5340

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TCGTGTGATA ACAATTAAAA GTACTGGAGG AGGTACAGCA AACTCTCCGG CACGACTTAT 5580

GCCTGATAAA ATACTCGATT TAAGATATAA ATTACGTGTA AATAATGTGC CGACACCAAG 5640

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AGCTGCAGAA AGTCATACTG TAAGTACAAA TCCATATACT ATCGATATCA TCATGAATAA 5760

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ACAAGTTATC GAGGAACATA AAAATGAAAT AATTGGTAAT ATTGGTGACC AAACGACTGA 6120

TGATGGCGTT ACTAGAATCA AAGATCAAGG TATACAGACC TTAAGTGGGG ATACTGCAAC 6180

ACCGGTTGTT AAACCAAATG CTAAAAAAGC AATACGTGAT AAAGCAACGA AACAAAGGGA 6240

AATTATCAAT GCAACACCAG ATGCTACTGA AGACGAGATT CAAGATGCAC TAAATCAATT 6300

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TGAAACAGCT AAAAATAATG GCATCAATAC TATTGGAGCA GTTGTTCCTC AAGTAACTCA 6420

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TCAACTTTAA AGATTCAAGC AATTTAATCC AAATTTAATC CAAAACCCAA ACAAATGGAT 7980

TCAGGGTAGG ACACCACTTA CAAATCCAA 8009

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10953 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

ACCCACCCCn TGGGGATAnT TTACCTGGTG GGGCCTTCGA TTGCCTTTAG GTGAAACCaG 60

AGATGAATGC TAACCATATT CATTCTGCTA AAGATGGTCG TGTTACTGCG ACAGCTGAAA 180

TTATTCATCG AGGTAAGTCG ACACATGTAT GGGATATAAA AATTAAGAAT GACAAAGAAC 240

AATTAATTAC AGTTATGCGT GGTACAGTTG CTATTAAACC TTTAAAATAA AAGAACTGCT 300

AGCTGAAATG TTATGAGATA TTCATAACTA CGGCTAGCAG TTTTTTTATG CGCTATATTG 360

TTGTAGTTTT AGAAATGCTT GTTCAATGCG TTCGGCAGCT TTACGGCCAC CCATAACATT 420

TCTACCAAAT GGTCCTAATT CTAAGTCTGC AAAGCATCCT GCGACAAATA GATTTGGTAT 480

CCATTCTAAT TTTTCGGAAA TAACAGGGTA ATTACATTCG TTGATAGGTG CATCATAATT 540

TTGTATTAAT TGCTTAATAA GTGGTTGTGA CATAAAATCT TGTTCAAAAC CAGTTGCAAC 600

CATAATCTGT TGATATGGAA CAGAATCATT TTCAGTGTTA ATTACACCAC CACTAATTTG 660

AGTGATAGGT GTTTTATGCa CATTTATACG ACCATTTTTA ATATGTTTTT TAAGGCGTAA 720

GTACAGTTCG TGAGGCATTG ATCCTTTATG ACGTTCGCGT TGTACAATGG CATTTCTTTC 780

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TTTGTCTTTT AAAATGTCAG GCATAAACGG AATATTTGTA CTGCCTATTG CAATAACGAC 1080

GCAATCTGTA GTGATAATTT GTCCATCTTC TAACTTGATA TGCCATTTGT CTTCTTGTTT 1140

ATCTAAAGTT TGAACTAAAC CTTGAACCAA GCAATCCTCT AATTGATATT GTTTAGAAGC 1200

ATGTGCAATA TGATCCATAA ACATTGTCAA TTCAGGTCGT TGATAAGGAC CATAAAAAGC 1260

ATTTGTATAT TGGTGCTGTT TAGCGAATTG TTTTAGATGG AACGGTTGTG GATGTACGTG 1320

ATGTACAATC GGTGATCTTA AATAAGGCAT TTCTATTCGA TTTGTATATG AGTTAAACCT 1380

TTGGCAAAAA GTTTCGTGTG GGTCAATGAT TGTTAATCGG TCTGTTGTTA ATCCGCTTGA 1440

TAATAGTTTT TGTGCGATTG CAGTTCCCTG TATGCCACCG CCGATAATTG TCCAATGCAT 1500

AATAAAACCT CTCTCTTTTT AAAACGTAAT AGTTACGATT TATAATTATT ATTATCATAA 1560

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CATTCCTAAT TTGGAATCAT CTTACTGCTG TTTGTTGTTG ATTTATATTC ATGATTTTGT 1740

TATATAATCT ACAATTTTGT GTCTTTTAAG TCTTCCGAAA TTTCATCGAC TTTAGTCTTT 1800

TTAGTATAAG GCGTTTTAAT ATTATATGCT GCTTTCATAA TCATATGACT TGAAAGAGGA 1860

GCAATAAAAT ATAAAAACGT ACCAAATAGT AATGACATTG CACCTAATGT TGATGCTTTT 1980

CCGGCAGCAT GTGCACGTGA ATATACATCT TCAAGTCTCA ATAATCCTAT AGCTGCTAGG 2040

GCGCTAATTA AAGCACCGAT GATAACAAAG ATAAGTGCAA GACTAATCAG TATGATTTTG 2100

ATCATGTTCA ATCACCTTAC CTTTGTCCAT AAATTTAGAG AATACTGCAG TACCTAAAAA 2160

AGCTAATATA CCAATCATCA TAATAACGAC AATCATGTAT TTAATATTTA ATAAAATACT 2220

GAATAATGCT ATAACTGCCA TTAATTGAAG ACCAATCGCA TCTAATGCGA CAACACGATC 2280

GGCAAGTGAT GGGCCTAGCA CAACGCGAAT GAGCATAGCT AACATAGAAA TGACAACTAT 2340

GATTAATGCA ATAACGATAA TAACATTATG ATTCATTATA TTTCGCCCAC CTCTCTTACA 2400

ATTTTCTCTA ATGATGTTTT AATACTTTCT ACTTCTTGCT CTTTAGTTGA AAAATCTATG 2460

GCATGAATAT AAATTTTTGT ACGATCGTCA CTTACACCAA GCACTACAGT ACCAGGTGTT 2520

AATGTAATTA AATTAGACAG CAAGACAATT TGCCAATCTT TTTTTAAATC TGTGTGATAA 2580

ACAAAGAATC CTGGTTCATT TTTAATCGAA GGTTTAATAA TAATTTTCAA AACATCAAAA 2640

TTAGCTTTAA TCAGTTCGAT TAAGAAAATA ATAACTAATT TAATAATACG ATATAGCGTG 2700

ATGACATAAA ATCTACCTGG TAACACTCTG TGTAAGAGGT AAACAAGAAC TAGGCCAAAG 2760

ATGAAACCTA ACACAAAGTT ATTTGTTGTG TAACTATTTG TCACAAACAA CCAAAACACT 2820

GCGATAATAA AGTTTAATAC TAATTGTACA GCCATGTTAT TTACCTCCTA ATACAGCTTT 2880

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ATCTGCTGAC AATCCATATA AAACAGTTAT CACAACTGCA ACGATTGCAA TCGTAGTTAA 3000

ATATTTGACG TCGACTTTGT TATTAAGATC ATATCCTTTT GGTTGACCGA AAAAGCCTTG 3060

TAGGAATATG CGAATGACAG AATATAATAC GACTAAACTT GATAATAAGA CGATGACACC 3120

ACTTAAATAA AATCCTCTTT CAAATGTTGA TTGGACAATA AAAAATTTTC CATAAAAGCC 3180

ACTGAGTGGG GGAATGCCAG CTAAACTTAA TGCTGCGATA AAGAATGACC AACCAAGTAC 3240

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CATAATTCCG ATAAGCAAGA ATAATGCAAG TTTTACTAAC ATGTCGTGCA ATGTATAGTA 3360

AATAGCCCCA ATCATACCTG ACTCTGTCAT CATTGCAACG CCGACTAAGA TCACACCTAC 3420

AGCAATCATG ACATTGTATA GGATGATTTT TTTAATGTTG GCATATGCAA CAGCACCGAC 3480

ACAACCAAAG ATGATCGTTA ATAGTGCTAA GAATAAAATG ACATAATGTG AAAAGCTTAC 3540

ATTATCACTA AAGAATAGGC TCAATGTTCT AGCGATTGCA TAAACACCAA CTTTTGTTAA 3600

CAAAGCACCA AAGAATGCAA TGATTGGAAT TGGTGGgCAT AGTATGCACT AGGTAACCAA 3660

ATATTGACTA AGCCACTGTC ATGCGCTGAA AGGTTAGCTA ATTTATTGCT TATATCTGCT 3780

AGATTCAATG TTCCTACTAC TGAATATAAA ATCGCTACAC CCATTACGAA GAAGGATGAC 3840

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TAATAATATC TTTCACGTTC AATACCAATT GTTTGGTATG AATATAAAAT CACAATAGCT 4080

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GCGTCGCAAT ACAAAAAACT AATCCGATAC CTATCAAGAT TTTAAAATCT AATGGGAAAA 4920

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ACGTGCTCTT GATAAAACTT AGATATCGAT TCAAAATGTC TATTTCCGTA TGCAATTAAA 5340

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TAATGTAATT AAACCAACGA GTGTGACAGT CCATACCCAA CCTTGCGATG CTGCGAAGAT 6720

TGGTGTCATT CGAGCGATTA AATATAACCC TGCTTTAACC ATTGTTGCTG AATGAAGATA 6780

AGCACTGACT GGTGTAGGTG CTTCCATTGC ATCTGGTAGC CAAATATAAA ATGGAAACTG 6840

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CATGATTCAA GGTGGCGATC CAACAGCTAC TGGTATGGGT GGCGAAAGTA TTTATGGCGG 8340

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TGATGGTGAA aCTACATTAG AAGATATTGC AAATACAAAA GTGGGACCAC AAGATAAACC 8640

ACTTCATGAT GTTGTAATTG AATCTATTGA TGTTGAAGAA TAATATCTAA ACATAATTAA 8700

CTACCAACAT TTTAAACTCG GATAAAGCTA ATTTATGAAT GGATTAGTAT ATATTCCAAC 8760

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TGATGGATAC GCATGCAACG ACACGTGAAG GTAAATACGC TGGACAAGAA AGACTGCCTT 10680

TAATTCACAA ATGGATAAAT GGTCGTATGC CACTTATCGG TATTGGTTCA ATTTTCACAG 10740

CTGACGAAGC TTTAGATGCA GTTGAAAATG TTGGTGTTGA CTTAGTAGCC ATTGGTAGAG 10800

AGCTACTACT GGATTATCAA TTTGTTGAAA AAATTAAAGA TGGACGGGAA GATGAAATTA 10860

AATTTAATGA AGGGTTTTAT CCATTACCAC GTA 10953

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

TTTGATAnAA AACTGAATnA ATTAAATGTA TCGATTCAAC CTAATGAAGT GAATTTACAA 60

GTTAAAGTAG AGCCTTTTAG CAnAAAGGTT AAAGTAAATG TTAAACAGAA AGGTAGTTTA 120

GCAGATGATA AAGAGTTAAG TTCGATTGAT TTAGAAGATA AAGAAATTGA AATCTTCGGT 180

AGTCGAGATG ACTTACAAAA TATAAGCGAA GTTGATGCAG AAGTAGATTT AGATGGTATT 240

TCAGAATCAA CTGAAAAGAC TGTAAAAATC AATTTwCCAG AACATGTCAC TAAAGCACAA 300

CCAAGTGAAA CGmAGGCTTA TATAAATGTA AAATAAATAG CTAAATTAAA GGAGAGTAAA 360

CAATGGGAAA ATATTTTGGT ACAGACGGAg TAAGAGGTGT CGCAAACCAA GAACTAACAC 420

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CAGCATTAAT AGCTGGTTTG ATTTCAATTG GTGCAGAAGT GATGCGATTA GGTATTATTT 600

CAACACCAGG TGTTGCATAT TTAACACGCG ATATGGGTGC AGAGTTAGGT GTAATGATTT 660

CAGCCTCTCA TAATCCAGTT GCAGATAATG GTATTAAATT CTTTGGATCA GATGGTTTTA 720

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TGATGTGGTT CAAGATAAAA TGGGATTAGA TAAATAAATA CTGTATTACA AATGAGCCGA 1740

TGCGTATGcA nTcgtTTTTT GTGTTTGTAG AAATAATTTA TAGTACAAAC GTAAAATGAT 1800

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ATAATGATGA TAAAATTAAT TTTAATTAGA TAGAGTTGCT TTGTGTTTTT AACGCAGATG 1920

CTACTACTTA TCTTAACAGT TGATTAAGTG AAATCATTTA ACAGCGAGAA TAATCAACCA 1980

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TGCCAACCAA GGACAACCAG CAGTACAACC AGCAAACCAA GGTGGACAGG CTAATCCAGC 2280

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AAAGCGAAAg cTCaAGGACT TGAAGCATTT GATAACATTC AAATCGACTC AACAGAAAAA 7740

CAAAAAGCTA TCGAAGAATT AGAAACTGCA CTAGACCAGA TTGAAGCAGG TGTAAATGTC 7800

AACGCTGATG CTACAACTGA AGAAAAAGAA GCGTTTACGA ATGCTTTAGA AGACATTTTA 7860

TCAAAAGCAA CTGaAGATAT TTCTGATCAA ACTACAAATG CAGAAATCGC TACTGTCAAA 7920

AATAGTGCGC TTGAACAACT TAAAGCACAA CGTATTAATC CTGAAGTTAA GAAAAATGCT 7980

TTGGAAAGCAA TCAGAGAAGT GGTTAACAAG CAAATAGGAA tAATTAAAAA TGCAGATGCA 8040

GATGCATCGG CGGAAAGAnA TTGCACGTAC GGGATTTAGG TAGATATTTT GGACCGATTT 8100

GCTGGATAAA TTTAGGGTnA AACCCCAACC AATGCCGAAG TTGCCTGAAT TACCA 8155

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1630 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

CTGTTTTATT TGCAGCACCC ATACTGGAAA TCACTTTAAT CCCTCGGTCA AGACACTCTT 120

TCATTAAGTG TACTTTGTAC ATTATTGTAT CACTTGCATC TACAAAATAA TCTATATCGT 180

AGTTATCGAA AATTTCTTCA TATGTCTCTT CTGTATAAAA CATATGTAAG GGCGTGACTT 240

TACAATCTGG ATTAATTAAT TTAATACGTT CTTCCATCAA AGAAACTTTA CTTTGTCCTA 300

CCGTTGTAGT TAAAGCGTGT AATTGTCTGT TTACATTTGT AATATCAACA TCATCTTTAT 360

CTATTAATAT AATATGACCA ATATTCGTTC TTGCTAATGC TTCAGCAGCA AATGAACCAA 420

CACCTCCAAC GCCAAGTATG ACAACAGTTT GTTGCTTCAA TAAATCTAAA CCTTGTTGTC 480

CAATCGCTAG TTCATTTCTT GAAAATTGAT GTTTCATTAT TTTACCTCTT TCACTGATTT 540

ATACATAAGT ACATAGTAAC TTAAAATTTT ATATTTAGCA TTATCACTTT GATTATTTTC 600

CCAAAATTCA ACGAGGAAAC ATTTATTAAA CGCTATAAAA CCCAACTAAT TCTTTATTAA 660

AAACTTAAAG AAACGCATAA AAATACGCAA GACAAAGTCT TGCGTATCGA TAGAGTCCGT 720

ATTGCCGTAG TTATAATAGC TTGATCATTC GGCCTGTTAT ATACAGGTGG GTGCCCTGTT 780

TCTTGTTTTG TACGTCCTTC ATATAAGGCG TGTACGCTGC AAGAAAACCC ATTGGGCTCC 840

CTTGATCAAA GAGTGTTAGG CCCAAATTAA AAAGCAAACT TACGAACAAC TCAGATGACT 900

ATCTTATGAT GTTATATTAC CACATAATTA AAATTAATGA AATTATAACA AACCAAAGTT 960

TATTGATTTT TTAAAATTTA GTGACGAATT CGCAAAGAAA GTTCTTCTAA TTGTTTATCA 1020

GAAACTTCAC TAGGCGCATT CGTTAATAAA CATGTAGCAG ATGCTGTTTT AGGGAATGCG 1080

ATTGTATCTC TCAAGTTTGT TCTATTAGTC AATAACATGA CTAATCGGTC tAATCCTAAT 1140

GCAATACCGC CATGTGGTGG TGCACCATAT TTAAATGCAT CTAGTaAGAA GCCGAACTGT 1200

TCCTgTGCTT GTTCTTTAGT AAATCCAAGA ACTTCGAACA TTTTTTCTTG TAACTCACCA 1260

TCATGAATTC TGATTGAACC GCCACCTAAT TCATAACCAT TTAATACTAT GTCATAAGCA 1320

TTTGCCTCAG CTTCtTCTGG CGCAGTGCCA AGCTTAGCAA TATCAGCTTC TTTTGGAGAT 1380

GTAAATGGAT GATGTGCTGC AACGTAACGT TTCGCATCTT CATCATATTC TAATAATGGC 1440

CAATCTGTCA CCCATAAGAA GTTTAATTTT GTTTCATCGA TTAAACCTAA TTCTTTAGCT 1500

AATTTGACAC GTAATGCACC TAAACTTTGT GCAACGACAT TTGGTttGTC TGCAACAAAC 1560

ATTACTAAGT CACCAGCTTC AGCACCAGTT AATGTAAGTA ATGTTTCAAC ATTTTCTGTT 1620

cAAAGAAACG 1630

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 732 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

CAATTGGACA TCTTGTATGA AAAGGACAAC CTTGCGGCGG ATTACTTGGC GAAGGTAATT 60

CTCCTTTTAA TATAATTCTA TTGTTATTAT GTTTATCAAT TTGTGGTATT GATGAAATCA 120

ACGCTTTTGT ATATGGATGT TTGGGATTTT CATAAATTTC TTTATCAGAT GCGATTTCAA 180

CTATATGACC TAAATACATA ACTCCAATGA CATCACTTAT ATGTTTTACT ACACTTAAAT 240

CATGTGCGAT AAATAAATAG CTTAAGTTAA ATTGTTCTTG TAAATCTTTT AATAAATTCA 300

GTACTTGAGA TTGAACAGAT ACATCTAATG CACTTACAGG CTCATCAGCA ACAATTAAAC 360

TCGGACGCAA AGCCAATGCT CTTGCAATTC CCACTCTTTG TCTCTGTCCA CCTGAAAATT 420

CATGTGCATA TTtATAATAT GCATCTTCAC TTAGGCCAAC ACATTTTAAT AAATATAGTA 480

CTTCTTTTTT TATTTCTTCT TTTGGCAATT TTTTATAATT TAAAATAGGT TCTGAAATGA 540

TATCTCCAAC CATTTGCATC GGATTCAATG ATGCATACGG ATCTTGAAAT ATCATCTGAT 600

ATTGTTGTCG TGATTTTCTG AGTTTTTTAC CTTGTAATCT TGTTATATCT TCACCATTAA 660

CAATTATTGA GCCTGAAGTT GCATCTTCAA GCCTGATAAT CACTTTACCT AACGTTGACT 720

TACCACAACC CG 732

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5838 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

AATATATTCA TATGTTTCAT CAACAATATT AGCTGCTTTT TGAATTAAAG CAATTTCGTC 60

AGCATCTTTG ACGTCTCTAA TTTTATCTAC AGTATTAGAA ATGCTTATTA ATGATATACG 120

GCTTTTATTT AATTCAAGGT ATGTATCATA ACTTACATGA TGCCCCTCAA AACCTACATT 180

TTCAAAATTT TCTTGGTGTA GCAATTCTTT AATCTCACCA ATAATAGTAG ATTTACGATT 240

AATAATTTCA TAATTTGGCG CCTGCTTAGT TGCTTGATCA ATATATCTAA AGTCTGTTAT 300

CAAATATTGT TTATCTTTAG ATATGATAAG TGCTCCACTG GTACCAGTAA AACCTGATAA 360

ATATCTTCTA TTGTAATCCG AAAGAATGaT AATCGCATCT AAATGTTTTT GTTCTAAAAT 420

CAACTTTATA CATTAAAATA ATATCATAAT AAGGATAAAA AATAATAGAT ATTGATTTTA 540

GGGAGATAGT AATGAAAAAA TTGGTTTCAA TTGTTGGCGC AACATTATTG TTAGCTGGAT 600

GTGGATCACA AAATTTAGCA CCATTAGAAG AnAAAACAAC AGATTTAAGA GAAGATAATC 660

ATCAACTCAA ACTAGATATT CAAGAACTTA ATCAACAAAT TAGTGATTCT AAATCTAAAA 720

TTAAAGGGCT TGAAAAGGAT AAAGAAAACA GTAAAAAAAC TGCATCTAAT AATACGAAAA 780

TTAAATTGAT GAATGTTACA TCAACATACT ACGACAAAGT TGCTAAAGCT TTGAAATCCT 840

ATAACGATAT TGAGAAAGAT GTAAGTAAAA ACAAAGGCGA TAAGAATGTT CAATCGAAAT 900

TAAATCAAAT TTCTAATGAT ATTCAAAGTG CTCACACTTC ATACAAAGAT GCTATCGATG 960

GTTTATCACT TAGTGATGAT GATAAAAAAA CGTCTAAAAA TATCGATAAA TTAAACTCTG 1020

ATTTGAATCA TGCATTTGAT GATATTAAAA ATGGCTATCA AAATAAAGAT AAAAAACAAC 1080

TTACAAAAGG ACAACAAGCG TTGTCAAAAT TAAACTTAAA TGCAAAATCA TGATAGGAGT 1140

CTTTTAATGC GTAATATAAT ATTTTATCTT GTACTTATTA TTGCTGCGAT TGGATTAGTA 1200

ATGAATCTAG ATGCCTTTAT TTTTTCAATC GTCAGAATGT TAATCAGCTT TGcgTAaTAG 1260

CTGGTATTAT TTATCTGATT TATTATTTCT TCATCTTAAC TGAAGACCAA CGCAAATATC 1320

GCAAAGCAAT GCgTrAaGTA TAAAAGAAAT CAAAGAAGAA AATAGATAAA AAAACGGAAG 1380

CACTTGTAGG TAAAATAGTC TACGTGCTTC CATTTTTTAT TCTAAAAACT ACTTTCTAAA 1440

CATCCATTCA TCTGAACGAT ATTTTTCAGT TAATTCTTCC ACTTCTGCCA ATTGAGCTTC 1500

TGtTAATTCA AGTGGCTTTA ATTCTATATT TAAACCTTTC TTAAAACCTT TCTCGAAAGC 1560

TTCTTCCATT TGACTAATAG TAATGTGTTC ATCTGAAATA TCATTGATGG CAACTGCTTT 1620

TTCAACGAAT GCCTCTTTCA TTTTTAATTT TAATCTTTCA TTTTTATAAA TrAACATATC 1680

AAACAGTTCA TCAATATCAA TATCTTGTAA AATCGAACCG TGTTGGAGGA TTACGCCCTT 1740

TTGTCTCGTT TGAGCACTCC CAGCAATCTT ACGGCCTTCA ACAACTAGCT CATACCAACT 1800

TGGTGCATCA AAACACACTG AACTTCGAGG TTGTTTTAAT TTTTGACGCT CTTCAGGCGT 1860

TTTAGGTACC GCAAAATAAG TATCAAATCC TAAGTTTTTA AATCCTTCTA ATAATCCTTG 1920

TGAAATCACT CTGTACGCTT CTGTAACTGT AGAAGGCATA TTCGGATGCG ATTCAGGCAC 1980

AATCACACTG TAAGTTAACT CTTTATCATG TAGCACCCCA CGGCCACCAG TTTGACGCCT 2040

TACGAGACCA AAACCTTTCT CTTTAACCTT ATCAATATCA ATTTCTTTTT GTAGCCTTTG 2100

GAAATACCCT ATTGATAATG TTGCAGGATT CCATGTGTAA AAACGTATAA CTGGATCAAT 2160

TTCACCTCTA GAGACAAAAT TTAATAACGC TTCATCCATT GCCATATTAT AATATGGGTC 2220

AAATGTATAA TATTTGATTC GCTAATTAAT CAATTTAACT AAATGAATAA TAATTGCAAT 2340

TCTTTAGTGA AATATTTTGA TAATTTGACC TAACAGTCTT ATAATTATAT TATCGTTTAA 2400

TTAGGGAGGA TGCAAGATGA GTGCTAGTTT GTACATCGCA ATAATTTTAG TTATAGCAAT 2460

TATTGCTTAT ATGATTGTTC AACAAATTCT TAACAAGCGA GCTGTTAAAG AATTAGATCA 2520

AAATGAATTC CATAATGGGA TTAGAAAAGC TCAAGTCATC GATGTTAGAG AGAAAGTTGA 2580

CTATGACTAC GGTCACATTA ATGGGTCTCG CAATATTCCT ATGACAATGT TCAGGCAACG 2640

ATTCCAAGGA TTAAGAAAAG ATCAACCGGT ATACTTATGT GATGCCAATG GGATTGCTAG 2700

CTATAGAGCC GCTCGTATTT TGAAAAAGAA TGGATATACA GATATCTATA TGTTAAAAGG 2760

CGGCTATAAA AAATGGACTG GAAAAATAAA GTCTAAAAAA TAGTTTTTGT AAATTTAATA 2820

TACGATTTAA TAAAATCTGA GTGTTAATTG ATCATCAATA ACAATACTCA GATTTTAATT 2880

TTTTAACAAA GTCTGTTACT ATATTTCTCT AGCTTCACTG ATCATTAAAC TTAGTTTCAG 2940

CATAATAAAG AAAGTTCAGC TCATTTTCAA TACGATTCAA TTACCGCAAT CTAAAAAATG 3000

AAAAGACAAT TTCTATGAAA GAATAATACC AAACCCTAAG AGTTATTACT TCGGTTTAGT 3060

TTTCTTGTTT AAATAGAAAT TGTCTTTTTC AATTGATTTT GAAACCATTA TCCTTAAATC 3120

TTCATACAAA GTTAGAATAA TAATTCTCGG AATATGTGTT TAATACTTTA TTTTTCCTGT 3180

TTAAGATTTT CAAACTTTAA TATTGGTTTA CGAGCAGCTG TAGCTTCGTC TAATCGATCA 3240

ATCACAGTTG TATGTGGTGC TTCTAGCacT TTATCAGGAT CATTTTTAGC TTCTTCAGCA 3300

ATACTAATTA ATGTATCGAT AAAATAATCA AGTGTTTCTT TAGACTCTGT CTCAGTCGGT 3360

TCAATCATCA TACCTTCTTC AACATTTAAT GGGAAGTATA TTGTTGGTGG ATGTACACCG 3420

AAATCTAATA ATCGCTTAGC CATGTCTAAA GTACGTACAC CAAATTCTTT TTGACGCACA 3480

CCACTTAACA CAAACTCGTG TTTACAATAT TGTTTATAAG GTATTTCAAA GTGTTTAGAT 3540

AAACGTGCTT TAATATAATT CGCATTAAGA ACCGCTGCTT CAGAAACCTC TTTAAGTCCA 3600

GTTGCTCCCA TAGTTCGAAT ATACGTATAA GCTCTTAAGT AAATACCAAA GTTACCATAA 3660

AATGGTTTTA CACGTCCGAT AGAATTTTTA ATGTCATTAT CATATTTAAA TTTGTCGCCA 3720

TCTTTAATAA CCATTGGCTT TGGTAAGTAA CTTGCTAGTT CTTTTACTAC ACCGACTGGA 3780

CCTGAACCAG GACCGCCACC ACCATGTGGA CCAGTAAATG TTTTATGCAA GTTTAAATGA 3840

ACAGCATCAA ATCCCATATC TCCTGGGCGA ACTTTGTCCA TAATAGCGTT TAAATTCGCA 3900

CCATCATAAT ATAATAGACC ACCAGCATTA TGGACGATTT CACGGATTTC CATAATATTT 3960

TTTTCGAAAA TACCTAAAGT GTTTGGATTA GTTAACATAA TAGCTGCTGT ATTTTCATTT 4020

GATTTAAATC CTGCAAATGa AGCTGAGGCT GGaTTCGTAC CATGCGCAGA ATCTGGcACA 4140

ATGACTTCAT CACGATGACC TTCACCATTA TTCTCATGGT AAGCTTTAAA TATCATCAAT 4200

GCAGTCCATT CACCATGTGC GCCAGCAGCT GGTTGTAATG TCACCTCATC CATACCAGTA 4260

ATTTCTTTTA ATTCTTCTTG CAAACTATAA ATAATTTCTA ATGAACCTTG AACTTGATCT 4320

TCATCTTGTA ATGGATGTGA TTCACTAAAT CCTGGTATTC TAGCAACCTT TTCATTAATT 4380

TTAGGGTTAT ACTTCATCGT ACATGAACCC AATGGATAAA ATCCGTTGTC TACACCGAAA 4440

TTTTTATTTG AAAGTTCAGT ATAATGACGT ACTAAGTCTA GTTCAGCAAC TTCAGGAAAC 4500

TCCGCTTTGT TTTTACGAAT AAATTTATCA TCTAACAATG ACTCAACAGA ATTTGTTTTA 4560

ATATCACTTT TTGGTAATGA ATATGCATAT CTGCCTTCAC GAGATCTTTC AAAAATTAAT 4620

GGACTTGATT TACTAGTCAT TTAACTCACC AGCCTTTTCT ACAAATGTAT CGATTTCATC 4680

TTTTGTTCTT AATTCAGTTA CAGCTATTAA CATGTGATTT TTAAAGTCGT CTGAAACAAC 4740

ACCTAAATCA AAACCACCGA TAATATTGTA CTTCACTAAT TCCTCGTTAA CTTGTTGAAT 4800

TGGTTTGTCA AATTTGACTA CAAACTCATT GmnAAGnTGT ACCATCTAAT ACTTCAAAAC 4860

CTTTTTTAAT AAATTGTTGT TTAGCATAGT TAGCATGTTC TATATTTTGA ACTGCAATAT 4920

CATAGATACC TTGTTTACCA AGTGCTGACA TTGCAATTGA TGaCGcTAAA GCATTTAATG 4980

CTTGGTTAGA ACAAATATTA GATGTCGCTT TATCGCGTCG AATATGTTGT TCACGTGCTT 5040

GTAATGTTAA TACAAAGCCA CGATTACCTT CATCATCTTG TGTTTGACCG ACTAATCTAC 5100

CTGGCACTTT ACGCATTAAC TTTTTCGTCG TTGCAAAATA TCCACAATGT GGCCCACCGA 5160

ATTGAGCAGG AATTCCGAAT GGCTGAGTAT CACCTACAAC AATATCTGCA CCAAATGAAC 5220

CTGGAGGTGT AAGTAATCCC AATGCTAATG GATTTGCATA TACGATAAAT AATGCTTTTT 5280

TATCTTCAAT AAAGCTATGA ATCTTTTCAA GATCTTCAAT TGAACCGTAA AAGTTTGGAT 5340

ATTGTACTGC AACAGCTGCT GTTTCATCAT CCACTGCTGC TTCTAATTTT TTCAAATCTG 5400

TAACAGTGCC ATCTAAATCG ATTTCCACTA CTTCGAATTC CTTACGCGTC TTAGCATAAG 5460

TATGAAGTAC TTGTAATGCT TGATAATGTA AACCTTTTGA GACTACAATT TTATTTTTCT 5520

TTGTTTGACT AAATGCTAAG ATACATGCTT CAGCAAAGCT AGTCATCCCA TCATACATAG 5580

AAGAATTTGC TACATCCATA TCTGTTAATT CACAAATTAA AGTTTGGAAC TCAAAAATGG 5640

CTTGTAATTC ACCTTGAGAA ATTTCCGGTT GATATGGCGT ATATGCTGTG TAAAATTCTG 5700

ATCTTGAAAT CATAGCATCC ACAACTGATG GCGCGTAATG ATCATAAACA CCAGCACCCA 5760

rAAATGATGT ATGCGTTTCT TTAGTGATAT tCTTGCTkGC AATGGGGATT TAAACnTCTA 5820

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

ATnATAATTG GCTTTGCTAA TAATTACTTC CCTGAATTAC aAGTATTAGC AAACGAAATA 60

AAATCTGATA TGGCTAGTTC ATTAAAACAA TGATATTTTT ATTTAAATTT TTaAAGCTTT 120

GTACGAAATT GTACAAAGCT TTTTTGGTGC GTATTGTATG GGCAACAACT TGACGATGAA 180

AATCCGTTAC AGGATTGGTA ATAGGAAATG TTAGCGAAAG ACAAGGGTAT CCATTGTAGA 240

TTAACAAAAG GACGTTTCCA CAAGTGTGGG TTATTCTCAC TAAAGCAATA CGCAGAGACA 300

ACTTACGTAA AATTTTGAAC TGACTAGAAC GGAACTTCTA CTCAATTATT GATAAAAATT 360

TTCAAAAAGA CTTGAATGTG CTGAGAATAC GAAGTTTATG GAAGGATTAT CAAAATATAA 420

ATGTGCATTC ATTTACAACC TTTATTGACA ATGATTCTCA ACTAATATAG TATATAATCA 480

AATCGTAATA GTTACGATTT GTTTTCTGCA ACTTTTTTGA AGTTTTAGTT GAGGTGAAAA 540

CAATAAAAGC ATCTAAGTGA ATGTAGTTAA CGGACAACTG CATTCGCTTG TAGAGCCACA 600

AGAAGCAACT TTAAATAAGG TTTACGGTTG CATTTTGATA CAACAACCGA TTACTAAGTC 660

ATGCTTTCCA CTTTGCGGGT TAGCATGACT TACCTAATAG ATAGAGCTAT TAGGTTCAGC 720

TTCTAAAAAA TTACAGTTTT AGAGGAATAC AGTTGcTTGc tTCGCAACAA CTGCATAAGA 780

GCCATGGTTT TCGCTTTTGC GAATTAGCAT GACTTACCTA CTAGATAGAG CTATTAGGTT 840

CATCTTCTAA AAAATTACAG GTTTAGAGGA ATACAGTTGT TTGcTTCGCA ACAACTGCAT 900

AAGAGCCTCT AGTAATTAAA ATTACAGAGG CTCTAAAAAT ACATCTAAAG GAGTGTCGTA 960

TGAATCGGCA GGTTATAGAA TTTTCTAAGT ATAATCCTTC GGGGAATATG ACGATACTTG 1020

TTCATTCAAA ACATGATGCT AGTGAATATG CATCTATCGC CAATCAGTTG ATGGCCGCAA 1080

CACATGTATG CTGTGAACAG GTAGGCTTTA TAGrATCAAC ACAAAATGAT GATGGTAATG 1140

ATTTTCACTT AGTTATGAGC GGTAATGAAT TTTGCGGTAA TGCGACGATG TCATATATAC 1200

ATCATTTGCA GGAAAGTCAT TTGCTTAAAG ACCAACAGTT TAAGGTGAAG GTGTCTGGCT 1260

GTTCGGATTT AGTGCAATGC GCAATTCATG ATTGCCAATA CTATGAAGTT CAAATGCCAC 1320

AAGCCCATCG TGTTGTGCCA ACAACAATTA ATATGGGTAA TCATTCATGG AAAGCAATAG 1380

TTCAACATTT GGTTGAAGCG TTTGTGCGTG AgcAACAATG GAGTCACAAA TATAAAACAG 1500

TAGGTATGAT GCTTTTTGAT GAACAACGTC AATTTTTACA GCCATTAATC TATATACCAG 1560

AAATTCAAAG TTTAATTTGG GAAAATAGCT GTGGTTCTGG TACAgcATCA ATTGGGGTTT 1620

TTAATAATTA TCAACGTAAT GACGCATGCA AAGATTTTAC AGTACATCAG CCAGGGGGCA 1680

GTATTTTAGT GACATCAAAG CGATGTCATC AATTGGGATA TCAAACTTCA ATTAAAGGAC 1740

AGGTTACAAC TGTAGCTACA GGaAAAGCAT ATATAGAATA AGGAGCCTAC AATGAATAAC 1800

TTTAATAATG AAATCAAATT GATATTACAA CAATATTTAG AAAAGTTTGA AGCGCATTAC 1860

GAGCGTGTAT TACAAGACGA TCAATATATC GAAGCATTAG AAACATTGAT GGATGACTAT 1920

AGTGAATTTA TTTTAAATCC TATTTATGAA CAACAATTTA ATGCTTGGCG TGACGTTGAA 1980

GAAAAAGCAC AATTaATAAA ATCACTGCAA TATATTACAG CGCAGTGTGT TAAACAAGTG 2040

GAAGTCATTA GAGCGAGACG TCTATTAGAC GGACAGGCGT CTACCACAGG TTACTTTGAC 2100

AATATAGAAC ATTGTATTGA TGAAGAGTTT GGACAATGTA GTATAGCTAG CAATGACAAA 2160

TTATTGTTAG TTGGTTCAGG TGCATATCCA ATGACGTTAA TTCAAGTAGC AAAAGAAACA 2220

GGTGCTTCAG TTATCGGTAT TGATATTGAT CCACAAGCCG TTGACCTAGG GCGCAGAATC 2280

GTTAACGTCT TAGCACCAAA TGAAGATATA ACAATTACGG ATCAAAAGGT ATCTGAACTT 2340

AAAGATATCA AAGATGTGAC GCATATCATA TTCAGCTCGA CAATTCCTTT AAAGTACAGC 2400

ATTTTAGAAG AATTATATGA TTTAACAAAT GAAAATGTCG TAGTTGCAAT GCGCTTTGGT 2460

GATGGCATCA AAGCAATATT TAATTATCCG TCACAAGAAA CAGCGGAAGA TAAGTGGCAA 2520

TGTGTGAATA AACATATGAG ACCACAGCAA ATTTTTGATA TAGCACTTTA TAAAAAAGCA 2580

GCTATAAAGG TAGGTATTAC GGATGTCTAA ATTATTAATG ATAGGCACTG GTCCgGTCGC 2640

AATGCAATTA GCGAATATTT GCTATTTAAA ATCAGATTAT GAGATTGATA TGGTTGGACG 2700

TGCCTCAACA TCAGAAAAAT CAAAACGCTT ATATCAAGCG TATAAAAAAG AGAAACAATT 2760

TGAAGTCAAA ATACAAAACG AGGCGCATCA ACATCTGGAA GGTAAGTTTG AAATTAATCG 2820

TTTGTATAAA GATGTTAAAA ACGTTAAGGG TGAATACGAA ACGGTTGTCA TGGCATGCAC 2880

AGCAGATGCT TATTATGACA CACTACAGCA ATTGTCGTTA GAAACTTTGC AAAGTGTCAA 2940

ACATGTCATT TTAATATCAC CGACATTTGG TTCGCAAATG ATTGTCGAAC AATTTATGTC 3000

TAAATTTAAT AAAGATATCG AAGTGATTTC ATTCTCAACT TATCTTGGCG ATACACGTAT 3060

TGTTGATAAA GAAGCGCCTA ATCATGTGTT GACAACAGGT GTAAAAAAGA AATTGTACAT 3120

GGGATCGACA CATTCAAACT CAACAATGTG TCAACGAATC TCTGCTTTAG CTGAGCAATT 3180

TTATGTGCAC CCACCACTAT TTATGAATGA CTTTTCATTG AAAGCCATTT TCGAAGGAAC 3300

AGATGTACCG GTTTATGTGT ATAAGTTATT TCCTGAAGGA CCGATAACGA TGACACTAAT 3360

CCGTGAAATG CGTTTAATGT GGAAGGAAAT GATGGTTATT TTACAAGCAT TTAGAGTGCC 3420

GTCAGTCAAC CTGCTTCAAT TTATGGTGAA GGAAAATTAT CCAGTACGTC CTGAAACTTT 3480

GGATGAAGGT GATATTGAGC ATTTCGAAAT CTTGCCAGAT ATCTTACAAG AATATCTGCT 3540

TTATGTAAGA TATACCGCAA TCCTCATTGA TCCATTTTCA CAGCCAGACG AAAACGGACA 3600

TTACTTTGAT TTTTCAGCTG TACCATTTAA GCAAGTCTAT AAAAATGAAC AGGATGTTGT 3660

TCAAATTCCA AGAATGCCAA GTGAAGATTA TTACAGAACG GCGATGATTC AGCATATTGG 3720

GAAAATGCTA GGTATCAAAA CGCCAATGAT TGATCAGTTC CTAACTCGCT ATGAAGCAAG 3780

TTGCCAGGCG TACAAGGATA TGCATCAAGA TCAACACTTA TCTTCTCAAT TTAATACAAA 3840

TCTATTTGAA GGAGATAAAG CACTCGTCAC AAAATTTTTG GAAATCAATA GAACGCTTTC 3900

ATAATAAGGG TTTGAAGTTT TATAATAGAA AAAAATTATT GAATTATGTT TGACATTTAC 3960

ATAAAAATAA GCAAATAATT GAGAAAAATA ATCATTACGA TTTGATTAAG TAATGCAACT 4020

TATCAATTTA GAAAGAGGAA AAGCAAATGA GAAAACTAAC TAAAATGAGT GCAATGTTAC 4080

TTGCATCAGG GCTAATTTTA ACTGGTTGTG GCGGTAATAA AGGTTTAGAG GAGAAAAAAG 4140

AAAACAAGCA ATTAACGTAT ACGACGGTTA AAGATATCGG TGATATGAAT CCGCATGTTT 4200

ACGGTGGATC AATGTCTGCT GAAAGTATGA TATACGAGCC GCTTGTACGT AACACGAAAG 4260

ATGGTATTAA GCCTTTACTA GCTAAAAAGT GGGATGTGTC TGAAGATGGG AAGACATACA 4320

CGTTCCATTT GAGAGATGAC GTTAAATTCC ATGATGGTAC GCCATTTGca TGctGACGCA 4380

GTTAAGAAAA ATATTGACGC AgTTCAAGAA AACAAAAAAT TGCATTCTTG GTTAAAGATT 4440

TCGACATTAA TTGACAATGT TAAAGTTAAA GATAAGTACA CGGTTGAATT GAATTTGAAA 4500

GAAGCATATC AACCTGCATT GGCTGAATTA GCGATGCCTC GTCCATATGT ATTTGTGTCT 4560

CCAAAAGACT TTaAAAACGG TACAAcAAAA GATGGCGTTA AAAAGTTCGA TGGTACTGGT 4620

CCATTTAAAT TAGGTGAACA CAAAAAAGAT GAGTCTGCAG ACTTTAACAA AAATGATCAA 4680

TACTGGGGCG AAAAGTCTAA ACTTAACAAA GTACAAGCAA AAGTAATGCC TGCTGGTGAA 4740

ACAGCATTCC TATCAATGAA AAAAGGTGAA ACGAACTTTG CCTTCACAGA TGATAGAGGT 4800

ACAGATAGCT TAGACAAAGA CTCTTTAAAA CAATTGAAAG ATACAGGTGA CTATCAAGTT 4860

AAGCGTAGTC AACCTATGAA TACGAAAATG TTAGTTGTCA ATTCTGGTAA AAAAGATAAC 4920

GCTGTGAGTG ACAAAACAGT CAGACAAGCG ATTGGTCATA TGGTAAACAG AGATAAAATT 4980

ACAGACATTA ATTTCGATAT GCCAACACGT AAGTATGACC TTAAAAAAGC AGAATCATTA 5100

TTAGATGAAG CTGGTTGGAA GAAAGGTAAA GACAGCGATG TTCGTCAAAA AGATGGTAAA 5160

AACCTTGAAA TGGCAATGTA CTATGACAAA GGTTCTTCAA GTCAAAAAGA ACAAGCAGAA 5220

TACTTACAAG CAGAATTTAA GAAAATGGGT ATTAAGTTAA ACATCAATGG CGAAACATCA 5280

GATAAAATTG CTGAACGTCG TACTTCTGGT GATTATGACT TAATGTTCAA CCAAACTTGG 5340

GGATTATTGT ACGATCCACA AAGTACTATT GCAGCATTTA AAGAGAAAAA TGGTTATGAA 5400

AGTGCAACAT CAGGCATTGA GAACAAAGAT AAAATATACA ACAGCATTGA TGACGCATTT 5460

AAAATCCAAA ACGGTAAAGA GCGTTCAGAC GCTTATAAAA ACATTTTGAA ACAAATTGAT 5520

GATGAAGGTA TCTTTATCCC TATTTCACAC GGTAGTATGA CAGTTGTTGC ACCaAAAGAT 5580

TTAGAAAAAG TATCATTCAC ACAATCACAG TATGAATTAC CATTCAATGA AATGCAGTAT 5640

AAATAAAGGA GCAATTAGAT GTTCAAATTT ATCTTAAAAC GTATTGCGCT CATGTTTCCA 5700

TTGATGATTG TAGTAAGTTT TATGACATTT CTATTGACGT ATATTACAAA TGAAAATCCA 5760

GCTGTGACAA TTTTACATGC ACAAGGGACG CCAAATGTAA CACCAGAGTT GATTGCAGAA 5820

ACGAATGAGA AGTACGGTTT CAATGATCCA TTATTAATTC AATATAAAAA TTGGTTACTT 5880

GAAGCGATGC AATTTAATTT TGGTACAAGC TACATTACAG GTGACCCAGT TGCTGAACGT 5940

ATTGGTCCAG CATTTATGAA TACATTGAAA TTAACAATAA TTTCAAGTGT TATGGTGATG 6000

ATTACATCAA TTATTTTAGG TGTAGTTAGT GCATTAAAAA GAGGAAAGTT CACTGATCGT 6060

GCGATACGTT CAGTGGCTTT CTTTCTAACT GCATTACCAT CATATTGGAT AGCTTCAATA 6120

CTTATTATTT ACGTTTCAGT GAAGTTAAAC ATATTGCCGA CTTCTGGATT AACAGGTCCA 6180

GAAAGTTACA TATTGCCAGT GATCGTTATT ACGATTGCCT ATGCTGGTAT TTACTTTAGA 6240

AATGTTAGAC GCTCGATGGT GGAACAATTA AATGAAGATT ATGTACTTTA TTTAAGAGCA 6300

AGCGGTGTGA AATCTATCAC ATTAATGTTG CATGTGTTGC GTAATGCTTT ACAAGTTGCG 6360

GTATCAATCT TTTGTATGTC TATACCAATG ATAATGGGTG GACTAGTTGT TATCGAGTAT 6420

ATCTTTGCAT GGCCTGGACT AGGTCAATTA AGTTTAAAAG CAATACTTGA ACACGATTTT 6480

CCAGTCATTC AAGCATATGT ATTAATTGTA GCGGTATTAT TTATTGTATT TAATACATTA 6540

GCAGATATCA TTAATGCGCT ATTAAATCCA AGATTAAGGG aGGGCGCACG ATGATAATTT 6600

TAAAmCGATT ATTmCArGwT AAAGGTGCAG TAATTGCTTT AGGCATTATT GTATTATATG 6660

TCTTTTTAGG ATTAGCAGCA CCACTTGTGA CATTTTATGA TCCTAACCAT ATCGATACAG 6720

CAAACAAATT TGCTGGCATG AGTTTTCAAC ATCTACTAGG TACTGACCAT TTAGGTAGAG 6780

TATTTGTTTC TGTACTTATT GGATCTATTT TAGGATTCTT ATCAGGATAT TTCCAAGGGT 6900

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CAATGATCTT GCAAATATCT GGCTTTTCAT TTTTAGGATT AGGTGTCAAA GCGCCTACTG 7260

CAGAGTGGGG CATGATGCTT AACGAaGCTA GAAAAGTGAT GTTTACACAT CCTGAAATGA 7320

TGTTTGCGCC AGGTATTGCC ATAGTGATTA TAGTGATGGC ATTTAACTTC TTATCCGATG 7380

CTTTACAAAT TGCTATTGAT CCCCGCATCT CTTCTAAAGA TAAACTTCGT TCTGTGAAAA 7440

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GACAGATCAA CCACTCGTGA GTGATGTGAA TTTTACATTA ACTAAGGGTG AAaCTTTAGG 7560

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TGAGCCGACA ACGGCTTTAG ATACAATTAC ACAATATGAT GTACTGGAAG CATTTATAGA 8040

TATTAAAAAA CACTTTGACT GTGCGATGAT TTTCATTTCA CATGATTTAA CGGTTATTAA 8100

CAAGATTGCA GACCGTGTTG TTGTGATGAA AAATGGTCAG CTTATTGAAC AAGGGACACG 8160

TGAATCAGTC TTGCATCATC CAGAACATGT TTATACGArt ATTkTATTAT CAACGAAGAA 8220

GAAGATTAAT GATCATTTTA AACATGTGAT GAGGGGTGAT GTACATGATT AAAATTAAAG 8280

ATGTTGAAAA GTCATATCAA AGCGCACATG TTTTTAAGCG TCGTCGAACA CCTATCGTGA 8340

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TGTTTGATGA AGCCATTAGT TCACTCGACA TGTCAATTCA AACACAAATA TTAGATTTAT 8820

TGATTCATTT ACGTGAAACG CGTCAGTTGA GTTATATTTT TATCACACAT GATATTCAAG 8880

CTGCCACGTA TTTATGTGAT CAATTAATTA TTTTTAAAAA CGGAAAAATA GAAGAACAAA 8940

TTCCGACAAG CGCATTGCAT AAAAGTGACA ATGCTTATAC AAGAGAATTA ATAGAAAAAC 9000

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GGTGGCGCAT TGATGGGACC TATTTCCGAT TTAGTAGGAT TTAAATGGAT GTATCTAATT 10140

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AAGGAAAATA AATCCAATAT CACGTTTGAA AAAACGCGAT TGTTCGGTAG CGTATTCTTC 11160

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GATACTTTAG CACATATTAC TTTGTATTGT ATGTTTTATA CATTAAAATT TAAAATGAAA 11280

AACATATCAT AAAATTGTTT TATAAAATGA AGCGCTTCCA TTGTGTTTTG TTTTGTAAGG 11340

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TGTAAACGGC ATTGCTGGTT ATGAAATGCA AGTTAAAGAA GCAATGCGTa ACTATATAGA 13920

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TAGGCGGTGG TCCAGTTGTC ATTATGATGG ATGCTACAAG TATTGCTCAC CAAGGTTTGC 14640

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ATTATAGGTC CATCAGGTAG TGGTAAAAGT ACATTTCAAA AGCAAATATG TAATTTGTTT 15300

AGTCCAACTA GTGGAGAACT TTATTTTAAA GGTAAACCCT ATAATGATTA TGACCCGGAA 15360

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TGCGACTATT TACATTCATT TTAAGTATTT TTATCGTAGG AATGGTTGAA ATGATGGTTG 17040

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CAGCAGCAGC ACTAATTATC GTAAAAGTAT TAGCTATTAC AGCGATGTTA TCAGCACCTA 17340

AAAATCGTGG TAAAATGATT GGACTTGTCT ATACAGGGTT TAGTGGTGCT AATGTTTTTG 17400

GTGTACCAAT TGGAACGGTT ATCGGCGATT TAGTAGGTTG GCGCTATACA TTTCTATTCT 17460

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GCGACGTTCA TTATGATACA TCGGCCAAGG CATTTTACCG CTTTTAGCAA AATTAGCTAA 18300

ATCATTTTGC ATTTGTCGAC TTAAAAATTT AAGGTGaGCA GTTGTTGGaT ATgAT 18355

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CGCAAAGAAG TACAAAAAAT GTTTTTACAA GAAGGTATTA AAACACCTCA ACCAATTATG 60

ACTGCTTATA ATCATAGTGA AAACGgTGTT TAGTAGTTTA TAATACATGG AGGTCATATT 120

TAATGGCGTC AAAATATGGA ATAAATGATA TAGTAGAAAT GAAAAAACAA CATGCGTGTG 180

GAACAAACCG TTTTAAGATT ATTAGAATGG GTGCAGACAT AAGAATTAAA TGTGAAAATT 240

GTCAAAGAAG TATTATGATT CCACGTCAAA CGTTTGATAA AAAACTTAAA AAAATCATCG 300

AATCTCATGA TGATACACAA AGATAGGAGA ATGATTAATG GCTTTAACAG CAGGTATCGT 360

TGGATTGCCA AACGTTGGTA AATCAACATT ATTTAATGCA ATAACAAAAG CAGGTGCTTT 420

AGCAGCGAAC TATCCATTCG CTACGATTGA TCCTAATGTA GGGATAGTAG AAGTGCCAGA 480

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TGAATTTACA GATATCGCTG GTATTGTGAA AGGTGCTTCA AAGGGAGAAG GGTTAGGTAA 600

TAAATTCTTA TCACATATTA GAGAAGTAGA TGCGATTTGT CAGGTCGTTC GTGCATTTGA 660

TAATATGGAA TTAGTACTAG CGGACTTAGA ATCTGTTGAG AAACGTTTGC CTAGAATTGA 780

AAAATTAGCA CGTCAAAAAG ATAAGACTGC TGAAATGGAA GTACGTATTT TAACAACTAT 840

TAAAGAAGCT TTAGAAAATG GTAAACCCGC TCGTAGTATT GACTTTAATG AAGAAGATCA 900

AAAATGGGTG AATCAAGCGC AATTACTGAC TTCTAAAAAA ATGCTTTATA TCGCTAATGT 960

TGGTGAAGAT GAAATTGGTG ATGATGATAA TGATAAAGTA AAAGCGATTC GTGAATATGC 1020

AGCGCAAGAA GACTCTGAAG TGATTGTTAT TAGTGCAAAA ATTGAAGAAG AAATTGCTAC 1080

ATTAGATGAT GAAGATAAAG AAATGTTCTT AGAAGaTTTA GGTATCGaAG AACCAGGATT 1140

AGATCgrTTA ATTAGGAmCA ctTATGAATT ATTAGGnTTA TCCACCATAA TT 1192

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AATATAGCTG CAATAGCATC TCGTTTCATT TGTATAATCA ATTCCGGTTT AAATATCAGT 60

GTGAACGTAA GCACGACACA GATTAAAAAT AACACTGCCG GAATGAGTCG TTTCAATCGT 120

CGCTtCCAAA ACTCTAGCAA ATCGATTTTT TGCGTCCGAT AATACTCACT TATCAACAAA 180

CTTGTTATTA AATAACCTGA AATAACGAAG AATGTATCTA CTCCTAAAAA GCCCCCACTT 240

AACCATTGTG CATTCAAGTG ATAAATAATG ATTCCTATAA CTGCGAATGC CCTCAATCCA 300

TCTAATCCAG GTAAGTATCG CGGGGAATAC ATTTTTTCTA AACGTTTAAA GTCTTTTGTA 360

TCCATGTTAA TAAACGCCCC ATTTATTTTT CTCTATTTTG TAGTATATCA CAATATTTTT 420

GAAAATAAAA TATTGCACTG aTTTTCATTA ATTGATTTAA CCCTTAATTA AGATAGTTTT 480

AAATTTTTTA TTAAGTAGAA AACAATTATT ACAGTTGATT TCATTACTGC AAACCACATA 540

TAAATTTGTC GATTTTACTA CATAACATAG ATTATCATAG ATTCTTGAAT TTTTAGCAAA 600

ATAACTGTTA TTTTCATTAT ATTTTTACAA AAAAAGGTTC GTTTTATATT TTATGCATCT 660

TACTGTAACA GAATCATTAA GATATGCTAT TCGAATATAC TTTTTCAAAA TTTATATAAT 720

GAATAAATTA ACATGTATTG AAAAAAAAGC GAAATGCAGC CTATCCTCTA ATGTAAACCA 780

AACGATATAT CTCGTCAGAC TTTATATTTA AACGCTATGT GTCACTTTTA AAATGAATAT 840

TACTAAGATT GTCATATCAA TTATTATTGC ATCGAATTAA TCTTTTAAAT TTCTGTAATA 900

ACGGAAGTCA TTATTAGAAT AAAAATACTG TGCACTAATA AATTTATCAA TTGTTCCTAA 1020

ATAAATACCA TCGATATTTT GTTCTTTACA TGTCATTATA ACTTTATCTA AAAGTTTTTT 1080

ACCTATTTTT AAATTCCTAT AACCTTTATC AACAAACATT TTTTTAAGTG CAGACATATT 1140

ATTATCTAGT CTAATCAAAC CTATAGTACC AACAATATTT TGaTGATTGT TTATTGCAAG 1200

CCAAAATgCC CTCCATTATT CAAATAGTTA TGTTCGATGT TCTCCAAATC AGGTTGATCA 1260

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AACAGCTGCG TTGATTTGTT GGTCAACAGT GTTTGTTGGA CCCCAACCTG GCATAGTTTG 1740

GAATAAACCT GAAGCACCTG ATGGGTTGTA AGCATTTACT TGACCATTTG ATTCACGAGC 1800

GATGATTGCA GCCCATGTAG AAGCTGAAAC ACCAGTACGT TGAGCCATGA TTTGAGCTGC 1860

TGATGAACCA GTAGCACCTG CAGTATTACC ATTGCTTAAT CTCACTGAAC TTGAAGTAGT 1920

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TTGtAATGTT GAAATATGGC TGTTTTATAC TGTAATGTGA AATATGTGCC CTTTAGAATC 2580

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TACAGCTTTC GTAATATTAC AGATTGTATT TTTGTTACAT AGCTGTAATA TATCTGACAT 2700

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GTGAATTGTC TTATCTTTTA TTAGCGCAAA TAAACTGCAG CTCAATTATA TTGTTCAACT 2880

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ACTGTTATTA TCCCATGAAT TTAAAAATAT CATTAGTATA TAAACGAAAC ACTTTACGAT 3000

AAATGATATC TGCAAGCCAA GCTGTTACAA ATGGTACAAC AAAGAACGCT ACTACAATTA 3060

GTAAGACACT CAACCAAGCA GAATCAACCT CCATAAATTT AAATGCATTA ATCGGTCCTA 3120

CCATTCCTAT AAAACCAAAT CCAGCTGACT CTTTCGTTCC ATGAATACCT ACTAATGCTG 3180

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ACCATTTTAT CTAACATTTG TGGGTTTCTA TTTATTTTAA ATCCTAACGC TTTATAAAAC 6600

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TTGCTCAGCT ATTTCAATTA TCTTCATACC TTGTCTTAAT TCTTCGCTAA CATCATCTTT 7260

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ATTATCACTC AGATCACCTT CArCGATTGA TAAATGCGGA TGTCCTATGT CTGAAAGTTT 7380

ACGATTATnC TTATTTCTAG TTAATGCACT TACATACCAT CCATCCTCTA ACAACTGTTT 7440

TACAACTGCA TTACCTTGCT TCCCTGTTGC GCCTATTACn AAAATATCTT TCAT 7494

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11802 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

AATTTATTTC GCCGTCCCAC CCCAACTTGC ATTGTCTGTA GAAATTGGGA ATCCAATTTC 60

TCTTTGTTGG GGCCCcGCCC CAACTCGCAT TGCCTGTAGA ATTTCTTTTC GAAATTCTCT 120

GTGTTGGGGC CCCTGACTAG AATTGAAAAA AGCTTATTAC AAGCGCATTT TCGTTCAGTC 180

AATTACTGCC AATATAACTT CGTAGATCAT AGAACATTGA TTTATTTCCC AGCCTATTCT 240

AGCAAAGGTA ATAATGATAT TAATAATGTA CAAAAAATAT AAATCAAATC GACATCCTTA 360

TAAAACATCA GAACCACTAA AAACAAAAAA GCACAAAATA AAATTAAATT TAAAATAAAC 420

GACCACTTTT CAAAAAAATC TCtTTTCaTa TTTCCACCCC TAATTTTAAT AAGCATTATT 480

TTATATTCTC TTTTAAGTTT ATTATTCAAA AGGAAAACAG AAATATCTTT CaATATTATT 540

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ATAAGTGAAC ATAGTTCTTT AGTTATAATA ATTAATTCAA CCAAAAGTCG ATTTGTTTTT 660

GCAATTGGTT TTCATTTCCT CTTAAAGATA TTTTCATTAA ATCTGTCAAA TCAATAGACG 720

CTATATTTTT CAACTTATCT CTATATTTAT TTTTAGTACG TCTTTCTAAA TTTCCCCATT 780

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GmATACCCAT ACAAAGAGGA TAAAATAAAA AACCTCGAAC TGaAATGATG ATCTTTTCAG 1740

CTCGAGGTTT AAATATTGGT GCCTTATTTA TATAGATTCG TTATATTATA TTCTCTATTT 1800

TCATTAACmT AATCCTTAAA GAGTTTTAAA TTAATACCTG CTAGATGATT CAAAAATGTT 1860

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TATTTGATAA AAAATCAATA AGTAATTGTG CGCCTTCAAC TTGAATATCT TTTACAACTG 2160

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TTTGCGATAG CCGTTGTAGG TACTTTCATC GCCGCAATTA TCTGTATTCC ATTAGCATTT 8460

CTAGGTGCAA ATAATATGGT AAAGCTACGC CCAGTTTCAG GTGTTAGCAA ATTTATTTTA 8520

AGTGTTATAC GTGTCTTCCC AGAAATTGTA ATGGCACTTA TATTTATCAA AGCTGTTGGC 8580

CCAGGTTCAT TTTCAGGTGT ATTAGCTTTA GGTATCCATT CCGTAGtATG CTTGGGAAAC 8640

TTTTAGCTGA AGATATTGAA GGTCTAGATT TCAGTGCTGT AGAATCATTA AAGGCCAGTG 8700

GTGCGAATAA GATTAAAACA CTCGTATTTG CAGTCATACC ACAAATTATG CCTGCCTTTC 8760

TATCACTCAT ACTTTATCGC TTTGAACTAA ACTTACGTTC AGCTTCTATA CTGGGGCTAA 8820

TTGGGGCTGG TGGTATCGGG ACACCACTCA TATTTGCCAT TCAAACACGT TCTTGGGACC 8880

GTGTAGGTAT TATATTAATC GGTTTAGTAC TAATGGTCGC AATTGTCGAT TTAATTTCCG 8940

GTTCAATCCG AAAACGTATT GTTTAACATT AAATCAGGAT ACTCCTAAAT AAGAAGTCCT 9000

ACCGTCTTAC GTTTCTCTAT TATAATAAAA ACAGCAGTGA AGAAAACTAT TGTTATAGTT 9060

AACTTCACTG CTGTTTTTAT AATATCTAAA TTTATTCTAT TTCAATTCCT TTAAATAACT 9120

TTTACCGAAC TCTGGTAATG TTACGTTGAA ATTATCTGCT ATAGTTGCAC CGATAGAACT 9180

GAATGTAGTA TCACTTTCTA GTGCATGACC ACCTTTAAAT TTCGGACTGT ACATAATTAC 9240

TGTAATAATT ACTAAATCGT CTTCTTTTAA GTTGCTAAAC AGTTCTGGCA AGCGATCATC 9360

GAAATCTTTA ATTGCTTGTG CATAACCTGG TTTATCACGA CGATGACCGT ATAATGCATC 9420

AAAGTCTACT AAGTTTAAGA AGCTAATACC TGTGaAATCT TTCTTAACAA TTTTCATCAA 9480

TTGATCCATA CCGTCCATGT TACTCTTCGT ACGAACCGCT TCTGTTACAC CTTCACCATC 9540

ATAAATGTCA TTAATTTTAC CGATGGCAAT AACATCATAA CCACCGTCTT TCAAATGATC 9600

TAAGACAGTT TTACCAAAAG GTTTTAACGC ATAGTCATGT CGATTAGATG TACGTGTAAA 9660

GTTTCCTGGT TCACCAACAT ATGGACGTGC GATAATACGA CCAATTAAAT ATTTAGGGTC 9720

TTTTGTCAAC TCACGAACCT TTTCACAAAT ATCATATAAC TCTTCTAATG GGATAATGTC 9780

TTCATGTGCA GCAATTTGCA ATACTGGGTC TGCACTTGTA TAAACAATTA AGTCACCAGT 9840

TTTCATTTGG TGCTCGCCCC ACTCATCGAT AATTTGCGTA CCCGATGCCG GTTTGTTAGC 9900

AACAACTTTA CGACCTGTCA TTTCTTCAAT TTGTTGAATT AACTCTTCAG GGAATCCATT 9960

AGGGTATACT TTAAAAGGTT GCATAATATT TAATCCCATA ATTTCCCAGT GACCAGTCAT 10020

TGTATCTTTA CCAACTGAAG CTTCACTCAA TTTAGTATAG TATGCTTCTG GTTGTTCAAC 10080

TGCATTTACT ACTGGTAATT TATCGATGTT CCCTAGACCT AACTTTTCAA GGTTTGGTAA 10140

AGTTTGATCG AAACCTTCTA AGGTATGTCT TAAAGTATGT GAACCTTCAT CTTTAAAATC 10200

AGCTGCGTCT GGCGCTTCAC CAATACCTAC TGAATCCATT ACGATTAAAT GTACACGATT 10260

AAATGGTCTT GTCATAGCTA TCACTCCCAA AATTTATATA TATTAGTAAT CTGAATCTGC 10320

TTCTAAACCT TGCATAATTT GAACACCTGC GCTCGCACCA ATACGTGTCG CACCTGCTTC 10380

AACCATTTTA TTGAAATCTT CTAAATTACG TACGCCACCT GATGCTTTTA CTTCTACATC 10440

AGCACCTACT GTATCTTTCA TTAATTTAAC GTCTTCTGCA GTCGCACCGC CACCTGCAAA 10500

ACCTGTTGAA GTTTTAACGA AGTCCGCACC AGCCGCTTTT GTTAATTCAC TCGCTTTTAC 10560

AATTTCGTCA TGGTCCAACA ATACCGTCTC AATAATCACT TTTACTGTGT GACCTTTCGC 10620

AGCTTTAACC ACTGCTTCAA TGTCTTGTTG TACATCATCA AAACGTCCAT CTTTTAATGC 10680

GCCGATGTTG ATGACCATGT CAATTTCATC TGCACCATTT TGAATTGCAT CTTCTGTTTC 10740

AAATGCTTTC GTTGCAGTTG TCGACGCACC TAATGGGAAT CCTATTACCG TACAAACGAG 10800

CACCTCTGAA TCAGCTAGTC GCTCTGCTGC ATATTTAACA TGTGTTGGAT TCACACATAC 10860

AGATTTAAAA TTGTATGctT TCGCTTCATC GATGATTTGA TCGATTTGCG TACGTGTTGA 10920

CTCAGGCTTC AATAAAGTGT GATCTATATA TTTCTCAAAT TTCATACTTA CTACTCCTCG 10980

TGTTATATAA TCTCTTTATT TAATTTTACT ATAAATACGA ATATATCTCG CGAATTTATA 11040

ATACTCATTA AACCTAAAAT AATTAAAATA ATACCGAAAT GTGAACTTAA TGCATCATTG 11160

CCTGGGAAAT TTAATGCTTT AAAATCGATT AGAGCCGCAG CAATCGCAAT ACCTACAGAT 11220

ACCGCCACAT TAATAATTAA ATTATAAAAA CCAATAGCCA CACCTGTCAT ATTAAGATCT 11280

ATTGTTTTAA TGGCTTCGTT AAGTAAAGGT GCATACATTA AAGCAAAGCT ACCTGCAAAG 11340

AATATCATAG AAATGACGAA GATTGAAATG TGATTACCTA CTGCAAATGC AGGTAAAATC 11400

AAGCTCAGTG CTATTAAAAT AATTGCTGTG ATAATCGCTT GTTTTGAATT CAGATATTCG 11460

CCGATTTTAC CACTTAGTGC ACCAACAATG ACTGCTACTA TATAACCCGG TACTAATAAC 11520

AGTGATGTTG TGTCTAGTTG CAGATGATAA ATTTGCTCCA TTATGAATGG GAACGTAAAA 11580

ATATAACCCA ATTGGATAGC ATACATTACA AATACTATAA ATAAAAATGA AGCATAACGT 11640

TTATTTTGGA AAAATGATTT ATTTACTAAT GGACGTTGCG CATTTTTAAT ATATAGCGCA 11700

AAAACGATAA TCGCAATTAA GGCACCAATC ATATATAACC AATTAAAGTT CGTAATAAAC 11760

AGCATGACTG TTGTAGCAGG GGATCCTCTA GAGTCGAnCC TG 11802

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTAAAGAAGA TGCGAAACAA GATGTTGATA AACAAGTTCA AGCTTTAATT GACGAAATCG 60

ATCAAAATCC AAATCTAACA GATAAGGAAA AACAAGCACT TAAAGATCGT ATTAATCAAA 120

TACTTCAACA AGGTCATAAC GACATTAACA ATGCGATGAC AAAAGAAGCA ATTGAACAAG 180

CAAAAGAACG TTTAGCGCAA gCATTGCAAG ACATCAAAGA TTTAGTGAAA GCTAAAGAAG 240

ATGCGAAAAA TGATATTGAT AAACGTGTAC AAGCTTTAAT TGACGAAATC GATCAAAATC 300

CAAATCTAAC AGATAAGGAA AAACAAGCAC TTAAAGATCG AATTAATCAA ATACTTCAAC 360

AAGGTCATAA CGACATTAAC AATGCGCTGA CTAAAGAAGA AATTGAGCAG GCAAAAGCAC 420

AACTTGCACA AGCATTGCAA GACATCAAAG ATTTAGTGAA AGCTAAAGAA GATGCGAAAA 480

ATGCAATAAA AGCCTTAGCT AATGCGAAgc GTGATCAAAT CAATTCAAAT CCAGATTTAA 540

CACCTGAGCA AAAAGCAAAA GCGCTCAAAG AAATTGACGA AGCTGAAAAA CGAGCACTAC 600

AAAACGTTGA GAATGCTCAA ACTATAGATC AATTAAATCG AGGATTAAAC TTAGGTTTAG 660

TTGAAGCAAC ACCTGAGCAA ATCCTAGTTA ATGGTGAACT CATTGTACAT CGTGATGACA 780

TCATTACAGA ACAAGATATT CTTGCACACA TAAACTTAAT TGATCAGCTT TCAGCAGAAG 840

TCATCGATAC ACCATCAACT GCAACGATTT CTGATAGCTT AACAGCAAAA GTTGAAGTTA 900

CATTGCTTGA TGGATCAAAA GTGATTGTTA ATGTTCCTGT AAAAGTTGTA GAAAAAGAAT 960

TGTCAGTAGT CAAACAACAG GCAATTGAaT CAATCGAAAA TGCGGCACAA CAAAAGATTA 1020

ATGAAATCAA TAATAGTGTG ACATTAACAC TGGAACAAAA AGAAGCTGCA ATTGCGnAAG 1080

TTAATAAGCT TAAACAACAA GCAATTGGAT CATGTTnAAC AATGGCACCT GGATGTTCCA 1140

TTCAGTTGAA GGAAATTTCA ACAACAAGGA ACAAGCGCCn GATTGGAACA ATTTGA 1196

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CAATCGTTTC AACGCTATTA TCTTTAGACA ACAATTGTAA GCGTGTATGT GCAGTTTCTA 60

AACAGTCTAT AATTCGAGTT CTTAATTCAG CTGGATCATC TTTAAAAATA AAATCCATCG 120

CTGCAACTTT GTAGACAAAT GTTAAATAGG TAAGTTCACT GTGACTCGTA ACGAAAATAA 180

TGTTACCAAC TGGGTCATGC TTACGAATTT CACTGCCTAA TTTGATACCA TTAATATCAG 240

TTGAAAGTTG AATATCTAAA AAGTAACAGC CTATGTCATT CATATTTTTA GCTTGCTCAA 300

GCACCTCATA AGGATTATCA GTTGCGAGGG CAATTTCCAT AGGCTTTTCT TCTATCATTA 360

TATAATTTTT AATAATGGTA ACCATGTTTT CTCTTTGTTT TGGATCGTCT TCGCAAATGA 420

AAATTTTCAT ACATTCACAT CCTTATGGCT AGTTGTTAAT AATTTCAACT TTTTGAATAA 480

AGAAACCATT TTCGATAATT GTATCTAATA AGACATTGTC TGCATTATCA GCAATTTCTT 540

TTAAAGTTGA TAGACCTAAA CCACGACCTT CACCTTTAGT AGAAAAACTT TCTTGGAACA 600

ATTCATGAAT GCGTGGTATA TCATCAGCGC ATTTATTCAT AACAATAAAC GTTACTGAAT 660

TTTCACTTTC AATAAATGCA ACGCGAATGA TAGGGTCATC AATTTCAGTT GATGCCTCAA 720

TTGCATTATC AAGAATAATA CCAATACTGC GACTTAAATC GATCATATTC AAGTTAATGC 780

TACTTACTTC ATCGGGTATT TCGATACTAA TCGGAATATT CATTTCTTGT GCACGTAAAA 840

TTTTCGCAGT AATTAAGCCT TTAATTTCAC GTACTTTAAG ATTCTCGATA CCATTTAATT 900

GTAGGCCAGG CATGTCATCT TCTCGAATGT ATTCTGAAAG TGTCGTTAAG ATATTGACAT 1020

AATCATGACG GAACTTGCGC ATTTCGTTGT TGATAGCTTC AATCTTCAAT GTATATTCAT 1080

AATAGGTTTC AATTTCTTCT TGATTACGTT TATATTTCAT CTCTTTAAGG AGAAATTGAG 1140

AAATAACAAA TGTTAATATA CTTAAAAATA TAGTGATACC AATAAAAATA AAAGAATACT 1200

GCCTTATTAC TTTAGCTTCA TCCGAGTTTA TTTGTGAATA AAAGAAAAAT AATGAAAAAG 1260

TAAGCAGTAA GATAGTCGAA ATAACTATTA AAAATCCTTT GTTTAGTATT AGATATGGTG 1320

TGCTAATTTT TTTGAGAACT CTATTTATTA TATATGAGAA TAGTATACTA ATAGTCACAT 1380

AAACTACAAA AAAGCTAGGG AATATTACAA ATATACTATC AGAAATTTTG GTGGATATAT 1440

GCATATATAA CTATATACCT GTAGTTAGCA CnGTnATAGG AATAATCnGG CGAGGTCCAT 1500

AATCCACCAA AATAGAATA 1519

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GTAGGAATCT CTTTGTCTTT TTGGGAGGAC ATTTAATATG AATGTATATT TAGCAGAATT 60

CCTAGGAACT GCAATCTTAA TCCTTTTTGG TGGTGGCGTT TGTGCCAATG TCAATTTAAA 120

GAGAAGTGCT GCGAATGGTG CTGATTGGAT TGTCATCACA GCTGGATGGG GATTAGCGGT 180

TACAATGGGT GTGTTTGCTG TCGGTCAATT CTCAGGTGCA CATTTAAACC CAGCGGTGTC 240

TTTAGCTCTT GCATTAGACG GAAGTTTTGA TTGGTCATTA GTTCCTGGTT ATATTGTTGC 300

TCAAATGTTA GGTGCAATTG TCGGAGCAAC AATTGTATGG TTAATGTACT TGCCACATTG 360

GAAAGCGACA GAAGAAGCTG GCGCGAAATT AGGTGTTTTC TCTACAGCAC CGGCTATTAA 420

GAATTACTTT GCCAACTTTT TAAGTGAGAT TATCGGAACA ATGGCATTAA CTTTAGGTAT 480

TTTATTTATC GGTGTAAACA AAATTGCCGA TGGTTTAAAT CCTTTAATTG TCGGAGCATT 540

AATTGTTGCA ATCGGATTAA GTTTAGGCGG TGCTACTGGT TATGCAATCA ACCCAGCACG 600

TGATTTAGGT CCGAGAATTG CACATGCGAT TTTACCAATA GCTGGTAAAG GTGGTTCAAA 660

TTGGTCATAT GCAATCGTTC CTATCTTAGG ACCAATTGCC GGTGGTTTAT TAGGTGCAGT 720

GGTATACGCT GTATTTTATA AACATACATT TAATATTGGT TGTGCAATTG CrATTGTTGT 780

CGAATCAATT TACTAAAATA AAAAGAAACG TAAATAGCAT AATTTAACAT GTTTGATTCA 900

TGGATTATGC TATTTTTTCG CCAAAATTTA ACAGATTTTG TACAATGGGT TAGCGATTAT 960

TTTTTAATAA AGGAGATACT ACTAATGGAA AAATATATTT TATCTATAGA CCAAGGAACA 1020

ACAAGCTCAA GAGCGATTTT ATTCAATCAA AAAGGGGAAA TTGCAGGGGT AGCACAACGT 1080

GAGTTTAAGC AATATTTTCC ACAATCAGGT TGGGTTGAAC ATGATGCAAA TGAAATTTGG 1140

ACATCTGTGT TAGCTGTAAT GACGGAAGTA ATTAATGAAA ATGATGTTAG AGCTGATCAA 1200

ATTGCAGGTA TCGGTATTAC AAACCAACGT GAAACAACGG TTGTTTGGGA CAAaCATACT 1260

GGCCGCCCAA TTTATCACGC AATTGTTTGG CAATCACGTC AAACACAATC AATTTGTTCA 1320

GAATTAAAAC AACAAGGATA TGAACAAACA TTTAGAGATA AGACAGGATT ACTTTTAGAT 1380

CCGTATTTTG CAGGTACAAA AGTTAAATGG ATTCTAGACA ATGTTGAAGG TGCACGAGAA 1440

AAAGCAGAAA ATGGCGATCT ATTATTTGGA ACGATTGATA CTTGGTTAGT ATGGAAATTA 1500

TCaGGaAAAg CtGCGCATAT TACTGATTAT TCaAATGCGA GTCGTACATT AATGTTTAAT 1560

ATCCATGATT TAGAATGGGA CGATGAGTTA TTAGAACTAt TACAGTACCT AAAAATATGT 1620

TGCCAGAAGT TAAAGCTTCG AGTGAAGTAT ATGGTAAGAC AATTGATTAC CACTTCTATG 1680

GTCAAGAAGT ACCAATCGCT GGAGTAGCTG GTGATCAACA AGCAGCATTA TTTGGACAAG 1740

CTTGCTTCGA ACGTGGTGAC GTGAAAAACA CATATGGAAC TGGTGGCTTC ATGTTAATGA 1800

ATACAGGTGA CAAAGCGGTT AAATCTGAAA GTGGTTTATT AACAACAATT GCTTATGGTA 1860

TTGATGGAAA AGTAAATTAT GCGCTTGAAG GTTCCATCTT TGTTTCGGGT TCAGCAATCC 1920

AATGGTTACG TGATGGATTA AGAATGATTA ATTCAGCACC ACAATCAGAA AGTTATGCGA 1980

CACGAGTTGA CTCTACTGAG GGTGTTTATG TTGTTCCAGC TTTTGTAGGT TTAGGAACAC 2040

CATATTGGGA TTCTGAAGCA CGTGGTGCGA TTTTCGGTTT AACACGTGGA ACTGAAAAAG 2100

AGCACTTTAT CCGTGCAACT TTAGAATCAC TATGTTACCA AACTCGTGAC GTTATGGAAG 2160

CAATGTCAAA AGACTCTGGT ATTGATGTCC AAAGTTTACG TGTCGATGGT GGTGCAGTTA 2220

AAAATAACTT TATTATGCAG TTCCAAGCAG ACATTGTTAA TACTTCTGTT GAAAGACCTG 2280

AAATTCAAGA AACTACAGCT TTAGGTGCTG CATTTTTGGC AGGTTTAGCA GTTGGATTCT 2340

GGGAGAGTAA AGATGATATC GCTAAAAACT GGAAATTAGA AGAAAAATTC GATCCGAAAA 2400

TGGATGAAGG CGAAAGAGAA AAATTATATA GAGGTTGGAA AAAAGCTGTT GAAGCAACAC 2460

AAGTTTTTAA AACAGAATAA ACTTGTAGAT TAGACTTTTG TATAAACATT GTGATACAAT 2520

CAATTTAAGT TAATATTTGA ATCGAGAAGC GAGAGATTTG TTCGAACATG TACAATTGAA 2580

GCATTGTCTA CTTTTAAGAG AGAACATATT AAAAAGAATT TAAGAAATGA TGAATATGAT 2700

TTAGTAATTA TTGGTGGCGG TATTACAGGT GCAGGTATTG CACTAGACGC GAGTGAAAGA 2760

GGAATGAAAG TTGCATTAGT TGAAATGCAA GACTTTGCAC AAGGAACAAG CTCAAGATCT 2820

ACAAAATTAG TCCATGGTGG TTTGCGTTAC TTAAAACAAT TCCAAATTGG AGTAGTTGCC 2880

GAAACTGGTA AAGAACGTGC GATTGTTTAT GAAAATGGGC CTCATGTTAC GACTCCAGAG 2940

TGGATGCTTT TACCAATGCA TAAAGGTGGA ACATTTGGTA AATTCTCAAC ATCAATTGGT 3000

TTAGGAATGT ATGATCGTTT AGCAGGTGTT AAGAAGTCTG AACGTAAAAA AATGTTATCT 3060

AAAAAAGAAA CTTTAGCTAA AGAACCATTA GTTAAAAAAG AAGGTCTAAA AGGCGGCGGT 3120

TACTATGTTG AATATCGTAC TGACGATGCG CGTTTAACTA TTGAAGTTAT GAAGCGTGCT 3180

GCTGAAAAAG GCGCAGAAAT TATCAACTAT ACTAAATCTG AACACTTCAC TTATGATAAA 3240

AATCAACAAG TAAATGGTGT TAAAGTTATA GATAAATTAA CTAATGAAAA TTATACAATT 3300

AAGGCTAAAA AAGTGGTTAA TGCAGCAGGT CCATGGGTTG ATGATGTTAG AAGTGGTGAT 3360

TATGCACGCA ATAATAAAAA ATTACGTTTA ACTAAAGGTG TACATGTTGT TATTGATCAA 3420

TCAAAATTCC CATTAGGTCA AGCAGTATAC TTTGATACTG AAAAAGATGG AAGAATGATT 3480

TTTGCAATTC CACGTGAAGG AAAAGCGTAT GTAGGTACTA CAGATACATT CTATGACAAT 3540

ATCAAATCTT CACCATTAAC TACACAAGAA GACAGAGACT ATTTAATCGA TGCGATTAAT 3600

TACATGTTCC CTAGTGTTAA TGTTACAGAT GAAGATATTG AATCAACATG GGCAGGAATT 3660

AGACCATTAA TTTACGAAGA AGGCAAAGAC CCTTCTGAAA TCTCTCGTAA GGATGAAATT 3720

TGGGAAGGTA AATCAGGTTT ATTAACTATT GCAGGTGGTA AATTAACAGG CTATCGTCAC 3780

ATGGCTCAAG ACATTGTTGA TTTAGTATCT AAACGCTTGA AAAAAGACTA CGGTTTAACA 3840

TTTAGTCCAT GTAATACAAA AGGTCTGGCA ATTTCAGGTG GCGATGTAGG TGGTAGCAAG 3900

AACTTTGATG CGTTTGTAGA GCAAAAAGTA GATGTAGCTA AAGGATTCGG CATTGATGAA 3960

GATGTTGCAA GACGTTTAGC ATCTAAATAT GGTTCAAATG TTGATGAATT GTTCAACATT 4020

GCGCAAACAT CTCAATACCA TGATAGCAAG TTACCATTAG AAATTTATGT AGAACTTGTT 4080

TATAGTATTC AACAAGAAAT GGTATACAAA CCTAACGATT TCTTAGTTCG TCGTTCTGGT 4140

AAAATGTATT TCAATATTAA AGATGTATTA GATTATAAAG ATGCTGTCAT CGATATTATG 4200

GCAGATATGC TTGATTACTC TCCAGCTCAA ATTGAAGCAT ATACTGAAGA AGTTGAGCAA 4260

GCAATTAAAG AAGCGCAACA TGGaAATAAT CAACCAGCAG TTAAAGAATA AtTAATTTGT 4320

ACAATCATAA ACTGGTGTCC TGTTTTAAGG GCATCAGTTT TTTTATACGA GATACATTAG 4380

GTTATTAAAG GTGTGAGATG ATGACTGAAA AACAATTTAA ATTAACTGTA CAAGATAATA 4500

CGAATATTGA AGTTAAAGTG AATTTTACAG ATGTAGATTC AAAAGGAATT ATTCATATAT 4560

TTCATGGTAT GGCTGAACAT ATGGAACGTT ACGATAAATT AGCACATGCA CTTTCAAAGC 4620

ATGGCTTCGA TGTGATACGT CATAATCATC GAGGACATGG TATTAATATT GATGAATCAA 4680

CAAGAGGGCA TTACGATGAT ATGAAACGAG TTATCGGTGA TGCCTTTGAA GTAGCGCAAA 4740

CAGTGAGAGG CAATGTTGAT AAACCATACA TTATAATCGG ACATTCAATG GGATCCGTTA 4800

TAGCTAGATT GTTTGTAGAA ACATATCCGC AATATGTTGA TGGTCTAATT TTAAGTGGTA 4860

CTGGTATGTA TTCATTATGG AAAGGTTTAC CAACCGTTAA AGTGTTACAA CTGATTACAA 4920

AAATTTATGG TGCTGAGAAA CGAGTTGAAT GGGTTAACCA GTTAGTATCA AATAGTTTTA 4980

ATAAAAnnAT ACGTCCATTA CGTACACAAA GTGATTGGAT TTCTAGTAAT CCAATTGAAG 5040

TAGATAaCTT TATTAAAGAT CCATATAGTG GaTTTAATGT GTCAAATCAA TTATTATATC 5100

AAACAGCCTA TTATATGCTA CATACATCAC AATTAAAAAA TATGAAAATG TTAAaTCATG 5160

CCATGCCTAT ATTATTAGTT TCAGGATATG ACGATCCTTT AGGTGATTAT GGTAAAGGGA 5220

TTTTAAAATT GGCGAATATA TATAGAAACG CTGGCATnAA AAATGTTAAA GTGAATCTTT 5280

ATCATCATAA ACGTCATGAA GTGTTATTTG AAAAnGATCA TGACnAAATT TGGGAAGACT 5340

TGTTTAAATG GTTGAATCAA TTTTATAAAA AATAAAGAAA GTGGAATTAA ATATGAATAA 5400

AAATAAGCCT TTTATTGTAG TAATTGTGGG GCCAACTGCT TGCAG 5445

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2569 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TGGCTTGAAC TACGCCAATA AGTCCCCCTA GTACAAGAAT GAATACCATG ATATCGACCG 60

CTTCTATCGT ACCTTCAACC ATGCTACTTG TTATTTGTTC TGGTCCAGCT GGATGTTGCT 120

TTAATCTTTC ATAAGTATTC GGAATTGATA CCGGCTTATT AATTGCACCT GATTTAAATT 180

GTTCAATCTT AATTTTAACC CCCATTTTGT CTAGTTCCTG TTGCGTACCC GGAACCTTTT 240

TCACTTGGTT ATGAGGGTTA ACTATCTTTA GTTCTTGGGA TGAAGGTTCG TAAGAAAGTT 300

TAGAATATGC ACCAGCAGGA ATAACCCATG TTGCTATAAC TGCAACAACC GTTAAAATGA 360

TAATTGTATT TTCCACGGTT TCATCTCCTT CGACATTTAA CCTAGCATTT CTACCTTAAA 480

GATTTTATAA ATATAAATTA AGAAAGTGCA CCCCGCATCA AAATAGAGGC ATTATTTTCA 540

GGGGGTGCAC ATAAATAATA AAAATCATGC ATTTGACATA TAGTAATTGA AAAGCGTTTC 600

AATTCAATTA CTTTTTAATC ACAGTACCTA CTTTACCCTC TAAGGCAGCA TCTAATTCAT 660

TTAATGATGT TATAAGCACA CTTCCTTTTG GATTGTTTTC AATAAATGAT ATGGCTGCTT 720

CAATTTTTGG TAACATACTT CCTTTTGCAA ATTGATTTTC GTCTATATAT CGTTTTAATT 780

CATCAACATT TGTTGTTTTC AAAGGCTGTT GGTTTTCAGT GTTAAAATTA ATATATACAT 840

AATCAATTGC TGTTAAAATA ATCAATTGAT CGCATTGAAT ATTAGCACCC AACAACGCAC 900

TTGTTTTATC TTTGTCTATA ACTGCATCAA TACCTTTAAA ACCATCATGT TGCTCTCTAA 960

TTACTGGTAT ACCTCCACCA CCAGCAGCAA TAACGAGTGT ATCATTTTTA ATAAGTGTTT 1020

TAATACTCTC TAATTCAATA ATAGAGATGG GTTGTGGTGA AGGAACAACG CGTCTATATC 1080

CTCTTCCAGC ATCTTCAACA AATATAAATC CTTTTTCTTT TTGAATTTGT TCAGCTTCTT 1140

CTTTGTTGTA AAATAACCCA ATTGGTTTTG AAGGATTGTT AAATGCCGGA TCATTTTCAT 1200

CAACTTCAAC TTGTGTCACT AGTGTTACCA CTTGTTTATC CATTCCAATA GAATGCAATT 1260

CATTTTGTAA GCTTTCTTGT AATTGATAGC CGATGTAAGC TTGACTCATT GCGCCACATT 1320

CAGCAAATGG AAATGCCGGA CCTTGGTTAT GTTCTGCAGC ATAGTTAAGT CCCAAATTAA 1380

TGCTTCCAAC CTGTGGTCCA TTACCATGAC TAATAACAAT CTCATGTCCT TTTGTnATTA 1440

AyCCTACTAA TGATTtCGCA GTATTTTTAA CAAGCTCGAG TtGgTyCTTG aGGTGATTTn 1500

CCTAAAGCAT TACCACCTAA TGCTACTACT ATTTTCGCCA TCATATTCAC TTCCTTATAT 1560

CATTTAAAAT TCACCCAATG TAGCAACCAT GaCTGCTTTG ATTGTATGCA TTCTGTTCTC 1620

AGCTTCTTGG AATACAACTG AAGCTTTACT TTCGAATACT TCATCTGTAA CTTCCATTTC 1680

TCGAATACCA TATTTTTCAA AAATTTGTTG ACCTATTTTC GTATCAGCAT TATGGAAAGA 1740

TGGTAAGCAA TGCTCAAAAA TAACATTTGG ATTACCAGTT TTATCCATTA TTTCTTTATT 1800

TACTTGATAT GGTTTCAATA ATTCAAGTCG TTCTTTCCAT ACTTCATCAG GTTCACCCAT 1860

TGATACCCAA ACATCAGTGT AAATTACATC CGAACCTTTT ACaCCTTGGT CaATATCATC 1920

TGTGATTAAT ATGTTGCCaC CATTTTCaGC GGCAATATTT TTACAGCGAT TTAATAATTC 1980

ATCTGTTGGA TTTAATTCTT TTGGACAAAC TAAATGGAAG TTCATACCCA TAATGGCAGC 2040

ACCTTGCATT AATGCATTTG CAACGTTATT ACGACCATCT CCAACATATG TAAAGTTAAT 2100

ATCTGCATAA TCTTTTTTTA AGACTTCTTT TGCTGTTAAG AAATCAGCAA GAACTTGAGT 2160

TTCTACTGTT CTTTGTGAAA AACCACGGTA TTCAATGCCA TCATACATTC CACCAAGCAC 2280

ACGTGCAGTA TCTTTAGTTG TTTCTTTTTT ACCCATTTGT GATCCAGTTG GGCCTAAATA 2340

AGTTACATTT GCACCTTGAT CATGCGCTGC AACTTCAAAT GCACATCGCG TTCTTGTAGA 2400

ATCTTTTTCA AATAACAGTG CAATATTTTT ATTTTTTAAC ATAGGCTTTT CAGTGCCAAT 2460

ATATTTAGCA CGTTTTAAAT CCTCGGAGAG TGTTAATAAG GTTCTACCTC TTGTCGTGAA 2520

AAGTCTAATA AAGTTAAAAA ACTTCTGTTT CGTAnATTTT TCATTAAnA 2569

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CCTGGAACCA TCCaATCGtG CaAATCtTGa AAGaGAATAC GCAACAACAA TTAAATGTAT 60

TGGAACACTA TATTCCAAAT GACCATCCAG CACTCGTTGA ATTAAAAATA TGGGAACGTT 120

GGTTACATAA ACAAGGTTAC AAAGACATCC ATTTAGATAT TACTGCGCAC CACCTAGATC 180

CTATTACACA GGTTTATTTA TTCAATGTCA TTTTGCTGAA AATGAATCTC GAGTTTTAAC 240

AGGTGGTTAT TACAAAGGAA GCATCGAAGG GTTTGGATTA GGATTAACAC TTTAAGTAAG 300

GGAGTATGCA CAATGTTAAG AATCGCCATA GCCAAAGGAC GTCTAATGGA TAGTTTAATT 360

AACTATTTAG ATGTAATTGA ATATACGACA TTATCAGAAA CATTAAAAAA TAGAGAACGC 420

CAATTATTAT TAAGTGTAGA TAATATTGAA TGCATTTTAG TAAAAGGAAG TGACGTGCCA 480

ATCTATGTGG AACAAGGAAT GGCAGACATA GGCATTGTTG GTAGCGACAT ATTAGATGAG 540

CGCCAATATA ATGTTAATAA TTTGTTGAAT ATGCCTTTTG GAGCATGTCA TTTTGCGGTT 600

GCAGCGAAAC CTGAAACGAC CAATTATCGT AAAATCGCAA CGAGTTATGT TCATACTGCT 660

GAAACATATT TTAAATCAAA AGGTATTGAT GTCGAATTGA TTAAATTGAA TGGCTCTGTT 720

GAATTGGCCT GTGTTGTAGA TATGGTAGAC GGAATTGTCG ACATCGTTCA AACAGGTACT 780

ACGCTAAAAG CGAACGGACT GGTTGAAAAG CAACATATTA GTGATATCAA TGCAAGATTA 840

ATAACTAATA AAGCAGCTTA TTTTAAAAAA TCACAATTAA TAGAGCAATT TATTCGCTCT 900

TTGGAGGTGT CTATTGCCAA TGCTTAATGC ACAACAATTT TTAAATCAAT TTTCATTAGA 960

AGCACCATTA GATGAGTCAT TGTATCCaAT TATTCGCGAT ATTTGTCAGG AAGTTAAAGT 1020

TTTAGaAATT AGTCATGAmC AAATTAAAGC AGCATTTGAC ACATTAGATG AAAAAACAAA 1140

ACAAGCATTA CAACAAAGTT ATGAAAGAAT TAnAGCATAT CAaGAAaGTA TtaAACAGaC 1200

GaATCAACAG TTAGAAGaAT CAGTGGaGTG tTrTGaAATA TACCATCCmC taGaAAGTGT 1260

CGGTATTTAT GTG 1273

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GTTGATAAAT TAAAAATGTT TTTATCAGAT ATTCAAAGTT ACCAACAATA TAGTAAAGAT 60

CATCCGGTGT ATCAGTTAAT TGATAAATTT TATAATGATC ATTATGTTAT TCAATACTTT 120

AGTGGACTTA TTGGTGGACG TGGACGACGT GCAAATCTTT ATGGTTTATT TAATAAAGCT 180

ATCGAGTTTG AGAATTCAAG TTTTAGAGGT TTATATCAAT TTATTCGTTT TATCGATGAA 240

TTGATTGAAA GAGGCAAAGA TTTTGGTGAG GAAAATGTAG TTGGTCCAAA CGATAATGTC 300

GTTAGAATGA TGACAATTCA TAGTAGTAAA GGTCTAGAGT TTCCATTTGT CATTTATTCT 360

GGATTGTCAA AAGATTTTAA TAAACGTGAT TTGAAACAAC CAGTTATTTT AAATCAGCAA 420

TTTGGTCTCG GAATGGATTA TTTTGATGTG GATAAAGAAA TGGCATTTCC ATCTTTAGCT 480

TCGGTTGCAT ATAGAGCTGT TGCCGArAAA GAACTTGTGT CAGAAGAAAT GCGATTAGTC 540

TATGTAGCAT TAACAAGAGC GAAAGAACAA CTTTATTTAA TTGGTAGAGT GAAAAATGAT 600

AAATCATTAC TAGAACTAGA GCAATTGTCT ATTTCTGGTG AGCACATTGC TGTCAATGAA 660

CGATTAACTT CACCAAATCC GTTCCATCTT ATTTATAGTA TTTTATCTAA ACATCAATCT 720

GCGTCAATTC CAGATGATTT AAAATTTGAA AAAGATATAG CACAAATTGA AGATAGTAGT 780

CGTCCGAATG TAAATATTTC AATTGTGTAC TTTGAAGATG TGTCTACAGA AACCATTTTA 840

GATAATGATG AATATCGTTC GGTTAATCAA TTAGAAACTA TGCAAAATGG TAATGAAGAT 900

GTTAAAGCAC AAATTAAACA CCAACTTGAT TATCGATATC CATATGTAAA TGATACTAAA 960

AAGCCCTCAA AACAATCTGT TTCTGAATTG AAAAGACAAT ATGAAACAGA AGAAAGTGGC 1020

ACAAGTTACG AACGAGTAAG GCAATATCGT ATCGGTTTTT CAACGTATGA ACGACCTAAA 1080

TTTCTAAGTG AACAAGGTAA ACGAAAAGCG AATGAAATTG GTACGTTAAT GCATACAGTG 1140

GATGGATTAA TCGATAAACA TATTATCGAA GCAGATGCGA AAAAAGATAT CCGTATGGAT 1260

GAAATAATGA CATTTATCAA TAGTGATTAT ATTCGATATT GCTGAAGC 1308

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GATGCCATTn ATnnGTATGC AAGAAGTTGT TCCGGGTTCA GGTGGATTaC CAGTTGGTAC 60

TGGTGGTAAG ACGTTACTAA TGCTTTCAGG CGGTATAGAC TCACCAGTTG CTGGGATGGA 120

AGTGATGAGA CGTGGCGTAA CAATTGAAGC GATTCATTTC CATAGTCCAC CATTTACAAG 180

TGATCAAGCA AAAGAAAAAG TTATTGAATT GACACGTATT TTAGCTGAAC GTGTTGGACC 240

AATTAAATTG CATATTGTAC CATTTACAGA ATTGCAAAAA CAGGTAAATA AAGTTGTACA 300

TCCAAGATAT ACAATGACTT CAACGAGACG TATGATGATG CGTGTTGCTG ATAAATTAGT 360

ACATCAAATA GGGGCTTTAG CTATTGTAAA TGGTGAAAAC CTAGGGCAGG TAGCCAGTCA 420

AACACTTCAT AGCATGTATG CAATTAATAA TGTAACTTCT ACTCCTGTAT TACGTCCTTT 480

ATTAACTTAC GATAAAGAAG AAATTATTAT TAAATCGAAA GAAATTGGTA CATTTGAAAC 540

ATCTATTCAA CCATTTGAAG ATTGTTGTAC AATTTTCACC CCTAAAAATC CAGTAACCGA 600

ACCAAACTTT GATAAGGTAG TCCAATATGA AAGTGTCTTT GATTTTGAAG AGATGATTAA 660

TCGTGCTGTT GAAAATATTG AAACACTTGA AATAACTAGT GATTATAAAA CTATTAAAGA 720

ACAGCAAACA AACCAATTAA TAAACGACTT TTTATAAATA AAATCCTAGA GTAAATTTAA 780

ACATAAGGGG ATGTTAAACT ATGGATTTGA ACTTAACGAT GATTATAATC ATAATTTTAT 840

TTGGTTTTAT CGCGGCGTTT ATAGATTCGG TTGTAGGGGG TGGCGGTTTA ATTTCTACGC 900

CAGCATTATT AGCAATCGGT CTACCACCAT CTGTGGCTTT AGGTACAAAT AAATTGGCAA 960

GTTCGTTTGG TTCTTTAACT AGTACGATAA AGTTTATAAG GTCCGGTAAA GTGGACTTAT 1020

ATGTTGTTGC CAAATTATTT GGTTTTGTAT TTTTGGCATC TGCATGTGGC GCATATATTG 1080

CAACGATGGT TCCGTCACAA ATATTGAAAC CTTTAATCAT CATTGCACTT TCGTCGGTGT 1140

TTATATTCAC ATTACTTAAA AAAGATTGGG GCAATACACG CACGTTTACT CAATTTACAT 1200

TTAAGAAAGC CATAATATTT GCAGCACTTT TTATATTAAT CGGCTTTTAT GATGGATTTG 1260

TAAGTGCAGC AGGAAATGCT AAAGTTTTGA ACTTTGCTTC TAATATAGGT GCGCTTGTAT 1380

TATTTATGGT ATTAGGACAA GTAGATTATG TAATAGGTTT AATTATGGCT A 1431

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

AATATTATTT TAAATTCAAT ATTTATTGGT GCATTTATTT TAAACTTATT ATTCGCCTTT 60

ACCATTATTT TCATGGAAAG ACGTTCTGCC AATTCTATCT GGGCTTGGTT ACTAGTCTTA 120

GTTTTCTTGC CTTTATTCGG CTTCATTTTA TACTTACTAT TAGGACGACA AATTCAACGT 180

GACCAAATTT TCAAAATTGA TAAGGAAGAT AAAAAAGGAT TAGAGTTAAT CGTTGATGAG 240

CAATTAGCTG CTTTAAAAAA TGAAAACTTT TCAAATTCCA ATTATCAAAT TGTAAAATTT 300

AAAGAAATGA TTCAAATGTT GTTATATAAT AACGCAGCAT TTTTAACAAC AGACAACGAT 360

TTArrrrtAT ACACAGACGG CCAAGAAAAA TTTGATGACC TAATACAAGA CATCCGTAAT 420

GCTACTGATT ATATTCATTT TCAGTACTAT ATTATTCAAA ATGATGAATT AGGTCGTACC 480

ATTTTAAATG AACTTGGTAA AAAAGCGGAA CAAGGTGTAG AAGTTAAAAT TCTTTATGAT 540

GACATGGGTT CTCGTGGACT GCGTAAAAAA GGCTTACGCC CGTTTCGCAA TAAAGGTGGA 600

CATGCTGAAG CATTTTTCCC ATCAAAATTA CCTTTAATTA ACTTGCGTAT GAACAATCGA 660

AACCATCGAA AAATTGTTGT AATAGATGGG CAAATTGGAT ATGTTGGTGG TTTTAATGTT 720

GGTGATGAGT ACTTAGGTAA ATCAAAAAAA TTCGGCTATT GGCGAGATAC GCATTTACGA 780

ATTGTCGGGG ATGCAGTGAA TGCATTGCAA TTACGATTTA TTCTAGATTG GAATTCACAA 840

GCCACACGTG ACCACATCTC CTATGATGAT CGTTATTTCC CAGATGTAAA TTCTGGTGGA 900

ACAATTGGCG TTCAAATAGC TTCTAGTGGT CCTGACGAAG AATGGGAACA GATTAAATAC 960

GGCTATTTGA AAATGATTTC ATCTGCTAAA AAATCGATTT ATATTCAATC TCCCTATTTC 1020

ATACCTGATC AAGCCTTTTT AGATTCTATT AAAATTGCGG CATTAGGTGG TGTTGATGTC 1080

AATATCATGA TTCCTAATAA ACCTGACCAT CCGTTTGTTT TTTGGGCTAC TTTAAAAAAT 1140

GCAGCATCCT TATTAGATGC CGGTGTTAAA GTATTTCACT ACGACAATGG CTTTTTACAC 1200

TCAAAAACAC TTGTTATAGA TGATGAAATT GCAAGTGTGG GAACAGCTAA TATGGACCAT 1260

AAATTAAAAC AAGCTTTTAT AGATGATTTA GCAGTATCTT CTGAATTAAC AAAAGCACGT 1380

TATGCTAAGC GAAGTCTTTG GATTAAATTT AAAGAAGGTA TTTCACAATT ATTGTCACCT 1440

ATCTTATAAA ATAGAAATAT GAGGAGTGTA aCTTTAATGC AACAATCAGA CGTCATTAGT 1500

GCTGCCAAAA AATATATGGA ATCTATTCAT CAAAATGATT ATACAGGCCA TGATATTGCG 1560

CATGTATATC GTGTCACTGC TTTAGCTAAA TCAATCGCTG AAAATGAAGG TGTTAATGAT 1620

ACTTTAGTCA TTGAACTCGC ATGTTTGCTT CATGATACCG TTGACGAAAA AGTTGTAGAT 1680

GCTAACAAAC AATATGTTGA ATTGAAGTCA TTTTTATCTT CTTTATCACT ATCAACCGAA 1740

GATCAAGAGC ACATTTTATT TATTATTAAT AATATGAGCT ATCGCAATGG CAAAAATGAT 1800

CATGTCACTT TATCTTTAGA AGGTCAAATT GTCAGGGATG CAGATCGTCT TGATGCTATA 1860

GGCGCTATAG GTGTTGCACG AACATTTCAA TTTGCAGGAC ACTTTGGTGA ACCTATGTGG 1920

ACAGAACATA TGTCACTAGA TAAGATTAAT GATGATTTAG TTGAACAGTT GCCACCATCT 1980

GCAATTAAAC ATTTCTTTGA AAAATTACTT AAGTTAGAAT CTTTAATGCA TACAGATACG 2040

GCGAAGATGA TTGCTAAAGA ACGTCACGAC TTTATGATGA TGTACTTGAA ACAGTTTTTT 2100

ACGGAATGGA ATTGTCACGA CTAGACATTG AAGTTGTAGT ATGATGATGC GATGTAATGG 2160

CGTGTTGTTG TGGAAGCTTG GTGTCATGCC ATGTTACTTT GATGTGTTGT TGTGGGAGCT 2220

TGGTGACATG TCATGCTACT TTGATGTGCT GGTACCACGA TGCGTCTTGA TGTAGTGCTA 2280

TGATGTGGCA TTGCGGTGTT ATGGTGTTAT AGACAGGTTT GGCGTTGATG CCATGTTACT 2340

TTGATGTGCT GGTACCACGA TGCGACTTGA TGTAGTGCTA TGATGTGGCA TTGCGGTGTT 2400

ATGGTGTTAT AGACCGGTTT GATGTTGATG CCATGTTACT TTGATGTGCT GGTGCTACGA 2460

TGCGACTTGA TGTAGTGCTA TGATGTGGCG TTGCGCTGTT ATGGTGTTAT AGCCAGGTTT 2520

GGTGTTGATG TCATGCCGTT ACGATTCTAT GATATGTTGT TGGGACGTTG CAATGTGTAT 2580

TATGCCGTTG TGACGTTATT ATTTCACACT GTTACATGTA TAAGTGAATT GCTGTGGAAA 2640

TTTGCGACAT ATACTGCTAC ACTGATGAAT CATTGTGTCA AGATGACATT GCGATGAAGA 2700

ATGACAACTC TGTTATTAAC CACTTTTTAC ATACTGAAAA CTCGTTAATA TTATTTCAAA 2760

TAAAAACAGC AGTAGGATGA CTTTCACATT TGAAATCATC TTACTGCTGT TTCTATTTAT 2820

CACATATTGT ATAATGTGAC ACTAAGTTTC GCTATTGAAG CGAAAAATAA TGTGCGCCCT 2880

ATAAAGTTAA AATTATCTTC AACTTTTAGG GTGCACATTA TTTGGACTTG CTAAGGTTAT 2940

TTCTTTTTCT TTTTAGACAC AACTTGTGTG TTTTTGCCTT TTTTATTGct GCCGCCGTTG 3000

TGCTCTCTTT CATACGCTTC AATGAAAGGT TGTACTTCTT TTTTAGCGAC TTTTTCATAA 3060

CCAAGTGCTG ATGCTGAGCT TAATGAAATC CAGATAATCA TAATTGGTGA AATGACCATC 3180

ATCATGTAAC CCATTTGACG TTGTTCGTCT GGCATCGTTT TACTTGATAC ATATGCTTGG 3240

ATAAAGTATA AAACACCGGC AATAATTGTA ATCCAAATAT CAGGACGTCC TAAATCGAAC 3300

CATAAGAAGT GTGGATATTT AAACAAACCA TCTACAAGTT GGTCTTTAAG TACAAAGTAT 3360

AATCCCATGA TGATTGGTAA TTGGATTAGC ATTGGTAAAC AACCCAACAT ACTCTTAATC 3420

GGGTTCATGT CATACTTTTT ATATACTTGC ATTAATTCTT GGTTTGCAGC CATTTTTTCT 3480

TCTTGTGTAC GCGnCaCGTT cACTTTTTCT TGAATTTTTT CAACTTCTGG CTTTGCAACT 3540

TTCATTTTTT GACGCATCAT ATGACTATTT TTATAGTTTG ACAACATGAA TGGTAATAAA 3600

ATAATACGAA TTACCAATAC AAGGATAATA ATAGCTAAAC CATAATTGTC GTTTAATAAG 3660

TTATTTCCCA ACCAATCCAA TACATTTTTC ATTGGATCTA CGAATGTATT GTAGAAAAAy 3720

cwCtACGTTT TTCAGGTTTA GAATAGTCAC AACCAGCCAA AAAGACCATA ATACCTAAAA 3780

ATAATGGTAG TAACGCTTTT TTCTTCATTT TTCCACCTCT ATCATTATAT TCACATAGGA 3840

TTTATTCTAT CACATTAATG AGTACGTATG AAACAATAAG TGGAAAAATT TAACTAATTA 3900

TTAAAAAAAT CTTTGAATCG ATTAACAGTC TTTTCAATAT TTTCACTTTT AGAAATGGCT 3960

GAAATGACTG AAATTCCATT GGCACCTGCT TCTACAATCG GCGCCACATT ATTAGTATTG 4020

ATACCGCCAA TAGCTACAAT CGGTAGTTGC GGATTCATTT CTTTAAACGT TGCAATCATT 4080

TCTGGACCTA CTGGTATATG CGCGTCATGC TTCGACGGCG TAGGATAGAT TGGTCCAACA 4140

CCTATATAAT CmACATGAGT TAAATCAGAT TTTGCATACT CATCTAAATC ACTAATACTA 4200

AGTCCAATAA TTTTATCAGT GAAATATTGT GCTATCTCTT TGACTTTCGC ATCATCTTGA 4260

CCGACATGTA TACCATCCGC GTTAATTTCT TTTGCCAAGG ATACATCATC ATTAACGATA 4320

AAAGGCACAT CATATTGATG ACAGAGATGC TGTAATTCTT TAGCTAATAC AAGTTTATCG 4380

TTTCCTTTTA AAGCTGATTC ACC 4403

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1808 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TGGAnCCAAT ATTAGAAATG ATTAAAACAT TAACAGGTAT TAATAGTCCT TCAGGAGnCA 60

TAACAAATAA AGGTGCGTTA TTAATAACAG TGCCAGGCAA AAATGATGAA GTACAACGCT 180

GTATTACTGC TCATGTTGAT ACTTTAGGTG CaATGGTTAA AGAAATTAAA GAAGATGGTC 240

GCTTaGCAAT AGAATTAATT GGAGGATTCA CGTATAACGC GATTGAGGGT GAATATTGCC 300

AAATTAAAAC TGATGCTGGT CAAATATATA CAGGAACAAT TTGTCTGCAT GAAACAAGTG 360

TTCATGTATA TAGAAATAAT CATGAAATAC CTAGAGATCA AAAGCATATG GAAATAAGAA 420

TTGATGAAGT AACTACATCA GAAGAAGATA CAAAGAGTTT AGGTATTTCA GTAGGTGATT 480

TTGTTAGCTT TGATCCACGT ACAGTTATCA CGTCATCAGG TTTTATTAAA TCTCGTCATT 540

TAGATGATAA AGCTAGCGTA CGgTtGATAC TACAATTACT AAAGAAATTA AAAGAAGAGC 600

AAATAATATT ACCACATACA ACGCAATTTT ATATTTCTAA TAACGAAGAA ATAGGTTACG 660

GTGCAAATGC ATCAATTGAT TCGAAAATCA AAGAATATAT TGCATTAGAT ATGGGCGCGT 720

TGGGAGACGG TCAAGCATCG GATGAATATA CAGTTTCTAT TTGTGCCAAA GATGCTTCAG 780

GTCCATATCA TAAGCAATTG AAATCGCACC TAGTTAATCT TTGCAAAATA AATAACATTC 840

CATATAAAGT AGACATATAT CCATATTATG GTTCAGATGC TTCAGCAGCT TTACATGCTG 900

GTGCGGATAT CAGACATGGT TTATTTGGCG CTGGCATTGA ATCATCTCAT GCAATGGAAC 960

GAACACATAT TGATTCTATT AAAGCGACAG AGAAATTACT ATATGCATAT TGCTTATCAC 1020

CAATTGAGTA AACAATTAGT GTTGACAAAT GTGaACGACC TATGTAATAT AATGAACTAT 1080

AAAAATAATT AGAATTTTCT AAAGAAATAG TAGCAGATAT GAAACGTAGC AAATAGAAAG 1140

CTAATGGGTG ATGGGAATTA GCACGCCATA TCTTGTGAAT TGGACTTTGG AAAACAATTG 1200

AATGAGTTTT GAAAGTGAAC ATGAATTATG TTAACTAAGG TGGCACCACG GTAACGCGTC 1260

CTTACAGGTA TATGCGTTAT GTGGTGTCTT TTTATTTAGA CAAAATGTAG TAGTTAATTA 1320

AAGGTAGCAA CAGAAAGTTA GTGGATGATG TGAACTAACA CCGAGATTAA TGAAATTGGG 1380

TTTTGTCTGC AACAGAAAAA TTATATATAG TAAAGAGTGA ACTATGAATA TTTCGAATAT 1440

TCGGTTAATT TAGGTGGTAC CACGCGTCAc nTCCTTTATA TTGATAAGGA TGCTGGCGCT 1500

TTTTTGAAAG GAGCGTATAG AATGGATATA TTTTATAAAA AAATAAAAGC AAATGTAACG 1560

CCCGAAGTTT TAGCACAACT TCATTCCAAG AAGaTCATTT TGGAAAGTAC AAATCAACAA 1620

CAAACTAAAG GTCGCTATTC AGTTGTTATT TTTGATATTT ATGGCACTTT AACTTTAGAT 1680

AATGATGTAT TATCAGTAAG TACTTTAAAA GAATCGTATC AAATCACTGA AAGACCGTAC 1740

CATTATTTAA CGACTAAnAT AAATGAAGAC TACCATAATA TTCCAAGATG AGGCAACTTA 1800

AGTCATTA 1808

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

TGGTCGTCAA TTTCTTGATT ATATCTATAA TCCTCATTTT CAATATTAGA GTCTGTAGAA 60

TCATCGATAT TATTATCATT CGCATGACTA GAAGCAGAAT CATTATTTTT ATCATTGCTT 120

TCTTCTTTTT TGAAGTCTTT ATTTATCAAG TAAATTTCTT CATCAAAATC AGCTTGTTGA 180

GATGTATCAT CTTTATTTTG ATTAGAAAAA TGTGTAGCCT TTGATCTTTT TCTTTGCCGT 240

CTTTTCTTAG ATGTATTCCT CGTAAATAAT TCTAATTCAT CTTTATCTTC ATTTGATTCT 300

TGTTGATCGT TCTTCGTTTT ATCATCCATC AATACTCACA CCCTTTAATA AGATGGTAAA 360

TGGGCACGGA ATCTTTCAAT AAATTTCTCT CCACGCTCTT CAAAAGTACT ATATTGATCC 420

CAACTCGCAC AAGCAGGTGA CAATAATACA ACATCATTTG GTTCTATAAT ATCTTGTACT 480

TTATCAACAG CGTCTTCGAC ATTGTTCGCT TCAATGACCG ATTTCCCTTG ACTATTACCT 540

AGTTTAGCAA ACTTAGCTTT CGTTTGTCCG AATACAACCA TCGCGCGAAC ATTTTCCATA 600

TAAGGAATGA GTTCGTCAAA TTCATTCCCT CGATCCAAAC CACCACATAA CCAAATGATT 660

GGTTGATTAA ATGAATTTAA GGCAAACTGT GTTGCTAGCG TGTTTGTTGC TTTGGAATCA 720

TTATAATATT TATTAGTTCT ATTAGTACCA ACATATTGCA ATCTATGCTC TATTCCTGAA 780

AATGTAGTTA AACTATCAAT AATTGCtTTA ATAGGTACAC CAGCanAATA CAAGCAAGCA 840

CAGCTGCTAA TATATTTcTA AATTATGTTC ACCAGGCAAT ACTAGAtCTT CAGTGTTAAT 900

AATaCGAACA CCTTTATaAA CGATAAAACC ATCTTtAATA TAAaTACCAT CArCTtCTTG 960

TTGAGTTGAG AAATACAATG TCTTAGCTTT TAATTCTTCC GACTCTATCA CTTGTCTTTG 1020

ATGATAATTA CAAATCAAAT AATCCTCTTC CGTTTGATTT TTATATATTT GCTTTTTAGC 1080

ATTTTGATAG TTTTCTAAAT TTTCATGGTA ATCTAGATGC GCCGAATAAA TGTTAGTAAT 1140

TATAGCAATG TGTGGTTTAT ACTTTTCGAT TCCAAGTAAC TGGAATGACG ACAACTCTGT 1200

AACTAAATAA TCTGTAGGCT TTACTTCTTG TGCTACTTTA GATGCAACAT AACCAATATT 1260

GCCGGATAAT CTTCCAGTTA AGCGACTTTT TTTAAACATA TCTCCAATTA GAGAAGTAAC 1320

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4280 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

TTTACACCAA TCAAAAAATC GAACTGATAT AAATAAGTAC AAAGCTTATC TATCAATCCG 60

ATTTAGTTAT AAAACAAAAA AAGCCACAGT AATGTGGCTT TTTGTTATAT TCAGTATCAA 120

AATGGTATCA ATAGCCATTT TCGGAAGTCA AGAATGGCTT AACAACGCGG TTTAAAGCTA 180

TCCAATACTA CCTTCCATTT CGAACTTGAT TAAACGGTTC ATTTCGACCG CGTATTCCAT 240

TGGAAGTTCT TTTGTAAATG GTTCGATGAA TCCCATAACA ATCATTTCTG TCGCTTCTTC 300

TTCAGAAATA CCACGACTCA TTAGATAGAA TAATTGTTCT TCAGAAACTT TTGAAACCTT 360

GGCTTCATGT TCTAATGATA TTTGATCGTT GAATACTTCG TTATATGGAA TTGTATCTGA 420

TGTTGATTCG TTATCTAAGA TTAATGTATC ACATTCAATA TTTGAACGAG CACCTTTTGC 480

TTTACGTCCA AAATGAACAA TACCGCGATA AATAACTTTA CCACCATTTT TAGAAATAGA 540

TTTAGAAACA ATTGTAGAAG ATGTATTAGG TGCTTTATGA ATCATTTTAG CACCGGCATC 600

TTGAACTTGT CCTTTACCAG CAAATGCAAT AGATAATGTA CTACCTTTTG CACCTTCACC 660

TAAAAGAACA CAGTTTGGAT ATTTCATCGT TAACTTAGAA CCTAAGTTAC CATCTACCCA 720

TTCCATATTT CCGTTTTCAT AAACAAAAGT ACGTTTTGTA ACTAAATTGT ATACATTGTT 780

CGCCCAGTTT TGAATCGTAG TATAACGAAC GTGCGCATCT TTATGCACAA TGATTTCCAC 840

AACAGCAGAG TGTAAAGAAC TAGTTGTATA AACTGGTGCA GTACAACCTT CTACGTAATG 900

TACAGAAGCA CCTTCATCAG CAATGATTAA TGTACGTTCA AATTGACCCA TGTTCTCAGA 960

GTTAATACGG AAATAAGCTT GTAGTGGCGT ATCTAGTTTG ATATTTTTAG GTACATAAAT 1020

GAACGAACCA CCTGACCATA CTGCTGAGTT TAACGCCGCA AATTTGTTAT CTGCTGCAGG 1080

TACTACAGAA GCAAAGTATT TTTTGAATAA TTCTTCATTT TCTTGTAAAG CACTATCTGT 1140

ATCTTTAAAG ATAATACCTT TTTCTTCAAG TTCTTTTTCC ATATTATGGT AAACAACTTC 1200

AGATTCATAT TGAGCAGAAA CACCAGCTAA ATATTTTTGT TCAGCTTCAG GAATTCCTAA 1260

TTTATCGAAA GTTCTTTTAA TTTCTTCTGG CACTTCATCC CATGAACGTT CAGCTTGTTC 1320

TGAAGGCTTT ACATAGTAAG TAATGTCATC GAAATTCAAT TCTGATAAGT CGCCACCCCA 1380

TTGAGGCATT GGCATTTTAT AAAACAATTT TAATGATTTA AGACGGAAAT CTAACATCCA 1440

TTCCGGCTCA TTTTTCATGT TAGAAATTTC TCTAACGATA TTCTCAGTTA AACCACGTTC 1500

TGATCTGAAA ATGGACACAT CATCGTCGTG GAATCCATAT TTATAATCCC CAACATCAGG 1560

TTTAATTCAT GATGTAAACC ATATTATAAC AATGACATGA CATCTTATAA AAATTTTTAT 1680

ACTTTTATAT GTCTAATATC AAAATTATCT ATGATTAACA GCATTCTATT CTTCTTCAGT 1740

CGTACCTTCT GCTTTACCTT CTTTAGCAAC AGTACCTTTT TCCAATGCTT TCCAAGCTAA 1800

TGTGGCACAT TTAATACGAG CTGGGAATTG AGATACACCT TGCAATGCTT CAATATCTCC 1860

CATTTCTTCT GTAATCACAT AGTCTTCACC AAGCATCATT TTCGTAAATT CTTGGCTCAT 1920

TTGCATTGCT TCTCCAAGTG AATGACCTTT AACAGCTTGT GTCATCATCG ATGCACTTGC 1980

CATTGAAATC GAACAACCTT CACCTTCAAA CTTAGCATCT TTTATAATGC CGTCTTCTAT 2040

ATCAAATGTT AGTCGTATAC GGTCACCGCA TGTCGGGTTA TTCATATCTA CTGTCATAGA 2100

CCCGTTATCT AATACACCTT TATTTCTAGG ATTTTTATAA TGATCCATAA TGACAGATCT 2160

ATATAATTGA TCTAGATTAT TAAAATTCAT AAGAGAAAAA CTCCTTCGTT TGTTTCAAGG 2220

CATTTATTAA CTGATCAACG TCTTCTTTCG TGTTGTATAT ATAAAAACTC GCTCTAGCTG 2280

TTGAAGACAC ATTTAACCAT TTCATTAACG GTTGCGCACA ATGATGCCCA GCTCTAACCG 2340

CTACACCTTC TGTATCTACG GCTGTAGCAA CATCGTGTGG ATGTACATCT TGTAAATTAA 2400

ACGTTATTAC ACCTGCACGA CGATCCTTTG GCGGGCCATA AATTTCAATT CCTTCAATTG 2460

CAGACATTTG CTCATAAGCA TATATCGTTA ATTCTTGTTC ATATTTATGA ATTGCATCAA 2520

AACCTATGCG TTCTAAATAG CGAATAGCTT CTGCAAGCCC AATTGCTTGA GCAATTAATG 2580

GAGTACCCGC CTCAAATTTA GTAGGTAAAT CAGCCCATGT TGCATCATAC TTACTTACAA 2640

AATCAATCAT GTCGCCACCG AACTCAATCG GTTCCATTTT TTGTAGTAAC TCACGTTTAC 2700

CAAATAATAC GCCAATACCT GTTGGTCCAA GCATTTTATG ACCACTAAAA CTATAAAAAT 2760

CAGCATTCAT TTCTTGCATA TCAAGTTTCA TATGTGGTGC TGctTGCGCC CCATCAACAC 2820

TGATAATTGC ACCATGTTGA TGAGCTATTT CTGCAATGGT TTTAACATCA TTAATTGTAC 2880

CGAGCACATT AGATATATGT GCAATAGCAA CGATCTTTGT TTTATCATTA ATCGTTTGCT 2940

TAATATCCTC GATGTTTAAT TCACCGTCAG CTGTCATTGG TATAAATTTC AATGTCGCAT 3000

TTTTACGCTT TGCTAACTGT TGCCAAGGAA CAATATTGGC ATGATGTTCC ATTTCAGTGA 3060

CAACAATTTC ATCGCCCTCT TCAACATTTG CATCACCATA GCTATGTGCT ACAAGGTTAA 3120

TCGACGCAGT TGTTCCGCGT GTAAAAATGA TTTCTTCAAA ATACTTCGCA TTAATAAAAC 3180

GACGAACGGT TTCACGGGCA TTTTCATAAC CATCAGTTGC CAATGATCCT AATGTATGAA 3240

CACCACGATG AACGTTTGAA TTATAACGCT TGTAGTAATC TTCTAAAACA TTTAACACTT 3300

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TTGTTGTATT ATCAATAATT TGGCTACCCT CATTCATTAA ACCTAGTGCC CAATTAATTG 4080

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TtAATTGATT TCCTTCACCA GATGCATTTG mTAAGTAATT TTCAACATAT GTGACTTCGG 4260

CGCTTTCTTC AGTAACGATG 4280

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15598 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

TCnGACTCGA ACGGTGmAAC TAttCCGTTG TaATTCCgGA GgAAsCAAGG TATGCCCATC 60

TGCaAAGAAA gaATGsAATG AACTTTTTGG AAATGTAGAA GTGGTAAATA AAGATAAAGG 120

ATATTACATT CTGAGAAGTA TAAAAGCTTG AAATGAAATG GATATTCTGT TATAGTTATA 180

TAATGTAAAA ATTTATGTTC AATAAGTGTG TACTTTTACG TTAAATAGAT AAGTTAATTA 240

AGAATAAATA TAGAATCGAA AATGGTGTCA TCATTAGTGT TGCCGTTTTC TTTTTGTCTT 300

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TGACTGATAC AGGTACGTTC GTTATCAATG GTGCAGAACG TGTAATCGTA TCTCAATTAG 780

TTCGTTCACC ATCCGTTTAT TTCAATGAAA AAATCGACAA AAATGGTCGT GAAAACTATG 840

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CATCTGGAGA GGCCATGATT GCCCCCGCAC GTGAATGAAT AGTTCCAGTA GGATAACCAC 13680

TCCATAAATG TGTACCGTAA ATTCTATCTA CATTTTCCAG ACATCCAGCA TCTATCATTT 13740

CTTGAGAACC ACCTGGCATG ATTTCTTCAC CGTACTGGAA TATTAATACA ACATTACCTT 13800

CTAATAAATG TTTATGTTCA TCTAAAATCT CTGCTACAGT AAGTAAAATT GCTGTATGAC 13860

CATCATGCCC ACACGCATGC ATACATCCTG GATTTTTAGA CTTATAAGGC ACATCGTTTA 13920

ATTCCTCGAC AGGTAACGCA TCAAAGTCAG CTCTTAATGC AATGGTAGGT CCTGTGCCCA 13980

AGCCTTTAAA TGTGGCTTTG ATACCATTGC GGCCGATAGG AGTTTCAATA TCACAAGATA 14040

ACTGGCTTAA TTGGTTAACA ATATAATCAT GTGTTTGAAA TTCTTCAAAA GATAACTCAG 14100

GATATTGGTG TAAATAACGT CTGAGTTGAA TTGTTTTATT TTCTTTATTA TTTGCTAGTT 14160

GGAACCAATC TAACACCCTT ATCACTACTT TCTAAAATAA TGTTTATAGT ATAACATTTT 14220

ATGAAATTAT CGTACTAAAT GATTGCTTTG AGATATTTTA TCTATGAATG ATAAGGCTTT 14280

CAAGTTATGT AGAATTACTG TATGATAAAG GTATTACCAA ACAATACTTA AGGGGGATTA 14340

TATACTGTGG TTCAATCATT ACATGAGTTT TTAGAGGAAA ATATAAATTA TCTAAAAGAA 14400

AATGGTTTGT ATAATGAAAT AGATACAATT GAAGGTGCAA ACGGACCAGA AATCAAAATC 14460

AATGGGAAAT CATACATTAA CTTATCTTCA AATAATTATT TAGGACTAGC AACAAATGAA 14520

GATTTGAAAT CaGctGCAAA AGCAGCTATT GATACACATG GTGTAGGTGC AGGCGCTGTT 14580

CGTACAATCA ATGGTACATT AGATTTACAC GACGAATTAG AAGAAACACT AGCAAAATTT 14640

AAAGGAACAG AAGCTGCAAT AGCTTATCAA TCAGGATTTA ATTGTAATAT GGCTGCTATT 14700

TCAGCTGTCA TGAATAAAAA TGATGCTATT TTATCAGATG AGCTTAATCA TGCATCAATT 14760

ATTGATGGAT GTCGCTTATC TAAAGCTAAA ATTATTCGAG TTAACCATTC AGACATGGAT 14820

GATTTACGTG CGAAAGCAAA AGAAGCAGTT GAATCAGGTC AATACAATAA AGTGATGTAT 14880

ATTGCAGAAG AATTTGGTTT ATTAACTTAT GTTGACGACG CTCATGGTTC AGGTGTTATG 15000

GGTAAAGGCG CTGGTACGGT TAAACATTTT GGTTTACAAG ATAAAATCGA TTTCCAAATA 15060

GGTACGCTTT CTAAAGCAAT TGGTGTCGTT GGCGGTTATG TAGCAGGTAC AAAAGAGTTA 15120

ATAGATTGGT TAAAAGCACA ATCACGACCA TTCTTATTCT CTACATCATT AGCACCTGGG 15180

GATACCAAAG CAATAACTGA AGCAGTTAAA AAGTTAATGG ATTCAACTGA ATTACATGAT 15240

AAATTATGGA ACAATGCACA ATATTTAAAA AATGGATTGT CAAAATTAGG ATATGATACA 15300

GGTGAGTCAG AAACTCCAAT TACACCAGTA ATTATTGGTG ATGAAAAAAC AACTCAAGAA 15360

TTTAGTAAGC GTTTAAAAGA CGAAGGTGTC TATGTGAAAT CTATCGTTTT CCCAACAGTA 15420

CCAAGAGGTA CAGGACGTGT AAGAAATATG CCTACAGCTG CACATACAAA AGACATGTTA 15480

GATGAAGCAA TTGCGGCTTA TGAAAAAGTA GGAAAAGAAA TGAAGTTGAT TTAATATTTA 15540

TTTATTCCCA CGGCAAATAT TGTCGTGGGC TTTTTTTAAT GTTTAGTTTA TTAACAGT 15598

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 661 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

AAGTAAATCA ACTTACTGGG ATAAGAATAA AGGCGATTAT AGTAACAAGT TGATTTTATT 60

CGAAAAACAT TTTGAACCGG TTCTGGGTAT CAAGATGCAA CATAGTGGAG GTCATAGCTT 120

TGGCCACACG ATTATTACGA TTGAAAGTCA AGGAGATAAA GCAGTTCATA TGGGTGATAT 180

ATTCCCAACT ACTGCACATA AAAATCCTCT ATGGGTAACG GCATATGATG ATTATCCTAT 240

GCAATCGATT CGTGAAAAAG AACGCATGAT ACCATATTTT ATTCAGCAAC AATATTGGTT 300

CTTGTTTTAT CATGATGAAA ACTACTTTGC TGTAAAATAC AGCGATAATG GTGAAAACAT 360

AGATGCATAT ATTTTACGTG AAACATTAGT TGATAATAAC TAAAATAAAG ATGTATTACT 420

AAACAAATTT TCAAAAATAA AAAATTGAGC CACATCCAAT CTTACTAATT AGGGTGTGGC 480

TCATTTTTAA GTTTTACgAT CCAAATCAAA TATGGaTAAA ATTCgTATTA ACGCTCTACa 540

ATGtTAATGA CTTCACCAGT ATATGCATCT GCATAAAAAT CATAATGAAT ATTTTGACCA 600

TTTTTAATAG TTGTAATTCC ACCTTGATAA ACTAAACGGT ATTTATCAGT TTCAGGATGA 660

A 661

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GCAGACGGTA CAGCAGTTAA AGTCGCACCA AaACTGTAGT GAATcTAATC GGTGcATTCT 60

TTTTAGGATT AGTTGTCGCG CTTATATATA TCTTCTTCAA AGTAATTTTC GATAAGCGAA 120

TTAAAGATGA AGAAGATGTA GAGAAAGAAT TAGGATTGCC TGTATTGGGT TCAATTCAAA 180

AATTTAATTA AGGATGGTTG CTACTTATGT CAAAAAAGGA AAATACGACA ACAACACTAT 240

TTGTATATGA AAAACCAAAA TCAACAATTA GTGAAAAGTT TCGAGGTATA CGTTCAAACA 300

TCATGTTTTC AAAAGCAAAT GGTGAAGTAA AGCGCTTATT GGTTACTTCT GAAAAGCCTG 360

GTGCAGGTAA AAGTACAGTT GTATCGAATG TAGCGATTAC TTATGCACAA GCAGGCTATA 420

AGACATTAGT TATTGATGGC GATATGCGTA AgcCAACACA AAACTATATT TTTAATGAGC 480

AAAATAATAA TGGACTATCA AGCTTAATCA TTGGTCGAAC GACTATGTCA GAAGCAATTA 540

CGTCGACAGA AATTGAAAAT TTAGATTTGC TAACAGCTGG CCCTGTACCT CCAAATCCAT 600

CTGAGTTAAT TGGGTCTGAA AGGTTCAAAG AATTAGTTGA TCTGTTTAAT AAACGTTACG 660

ACATTATTAT TGTCGATACA CCGCCAGTTA ATACTGTGAC TGATGCACAA CTATATGCGC 720

GTGCTATTAA AGATAGTCTG TTAGTAATTG ATAGTGAAAA AAATGATAAr AATGAAGTTA 780

AAAAAGCAAA AGCACTTATG GAAAAAGCAG GCAGTAACAT TCTAGGTGTC ATTTTGAACA 840

AGACAAAGGT CGATAAATCT TCTAGTTATT ATCACTATTA TGGAGATGAA TAAGTATGAT 900

TGATATTCAT AACCATATAT TGCCTAATAT CGATGACGGT CCGACAAATG AAACAGAGAT 960

GATGGATCTT TTAAAACAAG CGACAACACA AGGTGTTACA GAAATCATTG TAACATCACA 1020

TCACTTACAT CCTCGATATA CCACACCTAT AGAAAAAGTG AAATCATGTT TAAACCATAT 1080

TGAAAGCTTA GAGGAAGTAC AAGCACTAAA TCTAAAGTTT TATTATGGTC AGGAAATAAG 1140

AATTACCGAT CAAATCCTTA ATGATATTGA TCGAAAAGTT ATTAACGGTA TTAATGATTC 1200

ACGCTATTTA CTAATAGAAT TTCCATCAAA TGAAGTTCCA CACTATACTG ATCAATTATt 1260

TTTCGAATtA CAGAGTAAAG GCTTTGTACC GATTATTGCA CATCCAGAGC GGAATAAAGC 1320

AATAAGTCAA AACCTTGACA TACTATACGA TTTAATTAAC AAAGGTGCTT TAAGTCAAGT 1380

GACAACGGcG TCATTAGCGG GTATTTCCGG TAAAAAAATT AGAAAATTAG CAATTCAAAT 1440

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CGGATTTATT AGTAATGCGA AGTTAGTTGT TGATGATAAA AAAATTCCTA AACGAATGCC 1620

ACAACAAGAT TATAAACAGA AAAGATGGTT TGGGTTATAA ACAGCAAATG AGGGGTTTTA 1680

TGGCACATTT ATCTGTGAAA TTGCGGCTTT TAATACTAGC ATTAATCGAT TCACTGATAG 1740

TGACATTTTC AGTATTCGTA AGTTATTACA TTTTAGAACC GTATTTCAAA ACATATTCTG 1800

TCAAATTATT AATATTGGCA GCTATATCAC TATTCATATC GCATCATATT TCaGCATTTA 1860

TTTTTAATAT GTATCATCGA GCGTGGGAAT ATGCCAGTGT GAGTGAATTG ATTTTAATTG 1920

TTAAAGCTGT GACGACATCT ATCGTTATTA CGATGGTGGT CGTGACAATT GTTACAGGCA 1980

ATAGACCGTT TTTTAGATTG TATTTAATTA CTTGGATGAT GCACTTGATT TTAATAGGTG 2040

GCTCAAGGTT ATTTTGGCGT ATTTATCGGA AATACCTTGG AGGTAAGTCA TTTAATAAGA 2100

AGCCAACTTT AGTTGTTGGT GCTGGTCAAG CAGGTTCAAT GCTGATTAGA CAAATGTTGA 2160

AAAGTGACGA AATGAAACTT GAACCGGTAT TAGCAGTCGA TGATGACGAA CATAAACGCA 2220

ATATCACAAT TACTGAGGGT GTAAAAGTCC AAGGTAAAAT TGCGGATATT CCAGAACTAG 2280

TGAGGAAATA TAAGATTAAA AAAATCATCA TTGCAATTCC AACTATTGGT CAAGAGCGTT 2340

TGAAAGAAAT TAATAATATT TGCCATATGG ATGGCGTTGA GTTATTGAAA ATGCCAAATA 2400

TAGAAGACGT CATGTCTGGT GAGTTAGAAG TGAACCAACT TAAAAAAGTT GAAGTAGAAG 2460

ATTTACTAGG CAGAGATCCT GTTGAATTAG ATATGGATAT GATATCAAAT GAATTGACGA 2520

ATAAAACTAT TTTAGTTACG GGTGCAGGTG GTTCAATAGG ATCAGAAATT TGTAGACAAG 2580

TTTGTAATTT CTATCCAGAA CGTATTATTC TACTTGGCCA TGGTGAAAAC AGTATTTATT 2640

TAATCAATCG TGAATTGCGA AATCGCTTCG GwAAAAATGT TGATATCGTT CCTATTATAG 2700

CGGATGTGCA AAATAGAGCG CGTATGTTTG AAATTATGGA AACGTATAAA CCATACGCAG 2760

TTTATCATGC AGCAGCACAC AAGCACGTGC CGTTAATGGA AGACAACCCT GAAGAAGCAG 2820

TACGTAATAA TATTTTAGGT ACGAAAAATA CTGCTGAAGC TGCTAAAAAT GCAGAGGTAA 2880

AGAAATTCGT TATGATTTCT ACGGATAAAG CCGTTAATCC GCCTAATGTC ATGGGAGCTT 2940

CAAAGCGAAT TGCAGAAATG ATTATTCAAA GTTTAAATGA TGAAACGCAT CGAACAAATT 3000

TTGTTGCAGT GAGATTTGGT AATGTACTTG GATCGAGAGG ATCTGTGATT CCACTTTTCA 3060

AAAGTCAAAT TGAAGAAGGT GGGCCAGTTA CTGTGACACA TCCTGAAATG ACACGTTACT 3120

TTATGACAAT TCCTGAAGCT TCTAGACTAG TTTTGCAGGC AGGGGCATTA GCAGAAGGTG 3180

GCGAAGTATT TGTGCTAGAT ATGGGAGAAC CAGTGAAAAT TGTAGATTTG GCACGTAATT 3240

CCGGCGAAAA AATGTTTGAA GAGCTTATGA ATAAAGATGA GGTTCATCCT GAACAAGTAT 3360

TTGAAAAAAT TTATCGTGGC AAAGTACAAC ATATGAAATG TAATGAAGTT GAAGCGATTA 3420

TTCAAGACAT CGTCAATGAC TTTAGTAAAG AAAAAATTAT TAACTATGCC AATGGCAAAA 3480

AGGGAGATAA TTATGTTCGA TGACAAAATT TTATTAATTA CTGGGGGCAC AGGATCATTC 3540

GGTAATGCTG TTATGAAACA GTTTTTAGAT TCTAATATTA AAGAAATTCG TATTTTTTCA 3600

CGCGATGAGA AAAAACAAGA TGACATTCGA AAAAAATATA ATAATTCAAA ATTAAAGTTC 3660

TACATTGGTG ATGTGCGTGA TAGTCAAAGT GTAGAAACAG CAATGCGAGA TGTTGATTAC 3720

GTATTCCATG CAGCAGCTTT AAAACAAGTG CCGTCATGTG AATTCTTTCC AGTTGAGGCA 3780

GTGAAGACAA ATATTATTGG TACAGAAAAT GTCTTACAAA GTGCTATTCA TCAAAATGTT 3840

AAAAAAGTCA TATGTTTATC TACAGATAAG GCAGCGTATC CTATTAATGC TAGGGGTATT 3900

TCAAAAGCAA TGATGGAAAA AGTATTCGTA GCCAAATCAA GAAATATTCG TAGTGAACAA 3960

ACGCTTATTT GTGGTACAAG ATACGGTAAT GTGATGGCTT CAAGAGGATC AGTAATACCT 4020

TTGTTTATCG ACAAAATCAA AGCTGGAGAA CCTTTAACGA TTACAGATCC TGATATGACA 4080

AGATTTTTAA TGAGCTTAGA AGATGCGGTA GAACTAGTTG TTCATGCATT TAAGCATGCA 4140

GAGACAGGAG ATATTATGGT TCAAAAAGCA CCAAGCTCAA CGGTAGGGGA TCTTGCGACC 4200

GCATTATTAG AATTGTTTGA AGCTGATAAT GCAATTGAAA TCATTGGTAC GCGACATGGA 4260

GAGAAAAAAG CAGAAACATT GTTGACGAGA GAAGAATACG CACAATGTGA AGATATGGGT 4320

GATTATTTTA GAGTGCCGGC AGACTCCAGA GATTTAAATT ATAGTAATTA TGTTGAAACC 4380

GGTAACGAAA AGATTACGCA ATCTTATGAA TATAACTCCG ATAATACACA TATTTTAACG 4440

GTGGAAGAGA TAAAAGAAAA ACTTTTAACA CTAGAATATG TTAGAAACGA ATTGAATGAT 4500

TATAAAGCTT CAATGAGATA GGAGAGATTG ACGTTGAATA TTGTAATTAC AGGAGCAAAA 4560

GGTTTTGTAG GAAAAAACTT GAAAGCAGAT TTAACTTCAA CGACAGATCA TCATATTTTC 4620

GAAGTACATC GACAAACTAA AGAGGAAGAA TTAGAGTCAG CATTGTTGAA AGCAGACTTT 4680

GTCGTGCATT TAGCGGGTGT TAATCGACCT GAACATGACA AAGAATTCAG CTTAGGAAAC 4740

GTGAGTTATT TAGATCATGT ACTTGATATA TTAACTAGAA ATACGAAAAA GCCAGCGATA 4800

TTATTATCGT CTTCAATACA AGCAACACAA GATAATCCTT ATGGTGAGAG TAAGTTGCAA 4860

GGGGAACAGC TATTAAGAGA GTATGCCGAA GAGTATGGCA ATACGGTTTA TATTTATCGC 4920

TGGCCAAATT TATTCGGCAA GTGGTGTAAG CCGAATTATA ACTCAGTGAT AGCAACATTT 4980

TGTTACAAAA TTGCACGTAA CGAAGAGATT CAAGTTAATG ATCGGAATGT TGAACTAACG 5040

ATTGAAAATG GTGTACCTAC AGTACCAAAC GTATTTAAAG TGACATTGGG AGAAATTGTA 5160

GATTTATTAT ACAAGTTCAA ACAGTCACGT CTCGATCGAA CATTGCCGAA ATTAGATAAC 5220

TTGTTTGAAA AAGATTTGTA TAGTACGTAT TTAAGCTATC TACCTAGTAC aGACTTTAGT 5280

TAyCCCTTAC TTATGAATGT GGATGATAGG GGTTCTTTTA CAGAATTTAT AAAAACACCG 5340

GATCGTGGTC AAGTTTCTGT AAATATTTCT AAACCAGGTA TTACTAAAGG TAATCACTGG 5400

CATCATACTA AAAACGAAAA ATTTCTAGTC GTATCAGGTA AAGGGGTAAT TCGTTTTAGA 5460

CATGTTAATG ATGATGAAAT CATTGAATAT TATGTTTCTG GCGACAAATT AGAAGTTGTA 5520

GACATACCAG TAGGATACAC ACATAATATT GAAAATTTAG GCGACACAGA TATGGTAACT 5580

ATTATGTGGG TGAATGAAAT GTTTGATCCA AATCAGCCAG ATACGTATTT CTTGGAGGTA 5640

TAGCGCATGG aAAAACTGAA rTTAATGACA ATAGTTGGTA CAAGGCCTGA AATCATTCGT 5700

TTATCATCAA CGATTAAAGC ATGTGATCAA TATtTTAA 5738

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9062 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

ATCATCAACA AGAATGATAT TTTTCCCATC TACTATATCT TTTACCGCAG ATAACTTCAC 60

TCTCACACCT TGCTCACGTA ATTCTTGAGT TGGTTGAATA AATGTTCTTG CAACATATTG 120

ATTTTTAACT AGTCCCATTT CATATGGCAA ACCTATTTCT TCAGCATAAC CACTCGCAGC 180

TGATAGCGAT gAATTGGGTA CACCGATGAC CATATCAGCA TTTACAGGGC TTTCTTGGGC 240

TAATTTTTTA CCAGAAGCTT TACGTACTGC ATGGACATTT TTACCAGCTA TTGTTGAGTC 300

TGGTCTAGCA AAATAAATAT ATTCCATCGC AGAAATTGCA GTTGTCGTAT GATGTGTATA 360

AGATTTAACT GTAATACCTT TATCGTTAAT CACGACATAT TCACCTGCAT GAATATCTTG 420

AACAAATTCT GCACCTAACA CATCTATTGC ACATGTTTCA CTTGCAAGGA TGTATGTCCC 480

ATCTTTCATT TTACCTACAA CAAGTGGTCT GATAGCATTT GGATCTACTG CGCCATATAA 540

CGCATCTTTA GTTAAAATCG CAAATGTAAA ACCGCCTTTA ACTTTTCGCA AACTTTCTTT 600

CAACGCTTCC TCAAAAGTAG GAGCTTTACT TCGACGTATC AAATGCATAA TGACTTCAGT 660

ATCAGAAGAC GAATGGAAGA TAGCACCTTG TTTTTCTAAA TTCTGACGCA ATGATTTAGC 720

CGGTTGAATA TTTTCAATAC CTTTATTACC TGAAGTAGCA TAACGGACGT GACCAATTGC 840

ATGTTGATAT CCTTTTAATC GTTCCATTTG ATCATCTTTA ATCGCTTCAG TTAGTAAGCC 900

TAATCCTCGC TCGCCTTTTA ATTCATTTTG ATCAGAAACA ACTATACCTG cACCTTCTTG 960

ACCACGATGT TGCAAACTAT GAAGTCCCAT ATAtGTTAGT TGCGCTGCtT CaGGATGATT 1020

CCAAATACCA AACACGCCAC ATTCTTCGTT TAATCCTGAG TAGTTAAACA TTGaGCAATT 1080

GCCCCtTCCC ATATTTGTTT AATATCTGAA ACATTTTCAC TAATCTCTGT aTATGGTGTT 1140

GTTACCTTGr aATTATCACT ATCTGTTAAA AGTCCAATTT CTATTGCATT ATCAATATTT 1200

AAAGTTTTAC CTGATTTAAC AGAAACAACA TATCGGCCTT GCGTCTCACT AAACAATTGT 1260

GCATTTGTTA TATCTATTGA AGATTTTAAT CCTAAACCGT AATGCGCACT TAGTTTAGCT 1320

AAGGTAATCA GTAAGCCACC TTTACCAACT GTTTGAACAT GTGATAATAG TCCTTCACGA 1380

ATAGCGGTCT TGATTGATTC ACCTTTTTCA ACTTCTGAAC TCAAATCTAA TGACTCAAAT 1440

TCATGATTAA CTTTGCCATA AATTAACTTT TCAAGTTGAC TACCACCAAA GTCGTCCTTA 1500

GTATCACCGA TTAAATATAA TTTATCTCCA ACTTGAGGTT CAAAATCATT TAAATAATTT 1560

ACATTTTCAA TCAAACCTAC CATTCCAACA ACTGGTGTTG GGAAAATAGA AGTACCTTTC 1620

GTTTCGTTAT ATAAAGATAC ATTACCAGAA ACTACTGGTG TCTTAAGAAT GTCGCATGCT 1680

TCTGCCATAC CTTTCGTTGA ATCTATCAAC TGTTGATAGA TTTCTTTCTT TTCAGGAGAA 1740

CCATAATTTA AACAATCTGT CATTGCTAAT GGTGTTGCAC CCACGGCAAT TAAATTTCGA 1800

TAAGCTTCAG CTACTACCAT CTTTCCACCT TCATATGGAT TGTTATATAC ATAACGCGCT 1860

TCACCATCAA TTGTTGAAGC AATTGCCTTA TTTGTGCCTT CCACACGTAC TACCGATGCT 1920

TGAAGTCCTG GCTTAATTAT CGTATTGGCA CCAACTTGTT GGTCGTATTG ATCATATAAA 1980

TAGTGTTTAG ATGCTATAGT CGGATGCTTA AGTAATTTAA AGAAAGTATC TTTAACATCG 2040

ATGTGTGTAT AATCATTTTT AGAAGTATTA TAATCTTTTT CTTCTCCTTC TAAAATATAT 2100

ACAGGTGCTT CATCAGCTAG TGGTTCAACT GGAATGTCAG CATAAACTTC GTCATCATAT 2160

GTTAAAACAA AACGATTTGT ATCTGTAACT TCACCTATAA CAGCACTATC CAATTCGTGC 2220

TTATCAAATA AATCTAAGAA TTTTTGTTCA GTACCTTTTT CAACAACTAG TAACATACGT 2280

TCTTGAGTTT CTGAAAGCAT CATTTCATAA GGAGAAATAC CTGGCTCACG TGTTGGCACT 2340

TGTTCTAATC TCAAATGTAA CCCACTACCA CCTTTTGCCG CCATTTCAGA CGATGAAGAT 2400

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AGTGTTGCTT CCATTAATTT TTTACCTACA AATGGATCAC CGATTTGTAC AGAAGGTCGT 2520

CGACCAGTTT TCAAACCAAC ATAAATGACC GAATTACCTA CACCTTTTGC TGTGCCTTTT 2640

TGAATCATGT CGTGATTGaT AACACCAACA CACATTGCAT TAACAAGTGG ATTGCCATCA 2700

TAACGTTCAT CAAATTCGAT TTCACCAGCA GTTGTTGGaA TACCAATGCA GTTACCATAA 2760

CCTCCGATAC CCTTTACAAC ACCTTTAAGT AATCTTTGGT TTTGTTTATT ATCTAATTCT 2820

CCAAATCTAA GACTGTTTAA CAAATTAATA GGTCTAGCCC CAATAGAGAC AATGTCACGA 2880

ATGATTCCAC CAACGCCTGT AGCAGCCCCT TGATATGGTT CAATTGCTGA TGGATGATTG 2940

TGAGACTCTA CTTTAAATAC TACGGCTTGA TTATCACCTA TATCGACTAC CCCTGCACCT 3000

TCACCAGGCC CCATAAGCAC ATGGTcACCT GACGTAGGAA ATTGCTTTAA AAACGGTTTA 3060

GAATGTTTAT AAGAGCAATG TTCACTCCAC ATAACAGAAA AGATACCTGT TTCTGTAAAG 3120

TTAGGTTGTC TGCCTAAAAT ATCGCAAACT TTTTCATATT CTTGATCaCT TAATCCCATA 3180

TCTTGATATA CTTTTTCAAG TTTAATTTCT TCAACGCTTG GTTCGATAAA TTTAGACATG 3240

TTGTTCCCTC CAACTTTTTA CCATCGCTTC AAATAATTTC ACACCACTAT CAGTACCTAA 3300

CAACGTTTCT AAAGCTCTTT CagGATGtGG CATCATGCCA CATACATTGC CTTTTTCGTT 3360

AACAATTCCT GCAATATCAT CATATGAACC GTTCGGATTA TTCACATATT TCAGAATAAT 3420

TTGATTGTTA GCTTTTAATT GTTGATATAT TTCATCAGTA CAATAATAAT GACCTTCACC 3480

GTGAGCTACA GGATATATAA CTTTTTCACC TTGTTCATAA AGATTTGTAA ATGCCGTTTG 3540

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TAATGCACCA GGTAATAAGC CTATTTCAGT TAAAATTTGA AACCCATTAC AAACACCTAA 3660

TACTGGCTTA CCTTCAGCTG CAAGACGTTT AACTTCCGAA ATAATCGGsG CTACACTAGC 3720

CATTGCCCCA GATCTTAAGT AATCCCCGAA TGAAAATCCA CCAGGAATAA GTACGCCATC 3780

AAATCCACTT AGTGATGTTT CTCTATAATC TACATATTCC GCTTCAACAC CACTTTTAAT 3840

AGCAGCATTA AACATGTCTC TATCACAATT CGAACCTGGA AAAACAAGAA CCGCAAATTT 3900

CATTTTATGC ATTCTCCTTT TCATCATCTA ACACTTTATA GCTATATTCT TCAATCACTG 3960

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CCTCATCCAC TGTCATATAT AATACTTTTC CTACACGAAT ATCATTCACT TGTGCATAAC 4080

CTAAGTCATG TACAGCTCGA GTAAGCGTTT GTCCTTGCGT ATCTAATACT TGTGGTTGTA 4140

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TTGATATGTT TCAATCAGTG ATCCAGTGTT ATTTCTATAT ACATCTTTAT CAAAGTTTGC 4260

ATTGGTAGCT TTATCCCAAA TTCGACATGT ATCTGGAGAT ATTTCATCCG CTAACAAAAT 4320

ATCCATTAAT TGTTTCAACA CATTATTAAT CTTTAATGCT TTGGATTTTA GTATTTCAAT 4440

ATCTTCATCT GATGCTATAT TGAGCAATTT AACATGGTCA TCCGTTATCA ACGGATCATT 4500

TAACGCATCA TTTTTATAGA AAAATTCTAC AAGTGGTTCT CTAAAAACTT CACCATTTTC 4560

AAAACCTAAA CGCTTTGTAA TAGATCCACT AGCAATATTA CGAACAACTA CTTCTAATGG 4620

AATTATTTTC ACAGGCTTAA CTAATTGTTC TGTTTCAGAT AATTGTTTAA TAAAGTGACT 4680

TTCTATTCCA TTTTCTTGTA AATATTTAAA TATAATAGAA GTAATTTGAT TATTTAATCG 4740

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TAATGATTGT CCGGTAACTG CTAAAATATG AGTATCAAAT TGTGAATAAT CACATGCTTC 5160

AATTGAATAA TGTCCGGAAT TGTGAGGCCT TGGTGCTATC TCGTTCACAT ACAATTGGTT 5220

GTTACTATCT ATAAAAAAAT CAACTGTAAA TGTTCCAATG AAATGAATCG ATTGGATAAT 5280

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TGTTTCAATT GCTTTGTCAA TATCTGTAGA TTCTTTTACT GAAATGAACG GGACAACTTT 5640

GGTACCAGCA CTTTTTAATG TTTCTTTTTC AGTTAAGCGA TCTTGTAATA ACTGTATAGC 5700

TTGGTAACCT TGCGGAATAT TGTACTTTTC ACATAATAGT TTTAATTGTT GGGCTGAAAT 5760

GTTTTCAAAT TCATAAGTAA TCACATCACA TTTTTGTCCT AATTGATTGA GTGCCTTTTC 5820

ATCGTCATAC TTGGCTTGTA TAAATTCGTG TGCAACGTAT CTACATGGAC AATCTTCAGA 5880

AGGATCCAAT ACAACCACTT TATAACCCAT TTTTTGAGCT GATTGTGCCA TCATCTTTCC 5940

AAGCTGACCA CCACCAATAA TGCCAATAGT CGCACCAAAC TTTAATTTAT TGAAGTTCAT 6000

TTTGCATGTC CTCCACTTTT TGAATTAACG AAGATTCATA CTGATTTAGT TTTTCAACTA 6060

AAGAAGGATT TTGAATACTT AACATTCTTG CTGCAAGTAT ACCTGCGTTT TTAGCACCTG 6120

AAGAATCTAT ACCCTTTAAA CTTTTTGTTT CAATCGGCAC TCCAATAACT GGTAGCGTCG 6240

TTAATGATGC AACCATACCT GGTAAATGTG CCGCACCGCC AGCGCCTGCA ATGATAATGT 6300

TTATACCTCT TTCTCTCGCT TCAGAAGCAA ATTGAACCAT CATTTTTGGC GTACGATGTG 6360

CGGATACTAC TTGTTTTTCG TACGGAATTT CAAAATAATC CAACATGTTA CAACTCTCTT 6420

GCATAATTTT CCAATCGGAA GAACTGCCCA TAATGACTGC TACTTTCACT TTGTACACCC 6480

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TTCTCAACTT TCCTTTTAAA TATGAAGCAA TTTTTTCAAA AACGCTATTA GTCACAAAAT 9060

GT 9062

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

AAATATTTTT TCAAAACTAT GTGAAAATGG aCCATGTCtA aATCATGTAA TAATGCAGyA 60

CATAATGCCA ACGGTCTmTC TTTATTGTCC CATGCATCAT GACCAATAAA TGACTCATCA 120

ATTAATCGTC TAACTATTTC ATACACACCT AAAGAATGTC CAAAGCGACT ATGTTCTGCT 180

GTGTGAAAAG ATAGGTACAG TGTTCCTAGT TGTCTAATTC GACGTAACCT TTGGAATTCC 240

TCTTTAAAAA CTTTTTCTTC TACTAATTTT AAATCTACAT ATGCGTTAGT CATTATTCCC 360

CTCCTTTTCG TTTAATATAA TATTTAATTT ACTTAAAATG CTTTGTACAT AAGTGCTAAG 420

TCTAACTTTT CGCCATACAT TTCTGGCTCA TAAGAGCGTA AGATTGTAAA ACCTTGCTCT 480

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GATTCTGGTT TAACATAATG AGCTGATAAA TATAATTCTT CACCGTAAAT AAAGTTAGCA 660

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TTTAAATGAT GTTCATTATA TGAAGCTtCT AACAAGTGAT TAACTGTTGT CGCAGCGTAT 780

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GTGGCACCTA rAAAGTCTAA ACTATATTTC ATTTGCGTAA TTGCTGGTTC GCTTTTATTT 1200

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TTTTATCTAG AATCGGCAAA TAGTCATCGT CATATGAAGT AATAGTCTCT GCTGTATGTC 1440

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CCAAAGCTTT TACGCGACGC ACATTTTCTT CAAATACACC TGGTTTAAAA TCACGACGTG 2040

GCTAATGGGA AATATGGAAT AAATGTGATT TGGTGATCAA CACAATATTG TAATACTGCC 2160

TCATTTTCGC GATGCAATAA ATTATATTCT AACTGTACAA CATCAACGTA ACCATCTTTA 2220

TTTGCTTCTT TAAGTTGATC TAATGTGAAA TTTGATACAC CAATTGCTTT AATCTTCCCT 2280

TGTTCCTTAA GCTCTTGTAA TGCTGCAACT GCTTGATCTT TCGGAGTGTT GTTATCCGGA 2340

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ACCAATTCTT CTGATCGTTC TGGCCCATAA ATATATGCCG TATCTAATAA ATTAATACCA 2580

TGATTAATGG CTTGACGAAC AACATCTTTT CCTTGTTCTT CATCTAAGTT CGGATATAAA 2640

TTATGCCCAa CCTAtGCGTT CGTCCCAAGT GCGATTGGAA ACACTTCAAC ATCAGATTTA 2700

CCTAAGTTTA CAAATTGCTn CATTAGACCC AGCnCCTT 2738

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GATTAGATGA TATTTAACGA AAATTAaGrT GmAATACTtG AATGTArGAa GTCTGATGTC 60

GAAAATAGCT ATTAAAATAG AGTAGACGTA ATGtAAATGA AAGCACCTAA AATAGAAAAA 120

TTTCAAAAAT AGCGTAATTA TTATAATAAA TAGACTGCCA ATAAAATGCA ATTTTTCACT 180

TATAACATTC TTCAAAAAAT AATAGCAAAA TTATGTAAAA AATATCTTGT CATGGCAAGA 240

TTGGCTGTGC TATAATCTAT CTTGTGCTTA AGAACGGCTC CTTGGTCAAG CGGTTAAGAC 300

ACCGCCCTTT CACGGCGGTA ACACGGGTTC GAGTCCCGTA GGAGTCACCA TTTTTTAGGT 360

CTCGTAGTGT AGCGGTTAAC ACGCCTGCCT GTCACGCAGG AGATCGCGGG TTCGATTCCC 420

GTCGAGACCG TACAAATGCC TATCCAAGAG GATAGGCATT TTTTTGCGTT TAATATTATA 480

TTAATAAAAG ATATATGGAC GAATGATAAT CATATTGATT TATCTGTTCG TCCATTTTCT 540

TTAAAATGTA TGAACCTCAA GTAACTTAGT GGTTGGATAT GAAAGATAAA CGTAGACAAT 600

AAAATCTTTA TTAGACGTAC AAACATATGC TACTGTCAAC ATATTTCTTC GTTGTGATAT 660

GCCACCAGTC CTCCATAACA TCAATTGTTA AAGTAACGAA TAACGAATAA TGATATTTAT 720

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ATCCTGTGAT TTTTTACACA AACATAAACG ATAAAGAACA AAAAATGATA AAATAATATT 1020

AATGATTTAA GAAAAGAGGT TTATGCAAAT GGCTAGAAAA GTTGTTGTAG TTGATGATGA 1080

AAAACCGATT GCTGATATTT TAGAATTTAA CTTAAAAAAA GAAGGATACG ATGTGTACTG 1140

TGCATACGAT GGTAATGATG CAGTCGACTT AATTTATGAA GAAGAACCAG ACATCGTATT 1200

ACTAGATATC ATGTTACCTG GTCGTGATGG TATGGAAGTA TGTCGTGAAG TGCGCAAAAA 1260

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TGATCCGTCA CATCCTGAAT ATATTGTGAC GCGTAGAGGC GTTGGATATT TCCTCCAACA 1740

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TTATAACCAA TTAAATAATA TAAATCAAAT ATTCATTGTT GGTACAGCTA TTTCATTATT 2340

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CTATGAATAG TTACATTGAA GCACTTGAAG AAGGTGCATG GAAAGATGAG GAACTTGCGC 3000

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TCCAGGTAAA GTTGTATTGT TgtAGCGCAT AGAGGAACTG TTAGTAGCGG TACAGAAGGT 9240

TCTGGTCGCA CAATAGAAGG AGCTACTGTA TCAAGCAAGA GTGGGAAACA ATTGGCTAGA 9300

ATGTCAGTGC CTAAAGGTAG CGCGCATGAG AAACAGTTAT TTCATAATCA ACAGTCATTG 9360

ACGTAGCTAA GTAATGATAA ATAATCATAA ATAAAATTAC AGATATTGAC AAAAAATAGT 9420

AAATA 9425

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3886 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

AGTTGTAATG TCACATTTCC AGAGTCTGAA ATTATCTTTA TCACGTTACA TTTACTAGGC 60

TCTAAAATGA CTGAACATAC AGCATCTTCA ATTACCTTTG AATACCATGA TTTATCGCAA 120

AATATACATG AATTGATCAC TTGTGTTAGC CAAGAATTAG GCATTGATAT GTCAAAAGAC 180

AACAAGTTAC ATACCAGTCT GATCACACAT ATCAAACCAG CTATACATCG TATTAAATAC 240

GATATGCTAC AACCTAATCC TTTGAGGCAA GAAGTTATGC GTCGCTATCC TCAAATCATT 300

GAAGCCGTTA GCAAGCATAT TAGTCCAATT GAACAAGATG CTGCTATTCG CTTCAACGAA 360

GATGAATTAA CATACATTAC AATTCACTTC GCATCAAGTA TAGAGCGTGT TGCAACACAT 420

AAACAATCAA TGATTAAGGT TGTCTTACTA TGTGGTTCTG GTATAGGCAC GTCACAACTT 480

TTAAAATCAA AACTAAATCA CCTGTATCCT GaGTTnCACA TTTGGGAtGc CTATTcCATT 540

TaTcAATTGG aAGaAAGTCG ATTATTGCAA GATAACATTG ATTATGTCAT TTCAACAGTA 600

CCTTGTGAAA TATCAGCTGT ACCAGTTATT CATGTCGATC CATTTATCAA TCAACAATCT 660

CGTCAAAAAT TGAATCAAAT TATCAATGAC TCAAGAGAAC AACGAGTCAT GAAAATGGCA 720

ACTGATGGCA AGTCACTCGC AGATTTATTG CCTGAACATC GCATCATTAT AAATAAACAA 780

CCATTATCAA TTGAATCCGC AATTGCAGTG GCTGTGCAAC CTTTAATCAA TGATGGCATT 840

GTCTATTCAA ATTATACAGC TGCAATTTTA AAACAATTTG AACAATTCGG GTCATATATG 900

GTCATTAGTC CACATATTGC ACTTATTCAC GCTGGTACTG ATTATGTACA GAATGGTGTA 960

GGTTTCGCAC TAACATATTT CACTGAAGGG ATTATCTTTG GTAGTAAAGC TAACGATCCC 1020

GTTCACCTTG TAATTACATT AGCAACGGAC CACCCCAATG CACATTTAAA GGCATTGGGA 1080

CAGTTAAGCG AATGCTTAAG CAACGACTTA TATCGACAAG ATTTCTTAGA TGGGAATATT 1140

TTTAAAATTA AACAACACAT TGCTTTAACT ATGACAAAGG AGGCTTAATA ACGTGTCATT 1200

AGACATTTTG TCAACAACAC GCATCATTGT AAAAGAACAA GTAAATGATT GGACTGAAGC 1260

TATAACTATA GCTTCTCAGC CATTACTACA AGAACAAATT ATTGAACAAG GCTATGTTCA 1320

AGCAATGATT GATAGCGTTA ATGAACTTGG ACCTTATATC GTTATCGCAC CTGAAATTGC 1380

AATTGCACAT GCAAGACCGA ACAATGACGT ACATCAAGTT GGTTTAAGTC TATTAAAGTT 1440

GAATCAACAT GTGGCATTTT GTGATGAAGA TCACTACGCA TCTCTCATTT TTGTATTGAG 1500

TGCCATCGAC AATCATTCAC ACTTATCTGT ATTACAAAAT TTAGCAACCG TACTGGGCGA 1560

TAACCAAACA GTCCAGCAAC TATTAACTGC AACAAATGCA CAAGACATTA AAAACATTTT 1620

AAAGGAGCAT GATTAATATG AAAATTTTAG TAGTATGTGG CCACGGTTTA GGAAGTAGTT 1680

AAGTTGAACA TAGTGACATT ATGACAGCAA GTCCAGAGAT GGCTGACTTG TTTATTTGTG 1800

GTAGAGATTT AGCTGAAAAT GCCGAACGTC TAGGGGATGT CTTAGTTCTT GATAATATTT 1860

TAGATAAAGC TGAATTACAA CAAAAGCTCT CAGAAAAATT ACAACAACTT AACATGATTT 1920

AAAGGAGGTA CGACCTATGC AAGCAATCCT TAATTTTATA GTCGATATTT TAAGTCAACC 1980

AGCCATTCTT GTTGCACTGA TTGCCTTTAT AGGTTTAATC GTTCAGAAAA AACCTGCCGC 2040

AACGATCACT TCAGGAACCA TTAAAACGAT ATTAGGCTTC TTAATTTTAA GTGCAGGTGC 2100

TGATGTCGTC GTTCGATCTC TTGAACCATT CGGCAAAATA TTCCAACACG CATTTGGTGT 2160

GCAAGGTATC GTACCTAACA ACGAAGCTAT CGTCTCACTA GCCTTAAAAG ATTTTGGAAC 2220

AACAGCTGCA CTCATCATGG TCTGTGGCAT GATTGTTAAT ATTTTAATTG CCCGCTTCAC 2280

TAATTTAAAA TATATCTTTT TAACAGGTCA TCATACATTT TACATGGCTG CGTTTTTAGC 2340

AATCATTTTA ACAGTCAGTC ATATTAAAGG CTGGCTAACG ATTGTTATCG GCGCACTCGT 2400

ATTAGGATTA ATCATGGCAG TATTACCTGC ATTACTCCAA CCTACGATGC GAAAAATTAC 2460

AGGGAATGAC CAAGTAGCTT TAGGTCATTT TGGCTCAATC AGTTACTTTG CCGCAGTGCT 2520

GTAGGTCAAT TATTCAAAGG TAAGTCTAAA TCAACGGAAG AGATTAAATT TCCAAAAGGC 2580

TTAAGTTTCT TACGAGAAAG TACAATTAGT ATCTCGATTA CGATGGCATT ACTTTACTTC 2640

ATCGCATGCT TATTTGCGGG CGTTAGTTAT GTACACGAAT CTATTAGTGA TGGTCAAAAC 2700

TTTATTGTCT TTTCATTAAT TCAAGGTGTG ACATTTGCTG CTGGTGTATT TATTATTTTA 2760

ACGGGCGTTC GTTTAATCTT AGCTGAAATC GTCCCAGCAT TTAAAGGAAT TTCTGAAAAG 2820

CTTGTACCAA ATTCTAAACC TGCATTAGAC TGCCCTATTG TGTTCCCTTA TGCACAAAAT 2880

GCAGTATTAA TTGGATTCTT TGTCAGCTTT ATTACAGGTG TCATCGGTAT GTTTATCTTA 2940

TTCTTATTTG GTGGCGTCGT CATTTTACCT GGCGTAGTTG CACACTTCTT CTTAGGTGCA 3000

ACGGCTGCTG TATTCGGTAA TGCAAGAGGC GGTATTAAAG GTGCTATTGc TGGCGCCGCT 3060

CTAAATGGTA TCCTAATCAC GTTTTTACCA TTATTATTCT TGCCATTTTT AGGCGAATTA 3120

GGTGGTGCTG CAACAACATT CTCAGATACA GACTTTTTAG CTGTCGGTAT CGTGTTCGGT 3180

AACGCAGTAA AATATATGGG ATTATTTGGT GCGATTCTAT TTATTATTAT CGTAGGTGCG 3240

ACAACAATTT TATTAAAAGG CCGTCAAAAA GAACAGCAAT AGTGTTAACG TAGAAATATA 3300

AAACACCGTC ACATATTGAG TGAATGCCCC TTTtATCAAG AGGAAAGCCA CTTACTTATG 3360

GACGGTGTTT TGTATTATAT TAAATGATAC TTAGCCATAC TATCGACAGC TGCTAAAATT 3420

GCTTCTTCTT GTGTCGCAAT CGGTTCCCAA CCAAGTAATG TTTTTgCACG TTCGTTACTT 3480

CCTAGACTCA AAATAAAGTC TGGTAATTTT TTAGTAGAAA CTTTTTGAGC TATTTCAGGT 3600

CTCTTTTCTT TAATTAATTT TGCAATTTCC AACAAATTAA TTTGTCCATC AGCCGTCGCA 3660

ATAAATCGCT TGCCATTAGC TTGTTCATTT GTCATTGCCA AAATGTGCAG TTCAGCTACG 3720

TCTCTCACAT CAACAACATT TAACGGAATT TGCGGTACAC GTTTCATTGA ACCATTCAAT 3780

AAATTTTCTA ATAAATGAAA GCTTCCTGAA ACGTGTGCAT CTAATGATGG CCCAAAAATT 3840

GCAACTGGAT TGATTGTGGC AAATTCTACT GTTGTATTTT CATTCT 3886

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GTCATCTATC AAAAATTTGG TATACAGACC GACAATTATT AATTAATAAT TTAATTTCCC 60

AGGCAATACC AGTGATTAAA TATCCACAAA TACAACATAA AGAACAACCA TTAGAATCTA 120

TTTCACAACT TATATTGTCT AAGATGACAT CTAATCAATA GTGTTTAAAT TTCTCAGTGG 180

CTGTGAATGA GGTTTAAAAG TACTATAAAA CGTAAACTTT GATACTTTAA AATACGCAAA 240

AAACGGTAAA CCCTAATTCA TATTATAGAG TTTACCGTTT TATTTTTTAA CTTGCATCAT 300

AGTTATATTA ACATTATTGT TGGTAGTTTG GATCAGTAAC CATTGCTTGT CCAGTATAAT 360

CAACCGTTAC AATTGAATAT TTTCCaTTTG CATTTGGGTC TTTAAAACTA AACACATACT 420

TATAGTTGCC ATTATGTTCT TCAATAGAAT AATCATTATA CACTTTATTA TTACTACCAA 480

ATTTATTTGC TTCATTATTA GCCGCATTTA AAGCTGTTTG GAAATTTGGC AATTGCTGTA 540

AAGCTTGATT TTTATTTCCA TTAAACGGAT AAATTTGACG TGCAACCGGC GCGGCATTTT 600

GnCCATAATA TGGTGCAACG TAACTTGATT TTTGATTATT ATTCGCTTGG TTATTACTTG 660

ATTGGTTATT ATTTGTTTGG TTTTGGTCAT TGTTTGTTGC ATTTGAATTA GATTGTTGCT 720

GGTTATCGTT TGCACTATTA TCTTTATTAT CTTTGTTTAC GTCTTTACTA TCATCTTTAT 780

TATCTTTCTT ATCTTTAGAT GAATCATTTG TTTTTTTATC TTGTTGTTCA GTTTTCGCTT 840

TATCATCTTT TTCTTTATTA CCGTCTTTTT GTTGGTCACT ATCTTGACCA CATGCAGCTA 900

AAAATAATGA TAATGCTAGT AACCCTGTAA CTAATCTTTT CATACATATC TCCTCCTATA 960

ATTCGATATT CATTGAATAA TCTTGAAATA CATATCTACC ATGTGTATCT TTTCATGGCT 1020

TAAGGTTCTT TTTATTATAC CCTAATTTTT GTTCATTATT ATTTAATTTT TGTGAATTTT 1140

ATGtTTkCTA TAAATTTAAT TATTTTACTT TAACAATTCA TTACGCATTT AGCATTTCAA 1200

GGTATACACA ATATTTATTA CTATGATTTC ATTTTATCTG CTGCAAAAAC AATCATTATA 1260

ACTCTTTTTC CATAATTAAA TCTGTATCCG TTACATCACC TGTTTGAAAA TGATGTTCAC 1320

CAACCACTTT AAATCCATGA CGTTTATAAA ATGCTTGAGC ACGAGGATTA TGCTCCCAAA 1380

CTCCTAGCCA AATTTTATGT TTATTATGTT CTTGAGCAAT TTTTTCGGCC AATTCTATCA 1440

ATTGTGAACC TCTTCCGCCA CCTTGAAAGT CTTTCAAAAA ATATATGCGC TGCACTTCTA 1500

AATAGGTCTC CCCCATTTCT TCAGTTTGAG CACTATTAAT ATTCATCTTT ATATAACCAA 1560

CATTCGCACC ATCTTCTTGa TAAAAATAAT GAAATGAATC TACATGGTTA ATCTCTTGTG 1620

TAAATTTCTC TACAGTATAA TTGTCTTTAA AAAATTGATC AAAATCTTTG TCATCATAGT 1680

AAGAACCAAA CGTGTCATAA AATGTTCTAG TTGCTAATTC AACTAATTCA CTAGCATTTT 1740

GTTCTGAAAT TTCTTTGATT ATCCCAGCCA TATAAATCCT CCAATAAACA GTGATCGAAT 1800

CAAAATATTA CTTATGTTAT TTTTCAGCCA AAACTATTTA AAAATACATT AACACAAATC 1860

AATTACAAAT TGTATTGATT GTGTGTAACA TCAATAAATG ATACATTTAT TCCAGTAAAA 1920

TGGCCGTATT TTCAAAAGAG AAAAAGAGAG GATGTATCGT TGTGATAGAA ACATTTAAAG 1980

CGTTTGTAAT TGATAAAGAT GAGAGTGGTA AAGTGACACC AACTTTCAAA CAATTATCGC 2040

CTACTGATTT ACCTAAAGGA GATGTGCTGA TTAAAGTACA TTACTCTGGT ATAAATTATA 2100

AAGATGCTTT AGCGACTCAA GATCATAATG CAGTCGTAAA ATCGTATCCT ATGATTCCAG 2160

GAATAGATTT AGCTGGAACA ATTGTTGAAT cCGAAGCACC AGGCTTTGAa AAAGGAGAAC 2220

AAGTAATTGT AACGAGTTAT GACCTAGGTG TCAGCCATTA TGGCGGTTTT AGTGAATATG 2280

CGCGTGTAAA ATCAGAATGG ATTATCAAGC TTCCTGATAC TTTAACATTA GAAGAATCAA 2340

TGATATATGG CACAGCTGGT TATACTGCCG GTTTAGCAAT TGAAAGACTT GAAAAAGTTG 2400

GAATGAATAT TGAAGATGGT CCTGTACTCG TTCGCGGTGC TTCAGGTGGT GTCGGTACTT 2460

TAGCAGTACT CATGCTTAAT GAACTTGGTT ATAAAGTTAT CGCAAGTACA GGTAAACAAG 2520

ATGTTAGCGA TCAATTACTT GAACTTGGTG CCAAAGAAGT TATCGATCGA CTTCCTGTTG 2580

AAGATGATCA TAAAAAGCCA CTCGCATCAT CAACTTGGCA AGCTTGTGTA GACCCTGTTG 2640

GTGGCGAAGG TATTAATTAT GTTACAAAGC GTTTAAATCA TAGTGGGTCA ATTACAGTTA 2700

TTGGTATGAC TGCCGGTAAT ACTTATACTA ATTCTGTATT CCCTCACATT TTAAGAGGTG 2760

TAAACATTTT AGGAATTGAC TCGGTATTTA CTGCTATGAA ATTAAGACAG CGCGTTTGGC 2820

TTGATGAACT TCCAGAACAA CTTAACAAAG TAATTAAACA TGAAAATAAA GGGCGCATTG 2940

TTATCGATTT CGGTGTAGAT AAATAGTATT CATGAAAAAG ACATCCCGTT ATGCGAGATG 3000

TCTTTTTTAA TTTAGTATTT GATATACATA CCGCCTGAAT CTGGTTCGGT AGGTATAAAT 3060

CCAAATTTTG TATATAATTT ATCCGCTGGG TAGTCTGCAA TCAGAcTAAC GTATGTACTC 3120

TCAACAGCCA CACCTTTAAT ATATTGCATA ATATGCTCCA TAATTAGACT GCCGTAACCT 3180

TGACCTTGGT AACTTTTCAA AACTGCAATA TCAACAATTT GAAAAACAGT TCCGCCATCG 3240

CCAATCACTC TACCCATACC AATTAACCGA TCTTTATCAT ACAAGGTTAC TGTAAATAAG 3300

GCATTAGGTA ATCCTTTTTC aGCTGTTCGC GCGTCTTTGG ACTCATACCT GCGTTAATCC 3360

TTAATGCGCA ATAATCCTCG CAAGTCGGAA TATCATATGT CACTTTAACC ATTATTTACC 3420

CCACTTTTCA TCACACAATA TATCAACCTA GTATAAATGT TTATTTACAA TAGTCTTATT 3480

CGCTTCTTTA AACACTTCAT GATGACTTGA AACATAACCC TCTGCATTCG CATCTGGTTG 3540

GATATATGTT TTAGCAAGGT TCGCTGCATT TGCACCATCA CTAAATGCAC TTGCAATTAG 3600

ATGTGATTTT GCATCATGAT AAACAATATC TCCACACGCA TAGATACCAG GTATACTAGT 3660

TGTCGTATTA CCAAATCCTT TAACACGACA ATCATCATGC ATATCTAGCT TTGAAGATGT 3720

TtCACTCAAT AATGTATTAC AACGATCAAA CCCATGACTA ATAATGACAT CGTCAAATTT 3780

AACTGTATGC CTATCGCCAC TTTCAACATG TTCCAAAACA ACTTCACTTA TATGCGTTTC 3840

ATCATCATTG CCGACCAAGT ATTTAATACG TGTTTTTGGG CATAGTTTCA CATTTAAATC 3900

TGTCACCAAC GTTTTCATCG CTTCATGACC ACTTACATCT TCTTTTCGAT AAACAACTGT 3960

CACGCTTTTA GCAATCTTGG CAATATCATG CGCCCAATCT AATGCTGTAT TTCCTCCACC 4020

TGATATTAAT ACATCTTTAT CTTTGAAACG TCTGTAACTT TGTACAACAT AATGTAAATT 4080

AGTTAATTGA TATCTCTCTA CACCTTTAAC ATCTAATTGT TTTGGATTAA TAATACCCGC 4140

ACCAATTGCA ATGATAACTG CTTTCGATGT ATATATTTCT CCCGCTTCTG TTTCAACTTC 4200

GAAATGACGT TCTGCCTTTT TCCTAATATC TACCACACGT TCATTCAAAT GAACTTCCGG 4260

TTTAAAATAT AATCCTTGCT TAATTGTATC TTTTAAAATT TCATGACAAG GTTTTGGCGC 4320

AATGCCGCCA ATATCCCAAA TAATTTTTTC AGGGTAAATT CTCATCTTAC CCCCTAATTC 4380

AGATTGAACA TCTATCAATC TTACAGACAT ATCTCGCAAT CCAGCATAAA AGCTTGCATA 4440

CAAACCAGAC GGACCGCCAC CAATGATTGT AACATCTTTC ATTATGTGCC TCCTATGACT 4500

CTCTATATTC ATTTCTTTCA TTAACGTGCT CAAATTGATA ATTATTATCA TTTAAAGCCA 4560

TTATACTATT AATATTTATA TTGTTAAAAT AAATCGCATA GTTAGCCATG AATTATCAAT 4620

GAAAGATGTG TATATTTTTT AGTTCTAGTT ATATTATTTT TTAAAAGACT CATCACGTGG 4740

TTCTTTAAGA ATTGCTTGTC TTAAAAGGAA AAATAGCAAC AATAAACCTG CAAGCATACC 4800

TGTGTGCCCA ATACCTGCAA AGCCTGCnAA TGCTTCTGGA GAGTATGATT TACCAGTGAC 4860

TTGGAAGAAT CCTTTTGTC 4879

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1560 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

ATAATGTCTT AGaTTGATTG GGAGTTTTTT TAATTTTTTT GAAATTAAAT TAATCTGTAs 60

yTAATAAAAA ATTTGAATAA CTGACACAyT TTTTTGATCA TAGCTAyATA CTTTGTGAAT 120

TAATTCACAT TATAATAAGA GTGAAGATAA GAGTATTATA AATnATCTTT AAATAAATAT 180

ATGTGAAGTA AAAATTACAC GTTAGCATAT CGATTATGgT CATTTCkTTT AACATATTAA 240

CTgGGGaACG TTAAAAGTTA ACGGkTGATA TCyAACtAAA AACAAGGTCA CAGTAGTATG 300

TTTTAATCTG GCGTCTATTA CAAATAAAAA TTACATCTAT AATTATTCGT TTTCTTTTTT 360

GAAAGTAATA GCCAATTAAT ATCATACATA CTGGAGTGAC TATAAGGAGG ACATTATTAT 420

GAGAGCAGCA GTTGTAACGA AAGATCACAA AGTAAGTATT GAGGACAAAA AGTTAAGAGC 480

TTTAAAACCT GGTGAAGCGT TGGTACAAAC GGAATATTGT GGCGTTTGTC ATACCGATTT 540

ACATGTTAAG AATGCTGATT TTGGTGATGT TACAGGCGTT ACTTTAGGTC ATGAAGGTAT 600

TGGTAAAGTC ATCGAAGTTG CGGAAGATGT AGAATCATTA AAAATTGGAG ACCGTGTGTC 660

TATCGCTTGG ATGTTCGAAA GCTGTGGAAG ATGTGAATAT TGTACAACAG GTCGTGAAAC 720

ACTTTGCCGT AGTGTGAAAA ATGCTGGTTA TACAGTAGAT GGTGCAATGG CTGAACAAGT 780

TATTGTTACT GCAGACTATG CTGTGAAAGT ACCTGAAAAA TTAGATCCAG CAGCAGCGTC 840

TTCTATTACA TGCGCAGGTG TGACAACTTA TAAAGCTGTA AAAGTAAGTA ATGTAAAACC 900

TGGACAATGG TTAGGTGTTT TTGGTATAGG TGGTTTAGGT AACCTAGCTT TACAATATGC 960

TAAAAACGTT ATGGGGGCTA AAATTGTTGC CTTCGACATC AATGATGATA AATTAGCATT 1020

CGCGAAAGAA TTAGGTGCTG ATGCTATTAT TAATTCTAAA GATGTTGATC CAGTTGCAGA 1080

AGTTATGAAA TTAACTGATA ACAAAGGATT AGATGCAACA GTGGTAACTT CAGTTGCTAA 1140

TTTACCTGTT GATAAAATGA ACTTAGATAT CCCAAGATtA GTGCTTGATG GTATTGAAGT 1260

AGTAGGTTCA CTTGTTGGTA CAAGACAAGA CTTACGTGAA GCGTTTGAAT TTGCTGCTGA 1320

AAATAAAGTA ACACCTAAAG TTCAATTAAG AAAATTAGAA GAAATCAATG ATATTTTTGA 1380

AGAAATGGAA AATGGTACTA TAACTGGTAG AATGGTTATT AAATTTTAAA AATATCAACT 1440

GACTATATAG ATAAAGAAGG TAGTGCTCTG AACACTATCA TTATTAATCA AACCCCGAGG 1500

TTTTCCTGAA AAGATAGTGG nAAATCCCCG TGTTTTTTGG GTTTGAGGnG GTTGTnTGTA 1560

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11014 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

GTCCTGTnGC TGCAATGAAT ACGCCTAAAA ATCCAGGGAT GTAATGGATA CTTTGTGGTA 60

GTACTAATGA TAGAAATGAT AAAAATGAAA TCACAAAGGC TACGCTCGCA AAAGCTTGAC 120

ATGTACGCTT ATCGCCATAA TCTAACCCTG TACGTATATG TAATAAATAC TGTAATCCGA 180

TACTTAAATA CATAATTGCC ACGCATAAGA AGAATGGGAA GAATGTCTTT TCAAAGTCCG 240

GATATAGGCT GTTAGATAGG AAGACCATGA TGAACATATT AAACATCATA AACGAGACGT 300

CTTTGAATGT AACTTGACCA AATCGATTTG TAAAAAATGT TTGATGAGAC CACATTAACC 360

ATAAGAACAA ACTCATGACG ATGTATTTGA AAAATAAATC AGCTGAAATG GAACCGTTTT 420

GTGTTGTTAA AATCACATGT GCAATTTTTT GAATGGCATA GACGAAAATT AAATCAAAGA 480

ACAACTCATG GAATCCTGCA CGCTTTTCAG CTAAATGTTT TGGTGTTAAT GCATTAACCA 540

TAAAATTTTA ACTCCTTTAA GATGTGTAAT TAATTTACTA AGTATACTAT TTATTTTTTC 600

TAGTGAATAG GGGCAGATTT GGCGATGAAG TGGAAGGAGA GGTGACTGCA AGGTAATTGC 660

GGAATTAACA ATCATCAGCG ATTTAATATT TGACTGGAGA CGTCATGGTA ATAAAAAATT 720

GATGAGAAAT TGATGGTGAA ACCAGCTGTG AATAsCGaTG cAATGATrsA TAGaATTTAA 780

TTAGAGTCAT TACGCGaAAT GATTAATGAT AATTTGTGGT AAATCAAAGC aTAATTTTGT 840

ACTATAGATG AGGATGATAG AGCATATTTA AGAGGGTGAA ATGTTAAAGT GAAACCGTTT 900

ACGTTTCCGA TTGCCCAAAC AAATTACATC ATTGTATAAT ATGATTTGTT AAATGCATAA 960

CAAGAATGAA AATGTAACAT ACGTAGCAAT TGGTTTCATA AATTGGATGT TAGTGGCGTA 1020

TGACGAGAGT CGTATTAGCA GCAGCATACA GGACACCTAT TGGCGTTTTT GGAGGTGCGT 1140

TTAAAGACGT GCCAGCCTAT GATTTAGGTG CGACTTTAAT AGAACATATT ATTAAAGAGA 1200

CGGGTTTGAA TCCAAGTGAG ATTGATGAAG TTATCATCGG TAACGTACTA CAAGCAGGAC 1260

AAGGACAAAA TCCAGCACGA ATTGCTGCTA TGAAAGGTGG CTTGCCAGAm ACAGTACCTG 1320

CATTTACGGT GaATAAAGTA TGTGGTTCTG GGTTAAAGTC GATTCAATTA GCATATCAAT 1380

CTATTGTGAC TGGTGAAAAT GACATCGTGC TAGCTGGCGG TATGGAGAAT ATGTCTCAAT 1440

CACCAATGCT TGTCAACAAC AGTCGCTTTG GTTTTAAAAT GGGACATCAA TCAATGGTTG 1500

ATAGCATGGT ATATGATGGT TTAACAGATG TATTTAATCA ATATCATATG GGTATTACTG 1560

CTGAAAATTT AGTAGAGCAA TATGGTATTT CAAGAGAAGA ACAAGATACA TTTGCTGTAA 1620

ACTCACAACA AAAAGCAGTA CGTGCACAGC AAAATGGTGA ATTTGATAGT GAAATAGTTC 1680

CAGTATCGAT TCCTCAACGT AAAGGTGAAC CAATCGTAGT CACTAAGGAT GAAGGTGTAC 1740

GTGAAAATGT ATCAGTCGAA AAATTAAGTC GATTAAGACC AGCTTTCAAA AAAGACGGTA 1800

CAGTTACAGC AGGTAATGCA TCAGGAATCA ATGATGGTGC TGCGATGATG TTAGTCATGT 1860

CAGAAGACAA AGCTAAAGAA TTAAATATCG AACCATTGGC AGTGCTTGAT GGCTTTGGAA 1920

GTCATGGTGT AGATCCTTCT ATTATGGGTA TTGCACCAGT TGGCGCTGTA GAAAAGGCTT 1980

TGAAACGTAG TAAAAAAGAA TTAAGCGATA TTGATGTATT TGAATTAAAT GAAGCATTTG 2040

CAGCACAATC ATTAGCTGTT GATCgTGAAT TAAAATTACC TCCTGAAAAG GTGAATGTTA 2100

AAGGTGGCGC TATTGCATTA GGACATCCTA TTGGTGCATC TGGTGCTAGA GTATTAGTGA 2160

CATTATTGCA TCAACTGAAT GATGAAGTTG AAACTGGTTT AACATCATTG TGTATTGGTG 2220

GCGGTCnAAC TATCGCTGCA GTTGTATCAA AGTATAAATA ATAAGAAAAC AGGTTATCAC 2280

AACAGTATTA ATtACATGTT GGCATAACCT GTTTTTATTT GTTTATGGAT TTATTGGGTA 2340

ATATTAGTCA TTTGATGGTT TAATTGCAAA TGCTCTAACA GGGAACCCAG GTGCATCTTT 2400

TGGTTTAGGG CTGATAGCGT AAATGATGGC GCCACGAGTT GGTAATTGAT CTAAATTAGT 2460

TAATAACTCG ACTTGGTATT TATCCTGACC AAGAATATAA CGTTCGCCAA CTAAATCACC 2520

ATTTTTTACA ACGTCCACAG ATGCATCGGT ATCGAATGTT TCATGACCAA CAGCTTCAAC 2580

ACGACGTTCT TCAATTAAGT ACTTCAAAGC ATCTAATCCC CAACCCGGTG CATGTTGTTG 2640

TCCGTTCGCA TCTTTGTTTT CAAACTTTTC AATATTAGGC CAACGTTTTG ACCAATCGGT 2700

ACGAAGTGCA ACAAAAGTGC CAGGTTCAAT AGTACCATGC TCTTTTTCCC ATGCTTCTAT 2760

ATGCGCACGT GTTACGATGA AATCATTGTT GTTCGCTACT TCTGTTGAAA AGTCTAATAC 2820

AAAGTGAATT GGTGCATCAA TGTGAGTACC ATATTGCGTT ACAATATTCC AACGTTGCAC 2940

ATAGAAACCA TGATCTTTAA CCGTGAATAA AGTTGAAACT TCGCCTTTTT CAAACTCACT 3000

AAAACGTGGT ATTTCCGGAT CAAATGTATG CGTTAAATCA ACCCAAGTTG CTTGTTTTAA 3060

AGTATTTAAT TGTTGCCATA AAGGATATTG TGTCATAAAA TCACCCGTTT TTAGTTTATT 3120

ATATGATAAA TGCTGCGATT ATTCTTGGCG TTTAGCTTTA ACAGCATTCA CAAGCACAGT 3180

CAATGCATCT TTAACTTCTT CTTCTTTTCG CGTTTTTAAA CCACAGTCAG GGTTTACCCA 3240

GAATAATGAG CGGTCGATTT GTTGTAGTGA ACGATTGATT GCTGTAGTAA TTTCTTCTTT 3300

TGTTGGAATA CGTGGACTAT GAATATCATA TACACCTAGA CCAATACCTA AATCATAATT 3360

AATATCTTCA AAGTCTTTAA TTAAATCACC ATGGCTACGA GATGTTTCAA TTGAAATAAC 3420

ATCAGCATCT AAGTCATGAA TAGCATGAAT GATTTGACCG AATTGAGAAT AACACATATG 3480

TGTATGGATT TGAGTTTCAT CACGAACTGA AGACGTTGCA AGTTTAAATG ATAAAACAGC 3540

ATCTTTAAGA TATTGTTCGT GATATTCAGA GCGTAATGGT AAGCCTTCAC GTAATGCAGG 3600

TTCGTCAACT TGGATAACTT TGATTCCTGC AGCTTCAAGT GCTAATACTT CTTCGTTGAT 3660

TGCTAAAGCA ATTTGATCTT GAACGACTTT ACGTGGTAAA TCAACACGTT CAAATGACCA 3720

GTTTAGAATT GTTACAGGTC CAGTTAACAT ACCTTTAACT GGTTTATCTG TTAAGCTTTG 3780

TGCATAAACT GTTTCATCAA CAGTTAAAGG CGCTGTCCAT TTTACATCAC CATAAATGAT 3840

TGGTGGTTTT ACGGCACGTG AACCATATGA TTGCACCCAA CCGAATTTAG TTACTAAGAA 3900

ACCTTGTAAT TTTTCTCCGA AGAATTCAAC CATGTCATTA CGTTCAAATT CACCGTGAAC 3960

TAATACATCT AAGCCAATGT CTTCTTGAAT TTTAATCCAT CGAGCAATTT CATTTTTTAA 4020

GAATGTTTCA TATGCTTCGT CTGTAATGCG TTTGTTCTTC CAATCTGCAC GGTATTTTCG 4080

AACTTCTCGG CTtTGTGGGA ATGATCCAAT AGTTGTTGTT GGTAAATCCG GTAAGTTCAA 4140

ACGTTTTTGT TGTTGTTCAA TACGTTGCGC GAATGGTGAT TGTCTTGAAG TACGCACGCT 4200

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TAATTTATCA TATTTAACAC TATCGTTTTG ATTAAATAGG CGACGCAATG CATCTAATTC 4320

GTCTAATTTT TCAGTTGCAA AGCTTAAGCC TTCGCCAACA CTTGTATCTA ATGTTTCATC 4380

ATCTAAAGAT ACTGGAACAT GTAATAATGA AGATGATGGT TGAATGACAA GTTCATTAGT 4440

GTGTGCTAAC AATTTATCGA TTAAGACTTT TTTAGCTTCA ATGTCACTTG CCCATACATT 4500

ACGACCATCA ATAATTCCAG CGTATAATGT TTTTGATTTA TCAAAATCTC CAGCTTCAAT 4560

TTGTTTAAGG TTATAGCCAT TATCATGGAC AAAGTCTAAA CCTATACCAC CAACAGGTAA 4620

AACACCAGCT TTTTCGAAAT AGTCATAAGC TTCACGTGTA ATATTTTCAT AGCTTTCGCT 4740

GTCGTCTGTA ACTAAGATTG GCTCATCAAC TTGAATGTAC TCAGCACCTG CATCAATTAA 4800

TGATTCAAAC ACTTCTTTAT AAAGTGGTAA TAACGTTTTA ACTTTTTCTT CAAAAGTTTG 4860

GTGACCGCCT TTTGATAATT TAACAAAAGT AATCGGACCA ACAATGACAG GGTGAGCGTT 4920

AACGTTTAAA GATTGGGCAT ATTTAAAGCG ATCTAATAAT ACATTGCGAC TCACTTTAGG 4980

CTCAACATTG TCCCATTCAG GTACGATGTA ATGATAGTTA GTGTTAAACC ATTTTATAAG 5040

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TGCCCAATAA CTTTCGATGG CTTTTTTCCA TTCTCTTTTT CTACCTAATC TTGGGAATCC 5340

TAAGTTTGAT GTTTTAATTG TTGTCATAAT ATTGCCTCCT TGTGAGCAGT AATAGATTTT 5400

GAGTATGCTG CAAGTTCTAA TGAATCTTCG ACATTTTGAA ACGGTGTGAT AATGTATAAA 5460

CCATTAAAAT ATTCATGAAC AGTATCGATT AAATCCTTTG AAAGCTTAAG ACTTAGTTCT 5520

CGTGTTTTGG CTTTATCATC TTTAACTGCT TCAAATTGTT GTAAAATTTC ATCTGACATC 5580

TTGATTCCTG GCACTTCATT ATGCAAAAAG AGTGCGTTTT TGTAACTTGC GATAGGCATA 5640

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AATCTTTTGA CGGCACCATA TAATTTACGA ACATTAGGGT TAAAGGCGCC AgcGATGTTG 5820

AAGTGTGTAC GTTTCTTCAG CGCATCACCG TCAGTGTTAA TACCTTGATT AAATCTTAGA 5880

GCGAGTTCAG TTAATCCTTT AGAATTAACA TCATAGACAT TGGTTGCACC TGGTAAGTGA 5940

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GTTGCCAATG AATTATCTGC GAGTGTTACC GCATCTACAT TAGCTTTATC AAGTTTAGCG 6180

ATATTTTCAA AAAATCTATC CGTGTCTAAA TGTTTCGGTG TATCCAATTC GATAATAACG 6240

GTTGGACGTT CTTGAACCTT AGATGTTAAT GATTGTCTAA CTTTATTTTG AGATGGATTG 6300

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GCCTGACCAT TAACTAAGTA ATTTGTGTTT GAAGCGGTTA ATTGAGCAAT GATTGGAATG 6720

TCGTATTTCT TTCTCGTTCG TGAAATGACA TTTGTTAACT CTTCTAGGTC GTAATACGTT 6780

TCGAAAAGTA GCGCGTCAAC GCCTTCTTCA ATTAAGGTGT CTATTTGAAT TTCAGTATGA 6840

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CTCTTCTAAA AGTTCACGGT TAGGGTTGCC cTTCGTGCAT AATCATATTT AACATCGCCA 8220

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CTCCAATCTG AGCTTTATCT AATGCTTGGA TGATATCGCG TTCGATGTCT TCATAATTTT 8400

CAACACCTAG TGATAAGCGG ATTAAATACT CATCAATGCC ACGTTTATCT TTTTCAGCAT 8460

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AATGCAAAGT TTTAAGTCCA CGTAACAACA AATAACTATC TATTGGTGAA AGTGTTGCGC 8760

CAGTCATGTT GTGAAAATCA AACAACTGTT GCGCGAGTGA TTCATCTTTG ACGGTTACGA 8820

CACCTGCTAG TACATCGTTA TGTCCGCCAA TATATTTCGT GGCTGAATGT AAGACTATAT 8880

CAGCACCTTC TGCTAGTGGT GTTGAAAGAT AAGGTGTTAA AAAAGTATTG TCGATAATTG 8940

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CTTGTTCATA ATCTGTAAAA TCAACGTACT TAAATTTGAT ATCGTATTGT TGCTCGTAAA 9120

ATTCAAATAA TCTAAATGTG CCACCATATA AATCGAATGA AACTAAAATT TCATCATGAG 9180

GTTTAAATAG ATTACATATT AATTGAATGG CTGACATTCC ACTTGATGTA GCGAATGATG 9240

CAATACCATG CTCAAGTTTG GCAAAACAGG TTTCAAATGT TGAGCGTGTA GGATTTTTAG 9300

TACGTGTATA ATCAAAACCT GTCGATTGTC CTAGTTTTGG ATGCTTGTAG GCAGTAGATA 9360

AATGGATTGG ATTCGCTATA GCACCGGTTG AATCATCGGT TAATGTGATT TGGGCTAACT 9420

GTGTATCCTT CATATTAAGA CCCTCCTATA AGAAAAAATA AAAAAAGCTT CCGTCCTTCG 9480

TACCCGAATG AATCGGATAA AAAGGACGAA AGCTTATGTT TCGCGGTACC ACCTTTATTT 9540

GTTATTCCAT CGCTGAAATA ACCTTATTCA GTACGCATTA AAAGTAAATA TGCTTACTGA 9600

ACAATTATCA CAATTAAAGT CAGTAAGTAA GGATATAGTA ATGTGCTATC CCATACTTAT 9660

TAACAAAAAA TCGTGCGTAA AGAATCCAGT ACGCCATTTA ACATCAATGT TAATACTGTA 9720

TCGCTATAAC GGGCGAACCC GTAGACACCT CATATTGGCA TCAACACTCC AAGGCCATTT 9780

TCAAACACGC TTTCAAAATC TTCTCTCAGC TACTAAAGAC TCTCTGTATA AGCAGGGTGT 9840

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TCAAATAAAA AGTGATGTGA GTGAATTGTC AAAAAGTGAA GATCAACGTA TTACTAAAAC 10140

AAAAGATGAA CAAATTAAGC AAATAGATAT ATCGGATATC AAACCGAATC CGTATCAGCC 10200

CCGAAAAACT TTCGATGAAA ATCATTTAAA TGATTTGGCA GATTCAATTA AGCAATATGG 10260

AATTTTGCAA CCAATTGTGC TTAGAAAAAC AGTTCAAGGT TATTACATTG TAGTTGGTGA 10320

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TTTAACAGAT GAAGATATGA TGGAACTGGC GGTCATCGAA AATTTACAAC GAGAAGACTT 10440

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ACAAGAAGTA GCGAAACGAT TGAGTAAGTC GCGCCCGTAT ATAGCGAATA TGTTGAGGTT 10560

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TTCGTCAAAG TCGGAAACAG ACAAAGTAGA TATAACTAAG CCTAAATTTA TAAAGCAGCA 10800

AGAACGACAG TTGCGAGAAC AGTATGGTAC CAAAGTAGAT ATATCAATAA AAAAATCGGT 10860

TGGTAAAATC TCATTTGAGT TTGATTCACA AGAAGATTTT GTGAGAATAA TTGAACAATT 10920

AAATCGTAGG TATGGTAAAT AGTTACACAA TTTTATATAA TAACTCTTTG TGCAAGTGTA 10980

AATAAATTGT AATCAGTGAC ATTTGATTCT AGAT 11014

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6022 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

TCCCCTTATG GAATTTCACA TTCTAGTTTA CATAATATAT ATTATAGGAA GTTATATGTG 60

TGTAACGCAA AAgGTACCCT ACATCATAAT CATTATCTAA TATCGTCACA TAACTTACTT 120

ATGCTATAAT CATGGTATTA TATTGTTTGG AGTGATTTGA TGAGATTTGT CTTTGATATT 180

GATGGTACGC TTTGTTTTGA CGGCCGATTA ATTGACCAGA CTATTATTGA TACATTGTTA 240

CAATTACAAC ATGATGGTCA TGAACTTATA TTTGCATCAG CACGTCCGAT TCGTGATTTG 300

TTGCCAGTTT TACCATCAGT ATTTCATCAG CACACATTAA TTGGCGCAAA TGGTGCTATG 360

ATTTCACAGC AATCAAAGAT TTCTGTTATC AAACCAATTC ATACTGATAC ATATCATCAT 420

GCTGCACAAC TTGACGCTGn AGAACGCGAT TTTTGAGCGT TTAGATCCAC ATAAGCTGGC 540

CAGTTGTATT GATGTTGCAA ATATCGACAC GCCAATCAAG AkTATTTTAT TAAATATAGA 600

CCCGGCACAA ATTACAACTA TATTAGACGA GCTAGATAAA TACCATCAAG AATTGGAAAT 660

GATTCACCAT TCAAATGAGT ATAACATTGA TATAACAGCG CAAAATATTA ACAAATATAC 720

TGCATTACAA TATATATTTG ATGCAGATGT TAAATATATA GCATTTGGTA ATGACCACAA 780

TGATATTGTC ATGTTACAAC ATGCTAGTAG TGGCTATATT ATAGGACCAT CAGAAGCATA 840

CACACACGCA ATATTGAAAC TTGATAAAAT CAAACACATC AATAATAATG CACAAGCTAT 900

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GCCACTGCCC TTTACTTCAG CCTCATGCTG CGTTTCTGAA AATGATTTTA AGTTAATGAC 1380

GCATTCACTT TGATAATAAT TAAAGCCTCT TTCTATAGAA CGAATACTTG CAATATCAAG 1440

TAATCCCATT AATGaTACTC CTTTTTATTA TTATTTTTAA ATAAAGAaAA TAAAATAGAT 1500

AAGTGTCTAG ATTAAAATAC TTGATTTATC TATATTTTAT AACAAGTCTA GAATTATCGC 1560

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TAAGTTCGTA ATCGTTTGCG CTTTTAATAT ATTGATTACA TTTTGTTCAG CTATAACATC 1800

TAAATTTGAA GTTATCTCAT CACATATTAA AACGCGAGGC TGTGCTAATA ACGAACGCAT 1860

GACATTAAAT CTTTGTAATT GTCCGCCACT CACTTCGCTT GGTAATTTAG TCAATAATTG 1920

CGCGTTTAAC TCAAAAGTAG ATAAATGTTG TAATAATAAT TGATCCTGAG CAGTATTATC 1980

AGTTAGACCT CTGTAATAAT ATAACGCTTC TTTTAATGAG GTCTCAATCG TCCAATCAGG 2040

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CTCTCCTTTA ACAGGTTTAA ACAAGCCAAG AACCAATGAA GCGAGCGTAC TTTTACCACA 2160

GCCACTTTCG CCTAAAATAC CAACATTTTC TCCATCAGGT ATAGTAATAT TGATATCTTG 2220

CCCTCTTTAA TTGTGTTCTA TATTTAATTA GACGTTCAGT ATACGGATGC AAATGCTCAT 2340

ACTTGAAATG ATTAATATTA CCTCGTTCAA TGATTTGACC TTCTTTTAAA ACATAAATGT 2400

ACTGACAATA TTTCAATACA TGACTTAAGT TATGTGTGAT AATAAATAAT GTTTGACCAT 2460

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AACACTAATC GTTCAATCCA CCCTTTTTTG TATCCGGCAA ATAGACCTAG TGTAACACCT 3600

ATGACAACGA TAGCTATTAA TGTTAAAACA GTAACAAACA ATGTTGAACG TGCACCGATA 3660

ATAATTCGGG TAAATAAATC TCTCCCATAA TCATCAGTTC CTAATAAATG CAACCAACTA 3720

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AATCGTATTG ATAATAACAA CGAAGAAGCC AATAAATAAC ACGCATCCTT GAATAACAGG 4020

ATTTTCAATC ACTACAGTAC CACCTATTAG ACTGCCAAGT GAAATCCCTA GTAATGGGAT 4140

AATCGGCAAA ATTGTTGGTT TTAGTAAATC ATGAATTAAA ATATAACGTT CATTCATACC 4200

GCGTAATCTT GATGCTTGTA CGATATTACT TTGCAATAAC ATCAATAAAT TAGAACGCAC 4260

TAAACGAATG ATGTATGCAC ACATACCTAA AGATAGCGTG ATTACAGGTA ATATAAACTG 4320

ACTTAGTATA ACGCTATCTA TATTCATTAA ATTTGTGACA ATAAATAATA AAATAATACC 4380

GATAAAGAAC GCTGGTAAAC TAATCGATAG TGTTGAGATC ACTCTAATCA CTTTATCCGT 4440

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TACTAATGTT GAAAATGATA TGAGTAATGT TATGGGTGCA TAGTTGAATA ATATCTGTGT 4560

TACCGGTTCT TTTGATTCAA AACTTTTTCC TAAATTAAAA TGTAATAAAT GATTCATCCA 4620

ATGCCACCAC TGTACCAATA AAGAATCATT TAATCCCAAT TTATCTTTGG TTGCATTTAT 4680

TTGTTCCGTC GACACTTGTG CTACATCAAG ATGTAATATT TTATCAACAG GATTGCCTGG 4740

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GAAAATATTT TAATTGCCTT AGATCGCTTA AGTAATTATG CAGAACTACG TTTAAGTGTA 5940

GATACTAGTA ATATCGAGGC ACAAGTATTG AGCGCTAAAT TATCTACTAC ATACGGTAAA 6000

ATTGTTAAGC CAATTATCCT TT 6022

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 476 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CCATCAATAA TGTATACATG ATTGGCATCA TATTCCCCTT TAATTAGAGA GCTACGTACA 60

GTTTGTyTTA TTAAAGTAGA ACTAATAAAT AACCATCTCT TATGTGCACA AACACTTCCC 120

GCAACAATTG ATTCAGTTTT ACCAACCCGT GGCATACCTC TAATGCCAAT CAACTTATGA 180

CCTTCTTCTT TGAACAATTC AGCTAAAAAG TCTACTAACA AGCCTAAATC TTCACGCTCA 240

AATCGAAAGG TTTTCTTATC TTTTGCATCT TGCTCAATAT ATCTTCCATG TCTTACTGCA 300

AGACGGTCTC TTAATTCTGG TTTTTTAAGC TTTGTTATTT CAATTTCATT TATACCACGA 360

GCTATTTGCT CAAAACGTTC AACTTTTTCA AGATTGTCTG TTTTAATTAA AAGGCCTCGT 420

TTACCTTGAT CAACACCATT AATTGTAACA ATACTTATAC CTAACATACC TAATAA 476

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3633 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

AGAAATACAA CGAAGCATAT AAATATAACC GATCTTTTTT CTAATTGAAT ATTAAGTAAG 60

TGTATGTACT TTCTGGAAGT AGCACCTAGT rGGATTGTtC CTCCTACAAC AGGCCAAAAA 120

TTTTTATTTT TAACTGGCTT AACAGTGTTC AGTTTTTCAT ACTCTTCTCT ACTAATTTTG 180

GCGCACCTTT TTGGAATGAA CCAATTAATA AATGGAAAAA AGTATACAAG CCAAGTTCTT 240

ATTACATCGA CCATTAAATA CTCATCATCA TACTTAATAA CTCTGTATTT CGGATTTTTA 300

TTGATAATTT CGGTTTCACA AAGCAATAAT TATCACTTCC TATTAATAAC AAATTCACAC 360

TTATATGACC TTAAATATAT AACATGAATC TTTTTGTCTA TTATTGAAGA CATATTTATA 480

AAGAAAAATA GCATTGTCAT AATAACCCAA GCAATAAATA CTATAATATT TTGGATAGAT 540

AAACTAATCA rrACATCTAA GAACATGATT gATAATCCAC CACAGAAAAA ATAAGAAAAT 600

AGTACAAAGC AAAGATTCTT GAATGATGGA AAAATCATAA TTTTTCCATT GCTACTCCGA 660

TCATTATAGA TAGATAACTT TACTTTCTGA TTTAAATATA TATAAAACAC TAGAATACTT 720

AATAATAAAA CCGAACAAAT GATAATAACG CAATTTTTTT CTAAATGAGA ATCAGGTATA 780

TATATTTTAT CTCTAAACAT AGTGCCAAAT AAAAGTATGC TACCTATAGC TGGCCATAAA 840

GCTTTaTTTT TAACTGGTTT GACAATATTT AAATTATCAA AATCTTCTCT GCTGATTTGG 900

ACATATTTTT TTGGTATTAA CCAATTAATA AACGGAAAGA ACAAAACTAA CCAGGTGCTT 960

ACTAAATCAA TCATCAGATA GTCGTTTTTA TATTTAATAA TTCTATATCT GGGATTTTTG 1020

TTTACAACTC TAACCTCGCA AAGCAATATC TCCACTTCCG TCTCGTTGGT TTTATATCTA 1080

ATACACTTTC AGATACTTTA TAAGTGTTTT GTATTTTAGT AACATACTAT TTTCCTGTTT 1140

ATTACTTAAC TTACGAACTA CAATCTAAGT TTAGTAATTT CTATTGCTTT TTAAGTTTGG 1200

CATAAACCTT TTTATTACTA ATTGAGCCCA TGCTTATTAG AAAGAAAAAA ATTGTAATAA 1260

TAATCCACAT AATAAATACC AGTAGATTTT GAGGTTTTAT AGTCATTAGC CATATTAAAA 1320

ATAATATAGA ACAACCTCCT AATAATAGAT ATGTGAAAAC TATAAAACTT CCATCTTTAA 1380

AAGTAGGCAC TAATATAACC CTATTTTCAT TATCTAGATT ATCATCATAT ATCTTTAGTT 1440

TAAGCTTTTT ATTTAAGTAA ATGTAAAATG CTGCAATACC TATAAATCCT ATAAAACATA 1500

AAGATATTAA AATCTTATTA TCTAATTGAA CTTCAAACGT ATGTACATAT TTCCGTAAAA 1560

TAACTACAAA TAAAAACGAA CTACCAGTAA CTGGCCAGAA AATATTATTT TTATTTTGTT 1620

TATCAACATT TAAATTTTCA AGTTCCTTCT CACTAAGTTT TGCATACCTT TTGGGAATGA 1680

ACCAATTAAT AAAAGGAAAA AAGTATACAA GCCAAGTGCT TACTAAATCA ATTAACAAAT 1740

ACTCATCATT ATATTGAACG ACTTTATATC TCGGATTTTT ATTAATAACC TTAATATTAA 1800

AAAGCAAAAC TCACCACGCC CATTTCATTG GATTTATATG ATTGCTAATA ATATTTTTAG 1860

CTTCACTAAC AGCATTCCCA ACACTATCCA TGGATTTTTC TGTAGTTTTT TTAACAACAT 1920

CTATACTATT ATCGATTTTA TGCCCTACCC AGTCTACTTT ATCTTTTAAT CCAAAAATAT 1980

TATTTTGATA AATTAAATCT GTTCCTAATG CAAATACTGT ACTCATAGCC AAACCTGCTA 2040

AAATCACCCA TCCTACTGGA TTACTTCCTA AAACAAAAGT CGCTAATCCA GCTCCAACTG 2100

CTGTCCCTGC AGATCCAGCT GCAAGCGTgC ATACCATTAT GCGACAACGC CTCTCCAAAT 2160

CCTTTACCTA GGTATTTTCC GCCTTTTGCA AATTTACTAC CATTTTCTAT AAACACATTA 2280

CCTGATGTAC GTTTGACTTC CACAAATGAA TTTGGACCTG CTGGGCCTTT CACTCCACCT 2340

GCTGTATTGa TAAATACACC GAATTTACTT GcATTTATAC CGTCTTGCTC TAAAAGTGTT 2400

GACGTAATAT CTAATCCTAT ATCTCTTTTA ATACTGTCTT TATTGTCATT TATATATTTC 2460

AATATACTTT TCGGGATATC GTCTTCTGGA TGTTCTTTGG CATATGCCTT TATAACAGCA 2520

AAGTCTGCTT TATTTAAAGT TTCTTTCTCT GCTTTATGTT CAATTTTCCC CATAGCAACT 2580

TTCAAATATT TTTCATGACT TGCTTTGGCC CAATCAAGTT CTTTACCTGA AGGAATATTA 2640

AATTGATTTG TTGAAAAGTT CCAAAAATTC TGCGCTTGGG TAAGTCCTTG TTGGACAATT 2700

TTTTGAAATT CTTCAACTTC TTTAAATATT TCTGGTGATT TTTGATTAAA CTCACGCAAT 2760

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TTCGATGAAA TGGCTTGCTG ATTATCGGAA GCATGCTTTT TCAAATTGTT ATTCAAATTT 2880

TCATATCGCG TAATTTGTTG ACTTAATGAT CTGATATCTT CTTCAAGCTC TGATTCTTTT 2940

AAAGATATGC TATCAACCTC ACTCGTATAA CGTGACACAA AATTaTCGCA AGCTTGCTTC 3000

GTTAAATCAC TCAATGTTTT CATACTTGTT GATAATGGAA TTAACACCGT ACTAAAAAAT 3060

TGCTTAGCTG ACGTATACGC TTTCCCTTTA AGCGCATCAT CATTAATAAA TTGAGTAATT 3120

GCTTTTTCCA ACGCATCATA ATTTGAATTC ATTGTTTGAC TCAAATTCCC CACACTTGAA 3180

GCTTGGTTTC GAGATCTGTC TAAATACATG TCAATACTCA TCGGCATGCT CCTTTTTCAA 3240

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ATTTTAAAAC TCGGCGATGA TTATTTCTTA TGTAAAGGAG TCTAGATGCA GGTAAATTGA 3360

GATAACATGT CGCCTTTTTT CTTATTTTAG CATATGGATA TAATGGTGTC TTTGTATATT 3420

CGCAATTAAT CAATAAAAAT TATCTTTCAA TATTTTAATT TTATTGCGAC AACATCCTTA 3480

ACATTAAATA TATTAATATC TCAAAATATA TTCACTATTA AAATATGTCA TCAGTTGTTA 3540

AAAGTATTTC CTCATCATGC GAAATATCAA AACGTATCTA AAATACGAAT AAGTTTATAC 3600

AATCACACAA CATCATCATT CAAAATTTTA TTG 3633

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TGATACGAAt GCATTACAAT TCATATGCAA CATACAATTC CTTCTACAGC AAATGAAGTG 60

AAACAAATAG TTGATGTGAC ATCTGTAGCA GAAAATGATA CGCATTAGTC ATAAAATTAA 120

ATGGAAATGT CGATGAAGTG TATCAGCAAT TACAGCGATT AATTAAGAAT GCTAATGTCG 180

AAGAGAGTGA GAATACTGAC AATATTAATA GTCAAGATAC AAGTTATACA CCTCAAGTAA 240

AAGTAACAAC ACCAATTTTA GTGAAAGCAC CAATCGCTGG TCGTCGTATT TTACTTAAAG 300

AAGTAAGAGA TTCAATTTTT AGAGAGAAAA TGGTAGGTGA AGGCTTAGCA ATCAAAGCTC 360

ATGAAGAATC CAAAGTAATC GCACCGTTCA ATGGTTTAAT ATCTATGATT GTACCAACTA 420

AGCATGCAGT TGGTATTCAA TCAGAAGACG GTGTGGACAT AGTCATTCAT ATTGGCGTGA 480

ATACAGTTGA CTTGGAAGGT AAAGGGTTCA AGTGCTTTGT AAAGCAAAAT GATCATGTTG 540

AAGCAGGGCA AACGTTGTTG CAATTCGACC AGCAATATAT ACAACAACAA GGCTACAATG 600

CTGACGTTAT TGTCGTTATT AGCAACTCTG CCGATTTAGG AAAAGTAGAA CTGACAATGA 660

ATGAAATCAT TACGACTGAA GATGTTATTT TTAAAATATT TAAAAACTAG GAGTGTGTTG 720

TAATAATGAC AAAATTACCG CAAAATTTCA TGTGGGGTGG CGCTCTTGCC GCAAATCAAT 780

TTGAAGGTGG ATATGATAAA GGTGGTAAAG GGTTAAGTGT AATTGATGTT ATGACGAGTG 840

GTGCACATGG CAAAGCACGT CAGATTACAG AATCTATAGA TCCCAATCAC TATTATCCAA 900

ATCATGAAGG TATTGATTTT TATCATCGTT ATAAGGAAGA TATTGCCTTG TTTAAAGAAA 960

TGGGATTGAA ATGTTTACGT ACGTCGATTG CGTGGACACG TATCTTTCCG AATGGGGATG 1020

AAGATGTGCC AAATGAAGAA GGACTCGCCT TTTATGATCG TATCTTTGAT GAATTAATTG 1080

CACAAGGTAT TGAACCTGTT GTGACGTTAT CACATTTTGA GATGCCACTT CATTTAGCGA 1140

AACATTATGG TGGATTTAGA AATAGAGAAG TTGTCGATTA TTTTGTGCAT TTTGCGCGTG 1200

TTGTATTTGA AAGATATAAA GATAAAGTTA CATATTGGAT GACGTTTAAT GAAATTAATA 1260

ATCAGATGGA CACATCAAAT CCTATCTTTT TATGGACGAA TTCTGGGGTA GCATTGACAG 1320

AAAATGATAA TCCTGAAGAA GTCyTGTATC AAGTAGCACA TCATGAACTT TTAGCCAGTG 1380

CyTTAGCAGT TCGTCTTGGT AAAGaGATtA ATCCgAaGTT TAAGATTGGr ACmATGATTt 1440

CAmaTGTACC CmTTTATCCa TAwTCGTGTC ATCCGAAAGA TATGATGGAA GCACAAATTG 1500

CGAATCGCTT ACGTTTCTTT TTCCCGGATG TCCAAGTGAG AGGTTATTAT CCAAGCTATG 1560

CTAAAAAAAT GTTGGCACGA AAAGGATATG ATGTTGGATG GCAAGAAGGG GACGACAGTA 1620

TTTTACAGCA GGGCACGGTT GATTATATTG GCTTTAGTTA TTACATGTCT ACGGCTGTAA 1680

AACATGATGT TGATACTACA GTTGAAAACA ACATCGTCAA CGGTGGTTTG AATCATTCTG 1740

GATATACATT GAATGTGTTA TATGATCGTT ATCAGTTACC ACTTTTTATT GTGGAAAATG 1860

GTTTTGGTGC AGTTGATGAA GTGGTAGATG GACATATTCa TGATGATTAT CGCATTGAAT 1920

ATTTAAAAGC ACATATTACA GCAGCGATAG AAGCAGTTGA TCAAGATGGT GTAGATTTAA 1980

TCGGTTATAC ACCGTGGGGA ATCATTGATA TTGTTTCATT TACAACCGGT GAAATGAAGA 2040

AACGCTATGG TTTAATATAT GTTGATCGAG ATAATGATGG TCATGGCACG ATGGAACGCT 2100

TGAAAAAAGA TTCGTTCTAT TGGTATCAAC AAGTGATAGC ATCAAATGGA GATAAATTAT 2160

AAAGGTATAT TATAAGTATT TTAGGGTTAG AGCCCGAGAC ATAAATTAAT ATAGTAGGAC 2220

CTACAGTGTT ATAATGGCGG gCCCCCAACA CAAAGAATTT CGAAAAGAAA TTCtAcAGGT 2280

aATGCaAGtT GGCGGGGcCC AACACAGAGA AATTCGAAAA GAAATTCTAc AGGTAATGCA 2340

AGTTGGGGAA GGACAGAAAT AAATT 2365

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11050 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CTGCGATACG ATTTGTTGAA AGTGGGGAAA ACAAAAAAGT TATCATTACC AATTTAGAGC 60

AGGCATACGA AGCTTTGATT GGTAATAAAG GTACACACAT TCACATGTAG CACTTTATCA 120

CGCGACAAAA CATTAAATAT GTTTCTCCGT TGATTCAAAT GAAAAAGTTG TCTGCTGACA 180

CTTTGCAAGG TTTGAAGGAG TTTAACTTAT GACAGAAAAC TTTATTTTGG GTAGAAATAA 240

TAAATTAGAA CATGAACTAA AGGCATTAGC AGATTACATT AATATACCAT ATAGTATATT 300

ACAACCATAT CAAAGTGAAT GTTTTGTCAG ACATTATACG AAAGGCCAAG TTATTTATTT 360

TTCGCCACAA GAAAGTAGCA ATATTTACTT TTTAATTGAA GGTAACATTA TTAGAGAACA 420

TTACAATCAA AATGGAGATG TATATCGTTA TTTTAATAAA GAGCAAGTAT TATTTCCAAT 480

CAGTAACTTA TTTCATCCGA AAGAGGTTAA CGAATTGTGT ACAGCATTAA CCGATTGTAC 540

AGTTCTTGGA TTGCCTAGAG AATTGATGGC CTTTTTGTGC AAAGCTAATG ATGATATATT 600

TTTGACACTT TTTGCATTAA TAAATGATAA TGAGCAGCAA CACATGAACT ATAACATGGC 660

ATTAACAAGT AAATTTGCTA AAGATCGAAT TATCAAATTG ATATGCCATC TATGTCAGAC 720

AGTAGGATAC GATCAAGATG AATTTTATGA AATCAAACAG TTTTTAACTA TTCAACtCAT 780

TGAAAAACTT GTTGTTAAAG ATCATAAAAA TTGGTTAGTA AGCAAACATT TATTCAATGA 900

TGTATGTGTT TAATATACAA TGTAAAATGA ATAAGTTGAA CATGAGGTCT AACGTACATT 960

TATACGTTAG GCCTTTTTTG CTAGCATGAT GAATAATTTA AAATGTTAGT TAAATTTGAT 1020

TGTTGAAATT ACAGTAAAAT TTAAGGTGAT GAAAAATTTA GAACTTCTAA GTTTTTGAAA 1080

AGTAAAAAAT TTGTAATAGT GTAAAAATAG TATATTGATT TTTGCTAGTT AACAGAaAAT 1140

TTTAAGTTAT ATAAATAGGA AGAAAACAAA TTTTACGTAA TTTTTTTCGA AAAGCAATTG 1200

ATATAATTCT TATTTCATTA TACAATTTAG ACTAATCTAG AAATTGAAAT GGAGTAATAT 1260

TTTTGAAAAA AAGAATTGAT TATTTGTCGA ATAAGCAGAA TAAGTATTCG ATTAGACGTT 1320

TTACAGTAGG TACCACATCA GTAATAGTAG GGGCAACTAT ACTATTTGGG ATAGGCAATC 1380

ATCAAGCACA AGCTTCAGAA CAATCGAACG ATACAACGCA ATCTTCGAAA AATAATGCAA 1440

GTGCAGATTC CGAAAAAAAC AATATGATAG AAACACCTCA ATTAAATACA ACGGCTAATG 1500

ATACATCTGA TATTAGTGCA AACACAAACA GTGCGAATGT AGATAGCACA ACAAAACCAA 1560

TGTCTACACA AACGAGCAAT ACCACTACAA CAGAGCCAGC TTCAACAAAT GAAACACCTC 1620

AACCGACGGC AATTAAAAAT CAAGCAACTG CTGCAAAAAT GCAAGATCAA ACTGTTCCTC 1680

AAGAAGCAAA TTCTCAAGTA GATAATAAAA CAACGAATGA TGCTAATAGC ATAGCAACAA 1740

ACAGTGAGCT TAAAAATTCT CAAACATTAG ATTTACCACA ATCATCACCA CAAACGATTT 1800

CCAATGCGCA AGGAACTAGT AAACCAAGTG TTAGAACGAG AGCTGTACGT AGTTTAGCTG 1860

TTGCTGAACC GGTAGTAAAT GCTGCTGATG CTAAAGGTAC AAATGTAAAT GATAAAGTTA 1920

CGGCAAGTAA TTTCAAGTTA GAAAAGACTA CATTTGACCC TAATCAAAGT GGTAACACAT 1980

TTATGGCGGC AAATTTTACA GTGACAGATA AAGTGAAATC AGGGGATTAT TTTACAGCGA 2040

aGTTACCAGA TAGTTTAACT GGTAATGGAG ACGTGGATTA TTCTAATTCA AATAATACGA 2100

TGCCAATTGC AGACATTAAA AGTACGAATG GCGATGTTGT AGCTAAAGCA ACATATGATA 2160

TCTTGACTAA GACGTATACA TTTGTCTTTA CAGATTATGT AAATAATAAA GAAAATATTA 2220

ACGGACAATT TTCATTACCT TTATTTACAG ACCGAGCAAA GGCACCTAAA TCAGGAACAT 2280

ATGATGCGAA TATTAATATT GCGGATGAAA TGTTTAATAA TAAAATTACT TATAACTATA 2340

GTTCGCCAAT TGCAGGAATT GATAAACCAA ATGGCGCGAA CATTTCTTCT CAAATTATTG 2400

GTGTAGATAC AGCTTCAGGT CAAAACACAT ACAAGCAAAC AGTATTTGTT AACCCTAAGC 2460

AACGAGTTTT AGGTAATACG TGGGTGTATA TTAAAGGCTA CCAAGATAAA ATCGAAGAAA 2520

GTAGCGGTAA AGTAAGTGCT ACAGATACAA AACTGAGAAT TTTTGAAGTG AATGATACAT 2580

ACCAATTTAA AAATAGAATC TATTATGAGC ATCCAAATGT AGCTAGTATT AAATTTGGTG 2700

ATATTACTAA AACATATGTA GTATTAGTAG AAGGGCATTA CGACAATACA GGTAAGAACT 2760

TAAAAACTCA GGTTATTCAA GAAAATGTTG ATCCTGTAAC AAATAGAGAC TACAGTATTT 2820

TCGGTTGGAA TAATGAGAAT GTTGTACGTT ATGGTGGTGG AAGTGCTGAT GGTGATTCAG 2880

CAGTAAATCC GAAAGACCCA ACTCCAGGGC CGCCGGTTGA CCCAGAACCA AGTCCAGACC 2940

CAGAACCAGA ACCAACGCCA GATCCAGAAC CAAGTCCAGA CCCAGAACCG GAACCAAGCC 3000

CAGACCCGGA TCCGGATTCG GATTCAGACA GTGACTCAGG CTCAGACAGC GACTCAGGTT 3060

CAGATAGCGA CTCAGAATCA GATAGCGATT CGGATTCAGA CAGTGATTCA GATTCAGACA 3120

GCGACTCAGA ATCAGATAGC GACTCAGAAT CAGATAGTGA GTCAGATTCA GACAGTGACT 3180

CGGACTCAGA CAGTGATTCA GACTCAGATA GCGATTCAGA CTCAGATAGC GATTCAGACT 3240

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GCGACTCAGA CTCAGACAGC GACTCAGATT CAGATAGCGA TTCAGACTCA GACAGCGACT 3360

CAGACTCAGA CAGCGACTCA GACTCAGATA GCGACTCAGA TTCAGATAGC GATTCAGACT 3420

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GCGACTCAGA CTCGGATAGC GATTCAGATT CAGATAGCGA TTCGGATTCA GACAGTGATT 3540

CAGATTCAGA CAGCGACTCA GACTCGGATA GCGACTCAGA CTCAGACAGC GATTCAGACT 3600

CAGATAGCGA CTCAGACTCG GATAGCGACT CGGATTCAGA TAGCGACTCA GACTCAGATA 3660

GTGACTCCGA TTCAAGAGTT ACACCACCAA ATAATGAACA GAAAGCACCA TCAAATCCTA 3720

AAGGTGAAGT AAACCATTCT AATAAGGTAT CAAAACAACA CAAAACTGAT GCTTTACCAG 3780

AAACAGGAGA TAAGAGCGAA AACACAAATG CAACTTTATT TGGTGCAATG ATGGCATTAT 3840

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TTTTTTAGGC CGAATACATT TGTATTCGGT TTTTTTGTTG AAAATGATTT TAAAGTGAAT 3960

TGATTAAGCG TAAAATGTTG ATAAAGTAGA ATTAGAAAGG GGTCATGACG TATGGCTTAT 4020

ATTTCATTAA ACTATCATTC ACCAACAATT GGTATGCATC AAAATTTGAC AGTCATTTTA 4080

CCGGAAGATC AAAGCTTCTT TAATAGCGAT ACAACTGTTA AACCATTAAA AACTTTAATG 4140

TTGTTACATG GATTATCAAG TGATGAAACG ACATATATGA GATATACAAG CATAGAAAGG 4200

TATGCGAATG AACACAAATT AGCTGTGATT ATGCCCAATG TGGATCATAG CGCATATGCT 4260

AACATGGCAT ATGGTCATAG CTATTATGAT TATATTTTGG AAGTGTATGA TTATGTTCAT 4320

CAAATATTTC CACTTTCCAA AAAGCGTGAT GACAATTTTA TAGCAGGTCA CTCTATGGGA 4380

TTATCTGCTG TGTTTGAAGC GCAAAATTTA ATGGATCTAG AGTGGAATGA TTTTTCAAAA 4500

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CAAGACTTTT TATATCAAGA CAACTTAGAT TTTATCGATT ATTTATCACG CATAAATGTT 4680

CCTTATCAAT TTGAAGATGG ACCAGGAGAT CATGATTATG CATATTGGGA TCAAGCGATT 4740

AAGCGTGCTA TAACATGGAT GGTGAATGAT TAATTATTTC TTGGAAAATA TGTGGCTGCA 4800

TTAAATACAC AGAGTGAGAG ATACAAACTA TTTACGCACG ACTAACATTT CTAAGTGTTT 4860

AAATTATTTT TGTATTAATA TGATTGGCGC AATTTGCTGA TACACAAAAA TGTTTCTCGT 4920

GAAACTTAGA TTTAGCTTAT AGTTTTATCA TCATTTGTAT GACTTACATT ATAAATTTTA 4980

TTATAATGAG GTTAACGCTT TGAAAGGAGT CATCATCATG TCGACCAATA AAAACGATTA 5040

TGAGCATATG TTGTTTTATT TTGCATATAA AACCTTTATT ACTACCGCTG ATGAAATTAT 5100

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TGGTATTACT ATTAAATCAT TACTAGAAAT ATTAGAAATT TCTAAmCAAG GATCACATGC 5220

AACACTTCAA AAATTAAAAG AGCAAGGTCT CATTATTGAA AAAGTTTTAG AGACTGATCG 5280

ACGTGTCAAA AAATTATATT CGACGGATAA AGGCGATCAA CTCATTGCTG AATTGAACAA 5340

GGCGCAAGAT GAATTATTGC AAAATATATA TCAACAAGTC GGTTCGGATT GGTATGATGT 5400

GATGGAAGCA TTGGCTAAAG GgCGACCTGG cTTTGATTTT ATTAAGCATT TGAAAGATGA 5460

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TCAAAAAGTG TATAATAAAA ACATATAATT TAATTGAACT CAGTTTCAAC ACATCTTAGA 5580

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AACCATAAAA AATTCCCGAA CACCTTGTTA TAGTGCTCGG GAATTTTTTT ATGCTTTACT 5760

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ACCCTGTATA AGATTTATCA TTTACTGGCT TCTGAATAGC GTGTTGTAGG GCTTTTGTTT 5940

GCGTTTCTAC TTCTGCGGAT TTTTCGTCTT TTTCTTTTTT AAGTAGTCTT TTTAGCTTTT 6000

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TTTTATTGCG CTCAAGCTTA CTAAGTGCAC TTTGTTGCAT ATCAGCTAAT GATGGTTCGT 6420

CTTTAGAAGC ATCTATTGCA AGTGGCATAT TTTTATCTGC AAACAAACCA AGAACTTTAT 6480

CTTTATCAGA TTTTGATAAC TCCTTACTGT TCGTGGCAAG GTCGTAACCA TCTTTTTTGA 6540

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TGACTATGTC TTCAGTGTAA AAGAGGAATT TtGAGCAATT ATGTAGTTTT AGTTAnAAAT 7260

ATGTAAACAG AGTGATTTAG AATAACAAAA aATGAATATA TATGACAATT TGTTATAGAA 7320

AGCGTTAGAA TAGAAGCGTG TGAAAATATA GAATTAAATA TAATTTGAGG TGGAAAAATG 7380

ATACTAGTAA TGTTATCTCC ATTATTAATC ATATTCTTTA TAGTGTTGTC TATTTTAGAA 7440

GAGCGTAAAC GTACGAAGAA AAAGCAACTC GAGAAAGAAA AAGCAAATAC ACTAAATCAA 7500

AATACAAATG ACACGGAAAG TTCAAATCAA GAGCCGTCAT TGCAGCAGGA TAAAGAACAA 7560

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TGAAGATGAT TTTGTTATAG CAGAGAGTTT AGCATCTGAA CTTAAAAAAT GGAATTACGG 7680

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GCTTGTATTG CTAGATATTA ATTTGCCAAC GTTAAATGGT TTTCATTGGT GTCAAGAAAT 7800

CCGAAAAACA TCTAATGTGC CAATTATATT TATTAGTTCC CGTATTGATA ATATGGACCA 7860

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AGaTAAATAT GTAAGTAGrA CTGCTTTAAT TGaAAAATGT TGGGaATCAG AAAACtTCAT 8160

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CAATTATTAT GAAATATTCA ATACAGTTTA TTGATCAAAA AACAAAAATC CATTATGAAC 8820

CTTGTCATCA CGAAGTATTA ACTGACGTTA GATGGACCTC TTTAATGATA GAACAATTAA 8880

TAAATAATGC ACTTAAGTAT GCGAGAGGTA AAGATATATG GATTGAATTT GATGAGCAAT 8940

CCAATCAATT ACACGTAAAA GATAATGGTA TCGGTATTAG TGAAGCGrAC TTGCCTAAAA 9000

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TGTAAGTATA CTAGTAACAT TTTTTTACTA ATTTAAATGT TATTAGTATT TTTTTGTTTT 9240

AATATAGAAC TAACAAAGAA ATGAGGTGCA TGCCATGTTG CTAGAAGTGn AACATGTAAA 9300

AAAGGTTTAT GGTAAAGGTT TGAATGCTAC GACAGCACTT AATCAAATGA ATTTATCAGT 9360

TGGAGCTGGT GaATTTGTTG CaATTATGGG TGAGTCTGGG tCAGGGAAGT CTACACTACT 9420

AAATTTAATT GCtTCTTTTG ATGGACTAAC TGAAGGTGAC ATTATTGTGG ATGGCGCACA 9480

TTTAAATAAT ATGAAAAATA AAAGTAAAGC ATTGTATCGT CaACAAATGG TAGGTTTTGT 9540

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AATTTTAGCT GGTGCTAAAC GAAAAGATAT AGAACAAAGG GTACATCAGT TGGCAGTACA 9660

ATTACATTTA GAGGGATTCT TAAACAAGTA TCCTTCTGAA ATCTCTGGGG GTCAGAAGCA 9720

ACGCATTGCC ATTGCACGTG CATTAGTTAC TAAGCCGACG ATTTTACTAG CCGATGAACC 9780

TCAATTGGAA CAGACAATTT TAATGGTAAC TCATTCAAAT ATCGATGCGT CTTATGCAGA 9900

GCGAGTCATT TTTATTAAAG ATGGGCGTCT ATATCATGAA ATATATCGTG GTGAAGAAAG 9960

TCAATTAGCT TTTCAACAAC GAATAACAGA TAGCTTAGCA CTTGTGAATG GAGGAAGTGT 10020

CAATATATGA AGTTAAGATT GTTATGnACA TAGTGCGACG TCAATTTATT ACGCAGCGAC 10080

TTGTAATCAT TCCATTCATT TTAGCGGTAA GTGTACTATT CATGATTGAA TATACGCTTG 10140

TGTCAATTGG GTTAAATAGC TACATAAAAC AGAAGAATGA CTTCCTAGTA CCATTTATTA 10200

TCATAGCTAA TTTTTTTATG GCGCTTTTAA CTTTTATTTT TATTTTCTAT GCAAATCACT 10260

TTATGATGTC ACAAAGACGA AAAGAGTTTA GCATTTTTAT GACATTGGGC ATGACCAAGA 10320

AAAGTATGCG TTTAATTGTA GTGATGGAAA CTATCTTACA ATTTGTGATA ATTTCAGTCG 10380

TTAGTATTGC CGGCGGATAC TTACTTGGTG CGATATTTTT CTTGTTTATA CAGAAAATAA 10440

TGGGCAGTGA AGTTGCGACG TTAAGGTATT ATCCATTTGA CTCTGTAGCG ATGTTTATTA 10500

CTTTGATTAT CATTGCTGTA TTAATGGGCA TGCTACTTAT ATTCAACTTG TTTAGTATTA 10560

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ACAACAAGAT ACGACGTTTG GTGCCTTTTT TAAAATATGG ATTGTCATAG GATTAGTTAT 10740

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GGTATCAAAA GTTTACTATC ATCCACGGTA TTTTTTTGTG GTAGTTGGGA TGCGTGTACG 10860

TCTTAAAATG AATGCAGTCA GTCTTGCAAC AATCACTTTG CTGTGTACAT TTTTGATTGT 10920

AACGCTCACA ATGACATTAA CAACCTATCG TGATATGAAT CATACCATTA CGAAATTGAT 10980

TACGAATGAT TakGATTTGT CATTTAGCGA CAATTCTAAG TCACAAaTAG AACGTCAACA 11040

AACAATTGAG 11050

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 983 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CGACATAACG AGGCAAGGGT ACATGATACT TTAGCCTCGT TTTTGATATG TATTTTTCTG 60

AATATAAGGG CAATAGATGG TATTTTATAw TTTTTTTAAG GTAGTGATTA ACATAGATAT 120

TCAAGCGGAA CAGCATTATG CACCAGTATT AACGCATTTT TTAGATCCAA GAGGGCAATA 240

TATATTGGAA GTGATTTGTG GCAGTTATGA AGATTTAAAC GTATCTTTTT ATGGTGGACC 300

TAATGCTGAA AGAAAAAGAG CAATCATTTC GCCGAACTAT TATGAACCTA AAGAAAGCGA 360

CTTTGAATTA ACTTTAATGG AAATAGATTA TCCTGAAAAA TTCGTCACTT TAAAACATCA 420

ACATATTTTA GGGACATTAA TGTCTTTAGG TATCGAACGC GAACAAGTTG GAGATATAAT 480

TGTGaATGAA CGAATTCAAT TTGTTTTGAC AAGTAGATTG GAATCATTTA TTATGTTAGA 540

ATTACAACGT ATTAAAGGCG CATCAGTTAA ACTTTATACT ATTCCAGTAA CAGATATGAT 600

ACAATCTAAT GAGAATTGGA AAAATGAAAG TGCaCAGTTA GTTCTTTAAG GTTAGATGTT 660

GTTATTAAAG AAATGATACG TAAATCACGT ACGATTGCGA AACAACTAAT CGAAAAAAAA 720

CGTGTTAAAG TGAATCACAC TATTGTTGAT TCAGCAGATT TTCAATTACA AGCAAATGAT 780

TTAATATCCA TCCAAGGTTT TGGTAGAGCA CACATTACTG ACTTAGGTGG TAAAACTAAA 840

AAAGATAAAA CGCACATTAC CTATAGAACA TTATTCAAAT AGTAATGATT TAAGGAGGAT 900

AACAAATGCC TTTTACACCA AATGAaATTA AGAATAAAGA GTTTTCACGT GTaAAGAATG 960

GTTTTAGAAC CTACTGnAGT TGG 983

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

TTTTGCAAAG CTTATTTTAT GTCAAACAGA TAGTCAATGT GAAACAAAGG TTAGTACATA 60

TAATCATCCA GACTTTATGT ATATATCAAC AACTGAGAAT GCAATTAAGA AAGAACAAGT 120

TGAACAACTT GTGCGTCATA TGAATCAACT TCCTATAGAA AGCACAAATA AAGTGTACAT 180

CATTGAAGAC TTTGAAAAGT TAACTGTTCA AGGGGAAAAC AGTATCTTGA AATTTCTTGA 240

AGAACCACCG GACAATACGA TTGCTATTTT ATTGTCTACA AAACCTGAGC AAATTTTAGA 300

CACAATCCAT TCAAGGTGTC AGCATGTATA TTTCAAGCCT ATTGATAAAG AAAAGTTTAT 360

AAATAGATTA GTTGAACAAA ACATGTCTAA GCCAGTAGCT GAAATGATTA GTACTTATAC 420

TACGCAAATA GATAATGCAA TGGCTTTAAA TGAAGAATTT GATTTATTAG CATTAAGGAA 480

ATCAGTTATA CGTTGGTGTG AATTGTTGCT TACTAATAAG CCAATGGCAC TTATAGGTAT 540

GAATGGTTTC TTCGAAGATA TCATACATAC AAAGGTAAAT GTAGAGGATA AACAAATATA 660

TAGTGATTTA AAAAATGATA TTGATCAATA TGCGCAAAAG TTGTCGTTTA ATCAATTAAT 720

TTTGATGTTT GATCAACTGA CGGAAGCACA TAAGAAATTG AmTCAAAATG TAAATCCAAC 780

GCTTGTATTT GAACAAATCG TAATTAAGGG TGTGAGTTAG ATGCCAAATG TAATAGGTGT 840

TCAGTTTCAA AAAGCGGGAA AATTAGAATA TTATACACCT AATGATATAC AAGTAGATAT 900

AGAAGACTGG GTAGTTGTCG AATCTAAAAG AGGCATAGAG ATAGGTATTG TTAAAAATCC 960

ATTAATGGAT ATTGCTGAAG AGGATGTTGT GTTACCTCTT AAAAATATTA TTCGCATTGC 1020

TGATGACAAA GATATTGATA AATTTAATTG TAATGAACGA GATGCTGAAA ATGCATTAAT 1080

ACTATGTAAA GACATTGTAA GAGAACAAGG TTTGGACATG CGTTTAGTCA ATTGCGAATA 1140

TACATTAGAT AAATCGAAAG TTATTTTTAA TTTTACGGCG GATGATCGTA TTGATTTTAG 1200

AAAATTAGTA AAAATATTAG CGCAACATTT AAAAACACGT ATCGAGTTGA GACAAATTGG 1260

TGTAAGGGAT GAAGCCAAAT TGCTTGGCGG TATCGGACCT TGTGGTAGGT CGTTATGTTG 1320

TTCTACATTT TTAGGGGATT TTGAACCAGT ATCGATTAAG ATGGCTAAGG ATCAAAATTT 1380

ATCATTAAAT CCAACTAAAA TTTCTGGTGC ATGTGGTCGT TTGATGTGTT GTTTAAAATA 1440

TGAAAATGAC TATTATGAGG AAGTACGTGC ACAATTACCT GATATTGGTG AAGCAATTGA 1500

AACGCCTGAT GGTAACGGGA AAGTAGTTGC TTTAAATATA TTAGACATTT CTATGCAGGT 1560

GAAGCTTGAG GGACATGAAC AGCCACTTGA ATATAAATTA GAAGAAATAG AAACTATGCA 1620

TTAAGGAGGC ATTATTACAT TTGGATCGCA ATGAAATATT TGAAAAAATA ATGCGTTTAG 1680

AAATGAATGT CAATCAACTT TCAAAGGAAA CTTCAGAATT AAAGGCACTT GCAGTTGAAT 1740

TAGTAGAAGA AAATGTAGCG CTTCAACTTG AAAATGATAA TTTGAAAAAG GTGTTGGGCA 1800

ATGATGAACC AACTACTATT GATACTGCGA ATTCAAAACC AGCAAAAGCT GTGAAAAAGC 1860

CATTACCAAG TAAAGATAAT TTGGCTATAT TGTATGGAGA AGGATTTCAT ATTTGTAAAG 1920

GCGAATTATT TGGAAAACAT CGACATGGTG AAGATTGTCT GTTCTGTTTA GAAGTTTTAA 1980

GTGATTAATC AAGCACACTC AAATAGTGTT ATAATTATAA ATGAATATGG TTTGGATAAG 2040

TCTGAGACAA TGCATGTTTC AGGCTTTAAT TGTGTATAAA GTTTTGGTGA TTGCATAAGA 2100

GATGGCGGTA CTAAATGTTA TTATTAAGTG TGCACGCAgT ATCaTTAGTT ATAAAATGTA 2160

GCTGTTAAAA GTCAAAAATA CATCGAATGT AGTTAGGCAT ATAATATAAA AAGAGTTTTC 2220

AATTACTCAA TAGAAAAAGG TTGTCTTCAT AGGAGTTAAA AATGTTAAAA GAGAATGAAC 2280

GATTTGATCA ACTAATCAAA GAAGATTTTA GTATTATTCA AAATGATGAT GTTTTTTCAT 2340

TGGACTTATG TTCAGGCAAT GGGGTGATAC CCTTGTTATT GTTTGCGAAA CATCCACGAC 2460

ATATAGAAGG TGTTGAGATT CAAAAAACAC TTGTCGATAT GGCGCGACGC ACATTTCAAT 2520

TCAATGATGT TGATGAATAT TTAACAATGC ATCACATGGA TTTGAAAAAC GTTACTAAAG 2580

TATTTAAACC TTCACAATAT ACTTTAGTAA CGTGTAATCC GCCTTATTTT AAAGAGAATC 2640

AGCAACACCA ACATCAAAAA GAAGCACATA AGATAGCGAG ACATGAGATT ATGTGTACAC 2700

TTGAAGATTG CATGATTGCA GCCCGTCATT TATTAAAAGA AGGTGGCAGG CTAAACATGG 2760

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CTAAGAAAGT CGTTTTTATA TATAGTAAAG TAGGGAAATC AGCACAAACG ATAGTAGTAG 2880

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ATTGTAAAAT GTAGTGATGG AAGTTTATAT ACAGGATACG CTAAAGACGT TAATGCACGT 3060

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AAAACTTATA CCAGACAAAA GAAATTGCGA TTAATTAAGG AGCGATAGTA TGGCTGTATT 3240

ATATTTAGTG GGCACACCAA TTGGTAATTT AGCAGATATT ACTTATAGAG CAGTTGATGT 3300

ATTGAAACGT GTTGATATGA TTGCTTGTGA AGACACTAGA GTAACTAGTA AACTGTGTAA 3360

TCATTATGAT ATTCCAACTC CATTAAAGTC ATATCACGAA CATAACAAGG ATAAGCAGAC 3420

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ATTGCCCTTA ATTAGTGATC CTGGATACGA ATTAGTAGTG GCAGCCaGAG AAGCTAATAT 3540

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ACCTTCATAT GTATATACAT TTTTAGGATT TTTGCCACGA AAAGAGAAAG AAAAAAGTGC 3660

TGTATTAGAG CAACGTATGC ATGAAAATAG CACATTAATT ATATACGAAT CACCGCATCG 3720

TGTGACAGAT ACATTAAAAA CAATTGCAAA GATAGATGCA ACACGACAAG TATCACTAGG 3780

GCGTGAATTA ACTAAGAAGT TCGAACAAAT TGTAACTGAT GATGTAACAC AATTACAAGC 3840

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TAAAGCGAAC AATGAGATAT CGTGGTTTGA TGATTTATCT ATCAATGAGC ATGTTGATCA 3960

TTATATTCAA ACTTCACAGA TGAAACCAAA ACAAGCTATT AAAAAAGTTG CTGAAGAACG 4020

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GTTTTTTAAT GTAAAATAAA TACATTGAAA GTAATAAATA CCTTAACATT GAATAAGATG 4260

AAAATGAGAT GACGAGATAA ATGTTCGCGT CCGTTGAAAT GCATAGAAAT CTTAGATATT 4320

ATTTGAAGTG AGACATTACG AGGAGGAACA GTTATGGCTA AAGAAACATT TTATATAACA 4380

ACCCCAATAT ACTATCCTAG TGGGAATTTA CATATAGGAC ATGCATATTC TACAGTGGCT 4440

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GAACGTTTAT TAAAGCAAGG TGATATCTAT TTAGGTGAAT ATGAAGGTTG GTATTCTGTT 4740

CCGGATGAAA CATACTATAC AGAGTCACAA TTAGTAGACC CACAATACGA AAACGGTAAA 4800

ATTATTGGTG GCAAAAGTCC AGATTCTGGA CACGAAGTTG AACTAGTTAA AGAAGAAAGT 4860

TATTTCTTTA ATATTAGTAA ATATACAGAC CGTTTATTAG AGTTCTATGA CCAAAATCCA 4920

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TTACCGTTAC CTAAAAAAGT CTTTGCACAT GGTTGGATTT TGATGAAAGA TGGAAAAATG 5280

AGTAAATCTA AAGGTAATGT CGTAGACCCT AATATTTTAA TTGATCGCTA TGGTTTAGAT 5340

GCTACACGTT ATTATCTAAT GCGTGAATTA CCATTTGGTT CAGATGGCGT ATTTACACCT 5400

GAAGCATTTG TTGAGCGTAC AAATTTCGAT CTAGCAAATG ACTTAGGTAA CTTAGTAAAC 5460

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AGAACGAATA AGTATATTGA CGAAACAACG CCTTGGGTAT TAGCTAAGGA CGATAGCCAA 5700

AAAGATATGT TAGGCAATGT AATGGCTCAC TTAGTTGAAA ATATTCGTTA TGCAGCTGTA 5760

TTATTACGTC CATTCTTAAC ACATGCGCCG AAAGAGATTT TTGAACAATT GAACATTAAC 5820

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ATGCTGAACA TGTTAAGAAG TCAGATAAGC TTTTAAAAAT TCAAGTAGAC TTAGATTCTG 6120

AACAAAGACA AATTGTATCA GGAATTGCCA AATTCTATAC ACCAGATGAT ATTATTGGTA 6180

AAAAAGTAGC AGTTGTTACT AACCTGAAAC CAGCTAAATT AATGGGACAA AAATCTGAAG 6240

GTATGATATT ATCTGCTGAA AAAGATGGTG TATTAACCTT AGTAAGTTTA CCAAGTGCAA 6300

TTCCAAATGG TGCAGTGATT AAATAACTGT ATTTTTAAAA ATTAGGAGAG ATAATTATGT 6360

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AAACCGATGC ACCGTATCTT TCGCCACATC CGTATAGAGG GAAGCGAAAT GAACCGGCGA 7020

GAGTAACTTT AGTAGCTGAA CAAATTGCTG AATTAAAAGG CTTATCTTAT GAAGAAGTGT 7080

GCGAACAAAC AACTAAAAAT GCAGAGAAAT TGTTTAATTT AAATTCATAA AGTTAAAAGT 7140

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TGATATTGAT GCACAAACTG GGGTGATTGA AATTGGTCCA GGCATGGGGT CATTGACAGA 8040

ACAATTGGCC AGACATGCTA AAAGAGTATT GGCATTTGAA ATTGATCAAC GTTTAATACC 8100

TGTATTAAAT GATACACTAT CACCTTATGA TAATGTGACG GTGATTAATG AAGATATTTT 8160

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TATACCAATT GATGGCTACG TGGTGATGAT GCAAAAAGAA GTGGGCGAAC GCTTAAATGC 8340

TGAAGTAGGT TCAAAAGCAT ATGGTTCGTT ATCAATTGTC GTACAATACT ATACAGAGAC 8400

TAGTAAAGTA TTAACGGTAC CTAAATCTGT ATTTATGCCA CCACCTAATG TTGATTCAAT 8460

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CAACTTTGAG AGAGTATCTT ATACATACAC TGATGTGTTA ACTGaAAATG TTCAAGTTTC 9060

ATTTGAAGAG GATAATCATC ACGAATCAAT TGCACACTAA ATAAGACATA TAGAGATGTT 9120

AGACGTTTCT TAGTATAAGA AGTAAATATT ATGATAATTA TTTGAGTGTT GGGcATTATG 9180

TTCAATACTC TTTTTATTTA CAAAATGTTT AACACTGATG TTTCGCTTAT AGATTTTTCA 9240

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GGGTTGAAAA GATGAGATAT AAACGAAGCG AGAGAATTGT TTTTATGACG CAATATTTGA 10320

TG 10322

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5614 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GATTGATTAA ATGTTTTAAT CCACTTCAAT GCCTTCGATA AACTCTACAA TCGCGCTATT 60

CATATAATTA TTCGATTTCA TTTGTTCAGC ATATGTCTCA TTAAATCCAG ACATAACTTT 120

TTTAAAwGCG AAAATTGAAA TTGGTATCGT TACTAATAAG GCACTAGCCA TACGCCAATC 180

AATGAGCATT ATGTATAAAA AGATAGCAGC TGACAAAAGT AAGTTTCCTA TAACTTCAGG 240

AATCATATGT GCTAAAGGTA ATTCTATTGT TTCAACCTTA TCGACAAATA TATTTTTTAA 300

TTCACCTATT TTCTTAGATT CCaCTACGCC TAAAGGGAGA CGCATTAATT TTTGAGCTAA 360

TTTTTTACGA ATTTCAGATA AAATTTCATA TGCCGTAATA TGTGATAGCA TCGTTGACGC 420

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CGAATTAATC GTATATGTAT TGTTAATCAT CATTAAAATA ATTTTAAATA CTGCCCAATA 540

AGGAACTAAT CCAGAAAAGA CACTGATGAT AGACAACAAA ATTGATAACA TAATTTTCCA 600

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GATGATATAC ATAATATAAA TTTGTTATTT GTTAAAAATT AATACTTATT ACAAGTACAT 780

CATATATTAG TTGATAACGA TTATCAATGT CGCGTGGATT TGTGACACAT TTCTTTTAAA 840

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TCTAATGATC CTATGACTCA ACTATTAAAT CATTTTTCGA AATACTTAAT TCTAATATAA 1140

TTAAATTCAT TTATTGTAAT ATTGCAAAAA TACATTGCAC ACCTTGTTCA TCAATGCTAT 1200

AATTAATTAC ATAATAAATT GAACATCTAA ATACACCAAA TCCCCTCACT ACTGCCATAG 1260

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TAAATTGAAC ATCCGTCATA CACCTCCTCT CTGCGTTAAA GTAACGCCCG AGATGTTAGG 1440

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CAATGTGTAA TAATTTTAAC AGCAATAAAT AGACAACATA ATAATTTAAC GTATTAATGC 1860

CGCCAACAAT GATAAATTTT AAAATTTCAG CATGCGTTTG TGTTAGTTTC ATATGTGTAc 1920

TCCTCAACAT CAAAATATAT GCATAACTAC GTTCTCGAAC ATACTCGAAT ATGCGAGCCA 1980

ATCCGCTTCA CTTCAAATAT GCTTATTTCA ATCTTTATAC CCTTTCACAG CAAATTTAGT 2040

CTCTTTCCCC TCATCCTTAT ACGCCATTAT AATGTAACTG ATTTATCGCG TGACTCATTA 2100

GCACTATAGA GATTACTTTA GTTCACTAGT AATTTTATAT ACAATAAGAG CGACAACAGT 2160

AATGAGAGGA TGTCTACTAT GCAATTACAA AAAATTGTCA TCGCTCCTGA CTCATTTAAG 2220

GAAAGTATGA CCGCACAGCA AGTTGGCAAT ATTATAAAAC AGGCTTTTAC TAATGTTTAT 2280

GGGAATACCC TTCATTATGA TATCATTCCG ATGGCTGATG GTGGTGAAGG TACCACAGAT 2340

GCTTTAATGC ATGCAACAGG TGCCACTAAG TATACAGTCA TCGTTAATGA CCCTTTAATG 2400

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GTAAAGTTTA CTGATGTAAA CGGGGACTTA TTACAAATGA ATGGTGCTAA TCTTGCTCAC 2700

ATTGCACAAA TCGATATAAC CAATCTAGAT TCGCGATTAA AAGAGGTGAC CTTTAAAGTG 2760

GCCTGTGATG TTTCAAATCC TTTATTGGGT GAAAATGGTG CTACCTATAT TTATGGTCCT 2820

CAAAAAGGCG CTGATGCAAA GATGATACCA AAGTTGGATT TCGCAATGTC GCATTATCAT 2880

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GGCGGTATGG GCGCAGCATT ATTAGCGTTT TGTGAGACAA CTTTAACAAA AGGTATTGAT 3000

GTCGTCTTTG ACATTACAGA TTTTCATCAA AGAATTAAAG ATGCAGACCT CGTTATTACT 3060

GGAGAAGGAC GCATGGATTA TCAGACCATC TTTGGTAAAA CACCCGTAGG CGTTGCGTTA 3120

GCTGCAAAAC AATATCATAT TCCTGTCATC GCGATTTGTG GCAGTCTAGG CGAAAATTAT 3180

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CGTATTCTGA AATTACAATA ATGTCAAAGT AAATCATCAG CTTTATTATT TGCAGTTAAA 3360

ACTTGAATGA GGTGAAACCC ATGAAAAGAA CTGATAAATA CCGTGATTCA TATCAATACG 3420

ACAATCAAAA CCAAAATCAT CGTCGTCAAT CTGAAGACGC ATCGTATAGA CAACAATATG 3480

CTAAAGGCGA TCCTGAAGAA CACCCGGAAC GATACTATAA TGGTAGAGAT TATCGAAGAG 3540

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AAAAAACTGA TGACATTATT AAAAATTTAC AAAATCAAAT CGACAACTTG AAGCAGCAAG 3840

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CAGAGGCAAA TAATGCACTT AAAAACAATG CAAGCCAAGG TAAAATTGAA AGCATGTTAA 3960

ATGATATTAA TACAAAATTC GACAGTATTA AATCTAAATT AGAAAGCTTA TTTAAAGATG 4020

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TTATTGCTAA TTACGTTAGG CGTCATGACC GCTTTTGGCC CACTAACTAT AGATATGTAC 4320

GTACCATCAT TACCTAAAGT GCAAGGTGAT TTTGGTTCTA CTACATCAGA AATTCAATTA 4380

ACATTATCAT TCACAATGAT TGGTCTTGCA CTAGGCCAAT TTATCTTTGG ACCTTTATCC 4440

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TTAACTGGTG GTGGCGTCAT CGTGATTGCA AAAGCCTCTG CTGGTGATAA ATTTAGTGGC 4620

AACGCACTCG CTAAATTTTT AGCATCTTTA ATGGTAGTTA ATGGCATCAT CACTATTCTT 4680

GCACCATTAG CCGGTGGATT AGCTTTATCC GTAGCAACAT GGCGTTCTAT TTTCACAATT 4740

TTAACTATTG TGGCACTCAT CATTTTAATT GGCGTCGCTT CTCAATTACC TAAAACATCT 4800

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AAAAAACCAG CATTTATTAT TCCAATGCTA TTACAAGGwT TAACTTATGT AATGCTATTT 4920

AGTTATTCAT CTGCATCGCC ATTTATTACT CAAAAATTGT ATAATATGAC ACCCCAACAA 4980

TTTAGTATCA TGTTTGCTGT TAACGGTGTA GGTTTAATCA TTGTCAGTCA AGTCGTTGCT 5040

TTATTAGTAG AAAAATTACA TCGCCACATA TTATTAATCA TTTTAACTAT TATACAAGTG 5100

GTAGGTGTTG CTTTAATTAT CCTGACACTT ACATTCCATT TACCACTTTG GGTCTTACTC 5160

ATCGCATTCT TCTTAAATGT GTGTCCTGTG ACGTCAATTG GACCGCTTGG TTTCACAATG 5220

GCTATGGAAG AACGAACAGG TGGCAGTGGT AACGCATCAA GTTTACTTGG CTTATTCCAA 5280

TTTATCTTAG GTGGCGCTGT TGCACCATTA GTTGGCTTAA AAGGCGAATT TAATACATCA 5340

CCATATATGA TTATTATCTT CATTACAGCC ATTCTATTAG TCAGTCTACA AATCATTTAC 5400

TTTAAAATGA TTAAAAAGCA ACATGTCGCA TAACACTTCA ACATAATTAG AACCCTAGCA 5460

AAGATATCTA TCTTTGTCAG GGTTCTTCTT TATGAATTAT GAGATCGAAT CTTCAACTAA 5520

AATTACGCCT TCATAGCAAG GACATTTCTA TTCAATCACC CTTTAACAGG CATCCAAATT 5580

TcTGTAATAT ATTTTTCACT TGTAGTATCA CCAT 5614

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

AAAGACAATG ATATGAAGTA TATGGATATC ACAGAaAAAG TGCCAATGTC GGAATCTGAA 120

GTTAACCAAT TGCTAAAAGG TAAGGGGATT TTAGAAAATC GAGGGAAAGT TTTTCTAGAA 180

GCTCAAGAAA AATATGAGGT TAATGTCATT TATCTTGTTA GCCATGCATT AGTAGAAACA 240

GGTAACGGCA AATCAGAATT AGCAAAAGGC ATTAAAGATG GGAAAAAACG CTATTACAAC 300

TTTTTTGGTA TAGGAGCATT CGATAGTAGT GCTGTTCGTA GTGGGAAAAG TTATGCTGAA 360

AAGGAACAAT GGACATCACC AGATAAGGCG ATTATTGGTG GTGCAAAGTT CATTCGTAAT 420

GAATATTTTG AAAACAATCA ACTGAATTTA TATCAAATGC GATGGAATCC AGAAAATCCT 480

GCGCAACATC AATATGCGAG TGACATTCGC TGGGCAGATA AAATTGCCAA ATTAATGGAT 540

AAATCCTATA AGCAGTTTGG TATAAAGAAA GATGATATTA GACAAACATA TTATAAATAA 600

GACATCGGTG CTTAAAGGAG CTGGAACAAT TTATTGTTTC GAGCTCCTTT AGCGCATTCT 660

GAGTGTGTTA GTTAAATGGA TTTTAACCTA ACAAAAAACG CTATATAGCA TCAAATATGC 720

TATATCCCAC ATCATTGTTA CAAATGTACA TGATGTAAAT GAATATTGCT GTCTAAATGT 780

GCATGTAATA TACAATGGTG CAGATAATAC ACTTAAGTCC TTAAAAATGA AACGTTAgTT 840

CCAAGAGTCA TTTTTAAACA ATAGTGCATG TGATAAAATA GAAAAGAATG AAAAATATAG 900

AGGTGACAAT ATGAAGATAG CAATTATAGG TGCAGGCATC GGTGGATTAA CAGCTGCTGC 960

ATTATTACAA GAACAAGGTC ATACTATTAA AGTCTTTGAA AAAAATGAGT CAGTTAAAGA 1020

AATTGGCGCT GGGATTGGTA TCGGAGATAA TGTGCTTAAA AAACTAGGTA ATCATGACTT 1080

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AGATCGCCTG TTAACTACTG TTAAATTAAA AAGTAATACA TTGAATGTGA CGTTACCACG 1200

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TGCCCAATAT CGTAGTCGTT TATTTGTTGC AGTTAGAAAT CGTATTATGA AAATGATGCC 1980

AAATGCATTA GCAGCTGGAC AAACTAAATT CTTATATAAA TCGAAAGAAA AATAATACAA 2040

CAATATGAAA ACCCCCGTAT GTTGAAACGA GAGCTCAACA TATGGGGGTT CTTGTTTTTA 2100

TAATGTTATT ATAATAAATT CAATTATTAG TTAACGACAA ATTGTGGTTT CTCACCTTGA 2160

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CAATTAAATT AGATAACGTA GTTTTAAAGT TAATAGTATT AGAAAAAATT AATATTTTGA 3300

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CTATAAAGGA AAGCTCAAAG TTTTTTGATG ACATATGTAC TAGAATTAAG TTTCAAGACA 3420

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GTAATTTGTA TAATTTTCAG CAGCATCTGC ATGATGTGCT TGACCTACTA ATGCTGTGCC 3900

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AAGAATAAAA AAACTTTGAC TAATTTTGTA ATAAAAATTA GTCAAAGTTA CAATGAGATT 4140

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GGTATTATAT ATTCTTGGCC ATTATAATAT TTGACACACG CAATAATTGT GAATACAAAA 4260

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GCAGTAATTG TAATTGCATC AACCATTTTA GAGAGAGACT TCTTTGAGGA AGGCTTAACA 5880

GTTGAAGAAA TTGGTTTAGA TAAGCTTGAT TTAGAAAAAT ATTTAAAATA AATGATGGCT 5940

TGAAGATAGA AAAGGATATA GCATTATGCA AAAGCAATAA ATTGAAGAAA AGAGGTTTCT 6000

CATCAATAAG CGnAGGGGAC GATAGATGAT GAAAAGAAAA CCCACCTTTT TAGAATCAAT 6060

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AATTCAAGTA TTATTAATTA TTGCCTCAGC ATATGCCACA TGGATTGCAA AACGTGTAGG 6180

CTTAACATGG CAAGATTTAG AAAAAGGCAT TGCAGAACGT TTAAATACTG CAATGCCTGC 6240

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TGCAGGGATT GCACTTATTT CTATTGGTAA TCAATTGGGG ATTCCTCCAG GGATGGCAGC 6480

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AAGTGTATAA GTTACGTCCT GAAGTATAAC CACTTGAGAT TGAACGGCCA TTTGATGATG 8220

GAGCCATAGT TGTAGTTACT TGAACATTGT TGCTTGAAGT GCTGTAGCTT GCACCTAAAC 8280

CACCAGTACG GTAGCTGTTT GTGTTGTAAC TATTATAGTT ATTGTAGTTA TATGATTGAT 8340

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ATTGACTTGG ATGCCAGTTA CCTTTCCATG TGTAATGGTA GTTACCTTGT GCATCAATAG 8520

TGTAAGTATA GCTATATGAT GTTGGGTCGT TTGGATTATA ACCGTAGTTA TCTTGCTCAG 8580

AAGCATGAGC TTGATTTCCT GATGCAATTG CGATTGTAGC GAATCCTGCA GTTGCGATAG 8640

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GGATGAAAAT GTATATTTAA TGGATAAAAT ATCCTAATTT AGCATAAAAA AATGTTTTAA 9120

TAAAAGTATT ATTTGATATA ATCGATTTAT GTTTTGTTAC TGCTAAAAAA CATGTGGCG 9179

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1868 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CCTTCAGCCA TTTGACTTCG ACATGAGTTG CCTGTACATA TAAAATAAAT TGTTTTTTTA 60

GTCATAACAA TCTCCTAATT AATTAAAATA TGATAAGTGT TAGATACAAC CCTATGAGGG 120

TTATAAATAG TACTGGAATT GTAATGATGA TACCAGTTTT AAAGTATGTG CCCCAAGAAA 180

TCTTAACATC TTTTTGtGTT AAGACGTGTA ACCACAGTAA TGTAGCTAAA GAGCCTATCG 240

GTGTAATTTT TGGACCTAAA TCAGAACCGA TAACATTCGC ATAAATTAGG CCTTCTTTTA 300

ACATGCCATG GACATTTGAT TGACCAATAG CAATCGCATC TATTAAAACT GTAGGCATAT 360

TATTCATTAT TGATGATAAA AACGCTGAAA TGAAGCCCAT TCCCAAAATA GTGCTAAATA 420

GACCGTAATT GGAAATATAT TCTAATATTT TAGCCAATAT TAAAGTAATG CCAGCATTTC 480

TTAAGCCGAA TACGACGATA TACATACCAA TTGAAAATAA TACTATATTC CAAGGTGCGC 540

CCTTAATGAC TTGCTTAATA TTTACAGCAT TTGATTTACG AGCCAACATT AGAAAAATAA 600

AAGCAATGAT TCCAGTGAAA ATTGATACCG GAATTTTAGT AAATTTACTG ATTAGATAGC 660

CGAAAAGTAA TATAACTAGA ACAATCCaTG AAATTTTAAA TAGCTTTAAA TCATTAATGG 720

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TGTTCCTTTG GTATATTACA CGATATGACT ATGTAATTTA AATTTGGTTT TAGTATTAAA 1800

AGGGTATTAA AGATAAAATTA TAGATATTGA TTTTGCAAAA TATACTCTTT GTTCTGCATT 1860

GAAAAAGG 1868

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

ATTTATGAAA TCCATAGCnA TAAACATTAT TCTTGCATCG GCTATACAAA CAGTTACCGC 60

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GTTCTGAACC CAGCTCGCGT ACCGCTTTaA TGGGCGAACA GCCCAACCCT TGGGACCGAC 15180

GTGGAACTT 15249

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14051 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

GTGGCAATAT TTCTAGTTCT CGTTTTGATA AGATTTTAAA AGGATCTGTT GTGTTTGCAG 60

TGTCCTGATT TGAATTAGAT ACAAATTCAT TCACTAAAGA TGTTGTAAGT TTCATATCTA 120

CATATGTTTC ACCTTTATAT ACAGTTCGAA TAGCTAACAA TAATTGTTCA TCAGGTGCAT 180

TTTTCAATAT GTAACCTTTC GCACCATTAC GCAACACATG GAACAAATAC TCCTCATCAT 240

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ACACTCCAAA CATGCACCAA ACGTGTAAAT GGCCAACAAG CCATAATAGT GAAACCTAAC 2160

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CCTATATGAT ATAAATGCTC AGACACACCC ACTGCATCCA TCCATGGTTT CGGTATTAAC 2520

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CTCCATAGAA ATTCTCATTA TAAATTTCTT GACCAGTTTT CCCTGAACCT ACTGCAACGC 3360

CACAGCCTTC ACAGTTATCT CCAAAATGCT CGCCGCCGTA ATTGTATCCT GTACTACCTT 3420

GTGCGTGATA CGTATCTAAA TAGGTTTCTT TGTGTGATGT TGGAATAACA AATCGATCTT 3480

CATATTTGGC TAGTCCTAAT AAACGATACA TGTCTTTAGT TTGGCGCTCG GTTATACCTA 3540

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CCAATCAATA CCTAGTTCTC TTAGAgGCGT AAATGCTTCA TGCATGAGTT CTTGCAATTT 14040

TTCTGCATCT T 14051

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1885 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

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TACGAATTTA GAAAAATTAA TCGGCAAAAA AGCATTTTCT AAAATTGCAG AAGGCTTTAT 600

AGAAAAGCCG CAAGGTAAAT TAACACTTGC TACCGAGTCT GATAAACGAC CAGCTATAAA 660

GCAATCTGCT GAAGATGATT TTGACAAACT ATAAAAATTA AAAAGGACGG TATATAAACA 720

TGAAAGCAAA AGTATTAAAT AAAACTAAAG TGATTACAGG AAAAGTAAGA GCATCATATG 780

CACaTATTTT TGaACCTCAC AGTATGCAAG AAGGGCAAGA AGCAAAGTAT TCAATCAGTT 840

TAATCATTCC TaAATCAGAT ACAAGTACGA TAAAAGCCAT TGAACAAGCT ATAGAAGCTG 900

CTAAAGAAGA AGGAAAAGTT AGTAAGTTTG GAGGCAAAGT TCCTGCAAAT CTGAAACTTC 960

CATTACGTGA TGGAGATACT GAAAGAGAAG ATGATGTGAA TTATCAAGAC GCTTATTTTA 1020

TTAACGCATC AAGCAAACAA GCACCTGGTA TTATTGACCA AAACAAAATT AGATTAACGG 1080

ATTCTGGAAC TATTGTAAGT GGTGACTATA TTAGAGCTTC AATCAATTTA TTTCCATTCA 1140

ACACAAATGG TAATAAGGGT ATCGCAGTTG GATTGAACAA CATTCAACTT GTAGAAAAAG 1200

GCGAACCTCT TGGCGGTGCA AGTGCAGCAG AAGATGATTT TGATGAATTA GACACTGATG 1260

TTGAGGTGTC AAGAATTTGA AATTTATGAA TATAGATATT GAAACATACA GCAGTAACGA 1380

TATTTCGAAA TGTGGTGCCT ATAAATACAC AGAAGCTGAA GATTTCGAAA TTTTAATTAT 1440

AGCTTATTCG ATAGATGGTG GAGCGATTAG TGCGATTGAC ATGACTAAAG TAGATAATGA 1500

GCCTTTCCAC GCTGATTATG AGACGTTTAA AATTGCTCTA TTTGACCCTG CTGTAAAAAA 1560

GTATGCATTC AATGCTAATT TCGAAAGAAC TTGTCTTGCT AAACATTTTA ATAAACAGAT 1620

GCCACCTGAA GAATGGATTT GCACAATGGT TAATTCAATG CGTATTGGCT TACCTGCTTC 1680

GCTTGATAAA GTTGGAGAAG TTTTAAGACT ACAAAGCCAA AAAGATAAAG CAGGTAAAAA 1740

TTTAATTCGT TATTTCTCTA TACCTTGTAA ACCAACAAAA GTTAATGGAG GAAGAACrAG 1800

AAACCTACCT GAACATGATC TTGAAAAAtG GCAACAATTT ATAGATTaCT GTATTCGAGA 1860

TGTAGAAGTA GAAATGGCGA TTGCT 1885

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

TAATCCTTAG TTCACTGnCA AATTTCAAAA CACCAGTTCC CTCTATCTGC ATCCATAGAA 60

ACTGnATGTT TGTGTCAATA ACCGGATTAT ATTGTGATGn TGTTTGTAAC TCGATTAAGT 120

TATCATCTTT CGAAAAATTA TCTACTACCA TTATTCAACC ACCTTTCCTT CGAATAAACT 180

CCATTTACCA ACkCCACCAG TACCAAAGTT TCTAACTAAA AATTGATGTG CAGACGGGAA 240

GTTATTACGT CTTAATACTT GTGTTGTATT ACCTGGTGTA TTCGATTTTA CTTCTAATAT 300

CCAACCTGCA ATACCTTTAA AGTCTTTAGG AAAATCAGTA AATCGGTTTG ATTCTTCAGT 360

AGTGATATAG AAATCTAAAC CAACGATTTT TAAATCTGAT AATTTTGTAA TACTCTTAGG 420

GATATGTTCC CAATAACCGG CGTTTTGCGG GCAGAAATTC CATGCTCCGT TGTTTTTCTT 480

ATTGAAAATG TCAATGACAC GTTCGAATTT AAGCATATTT CTACCTGTGC TGTTTCTGGt 540

AAGTACTTGT CTTAGAGCAC CATTATAGTG TCCAGGCAGT ACATCCAAGA ACCACCCTGC 600

ATCTCTAAAC GCTTTCGGTA ACGGGAAATC TAATGCATTT TGTGTGTCTT GaCGTATAGA 660

TATAGTAATG ACCAACTTCC GTAATATCAC TTAGATATGC TGGGTTCTGT ATTGGTAACG 720

GTTTAACACG TCCGCCTGAA TCAGTCATTG ATACTTGAGG TGCGATGTTT TTCAAGAATT 780

TAGTTACCCC GATTAGAAGT GCTTTACGTC CTGTTTCTAG ATCGTAATAC ATATCTAGAC 900

CCTCAGCCTC TTGGAAATCT CCTTTAAAGT TGTTATTCAC ACCGCCTATA TCGATGCGAC 960

GTTTAAATAA CAATTCTTTC GTTTTGATAT CGAAGCCTTG TAAGTAGTTA GGGTTGGCTG 1020

TATTCGAATC ACCTGTATAC CAATATAAGA TACCTGCATC ATAAGTGATA CCTTGCATAG 1080

GTTGTGTATC TGAAGTGTAT TCCATAGGTA TATCCATTTG ATACAATACT TTGTCTATAC 1140

CTTTATCAAT ATCGTCAGCA CTTCTAACCT CAACAAAGTT CAACGAATTC TTAAGTTGTC 1200

TTTCAGTGGG TTTATATTCA CGTCTAAAAA TCATTAAATT TTCTACCGGA TTATAAATCG 1260

CTGACGTATA TCTGTCGTTA AATATATTCG GCATGACATC TTGCATTTCA TTACCATAAG 1320

TTATTTCTCC AGTTCTATAT TGGAAACGTA CAAACTTGTT GTTTTTGTTA CTGTCCAATA 1380

CAGCTGAATA AATCCATAAT TCTCCATCAA TGTATCTATA CGCATTGTGT GTACCGTGAC 1440

CGCCGTTTTT AACAAGCAAT CTATCAATAA ATTGTCCGTT GGGCTTCAAT CTAGATAACA 1500

TGTAATGATT ACCTGGACGA GCTTGCGTCA TATAAATAAT TTTCGTTCTA GGGTCTACCC 1560

AAAATGATTG CATTACTGCA TTTGTATATG GCGATAAATC AGTGATAAAT TCCGGTTCTT 1620

GCTCTTTTGG TTCGAATCGG TATTCTGTCG CTCGATATTC TTTATAGTGT TCATCTACAG 1680

CTTTCTCAAC CTTTTTAGTG AAAACATCTA GTGTTGAATA ATCATGATAC AAACGATCTT 1740

GCAATGTCTT ATGACCATAA CCTGTATTAT CAACGCGCGC GTCTTTTAcT TCGTTGATAC 1800

CGTCGCCGTT ATGACCTAGT ACCATGTTGC TAAATCGACC GTTTAAATAT GTTAAAAAGT 1860

CAGAGACGTT ACTTGTAACA TTTAAATGTT CATACTTTAT TTGTTCTCCA TCATGTGCGA 1920

ATACCTCTTT ATTTCTGTGG TATTCAAGAG AGAAATTAAA ATCCGTCAGC ATGTCTGAAA 1980

TAAGTTTAAA GTTATACTCA TTTTCATCTA CATATCTGTA GTCAAAGACT CTACTTAAAT 2040

CTGTAATTAG TTTATTACTC ATGTTTTCCT CCTTTACTAT CCATAAAACT GATmATAATT 2100

TTTAATAAGC TCATACATAA TAACTTCATG ACCTCTTTCA TTAGGATGTA ATCCATCAGG 2160

CATGCTAGAT TTTCTAAATG CTGGATTATA TGGTTTGAAA TAATCTGTGT GATAAGCATC 2220

ATATACTGGT ACATCCAATT CACTACAAGC CAATATCTGA GCATTGACAT AATCCTCTAA 2280

AGTTAACCCT AGTTTGTTTT TGTCCGTATC TTTACGGCGT ATCGTTGTAC CACTCATAGG 2340

GCATTGCCTA GTAGCTGTCA TTACAAGTAT TTTTGAAGCT GGATTATTTT TCCTGATAAC 2400

TTCAATTGCA GAACAAAAGG CGCCGTAAAA CGTTTTAGTG TCGGTTTTAT CAGTGCCTAT 2460

CGGTACGCCT GCCCAATAAC CATGTAACCA GTCATCATCT GTACCTTGTA ATATGATTAG 2520

GTCTCCTCTT ATTTGCTCTG CTTGTCTaTA AATGCTGTTT TCTaCCGCTT CTTTACCTAT 2580

CTTGCCTAAC ATTTCT 2656

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4854 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

AAAATGAGGG TTCTAGCGGA AATTACCAAA AGCGTGGTTC ATACTATGGG CAGCGTAATC 60

GTATTTCAAA AGAAAAAACA CCTAAATGGT TAGaAAATAG AGATAAACCT AGTGAAGAAG 120

ATTCGGCTAA AGATAATAGC GTAGATGATC AACAATTAGA GCAAGATCGA CAAGCATTTC 180

TAGATAAATT ATCTAAAAAA TGGGAGGAGG ACAGTCAATA ATGAAGCAAT TTAAAAGTAT 240

AATTAACACG TCGCAGGACT TTGAAAAAAG AATAGAAAAG ATAAAnCAGA AGTAATCAAT 300

GACCCAGATG TTAAGCAATT TTTGGAAGCG CATCGAGCTG AATTmACGAA TGCTATGATT 360

GATGAAGACT TAAATGTGTT ACAAGAGTAT AAAGATCAAC AAAAACATTA TGACGGTCAT 420

AAATTTGCTG ATTGTCCAAA TTTCGTAAAG GGGCATGTGC CTGAGTTATA TGTTGATAAT 480

AACCGAATTA AAATACGCTA TTTACAATGC CCATGTAAAA TCAAGTACGA CGAAGAACGC 540

TTTGAAGCTG AGCTAATTAC ATCTCATCAT ATGCAACGAG ATACTTTAAA TGCCAAATTG 600

AAAGATATTT ATATGAATCA TCGAGACCGT CTTGATGTAG CTATGGCAGC AGATGATATT 660

TGTACAGCAA TAACTAATGG GGAACAAGTG AAAGGCCTTT ACCTTTATGG TCCATTTGGG 720

ACAGGTAAAT CTTTTATTCT AGGTGCAATT GCGAATCAGC TCAAATCTAA GAAGGTACGT 780

TCGACAATTA TTTATTTACC GGAATTTATT AGAACATTAA AAGGTGGCTT TAAAGATGGT 840

TCTTTTGAAA AGAAATTACA TCGCGTAAGA GAAGCAAACA TTTTAATGCT TGATGATATT 900

GGGGCTGAAG AAGTGACTCC ATGGGTGAGA GATGAGGTAA TTGGACCTTT GCTACATTAT 960

CGAATGGTTC ATGAATTACC AACATTCTTT AGTTCTAATT TTGACTATAG TGAATTGGAA 1020

CATCATTTAG CGATGACTCG TGATGGTGAA GAGAAGACTA AAGCAGCACG TATTATTGAA 1080

CGTGTCAAAT CTTTGTCAAC ACCATACTTT TTATCAGGAG AAAATTTCAG AAACAATTGA 1140

ATTTTAAAAT GATTGGTGTA TAATGAATAC AAATCTAAAT CGTTTAAATG ATTGAAGACA 1200

AGATGATCTA ATCAATATTA CACAGAAAGC CATTGTTTGA TGAGAATATG GTTAATAAAT 1260

TAGATGATTA CTACTTCATT TATGGTATTT GTAATGAATA CCCGGATCAA GACCGTTATC 1320

CTCGTCCCTT GTATAGGGGC GGGATTTTTT GTTTTTTTCA GACATAAATG TTTGTTGGTG 1440

TCATAAATTC CCTGTTTATT GTTAATAGGT TTAATGTTAA AACGATGATT GTTGTTCAAT 1500

TTTTTAACGA GGTCAGATAA AAGTATTTAT AAAGCAAATA GGAGGGTTTA ACATGGAACA 1560

AATTAATATT CAATTTCCAG ATGGTAATAA AAAGGCGTTT GATAAAGGTA CTACTACTGA 1620

AGATATAGCA CAATCAATTA GTCCTGGATT ACGTAAAAAA GCTGTTGCCG GCAAATTTAA 1680

CGGGCAACTT GTAGATTTAA CTAAACCGCT TGAAACTGAT GGATCAATTG AAATTGTGAC 1740

ACCAGGTAGT GAAGAagcGT TAGAGGTATT ACGTCATTCT ACTGCACATT TAATGGCACA 1800

CGCGATTAAA AGGTTATATG GTAATGTTAA ATTTGGTGTA GGTCCTGTAA TAGAAGGTGG 1860

ATTCTACTAT GACTTCGACA TTGACCAAAA CATCTCATCT GATGACTTTG AACAAATTGA 1920

AAAAACAATG AAACAAATCG TTAACGAAAA TATGAAAATC GAACGAAAAG TGGTTTCACG 1980

AGATGAAGTG AAAGAGTTAT TCAGCAATGA TGAATACAAA TTAGAATTAA TCGACGCGAT 2040

TCCTGAAGAT GAAAATGTAA CATTATATAG TCAAGGTGAT TTTACTGATT TATGTCGTGG 2100

AGTTCACGTT CCATCAACAG CTAAAATTAA AGAGTTTAAA CTATTATCTA CAGCAGGTGC 2160

ATACTGGCGT GGAGATAGTA ACAACAAAAT GTTACAACGT ATATACGGTA CTGCTTTCTT 2220

TGATAAAAAA GAATTGAAAG CACATTTACA AATGTTAGAA GAGCGTAAAG AACGTGATCA 2280

TCGTAAAATT GGTAAAGAGT TAGAACTATT CACAAATAGC CAATTAGTTG GTGCTGGTTT 2340

GCCATTATGG TTACCTAACG GTGCAACAAT TAGACGTGAA ATTGAACGTT ACATTGTTGA 2400

TAAAGAAGTT AGCATGGGAT ATGACCACGT TTATACACCA GTACTTGCTA ATGTTGATTT 2460

ATACAAAACA TCTGGTCACT GGGATCACTA TCAAGAAGAT ATGTTCCCAC CAATGCAGTT 2520

AGATGAAACT GAATCTATGG TATTACGTCC AATGAACTGT CCACATCATA TGATGATTTA 2580

TGCGAATAAA CCACATTCAT ATCGTGAATT ACCTATCCGT ATCGCTGAGC TAGGAACGAT 2640

GCATAGATAT GAAGCAAGTG GTGCTGTATC AGGATTACAA CGTGTTCGTG GTATGACTTT 2700

AAATGATTCA CATATCTTTG TTCGACCTGA TCAAATTAAA GAAGAATTCA AACGCGTTGT 2760

AAACATGATT ATTGATGTGT ATAAAGACTT TGGTTTCGAG GATTATAGCT TTAGATTAAG 2820

TTATAGAGAC CCTGAAGATA AAGAAAAGTA CTTTGATGAT GATGATATGT GGAATAAAGC 2880

TGAAAATATG CTTAAAGAGG CAGCGGATGA GCTTGGCTTA TCGTACGAnG AAgCGATTGG 2940

TGAAgCGGCA TTCTATGGTC CGAAACTAGA TGTTCAAGTT AAAACAGCGA TGGGTAAAGA 3000

AGAGACATTA TCAACAGCAC AACTTGATTT CTTATTACCA GAACGTTTTG ATTTAACTTA 3060

TATTGGTCAA GATGGTGAAC ATCATCGTCC AGTTGTTATT CATCGTGGTG TTGTATCAAC 3120

AGCGCCAAAA CAAGTTCAAA TCATTCCAGT TAACGTTGAT TTACATTATG ATTATGCGCG 3240

CCAATTACAA GATGAATTGA AATCTCAAGG CGTTCGTGTA AGTATTGATG ACCGTAATGA 3300

AAAAATGGGT TATAAAATCA GAGAAGCTCA AATGCAAAAA ATACCTTATC AAATCGTAGT 3360

TGGGGATAAG GAAGTTGAAA ATAATCAAGT GAATGTGCGT CAATATGGAT CGCAAGACCA 3420

AGAAACAGTT GAAAAAGATG AATTTATCTG GAATCTAGTT GATGAAATTC GTTTGAAAAA 3480

ACATAGATAG ACAGTTGTCG CAATAAAATG CTTTAAAACT TTTATTGCGT ATCAAGTTTT 3540

ACAGGGTTGA TTATGCGTGA TGAATCCTGT ATATTACAAG TTAGTTAAAA TATTAAATTG 3600

AGTTAGAGGT TGCATGTTTA ATTAGTAACT TGTCAGAAGT ATTTATGGTA CATAAGTTGA 3660

ACAAGTGAAA GGTAAAGATG CCGAAATAGA TATAAACCAT AAATTATATC TATTGGGACA 3720

GTTTTCGAAT AGGAACTGTA CTGTCACAGA ATGTGATGTG CTACCTTATA TAGATAATTG 3780

CCAAAGTGGT TGCATATCTT AAAGGTATGT AGCCACTTTT TTACTTTTAA TATCACTATG 3840

TTCTGTAAAA AAGGGTATGA AAGTGAATAA AGGTTATTTA TTTCTTGGCC TCTAAAACAT 3900

GGAAAGGGAG CTTATATGTC AAAAGTTCAA AATGAAAGTA ACAATGTTGT CAAAAGGGGA 3960

CTTAAAGATC GTCATATTTC TATGATTGCG ATTGGGGGTT GTATTGGTAC AGGTTTATTT 4020

GTAACTTCTG GTGGAGCAAT TCATGATGCA GGTGCTTTGG GTGCATTAAT AGGATACGCA 4080

ATTATCGGAA TAATGGTATT TTTCTTAATG ACGTCACTTG GCGAAATGGC TACGTATTTG 4140

CCAGTATCAG GTTCATTTAG TACATATGCT ACAAGATTTG TTGATCCATC TTTAGGGTTT 4200

GCGCTTGGTT GGAACTATTG GTTTAACTGG GTAGTGACTG TAGCAGCAGA TATTACGATT 4260

GCAGCACAAG TCATTCAATA TTGGACACCA TTGCAAGGCA TACCCGCTTG GGCATGGAGT 4320

GCGTTGTTCT TAGTTATAAT TTTTAGTCTG AATTCGTTAT CAGTTCGCGT CTATGGTGAA 4380

AGTCAATACT GGTTGGCATT GATAAAAGTG GTTACAGTTA TTGTTTTCAT TGCAATTGGT 4440

TTATTAACGA TTGTCGGAAT CATGGGTGGT CATGTTGTAG GATTCGAAAT ATTTAATAAA 4500

GGTGAAGGTC CAATTCTTGG TGGCAACTTA GGAGGAAGTT TGTTATCAAT TCTAGGTGTA 4560

TTCTTAATCG CTGGTTTCTC ATTCCAAGGT ACTGAGTTAA TTGGTATTAC GGCTGGTGAA 4620

TCAGAAAATC CTGAACGTGC TGTGCCGAAA GCAATTAAAC AAGTATTCTG GAGAATTTTA 4680

TTATTTTACA TTTTAGCCAT TTTTGTTATC GGTATGTTAA TTCCTTATGA TAGTAGTGCA 4740

TTAATGGGGG GTAGTGATAA TGTAGCAACG TCTCCATTCA CATTAGTGTT TAAAAATGCT 4800

GGATTTGCGT TTGCAGCATC ATTTATGAAT GCAGTCATTT TAACGTCTGT GTTA 4854

(2) INFORMATION FOR SEQ ID NO: 107:

(A) LENGTH: 2488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

ATCAAAAATT GATTGTTTTC nATTTTTTGT TTCAGCGCGG GATCTTTTAC GTCTTTTGTG 60

AAAACGaTTT TATTATTAAC TACTTTTACT GGATAACTTT TGTATGTCGA GTCAGTAGCA 120

TTTTTTCTAT CGTTTGTAGT TGTGTCATAT TCACCAgTTA TTTTATGTGT GTTCTTATCT 180

ACCTTTAACA ACATACGGTC TTCTTTTAAA AGCTCATCTG ATCCAACAAC TGAATAAGAG 240

GATTCTATAT ACCATGTGTC TTGATCATTA TTTTCATAAT GGGGATTATC GTGACCATCA 300

ATTTCATAAA GCGTTTCTAA GTTTTTAATA GGATACGTAC TTAGTACTTT TTTAAGACCA 360

TCTTTCAAAT GAATTTGTTC CCACTTCATT GCCAAAAACA TATCGCCACT GACTACAATT 420

GAAATAATAA TAATTGCTGC TAAGTTTAAC CAGAAAATTT TATGTGCTTT CATACATTCC 480

CACCGTTTCT CAAAATACTT CATTAACACT ATAATAATAT ATTTTGAAAA ATATTTACAT 540

CAGTATTAAA GTGAATATCA AATTTTAAAT TTATGAAAAT AATAGATATT TATAAAAAGC 600

GGAAAAGAGA TACAATAAAA AACTGCATGA CGTTTGAGAC GTCACACAGT GTAACTAAAA 660

ATTTAAAAAG TTGTTGCTAA TTTTTCAGCA TTATTAATAC TAGTTGCTTT AATTTCTTCA 720

GTCTTATGAG GTTCAGCATT GTGTCCTTCA ATAATGATTG TTTCATATGA TGGCACACCT 780

AAGAATGTCA TAATTGTTCT TAAATAACGG TCACCCATTT CAAAATCAGC AGCAGGTCCT 840

TCAGTATAAT ATCCACCACG TGATTGAATG TGTAATACTT TTTTGTCAGT TAGTAAACCT 900

TGTGGTCCTT CAGCAGAATA TTTAAAAGTT TTACCTGCAA TTGAAATAGC ATCAATATAT 960

GCTTTAACTA CAGGTGGGAA AGAAAGGTTC CACATAGGCG TTACAAATAC ATATTTATCT 1020

GCACTTAAAA ATTCTTCTAA AATGTCACTC AATCTTGAAA CTTTCATTTG TTCATCATCA 1080

GTTAACGTTT CGCCATTACT CATTTTTCCC CAACCAGTTA ATACATCTTT GTCAATAACT 1140

GGAATATAAG TTTCArATAA ATCAATATGT TTCACTTCAT CATCAGGATG TTGTTGTTGA 1200

TATGTTTCGA TAAATGCTTT ACCAGCCGCC ATAGAATTTG ATACCAGTTC ATTAAAAGGG 1260

TGTGCTGTAA TATATAATAC TTTTGCCATT TGAAAATTCT CCTCTGkTTC TGTTATTTTC 1320

TTAAGTATAA TTATTATACT CGATATAAAA TTTAATATCA ATCAAAATAT TCAAATTACC 1380

ATCATTTTCT TCATCTATAT nTGGCAGTAC TACTAAAGTA TGAGTGCATT TAATTATGAa 1440

ATAGTTGATT TaGAATAtAT ACTTAATACC CAAAATATAT GAAGGATGGA TGCCACTATG 1500

ATTATTTATA TAGATGACAT TCAAAAATGG TTTAACCAAT ATACCGATAA ATTGACACAA 1620

AATCATAAAG GACAAGGACA CTCAAAATGG GAAGACTTTT TTAGAGGGAG TCGGATTACT 1680

GAGACTTTTG GTAAATATCA ACATTCACCA TTTGATGGTA AGCATTATGG CATTGATTTT 1740

GCATTGCCAA AAGGTACACC AATTAAAGCG CCGACGAATG GTAAAGTAAC ACGTATCTTT 1800

AATAATGAAT TGGGCGGCAA GGTATTACAG ATTGCCGAAG ACAATGGAGA ATATCACCAG 1860

TGGTATCTAC ACTTAGACAA ATATAATGTC AAAGTAGGTG ATCGAGTCAA AGCAGGTGAT 1920

ATTATTGCAT ATTCAGGCAA TACAGGTATA CAAACGACAG GCGCACATTT ACATTTTCAA 1980

AGAATGAAGG GTGGCGTAGG TAATGCATAT GCAGAAGATC CAAAACCGTT TATCGATCAG 2040

TTACCTGATG GGGAACGTAG CCTATATGAT TTGTAGTTAT AGAAGGGTGC CCGCAGTCTA 2100

AAAAATTAAG CAATCATTGT GTGAGTATGA TACTTACATA ATGGTTGCTT TTTTCAATGA 2160

AAATCGTAAT GCTAAGTCAT ACTTGTTTGA TTTAGATATT ACTTAAAATG TAAGACAAGG 2220

TTGTTAGCAT TGGCAGTGAA ATATCGCACA TAAAAAACAT TATTGTCACA CTAGAAAATA 2280

GTTGTGCACT ATATCAATTT TCTGTATAAA AGTTTAATTC TGACAGTAAT GTAAACGTTT 2340

ACAATTTATG ATTGACATTA ATAATGACTG AATATATGAT TTATGTAAGT ATTTGTGCAA 2400

CGTTTTCACA AAGTGTATTG CACaAyCAAA CTGtAAACaA aGTATGGGGg GCCATAACAT 2460

GGCAGAACTA AGTTAGAGCn TATTAAAA 2488

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4093 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TTTTCTTTAT TTCAAmCTGT ATATTaATGA TGTCACTTCA TTTGATACGA TTCTTGATAA 60

CCTATTCAAA ATTCCGCCAA ATAACATAAA TATTATATAA ATGCCGATAC TTTTAATCAT 120

TTTCTACTTT TTCTTCGATA CGGAAACTTG TTTTCGAATT GAACACTTCA CCAGCTTTTA 180

AAATTGACGG TGCTTTTTCA CCATATAAAT TAATATCATT TGGTAAAAAT TGTGTTTCTA 240

ATGTAAAGCC AGAATGTGGT TTATAAATAT TAAATGGACT ATCCCACTCA TCAGGCTGGT 300

TAAAAGTAAA GAACACAACA TGAGGCATAT CTGTATCGAC CTCTAACATA AATTCATGAT 360

TTTCAACATA CATTTTATGT TCACCAACTG TAAATGGGTG ATCGAGACCA CCAAAACGTG 420

TATCTTCAAA CACTTCATGT AAATCTAGAA TATCACCTGT AACAATATTT CGCTCATCTA 540

ATACATACAT ATCTAATTGA TTACTTGAAA TGCGATGATT ATCAACGACA TTATTATCTC 600

GATTCAAATT GAAGTACACA TGATTCGTAG GACTAAACAA TGTGTCTTCT GATGCAACTG 660

CTTCGTATTC AATCGACCAT TGGTGATCCG CATCATAAAT ATGTGTAATC GTCACATCGA 720

TATCACCCGG GAAATGATCA TCAGCTGATT TCAACACCGT CTTAAATATA ACTTTAATTT 780

GAGCAATTTC ATTTCTAATT TCATAATCAA ATAACTTATT GTCCAAACCA TGACATCCAC 840

CATGTAAATG ATGTTCACCG TTGTTTTTTT CTAACTGATA TTCTTTACCT TTCAACTTAA 900

ATTTAGCATT ATCAATTCTA CCGCTATATC TTCCTATAGA AGCACCAAAT TTAAAAGGAT 960

TACTATGATa AAATTCATCC GCTTCAACAA CATTTCCAAG AACAATATTA TTATCATGAT 1020

ATTTCCAAGA CACTACTCTT GCTCCATAAT TCGTAAAAAT AATTTTAGTT TCATCATTAT 1080

CAATTTTGAT TAAATCTACA CCTTGTCTTT GGTGCTCAAC TTCAACTATC ATTTTTACTT 1140

CTCCCTTCTA ACCACAAGTG TTCAAGCTCT GCTGGGTAGC AACATTACTA AAACACCTAC 1200

AATACAAATG ATTGCACCGA TAACATCATA TTTATCTGGC ATTTGTTTAT CTACGACCAT 1260

CGCAAAAATC AAACTCATGA TGATAAATAC GCCACCATAT GCTGCATATA CTCTTCCGAA 1320

TGATGGAAAT GATTGAAATG TCGCAATGAC ACCATATAAC ATGAGTATCG CACCGCCTAT 1380

TAGCCCAACA AGTGAAGACT GTCCTTCCCT AAGCCACAGC CAAATCAGGT ATCCCCCACC 1440

TATTTCACAT AAGCCAGCTA ATATAAATAT AAAAATCGGA TATAACATGA AATCACTCCA 1500

TCACACATTT GCTATCAATA ATCTATCGGC TACATATCAT TTGTTTACAT TTCTTCTTAC 1560

TTCACATTCC CATTTTAAAA AGTTCGTTTT CACATTCATA TTGTACACTT TTTTAGACAT 1620

TATTCTATAG CTAAATATAA AAAAATAAGA GTAACACGCT TTCATCATCA TTTTATATGA 1680

TAAATGTGTG TCACTCTCAT CAATTTTATT TTTTAAATAC ACGTTTCATT GAATTAAATA 1740

AGCCACGTTC AAATGTAAGT ACTGAATCTT TATATGTTTT AATTGCAATC CATATCAAGA 1800

CAGCTACCAT TACAATTGAG ATTAAAGAAC TTAAGATGAC CTCATATATT TGAAGCCCTG 1860

AAGTTTGAGC GCGTACAACT AATTGAAATG GCGCTAAAAA CGGAATATAA CTTGTGATTA 1920

AAGCAAGTTG TCCATCAGGA TTATTTATCG TGAATATCGC GATATAAAAT GCAATCATAC 1980

CAAGTAATGT CAGTGGCATC AAAGATTGAT TTAAATCTTC TATTCTAGAT GTTAATGATC 2040

CGAGGATGGC TGCAAGTAAT ACATACGCCG TAATTCCAAC AATACTACTT ATAATTCCGA 2100

CAATAATAAT TTGCCAAGAC AATTGATTCA TTTCCACGTT AAAACCTTGT AGCAAGTCTT 2160

TTAAGTCAAA GGCAAAAATG CATATAACTG CCATCAATAC AATTAAAATA ATCTGAGTCA 2220

TAATAATCAT TTCAATGACA CGCGATGTTT TCTCACTAGC AATTTCCATA GCTATTTGAG 2340

ATGCATAATT TAAAACAATG AAGAACATTA GAAAGATAAT GCCATmaGcT AAAGCATAGT 2400

TGAAAATCTT TTGTCCTTCT GATACTTTAT CGACTTCATC ATTAGAAATC ACCTTATTAT 2460

CAACTTTACT TTGTGCTTGT AATTTTTGTA AGTCTTCTTT GTTGATATTT AATTCCCCGG 2520

CTACCATATT TGTTTGAATA GCTGTAAGCA GTGCTTGTAC TTTTTGTGAA TCTTCATGAC 2580

TTACTCGCTT CTCACTAATG ATTGTCCCTT GTAACGTGCG ATTTTGATTC ACCTTGATAA 2640

TATAAGCTTT ATCAAGTTTA TGTTTTTTTA CTTCTTTTTC AGCATCTTCT ATAGAAACTT 2700

TAGTAAACTT AGCATCACTA TGAAATGTAT TCGCCTGTTG CTTGAAAACC TTATAGATTT 2760

GTTCATTCGG TGCTGCTACA CCAATTTTAT CTGGACCATC ATCAAACATG TTAATAATCT 2820

TATCAATGTT AGATAGGCCA ATCATTAAGG CAGCAATAAT AATCATAAAA ATTACAAATG 2880

ATTTAGCTTT AATTTTTTTG ATATATGTCA AAGTAAATGT CGCCCAAAAC TTATGCATCC 2940

TTGCCACCAA CCTTCTCAAT GAATATATCT TGTAATGATG GTTCTACAAC TTGGAATCGT 3000

TTAACATAAC CTTGATGTGC CACAACTTGA TAAATATCTT TGGCTACGTC TTCATTCTCA 3060

ATCGTCAACT GAAGACCTTG CTTCATGTTT TCACTATGAA TGATGCCTCT AATGTTTGTT 3120

AAATCTGGTA GTGTTGTTTC TGATTCAATG ACAACTTTCT TGTTACCATT AGATGCACGT 3180

ACATGATTGA TATCACCAGA AACAACAAGT TGACCTTTAT CTAAAATACA AACATCATCA 3240

CATAATTCTT CAACATGCTC CATACGGTGA GAACTATAAA CGATTGTACT GCCCCAATCA 3300

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CGCTCAAGCC AATACGATAT TTGCTGTTGT ATTTCTGTTT TTGACATTCC CTTTAAAGTT 3540

GCCAAATATT TCAATTCTTC TTCAACTGTC AATTTCCCAT GTAAACCGCG TTCTTCCGGT 3600

AAATAACCAA TACGATTGTA CATTGTTTTA TCTAGTTTTT TACCGTTATA CGTrrTGTGT 3660

CCTTCAGTTG GTTCACTTAA GCCTAAAATC ATACGAAATG TCGTTGTTTT ACmTGCACCA 3720

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TAAAATGAAT TTATTTTTAA AATTTCTGAA ATTGAAAAAT TTAAATAGTG CCATTTTTGC 3960

ATGTTAAGTA TCATTAGCAC TAGATATGTT TTTTCCATGC CTTTATTGCC TTATTTGTAA 4020

CTTnCCGGTG TTT 4093

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

TGCCAAACTA CCTTTTGACA GTCGTTGCTG TACTTCAGGA TGATCAATCA CATATnTTAC 60

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AGCATTCAAT ATTTGATGAT TGTTGAAATG AATCATTCAT ACTATTGTAA CTTTTGAAAA 14100

TGTCATTCAC TTTAGATAAG TGTGATATGT TAAAATATGT CCTGAGGTGA GATTGAATGG 14160

AATGGTCGCA AATTTTTCAT GACATAACAA CGAAACATGA CTTTAAAGCT ATGCATGATT 14220

TTTTAGAAAA AGAATATTCG ACTGCAATCG TATACCCTGA TAGGGAAAAT ATATATCAAG 14280

CGTTTGATTT AACACCGTTT GAAAATATCA AAGTTGTTAT ATTAGGACAA GACCCGTATC 14340

ATGGTCCAAA CCAAGCACAT GGATTAGCAT TTTCAGTGCA ACCTAACGCA AAATTCCCTC 14400

CATCTTTACG TAATATGTAT AAAGAATTAG CAGATGATAT TGGATGCGTT AGACAAACAC 14460

CGCATTTACA AGATTGGGCA AGAGAAGGCG TCTTGTTATT GAATACAGTT TTAACCGTAA 14520

GACAGGGTGA AGCAAATTCT CATCGTGATA TTGGTTGGGA AACATTTACT GATGAAATTA 14580

TTAAAGCAGT GTCTGATTAT AAAGAACATG TTGTCTTTAT TTTGTGGGGG AAACCTGCAC 14640

AGCAAAAAAT AAAGCTTATC GATACATCTA AACATTGTAT TATAAAATCA GTGCATCCTA 14700

GTCCACTGTC TGCATATAGA GGATTCTTTG GATCAAAACC GTATTCCAAA GCGAATGCCT 14760

ATTTAGAGTC AGTAGGAAAA TCACCAATTA ATTGGTGTGA AAGTGAGGCG TAGATGTTGA 14820

ATAGAGAAAC TTTAATAGCA CGAATTGAGC AAGAATTAGT ACAAGCAGAG CAGGCACAGC 14880

ATGACCATGA CTTTGAAAAA CATATGTATG CCATACATAT ATTAACATCT TTATATGCTT 14940

CAACATCAAA TACACCACAT ATTGGTGAAC AACAAATGAA TCGTCGTATT GCTAACCATA 15000

ATCAAATGCC ACAATCACAA ATAACGCAGC CAACTCATCA AGTGACAGTT GCTGAAATTG 15060

AAGCGATGGG TGGTAAAGTA AATACGCATT CAGCACATCA TCATAATAAG TCATATTCAC 15120

AACCTTCAAA CCAACAACAA AGATTAGCGA CAGATGATGA CATTGGCAAT GGTGAATCCA 15180

TATTTGATTT TTAAAAAGCA ACAATGAAAC ATAATTACTT AATAGCTTGT TAAGTATGTA 15240

GGTTAATAAT CAAGACGCAT ATACTTTTAT TCGAGTGTTC GGATTTAAAC ATTTATTAAT 15300

ACTGAATTAT ATAAGGAGAG GTAGCAATGA AATTATTTAT TATTTTAGGT GCATTAAACG 15360

CGATGATGGC TGTCGGTACA GGTGCATTTG GTGCGCATGG TTTACAAGGA AAAATAAGTG 15420

ATCACTATTT ATCAGTATGG GAAAAAGCAA CGACGTATCA AATGTACCAT GGCTTAGCAT 15480

TATTAATTAT AGGTGTAATT AGTGGTACAA CTTCAATCAA TGTTAACTGG GCTGGCTGGT 15540

TAATATTTGC TGGTATTATT TTCTTTAGTG GATCATTATA TATTTTAGTA TTAACTCAAA 15600

TTAAAGTTTT AGGTGCGATT ACGCCAATTG GTGGCGTATT GTTCATCATT GGATGGATAA 15660

TGTTAATCAT TGCGACATTC AAATTTGCTG GTTAAATTTT AAAACTTTAG ATTACCTATG 15720

TGGGTATAGA ATACCTTCGA GGTGAGTTTT TATTTATGGA AAAAAAGAAT AAGCAAATAG 15840

ATAGAGGCGA TTTAAAACAA AACCTATCTG AAAAGTTTGT ATGGGCGATT GCATATGGTT 15900

CATGTATCGG ATGGGGCGCA TTCATCTTAC CAGGAGACTG GATTAAGCAG TCAGGTCCGA 15960

TTGCAGCATC AATTGGTATA GTTATTGGTG CATTATTAAT GATATTAATT GCGGTTAGTT 16020

ATGGCGCATT AGTAGAGAGA TTTCCAGTAT CAGGGGGCGC GTTTGCCTTT AGTTTCTTAA 16080

GTTTCGGCAG ATATGTGAGT TTCTTCTCAT CATGGTTTTT AACTTTTGGT TATGTCTGTG 16140

TCGTTGCTTT AAAtGCGACC GCATTCAGTT TACTAGTTAA ATTCTTATTG CCAGATGTCT 16200

TAAATAATGG GAAACTATAC ACCATTGCGG GCTGGGACGT TTATATTACG GAAATCATTA 16260

TTGCGACCGT ATTACTACTT GTATTCATGC TAGTAACGAT TCGTGGCGCA AGTGTATCTG 16320

GATCATTACA ATATTATTTC TGTGTGGCGA TGGTAATCGT CGTATTATTG ATGTTCTTTG 16380

GTTCATTCTT TGGTAATAAT TTTGCACTTG AAAATTTACA ACCGTTAGCT GAACCTAGCA 16440

AAGGATGGTT AGTGTCTATT GTGGTTATTG TATCCGTGGC ACCATGGGCA TATGTTGGAT 16500

TTGATAATAT TCCACAAACA GCAGAAGAGT TTAACTTTGC ACCAAACAAG ACATTTAAGC 16560

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GTTGGTTATC AACAAGTCAT CAAAGTTTAA ATGGGCAGTT GTGGTTAACA GGTGCTGtTA 16680

CACAAACAGC ATTTGGTTAT ATTGGATTAG GTGTATTAGC AATTGCAATT ATGATGGGTA 16740

TATTTACTGG TTTAAATGGA TTCTTGATGA GTTCAAGTCG CTTGTTATTT TCTATGGGAC 16800

GTTCAGGTAT TATGCCAACA ATGTTTAGTA AATTACATAG TAAATACAAA ACACCATATG 16860

TCGCAATCAT ATTCCTAGTA GGAGTGTCGT TAATTGCACC TTGGCTAGGA AGAACTGCAT 16920

TGACTTGGAT TGTAGATATG TCATCTACTG GTGTATCCAT TGCCTACTTT ATTACATGTT 16980

TGTCTGCAGC GAAATTATTC AGTTATAACA AACAAAGTAA TACGTATGCA CCGGTTTACA 17040

AAACGTTTGC TATTATCGGC TCATTTGTAT CATTCATTTT CTTAGCGTTG TTATTAGTGC 17100

CAGGTTCTCC TGCAGCACTG ACTGCACCGT CTTATATTGC ATTACTTGGA TGGTTAATCA 17160

TCGGTTTAAT ATTCTTTGTG ATTCGATATC CTAAATTGAA AAATATGGAT AATGATGAAT 17220

TAAGTCGCTT GATTTTAAAT AGAAGTGAAA ATGAAGTTGA TGATATGATT GAAGAACCTG 17280

AAAAAGAAAA AACTAAATAA TAAAAGAATC GCACAATAAA CCTTCTTCAT TCGGAGGCGT 17340

ATCGTGCGAT TTTTTGTATT ATAAATTGAC ATTTAAGACG AGGCAGCTGA ACCTTATATA 17400

TAATTGCTAA GAGTTAGGGC TGAGCCATTT CTAACAAATA TTTATAATCG TTTAAAAGAT 17460

TTCACGAACC CAGAAACAAT TAATTTGGAA ATTTGGTCGG CGAATAATAA ACCTAATGCG 17520

AAGACTAAAT TTTTTGTAGC ATCGTATGCT AAGCCACCAG GTACTAATGG AATGATACCC 17640

GTTACCATAA AAATGATGGC AGGTTCTTTT TGTTTACGAG CCATATAATG ACTTAACAAG 17700

CCTAATGCTA AACTACCAAA GAAACTAGAG TATATAGTGT GCACATTAAA GCCGTTGAAG 17760

AATAAGGTGT AAACCATCCA TCCACACGTA CCAACGAAAC CACATGATAG ATATAATTTT 17820

CTAGGTGCAT CAAAAATGAC GCAGAA 17846

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5544 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

ATTGACACTT GGTGAAAGTA ATATCGCCGC GCTATTTTGG CAAAATGGAC ACTTAGAACC 60

TGAGTTACAA GATGAACAGC CAATTAATAT ATTAGGATCT GkTCAAATCA ACGAATGGAA 120

TGGTAATCAA TCACCGCAAA TAATTATTCA AGATATTGCG ATGAATGAAC AGCAAATATT 180

AGATTATAGA AGTAAGCGAA AAAGTTTACC TTTTACAGAA AATGATGAAA ATATTGTCGT 240

GCTTATTCAT CCTAAAAGTG ATAAAGTAAA TGCGAATGAA TATTATTATG GTGAAGAAAT 300

TAAACAACAA ACTGATAAAG TAGTATTAAG AGATTTACCA ACGTCAATGG AAGACTTGTC 360

TAATTCCTTG CAACAACTGC AATTTTCTCA ACTTTATATA GTTTTGCAAC ATAATCATTC 420

GATTTACTTC GATGGTATAC CTAATATGGA TATTTTTAAA AAGTGTTATA AAGCATTAAT 480

AACTAAACAA GAAACAAATA TCCAGAAAGA GGGTATGTTA TTGTGTCAAC ATTTAAGTGT 540

GAAACCAGAT ACACTTAAAT TCATGTTGAA AGTTTTCTTA GACTTAAAAT TTGTAACACA 600

AGAAGATGGT TTAATTCGAA TCAATCAACA ACCTGATAAA AGATCGATTG ATTCCAGCAA 660

AGTATATCAA TTAAGACAAC AACGTATGGA TGTTGAAAAG CAATTATTAT ATCAAGATTT 720

TTCAGAAATA AAAAATTGGA TAAAGTCACA ATTGTCGTGA GCAATTTAGG AGGAAATATT 780

AATGGATTTA AAGCAATACG TATCAGAAGT TCAAGATTGG CCGAAACCAG GTGTTAGTTT 840

CAAGGATATT ACTACAATTA TGGATAATGG TGAAGCATAT GGCTATGCAA CAGATAAAAT 900

TGTAGAATAC GCAAAAGACA GAGATGTTGA TATCGTTGTA GGACCTGAAG CGCGTGGCTT 960

TATCATTGGC TGTCCTGTAG CTTATTCAAT GGGGATTGGC TTTGCACCTG TTAGAAAAGA 1020

AGGGAAATTA CCTCGTGmAG TCATTCGTTA TGAGTATGAC CTAGAATATG GTACAAATGT 1080

ATTAGCTACT GGTGGTACGA TTGAAGCAGC AATAAAATTA GTTGAAAAAT TAGGCGGTAT 1200

CGTAGTAGGT ATTGCATTTA TAATTGAATT GAAATATTTA AATGGTATTG AAAAAATTAA 1260

AGATTACGAT GTTATGAGTT TAATCTCATA CGACGAATAA TAAATAATAT AATTTTATCA 1320

AATGAAATCC TTCATCAAAT GTATAAGAAC CAATGACTTA ATTAAAAAAG TTGTTTAAGT 1380

TTTCTTAACA TGAGATGTTA GGATTTTTTA TTTACTGAAA ATGTTAGATG ATTGAGCATT 1440

ATACCTTAAT AACATCGTTT ATTTATTTCA TAAATTGTAG TATCATAGAA CTAATATTTA 1500

AAAAATGAAA CAGTAGATTT AGGTCGAATT TTTGTAAAAG TTTTAAAAGT AGGAATAGTA 1560

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TCATTGTTTA AGGCGAAGTA ATAAATATGA ATGGGGTGTA TCATATAATG AACAACGAAT 1740

ATCCATATAG TGCAGACGAA tTCTTCACAA AGCAAAATCA TATTTGTCAG CAGATGAATA 1800

TGAGTATGTT TTAAAAAGCT ATCATATTGC TTATGAAGCA CATAAAGGTC AGTTCCGAAA 1860

AAACGGATTA CCATACATTA TGCATCCTAT ACAAGTTGCA GGTATTTTAA CAGAAATGCG 1920

ATTAGACGGA CCGACGATTG TCGCAGGTTT TTTGCATGAT GTAATTGAAG ATACACCGTA 1980

TACATTTGAA GATGTAAAAG AAATGTTCAA TGAAGAAGTT GCTCGAATTG TTGATGGTGT 2040

GACGAAGCTT AAAAAAGTAA AATACCGCTC AAAAGAAGAA CAACAAGCTG AAAATCATCG 2100

CAAGTTATTT ATTGCGATTG CCAAAGATGT ACGCGTAATT TTGGTGAAAT TAGCAGACAG 2160

ATTACATAAT ATGCGTACCT TGAAAGCCAT GCCGCGCGAA AAACAAATTA GAATTTCTCG 2220

AGAAACATTA GAAATTTATG CACCATTAGC ACATCGTCTT GGTATTAATA CAATCAAATG 2280

GGAACTAGAA GATACGGCTC TTCGTTATAT TGATAATGTG CAATATTTTA GAATAGTCAA 2340

TTTAATGAAG AAGAAACGTA GTGaACGTGA AGCGTATATC GAAACGGCTA TTGATAGAAT 2400

ACGTACTGAA ATGGACCGAA TGAATATCGA AGGCGATATA AATGGTAGAC CTAAACATAT 2460

TTACAGTATT TATCGGAAAA TGATGAAGCA GAAAAAACAA TTTGATCAAA TTTTTGATTT 2520

GTTGGCGATA CGTGTTATTG TCAATTCTAT TAATGATTGT TATGCGATAC TTGGGTTGGT 2580

GCATACGTTA TGGAAACCGA TGCCAGGACG TTTTAAAGAT TATATTGCAA TGCCTAAACA 2640

AAATTTGTAT CAGTCATTGC ATACTACAGT AGTAGGCCCA AATGGAGACC CGCTCGAAAT 2700

CCAAATACGA ACGTTTGATA TGCACGAAAT TGCTGAGCAT GGTGTTGCAG CACACTGGGC 2760

TTACAAAGAA GGTAAAAAAG TAAGTGAAAA AGATCAAACT TATCAAAATA AGTTAAATTG 2820

GTTAAAAGAA TTAGCTGAAG CGGATCATAC ATCGTCTGAC GCTCAAGAAT TTATGGAAAC 2880

TGAGTTGCCA TATGGTGCTG TGCCGATTGA TTTTGCTTAT GCGATTCACA GTGAAGTAGG 3000

TAATAAGATG ATTGGTGCCA AGGTGAATGG CAAAATTGTA CCAATTGACT ATATTTTACA 3060

AACAGGCGAT ATTGTTGAAA TACGTACTAG TAAACATTCA TATGGACCAA GTCGTGATTG 3120

GTTGAAAATT GTTAAATCGT CTAGTGCCAA AGGTAAAATT AAAAGTTTCT TCAAAAAACA 3180

AGATCGTTCA TCTAATATTG AAAAAGGCCG AATGATGGTT GAAGCTGAAA TAAAAGAGCA 3240

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TAACTTTGCA AATGAAGATG ATTTATTCGC AGCTGTAGGA TTTGGCGGCG TGACATCCTT 3360

ACAGATTGTT AATAAATTAA CTGAAAGACA ACGTATTTTA GATAAACAAC GTGCTTTAAA 3420

TGAAGCACAA GAAGTTACGA AATCATTGCC TATTAAAGAC AACATCATTA CTGATAGTGG 3480

TGTCTATGTA GAAGGTTTAG AAAATGTACT TATCAAGTTG TCAAAATGTT GTAATCCTAT 3540

ACCaGGTGAT GATATTGTAG GTTATATCAC CAAAGGTCAC GGTATTAAAG TACATCGCAC 3600

TGATTGCCCA AATATTAAGA ACGAAACTGA ACGACTAATT AATGTTGAAT GGGTAAAATC 3660

AAAAGACGCA ACTCAAAAAT ATCAGGTTGA TTTAGAGGTA AtGCGTATGA CCGAAATGGC 3720

TTGTTGAATG AAGTACTACA AGCTGTTAGC TCGACAGCCG GCAATTTAAT TAAAGTTTCA 3780

GGACGTTCAG ATATTGATAA AAATGCAATA ATAAATATTA GTGTCATGGT GAAAAACGTG 3840

AATGATGTTT ATCGTGTGGT AGAAAAGATC AAACAACTTG GTGATGTTTA TACAGTAACA 3900

AGAGTTTGGA ACTAGAGGTG CAAAATATGA AAGTAGTTGT ACAAAGAGTT AAAGAAGCAT 3960

CGGTGACGAA TGATACATTA AATAATCAAA TCAAAAAAGG ATATTGTTTA TTAGTCGGTA 4020

TCGGTCAGAA CTCTACAGAG CAAGATGCAG ATGTAATTGC AAAGAAAATT GCTAATGCAA 4080

GATTATTTGA AGATGACAAT AATAAATTAA ACTTTAATAT CCAACAAATG AATGGTGAAA 4140

TACTATCAGT TTCACAATTT ACTCTCTATG CAGATGTAAA AAAAGGTAAC CGTCCAGGTT 4200

TCTCAAATTC TAAAAATCCT GATCaAGCGG TAAAAATTTA TGAGTATTTT AATGcaTGCG 4260

CTACGAGCGT ATGGTCTTAC TGTGAAAACA GGTGAATTTG GAACACACAT GAATGTTAGC 4320

ATAAATAATG ATGGTCCAGT CACTATTATT TATGAAAGTC AGGACGGCAA AATTCAATGA 4380

AAAAAATAGA GGCATGGTTA TCTAAAAAGG GTCTTAAAAA TAAACGTACT CTAATAGTAG 4440

TGATTGCCTT TGTCTTATTT ATCATCTTTT TATTTTTATT GCTGAATAGC AATAGTGAAG 4500

ATAGTGGGAA CATCACGATA ACTGAAAATG CTGAATTACG TACAGGTCCA AACGCTGCGT 4560

ATCCAGTCAT ATATAAAGTT GAAAAAGGTG ACCATTTTAA AAAGATTGGT AAAGTAGGTA 4620

AATGGATTGA AGTTGAAGAT ACATCCAGTA ATGAAAAAGG TTGGATAGCT GGATGGCACA 4680

TAGTGCTTGA TCCTGGTCAT GGAGGTAGTG ACCAGGGTGC TTCAAGCAAT ACTAAATATA 4800

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CAAATGGAAT GACaGTTTAT TGGTATCATG ATAATCAAAG AGCTTTAGCA GATACGTTAG 5040

ACGCTACGAT TCAGAAGAAA GGTCTACTTT CTAATCGCGG TTCAAGACAA GAAAATTATC 5100

AAGTGTTAAG ACAAACAAAA GTTCCTGCTG TTTTATTAGA ATTAGGTTAT ATTAGTAACC 5160

CAACTGATGA AACGATGATT AAAGATCAAT TACATAGACA AATTTTAGAA CAAGCAATTG 5220

TTGATGGCCT TAAAATTTAT TTTTCTGCGT AGGGCTTGCA AAAATATGTG AAAGTAGTTA 5280

TCATTGATAT TGAATTTTAT AACTAAAACC GTTAGTATTC TTGAAATGGT AAATGAAATA 5340

GGTAGCAATC TAACTAAGAT TGTGTAGGAA TATAATCCAT AGACTGAAAG ATTATGCTGA 5400

GTAGTTTATA TACATTGAAC ACAAGAAGAG GTGCTTTATG AAAAGTAAAG CCGTTAAACG 5460

TACGTTaAAC GTTTTGAGTG GGTTTATTAA ATGCACGCTT ATAAAAAGTA ATGATGATTA 5520

CAATTAGGCA TGTTTTTTAA ACCA 5544

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1067 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AAAAGATTGC AAATATAAAT GGCATGTTTA ATATGTTAGA ACAACAAATC ATTCATAGCC 60

AAGATATGGC TCATTTTAGA AGTGAATTTT TTTACGTCAA TCATGaGCAT CGAGAAAACT 120

ATGAAgCACT CCTAATTTAT TACAAAAATA GTATCGACAA TCCTATTGTA GATGGTGCAT 180

GTTATATTTT AGCCCTACCT GAAATTTTCA ATAGTGTTGA TGTTTTCGAA TCAGAGTTAC 240

CATTTTCATG GGTATATGAT GAAAATGGCA TTACCGAAAC AATGAAATCA CTTAGCATTC 300

CATTACAATA TTTAGTTGCA GCAGCTTTAG AAGTAACTGA TGTGAATATA TTTAAGCCTT 360

CAGGATTTAC AATGGGAATG AATAATTGGA ATATTGCTCA AATGCGAATC TTTTGGCAAT 420

ATACAGCAAT TATTAGAAAA GAAGCACTAT AACATTAATA ATTAATTAGC TATAAAGATG 480

ATTCACAACA ATCATCTTTA TAGCTTTTTT ATGTCTAATT ATTTTTGAGG AAAATmACAA 540

AATTTTATGT TTTCAAAAGT AAACAATCAA AAGATGTTAG AAGATTGCTT CTATATAAGA 660

AAGAAAGTGT TTGTAGAAGA ACAAGGCGTC CCTGAGGAAA GTGAAATTGA TGAATATGAA 720

TCTGAATCTA TTCACCTCAT TGGATATGAT AATGGACAGC CAGTTGCCAC TGCTCGAATA 780

CGCCCTATTA ATGAAACAAC TGTCAAAATA GAACGAGTAG CTGTGATGAA ATCACATCGT 840

GGACAAGGAA TGGGTAGAAT GCTTATGCAA GCTGTAGAAT CATTAGCTAA AGATGAAGGT 900

TTTTACGTAG CTACTATGAA TGCCCAATGT CATGCTATCC CATTTTATGA AAGTTTAAAC 960

TTTAAAATGA GAGGTAATAT ATTTCTTGAG GAAGGCATCG AGCATATTGA AATGACAAAA 1020

AAGTTAACCT CGCTTAATTA AAAAAAGTTG TATCTATTTT AGAAACA 1067

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18613 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

AAGACGtAtG ATAACAACAA TACgTGTAGT GAAAGATTTT AATCTACATA TTACTGACAA 60

AGAATTCATT GTATTTGTTG GACCATCGGG ATGTGGTAAA TCAACAACAT TACGAATGGT 120

TGCTGGACTA GAGTCTATCA CATCTGGAGA TTTTTATATT GATGGGGAAC GCATGAACGA 180

TGTTGAACCA AAGAATAGAG ATATTGCGAT GGTATTTCAA AACTATGCAT TATATCCACA 240

TATGACTGTT TTTGAAAATA TGGCATTTGG GCTAAAGCTA CGTAAAGTAA ATAAAAAAGA 300

GATTGAACAA AAAGTTAATG AAGCAGCTGA AATATTAGGA TTAACTGAGT ATCTTGGTCG 360

TAAACCAAAA GCGTTATCTG GCGGACAGCG TCAACGTGTT GCTTTGGGCA GAGCTATTGT 420

TAGGGATGCG AAAGTCTTTT TAATGGATGA ACCATTATCG AATCTTGATG CGAAyTtCGA 480

GTACAAATGC GCACAGAAAT ATTGAAATTA CATAAGCGAC TTAATACTAC GACAATTTAT 540

GTTACACATG ATCAAACTGA AGCATTGACG ATGGCTAGTC GAATTGTTGT TTTGAAAGAT 600

GGCGACATTA TGCAAGTCGG CACACCTAGA GAAATATATG ATGCCCCTAA TTGCATATTT 660

GTGGCGCAAT TTATCGGCTC ACCAGCAATG AATATGTTGA ATGCTACAGT TGAAATGGAC 720

GGATTGAAGG TAGGAACACA CCATTTTAAA TTACATAATA AAAAATTTGA AAAGTTAAAA 780

GCTGCTGGCT ACTTAGACAA GGAAATTATT TTAGGTATTC GAGCTGAAGA CATTCATGAA 840

GAACCAATAT TTATTCAAAC TTCTCCAGAG ACACAATTTG AATCTGAAGT AGTTGTATCC 900

AAATTAGATT CAAGAACTCA AGTGATGGCG AACGACAAGA TTACACTAGC ATTTGATATG 1020

AATAAGTGTC ACTTTTTTGA TGAAAAAACA GGAAATCGTA TCGTCTAAGG GGGAGTATTC 1080

ATGTCTAAAA TTTTAAAATG TATCACGTTA GCCGTGGTAA TGTTATTAAT CGTAACTGCA 1140

TGTGGCCCTA ATCGTTCGAA AGAAGATATT GATAAAGCAT TGAATAAAGA TAATTCTAAA 1200

GACAAGCCTA ACCAACTTAC GATGTGGGTG GATGGCGACA AGCAAATGGC GTTTTATAAA 1260

AAAATTACGG ATCAATATAC TAAAAAAACT GGCATCAAAG TAAAGCTTGT AAATATTGGT 1320

CAAAATGATC AACTAGAAAA TATTTCGCTA GACGCTCCTG CAGGAAAAGG TCCAGATATC 1380

TTTTTCTTAG CACATGATAA TACTGGAAGT GCCTATCTAC AAGGCTTAGC TGCTGAAATC 1440

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GACAATAAGC AACTAGCATT GCCAGCTATC GTTGAAACAA CCGCACTTTT TTATAATAAA 1560

AAATTAGTGA AAAATGCACC GCAAACGTTA GAAGAAGTTG AAGCTAATGC TGCCAAACTA 1620

ACTGATAGTA AAAAGAAACA ATACGGTATG TTATTTGATG CTAAAAATTT CTATTTTAAT 1680

TATCCGTTTT TATTCGGCAA TGATGATTAT ATTTTCAAGA AAAATGGCAG TGAATATGAT 1740

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TGGTACGACA AAGGGTATCT TCCTAAGGCA GCAACACATG ATGTCATGAT TGGTCTTTTT 1860

AAAGAAGGAA AAGTAGGACA ATTTGTCACT GGACCGTGGA ACATTAATGA ATATCAAGAA 1920

ACGTTTGGTA AAGATTTAGG AGTAACAACA TTACCTACAG ATGGTGGCAA ACCTATGAAA 1980

CCATTTCTAG GTGTACGTGG TTGGTATTTA TCTGAATATA GTAAACATAA GTATTGGGCT 2040

AAAGATTTAA TGCTGTATAT CACTAGTAAA GATACATTAC AAAAATATAC AGATGAAATG 2100

AGCGAAATTA CTGGACGTGT TGACGTGAAA TCATCTAATC CAAATTTAAA AGTGTTTGAA 2160

AAGCAAGCAC GTCATGCTGA ACCGATGCCT AATATTCCTG AAATGCGACA AGTTTGGGAA 2220

CCGATGGGCA ATGCAAGCAT ATTTATTTCA AATGGTAAGA ATCCTAAACA AGCGTTAGAT 2280

GAGGCGACGA ATGATATAAC GCAAAATATT AAGATTCTTC ATCCATCACA AAATGATAAG 2340

AAAGGAGATT AGTTATGACG AAACGTAACC CTAAATTAGC GGCATTATTA TCTGTTATAC 2400

CTGGTTTGGG ACAGTTTTAT AATAAAAGAC CCATTAAAGG GACGATATTT TTTATCTTTT 2460

TCATCAGTTT TATTTCTGTT TTTTATAGCT TTTTAAATAT TGGTTTTTGG GGATTGTTCA 2520

CATTAGGGAC AGTACCTAAG TTAGACGATT CTCGTGTCTT ACTTGCACAA GGTATTATTT 2580

CTATCTTACT CGTTGCTTTC GCAATCATGC TATATATCAT TAATATTTTA GATGCATATC 2640

GTAATGCTGA ACGATTTAAT CGCAATGAGG AAATAAAGGA TCCGAAGcGC GTATGGTGGC 2700

TGTAGTTGTA TTTCCATTAA TAyyTATGTT TGGAGTAGCA TTTACAAATT ACAATTTATA 2820

CAACGCGCCT CCGAGACACA CATTAGAATG GGTTGGTTTA GATAACTTTA AAACGTTATT 2880

CACAATTGGC GTTTGGCGTA AAACATTTTT CAGTGTTATT ACTTGGACAT TAGTATGGAC 2940

GCTTGTTGCA ACGACACTTC AAATTGCATT AGGGCTGTTT TTGGCAATTA TTGTAAATCA 3000

CCCTGTCGTC AAAGGTAAGA AATTTATCCG TACTGTGTTA ATCCTACCTT GGGCTGTACC 3060

ATCATTTGTG ACAATTTTAA TATTTGTAGC GTTATTTAAT GATGAATTTG GTGCGATAAA 3120

TAATGATATT TTGCAACCTT TATTAGGTGT AGCACCAGCA TGGTTAAGTG ATCCGTTTTG 3180

GGCAAAAGTG GCATTAATCG GCATTCAAGT ATGGCTTGGA TTCCCATTTG TCTTTGCACT 3240

GTTCACTGGA GTACTGCAAA GTATTTCATC AGATTGGTAC GAAGCAGCAG ATATGGATGG 3300

TGCGTCTAGT TGGCAAAAGT TTAGAAACAT CACATTCCCG CATGTCATTT ACGCCACAGC 3360

GCCATTGTTA ATTATGCAAT ATGCAGGTAA TTTCAATAAT TTTAATCTTA TTTATCTATT 3420

TAATAAAGGC GGTCCACCAG TGTCAGGGCA GAATGCTGGT AGTACAGATA TCTTGATATC 3480

TTGGGTGTAT AATCTGACAT TTGAGTTTAA CAACTTCAAC ATGGGTGCAG TTGTGTCATT 3540

AATTATTGGA TTTATTGTTG CTATTGTCGC ATTTATTCAA TTCAGACGTA CAAGTACGTT 3600

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CATTTAAAAA TTATGCATTC TTACTATTCG ATGACAGTAG TCAATACCTG ACTTGGTATA 3840

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CAGCATATGC TTTTTCTAGA TATCGCTTTG TTGGTCGTAA ATACGGGCTG ATTACATTTT 3960

TGATTTTACA AATGTTCCCT GTATTAATGG CAATGGTCGC AATCTATATT TTGCTAAATA 4020

CAATTGGATT ATTAGATTCT TTATTTGGAC TAACACTGGT ATATATTGGT GGATCAATAC 4080

CGATGAATGC CTTTTTAGTG AAAGGTTACT TCGATACGAT TCCAAAAGAA CTTGATGAAT 4140

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CTAAGCCGAT TTTAGCAGTT GTTGCTTTGT TCAATTTTAT GGGGCCATTT ATGGACTTTA 4260

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GGGTGTGGTG GTATTGCGAA TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAAATGTT 4620

GAAATGATCG CATTTTGTGA CGTAGACATT TCGAAAGCAG CGAGTGCGGC AGAAGCATAC 4680

GGAACTGACA ATGCAAAGGT TTATGATGAT TACAAAGCAT TGTTAAAAGA TGACACGATT 4740

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TTGAAAAGCG CATTGTTCTT CTATTATkTA TTtACGAAAT TATCATTAAT CAGTGTGTTA 18600

GTACTGCACT TAA 18613

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AAAGTTTTAA AAGGGGTGAG ATACTTGGCG AATAATCCAT TCCAGCTTTG CGTTTAAAAG 60

GAATTATACT TGCCATTGTC GGTGCTTGTT TATGGGGATT AGGTGGTACT GTTTCTGATT 120

TCTTGTTCAA ATATAAGAAT ATTAATGTCG ATTGGTACGT CACTGCTCGA CTTGTAGTCA 180

GTGGTGTTTT CTTACTTATT ATGTACAAAA TGATGCAACC CAAACGTTCA ATATTTAGCG 240

TATTCCAAGA TCGACGTATG TTAGGCAAAT TACTTATCTT CAGTATACTG GGCATGTTAG 300

TAGTACAATA TGCTTATATG GCATCTATTA ATACAGGTAA TGCTGCGATT GCAACATTAC 360

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TAACATTATT TGATGTGCTT GCTATTATCA TGACACTATT AGGAACATTT TTATTATTAA 480

CAAATGGTTC ATTTTCTAAT TTAGTCGTCA ATCCTGCAAG TTTATTCTGG GGTATTTTAG 540

CTGGTGTAGC ACTCGCTTTT TACACAATTT ATCCTTCAGA CCTACTTAAC CGCTTCGGTT 600

CGATTCTAAT TGTCGGGTGG GCAATGCTTA TTTCTGGTGT TGCGATGAAT TTACGCCATC 660

CAATTTGGCA CATTGATATC ACTAAATGGG ACATATCAAT TATATTATTT TTAATCTTTG 720

GTATTATCGG TGGTACCGCA CTCGCATTTT ATTTCTTTAT CGACAGTTTA CAATACATAT 780

CAGCGAAAGA AACAACATTA TTCGGAACTG TTGAACCTGT CGTAGCCGTT ATCGCAAGCA 840

GTCTATGGTT ACATGTGGCA TTCAAACCAT TTCAAATCGT AGGCATCATT CTTATTATGA 900

TTTTAATTTT ATTACTATCA CTTAAAAGAC AACCTGAAAC ATTAGATGAA TAAGAAAACT 960

CTGATAATCA CTTTAGCAAG TAACTATTAT TTAACAACGT AGTTACCTTA TAGGTGATAT 1020

CAGAGTTTTT TATTTTAGTT AATAATATTT TTCACTTGGT ATAAAAAaGC GTCGTCGCTC 1080

TGGTAATCGG AAATACTGGA ATAAAATATG GAATTGGGTA ATAATCCCAG GTAnTAAAAG 1140

TCCATGTTCC GATAnCCTnT CCGCAnCTCC AACCAAATTT GCCGATAAGG TTCCAAAAGG 1200

CATCCTGGGG GTAC 1214

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9458 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

ATTTTGGTTT CATTCACGAT GGGGTnATAC AGCAAACACA nCTAAAATAA CTATCAATAG 60

CTTAGACAAT AAAAAATATG CCACTACAAT CGCTAATATT ACGATTAAAA AAGAAGCGTT 180

AACGATTACT TTCATCGTTG TTCTATCTCT GAACATCATA TTAAAGACAA CTAGACTAAT 240

TGATAATGAA ACAGCAAAAA AAGTAATAGC TAACACTAAT TTCATCATAA ATAGACAGAC 300

TAAACCTATG ACTAATAATG TATTAGAAAT TACAGCTGAC GTTTTTAACA TTCTCGaATT 360

AATATGCACT CACCCTTTTT ATTTAAATAA CTTACATAAT CATAATAATA CATGATGTTT 420

CATAGGCCTG TCGATGATTG ATTCACAATA GCACGTGATT TTTTTGTTTT TCAATATTAT 480

TCATTTATTC CATCAAAAAC ACCCTTTTTA ATTTTTACAA AAATTAAAAA AAGTGCTCCT 540

ACACTGCTTG CATGTAGAAA CACTTTTTCA TTGTAATGTT ATTCTTCTCG AGACATACCT 600

TTTAGCATAT TAAGCATGTA TGTTAAACTA CGGTTCATGT CGTCATCTTT CAATACGCCC 660

AATAGACTTC TTATAGTTGT CTTAGCATTT GGACTCGCTT GATTGGCAAC GTGTAATCCT 720

TTATTAACTT TATTTAGGAA GTCGCTTAAA TCTGATACAT TGAGTTCACC TAATAAAAAT 780

ACCATTGAAG CCATATTAGA TAATAGCCCT GTATAAATAT CTTTATTAAG TTCAACTGCA 840

AATTTATTTA TGATGACTTG ACGTCCTCGA ATTGCACCAT TTAAAGCATC TAATAGTTTT 900

GCATCATCTA ATGTTTTAAT AAGCTTGATT GCTTTTAATA TACTATCTTT ATTCGCTGCA 960

ATTGCCTCTG TAACTTCATT TAAACTTTCT AACTTAATTT GTTCTTCTGA TTTTTCTAAG 1020

CGTCTAATTT TAGAAGATAT TCTCTCAGCC ATTATTTATC CACCTGATTT CCCGGGAAAA 1080

CATAATCTGA ACGTTCCCAT TTTTTCTGTA CTTGAACACT GTACTGCGGT TGACGTTTTT 1140

TATTGACACG GAAATTATTA GGGTTCAACG GTGACTTACC ACGTTTCGTA ATTACCTCCA 1200

AACGACAGCT AGTACGTTTA TAAGATGGTG TATCCGTGTA TTGATCAACA TCACTaTTAG 1260

TTAATAAGTT AATTGCACCT AGATCTCCAT TTTCCATCGC aTCaTTATTT AATGGAATAT 1320

AGATTTCTTT ACCTTTAACA CGATCTGTCA CGTGAACTTG TAATACCGCT TCTCCTGTyT 1380

CAGAAATCAG CTTAACTTCT GCACCTTCAT GAATGCCTCT ATCTTCAGCA AGCTCTGGAG 1440

AAATTTCAAC AAATGCACGT GGCACTTTGT ATTTAATCAT TGGTGTTTGA TAAGTCATAT 1500

TACCTTCATG GAAGTGCTCT AACAATCGAC CATTGTTTAC ATGAATATCA TAAATTTCAT 1560

CTTGCTTAAA GTAATTATCA AATGATAATG GGAATAATTT TGCTTTACCA TTATCAAAAT 1620

TGAATCCTTC TAAGTATAGA ATAGGCTCAT CAGTACCATC AGGTTGTACT GGCCATTGTA 1680

AACTATTGAA TCCTTCTAAA CGATCATAAC TTACCCCAGC ATATAGAGGT GTTAAGCGTG 1740

CTACTTCATC CATAATTTCA CTAGGATGCT TGTAATTCCA ATCAAATCCT AATCTATTAG 1800

CAATTGCTTG GAAAATTTTC CAGTCAGGTT TTkAATCACC AAGAGGTTCT AATGCTTGGT 1860

TTGCTGGCAA TACAACATCT GCGTATGTTG CTGTGAATGT TAAAAATTCA TCTTGGACTA 1980

CCATGAAATC TAATTTTTCA AACGCAGCTT GTACAAAATT AATATTTGAA TCCACAATAC 2040

CCGTATCTTC ACCATATAAG TACAATGAGT GTACTTCTCC GTCATGTATA CCTTCTACCA 2100

TTTCATGATT ATCTTTACCA GCTTTTGGAT TCAATTTAAC GCCATATTCT TTTTCAAATT 2160

TAGCGCGAAT ATCATCCGCT TCAATACTTT GATAACCAGT AATCTTATCA GGCATACTTC 2220

CCATATCACT ACATCCTTGA ACATTATTAT GTCCACGTAA TGGATACGCA CCAGTACCAG 2280

GACGACGATA ATTACCTGTT ACTAATAATA AGTTTGAAAT CGCTGTACTT GAGTCACTAC 2340

CAATGTCTTG TTGTGTAATA CCCATTGCCC AACAAATTAC AACAGATTCA GCTTTAGCAC 2400

ATTCTTCAGC AAATTTAATC AATTCTGATT CAGGAATACC TGTTGCTTCT TCAGCAAAAG 2460

CCATTGTAAA TGTTTCTAAT GATTTGTAAT ATTCATCAAA ATCATCTACC CACTCATCAA 2520

TAAATGCTTT ATCGTGTAAA TCATGATCAA TAATATACTT AGTCACTGCA CTTAACCACG 2580

CTAAATCCGT ACCTGGTTTA GGTTGATAAA AACGATCCGC ACGTTCTGCC ATTTCATGTT 2640

TTCTAATATC AAATACATGT ATTTTTTGAC CAAATAATTT TTGTGCACGT TTCATGCGTG 2700

ATGCGATAAC TGGATGAGCT TCGGCTGTAT TAGTACCTAT CAATACAGAC ATTGCCGCTT 2760

TTTCTAAATC TTCAATACTA CCTGAGTCAC CGCCGTGTCC AACCGTTCTA AATAAGCCTT 2820

TTGTTGCAGG TGCTTGGCAA TATCTTGAAC AGTTATCAAC GTTATTTGTG CCAATAACTT 2880

GTCTTGCTAA TTTTTGCATT AAATACGATT CTTCATTCGT CGCTTTAGAA GAAGAAATGA 2940

ATGATAGTGC ATCTGGGCCA TGCTTTTCTT TAATAGCTGT AAAATTATCT GCAATGACGT 3000

TTAAAGCTTC ATCCCATTCT ACTTCATGGA ACTCACCATT TTTCCTTACT AGTGGTTTAG 3060

TTAATCGTTG ATCTGAATTA ATATGTCCCC ATGAAAACTT ACCTTTAACA CAAGTCGCAA 3120

TTTTATTTGC TGGAGAATCA TGTGATGGTT GTACTTTTAA AATTTCTCTA TCTTTAGTCC 3180

AAACTTCAAA TGAACAACCC ACACCACAAT AAGTACACAC TGTTTTAGTT TTCTTAATAC 3240

GCTCTTTACG CATTTCTGCT TCTGAATCTG AGATTGCAAA TAGTGGACCA TAACCAGGTT 3300

CTGCTTTTTT AGTTAAATCA ATCATTGCTG CTAATGAACC AGGTTCCGTA TCAGTCATAT 3360

AACCCGCATT ACCTTCCATA TTCACTTCCA TCATGGCATT ACATGGACAT ACCGTCGCAC 3420

ATTGACCACA AGATACACAT GAAGACTCAT TAATCGGTAC ATCATTATCC CAAATAACAC 3480

GTGGATGTTC ACGATCCCAA TCAATTCTAA TAGTTTCATT CACTTCGATA TCTTGACATG 3540

CTTCTACACA ACGCCCACAT AAGATACATT GATTTGGATC ATAACGATAA AATGGGCCGT 3600

AATCTTTTTC GTATGGCTTC TCTTTATATT CATACGTTTG ATGCTGAAGC CCCCATGCAT 3660

TATGCTTTTC TAAAATTCGA TCAAGCGCTT CTTTTTGAGC ATCTTTCACA TCATTGTTCA 3780

CAGTATTTAC AGTCATTGGA CGATCAATCA CCGTACTACA TGAACGTTCA ATTTTACCGT 3840

CAATCTCAAC AGTACATGTA TCACATGTTT GAATTGGTCC CATCGACTCG TTATAACAAA 3900

TTGAAGGTAC AAAAGTATCT TGTGATTTAA TAAATTCAAG TAAATTCGTA CCTGGTTCTA 3960

CAAGATAATC TTTTCCATCA AGTGTAACCA CCAAATGTTC TTGCATATTA CTCACCCCGT 4020

CTATATATAT TTTCCGTAAA TGACTTTTAA TAAATTGCTC ATATCCACCT AAAATAACGA 4080

TGCCCCACAC ATCTTTCAGA TAGAATTAAT TTAATTGTAT TACTTTATGT ACTAGTTGTT 4140

AAGTAAAATT TTGTATTTTG CCTTTTTACA ATCATTTTTA TTTGAAATAT TTTGCGCGAA 4200

ATTAAATCAT CTTTTTGTTT AATTGAAAAT AATTATCATT ATTAGTTTTC CAATTATCTG 4260

TTTCACGCTT TTTGCCATAT CTTTCACAAC CTTATTAATG ACAATATTTA ATAATCACCT 4320

CACCTAAAAA TCGTTATACT ATTTATAAAT ACCCTTTTTC TGAAAATTAA TAACCCAAGT 4380

TTGATAAATA TCTACTATCA TTTAGAAGGT AATATTTATC TTTAAATTAA ATTTGTAATG 4440

GATTAATTTA TAAAAATCAA ATCAGGCATT AAATAAAATA GCCCATAAAT ACAAAGTGTT 4500

ATCACCTTCT ATTTACGGGC TATTAGTTCT ATTCGTTATT CTATTTACAG ATCATTCTAT 4560

CTAATTAATT TGTGTACAAT TTTGATAACT TATTTTCCCT TAGTTTACTA CTCTAGATTA 4620

TCTTTTAATA ACTTAGTACT TTCAGCTTTT GACTGCTCAC TAGGAATGAA GTAGTACAAT 4680

CCGTCACTTT GAATGCCGCC TTGACCACTC AATTGATGTT TATTAATCGT GTCATTAGCA 4740

TCTTTATAAT TGCTTCTAAT CGTATTCAAA TCACCTAATG TTAAATCTGT TTTAACATTA 4800

TTTTGAATTT CATTCATTAG ACTATTAAAA TGTGTAATCG ATGATGGGCT TGCAATCTTA 4860

TTGGCCATCG CTTCAAGCAC AATTTGCTGA CGTTGTTGTC GACCAAAGTC ACCACCAGCA 4920

CCTTCTTCTT TACGACTTCT AATAAACTTC AATGCTTGAT CACCATTTAC ATGTGTCTGC 4980

TGTCCTTTTG TAAAACGAAC ACCATCAACA GTGAATGTAT CATTACTTAC TACATCAACA 5040

CCGCCGATGC TATCTATCAT ATTATGCAAA CCATCCATAT CGATTGTCGC ATAATGATCA 5100

ATTGGCACAT TCATTAATTT TTCAAGTGAT TTAACAGCCA TATTTGGTCC ACCATATGCA 5160

TAGGCATGTG CAATTTTTTC AGTAGTACCA CGGCCAACAA TTTCCGCTCT TGTATCACGC 5220

GGTATACTTA CTATTTCAGT TTTCTTCGTT TTAGGGTTGA TAGATAAAAT CATAATACTA 5280

tCACTACGCT CTCCGCCACC CTTTTTCTTA CGATCAGCAT CTGAATCGAC ACCAAATAAA 5340

GCGATTGTGA ATGGATCACC ATCGTTTAAA CTCACTTTTT TATCTCTTAA TTCTGAATGA 5400

TTGCGATCTA ACGGATTGTG TATCTTATTA CCAGTAATAA AAATTTTAGC AGCTACATAC 5460

GGTAGGCTCA TTTTACTTTT AGACGAACGT TTCAATCCCA CCACTCCTTT ACTATTCCTT 5580

ACATACTTTG TCTGTTTTCT CTATTTATTA TATAGTAAAA TAATTTTTTT ACTATACTTC 5640

TGTAGACGTA TAACTATTTT TTATCATTTT TTATCTCTAG AGAATATCTA TCTGTATTTT 5700

TGATAACCAC CATTTGCATT TAAAATTTTA AGTACCGTTT CATGACATGC TTTATTACTT 5760

ATAATAAAAG GTGCACCCTT TAAATGATCA ATTGCCTTAC CATCTAAAGT CGTCATTTTT 5820

AGATTCAATA GTTCTGCAAA TAAAAACTGT GCAGCAATGT CCCAAGGTTT AGGATTTGTA 5880

TTAATATGTG CCCCAAATTG ACCTTTTGCC ACTCGCATAG AATCTAATCC GCAAGCACCA 5940

ACTAAACGAT AACTAAATGA GGCGTCAAAT AAATCTTGCA CCGTATCTAG ATTCATCACT 6000

TGTGCATTAA ACGATATAAT AGCGTCTTCC AATTTTAACG ATGGTGGTTC TTCCATCTTA 6060

ATTCCATTAC AAAAAGCACC TTCTCCTCGT ATTGCTTTAT AAAGCTTTTT ATGCGGATAA 6120

TCATATACGT ACGATAACAT TGGTTTACCT TCATAAAAAT ACGCCAATAT AATACAATAA 6180

TCTTCTTGCT GTTTTACTAA ATTGGCAGTT CCATCAATGG GATCCATAAT CCATAAATGA 6240

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AAATGTGTTG CTAAAAATTG TTGGAATTGT TGTTGAATCT GTTTATCTAC ATTTGTAACT 6360

AAATCAAATC GATGACGCTT AGTTTCTGTA GTCATTTCCA TAATTAATTG CGGAATAACA 6420

TTGTCTATTT GTTTCAACCA CGAACATATT AACTTATCTA TTTGCTGTAA TGTTTTATCT 6480

GTCATTTCGT CCACCACTTC TCATATCATT ATCATTTTAT TATTACCCTA TATTAAAAGA 6540

ATCAACAATA CAACTGAAGA CTTCTTCATT TTATGCATAA AAAAATCGGC TAGTCACGTG 6600

CTAGCCGACA AATAGAAAGG AAAGTAAGTA ATAAATATTG AAGATGTTGT GATGTAACTT 6660

GAACGATTAA AAGCTATCTG TTATATAGCT CTACCCCTTT GTTTAATCGC TCCCCCTGTT 6720

ACAAGTAATA TCATAGCACA ATCTTTTTTA AAATGTAAGC GTTTTCCACA AAATTTTTAC 6780

GATTTTTTTA AAAAGATATT GAAAATGTCC TCATTGTCAC TCTTATGTTA TACTTTGTGT 6840

AATATATCAT CTTTTAGGAG GTGGCTGTCA TGAATAAAGC TGAAAGGCAA AATTTAATAA 6900

TTACTGCAAT TCAACAAAAT AAAAAAATGA CCGCTTTAGA ATTAGCTAAA TATTGCAACG 6960

TATCCAAACG CACAATTTTA AGAGATATTG ATGATTTAGA AAATCAAGGT GTTAAAATTT 7020

ATGCGCATTA TGGGAAAAAT GGTGGTTACC AAATACAACA AGCACAATCT AAAATTGCAT 7080

TAAACTTATC TGAAACACAA TTATCAGCCT TATTTTTAGT GCTTAATGAA AGTCAGTCGT 7140

ACTCGACATT ACCATATAAA AGCGAAATCA ACGCAATTAT AAAACAATGT TTAAGTCTTC 7200

CACAAACACG CTTAAGAAAA TTGCTTAAAC GCATGGACTT TTATATTAAA TTTGATGACA 7260

ATGTGATGTT AGTAGATCAT AGGGTTGATG ATAATATTAA AGCTGAAAAC GTTATATTTA 7380

TTGGCCTTTT GTGTAAACAT GGACATTGGC ATGCAGTCAT TTATGACATT GCTCAAGACA 7440

AAACTGCCGA ACTCGAAATT GAAAATATTA TAGATATTTC GTATTCATTC GGTAAGACGA 7500

TTCAAACCAG AGACATATCC ATTGATAACT ATCATCAATT TTTAAACCCC ATCGATTCCT 7560

AAAAAACAGC AGTAAGATGA TTTTCAATTA GAAAATATCT TGCTGCTGTT CTCTATTTAT 7620

ACAATACTTC GTATTGAATG GnTTCGCTTT CCTAGGGTGC CGTCTCAGCC TTGGTCTTCG 7680

ACTGGCACTG CTCCCTCAGG AGTCTCGCCA TTAATACTAC GTATTAACAT GTAATTTTAC 7740

TTTGAAATAC TTAAAAAAAT AAAACACTTT GCCCAACTTA CACTACCAAT AGAAACTGCT 7800

GTTAGAATTC CTCAAAATGA TATTTCGCGA TATGTTAATG AAATTGTTAA AAAGATAGCT 7860

GATAGCGAAT TCGATGAATT CAGACATCAT CGTGGCGCAA CATCCTATCA TCTAAAAATG 7920

ATGTTAAAAA TCACCTCATA TTCATATACT CAATCTGAAT TTTCTGGCCG TAGAATAGAA 7980

AAATTACTTC ATAACAGTAT TCGAATGATG TGGTTAGCTC AAGATCAAAC ACCTTCTTAT 8040

AAAACTATTA ATCTTTTTAG AGTGAATCCT AATACTGATG CGCTAATTGA ATCTTTATTT 8100

ATTCAGTTTC ATAATAAAAT GCATATCAAA AAAGCTGATT TCTATCAAAT AATTAATAGA 8160

AATCAGCTTT TTTCaTTGCC TAAAAACTTA ATGTCCCGAC CTCTTTATCT ACGCATAAAT 8220

ACTTATTACT GATATAACGA AAGAAACAAA ATTATTTGCT ATATGTAATG CAATTGTTGA 8280

ACCTAGGTTT CTTCCAGATT TTAAATAAGT GAAAACTAAT ATGATGGATA GTATGAGATA 8340

TGGACCAAAC TCAAACGGCG ACTTTGCATC AGTCACATGA ATAAATGCAA ATAAGAACAC 8400

CGAAACAATA CTCATAGCTA TAAAATTAAA CTTCTTACCT AATTCTCCAA TTAAAATATG 8460

TCTAAATACG ATTTCTTCAA CTATTGGACC TACAATCACA ATTAATAAGA ATGCTACAGG 8520

TAAAAATGCA GGCACTTCAA ACATTTTATT TAGCTCAAGT TCATTGGCTG TTtCACTATA 8580

TTGCAAATGT TTAGGTAGAA ACTGTGTCAT ATATTCATAT GTATAAATTA AGATGAGAGC 8640

AATAATATAC GTTATTGACA ATCTAAGCCA ATATTTTTTG ATATACGCAA AACCAGCTCG 8700

AAGCCTTGAT GGCATCACTT TTAAATGAAA TAAATAAAAT GCGCCAATCC CAATCGTATA 8760

TGCTAAAGCT TGTGTGATAG TCGCTACAAA TATCAGATTA CTATCGATTT CATAATAACC 8820

AAACAAAATT GGTCCTATGT AAGCTGCAAT TGTGAGTGCA TAAAATATAA CACCTATAAT 8880

TGGAATTATA AGCAAATCTC TCCATGCTAT ATCTTTAAAC GTGTATTTCT TTTTTTCATT 8940

TTCCaCTGTT ATATCCtTTC CTGTTTAATA ATTGATTTTT GGAGGTACTT CTACATGATA 9000

AACGAAACTA AGTATATGAG ACAACAAATT ACTAATTTGA TTCAAATCAT TGATACGATT 9060

ATAGTTACTA ATGAATTGAA TAAGTTCAAA GGCTTTGAAA CATCATATAT AATAAACGAA 9180

AATCAAGTTT CCTATTATGA AATTATAACA CTACTTAATA AACGTCCCCT CgACAAGTCG 9240

ACTATGGTAA CAAAATTCAA TATCTTAATT TTTATCATAC AGAACTATCT AACGCATTAT 9300

TTGCAATTAA ATTTGCCCAT TAACCTATTT TTCATAAAAT GTCATTTAAA CAAGTTATTT 9360

ATTAAAATTC ACTTTATTAC ATAAATTATA CAATTArAAA GTTTCTTCAA ATTGTAAAGA 9420

TGCATTAATC GAGTTATAAT CATAATGATT AAGATGGT 9458

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 910 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

AnGCGTATCA TGTCACGCAT TTTAACTACT TCTTTACCAC AAGATTATAC AGTCACATTA 60

GTTGATCGTA TGCCATTTCA TGGATTGAAA CCAGAATTTT ATGCTTTAGC TGCGGGCACG 120

AAATCAGATA AAGATGTTCG TATGAAATTC CCTAATCATC CACAAGTGAA TACAGTTTAT 180

GGTGAAATTA ACGACATAGA TTTAGATGCT CAAATTGTCT CAGTCGGTAA TTCTAAAATT 240

GATTATGATG AGCTAATCAT TGGTTTAGGA TGTGAAGATA AATATCATAA CGTTCCAGGA 300

GCCGAAGAAT ATACACATAG TATTCAAACA CTCTCAAAGG CTCGGGATAC TTTCCATAGT 360

ATTAGTGAAC TACCAGAAGG TGCTAAAGTC GGTATCGTTG GTGCTGGATT AAGCGGCATA 420

GAACTTGCCA GCGAATTAAG AGAAAGTAGA TCAGACTTGG AAATATATCT TTATGACCGT 480

GGGCCGCGAA TTTTAAGAAA TTTTCCAGAA AAATTAAGTA AGTATGTTGC GAAATGGTTC 540

GCCAAAAATA ATGTTACCGT TGTTCCAAAT TCAAATATTA ATAAAGTTGA ACCTGGTAAA 600

ATATATAACT GTGATGAACC TAAAGATATT GATTTAGTTG TATGGACAGC AGGAATTCAA 660

CCTGTTGAAG TTGTTCGTAA CTTGCCGATT GATATAAATA GTAATGGACG CGTGATAGTT 720

AACCAGTATC ATCAAGTACC AACATATCGT AACGTCTATG TAGTTGGTGA TTGTGCTGAT 780

TTACCACATG CGCCAAGTGC TCAGTTAGCC GAAGTTCAAG GTGATCAAAT TGCCGATGTG 840

CTTAAAAAGC AATGGCTAAA TGAACCATTA CCTGACAAAA TGCCGGAACT AAAGGTACAA 900

GGTATCGTTG 910

(2) INFORMATION FOR SEQ ID NO: 116:

(A) LENGTH: 10182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

TTTTTGATTC AAAGTGGTGA TTTAACAAGC ATTTTAAATA GCAATGATTT GAAAGTCACA 60

CATGATCCTA CCACTGATTA TTATAATTTA TCTGGTAAGT TGTCGAACGA TAATCCAAAC 120

GTTAAACAAT TAAAACGTAG ATATAATATT CCTAAAAACG CATCAACAAA GGTGGAATTA 180

AAGGGAATGA GTGATTTAAA AGGCAATAAT CATCAAGATC AGAAACTTTA TTTTTATTTT 240

TCAAGTCCTG GAAAAGACCA AATCATTTAT AAAGAAAGCC TTACTTATAA TAAAATAAGT 300

GAACATTAAT ACTTATGCTG TAATTATAGA AACATCCAAA TCATCTATTA nAATCCTATA 360

TTATAAAAAnC ACCTCACATA ACTCGTTCAA CTGTACCAAA CCACATTACA TTAGATTTTA 420

GGCTAACTAT TGTGATGTAC ATCAAAAACG AATTTGTGAG GCGTTGTATA TTTTACAAAG 480

GTGACTAGCG TTTCGTATAG CATTTCCAAC ATTACTACAC TCAAGCGTCA CGCTAAAGTT 540

CGAAATCGAA TCCTTTCATT CAACAAAAGC TCATATCCAC TACAAACTTC ATATCAAGCG 600

TATAAACTAT CTTGTGATAC TATCTCGATC ATATCTATAG TATGCATTTG TGTTCCGTTT 660

CACTGAAGTA TATGTATCAT CAGTTAAGTA TAAACCGTCA TCCTTCAATG TTACTTGATA 720

AGCATATTTC CGTGCTAACC AGGCAATATC TATATAATTT TCTCCTGCGT TTTCATAACT 780

TCTTAAATCT TCAATATGTG CACTAACTTC AGGGaAAATG ATTCTAACAA CACTTTCATC 840

AACCCAATAT TTGTCATGCA TCCATCGCAC TTGATCTGCC AATAAAGGTA ACTGCACATC 900

ATTGAAATAT AGACGAAAGC CGTCACTATC ATACATTTGC CGATATGGTA ATGGCTGTTT 960

TCTAATCACT AACACCTCGC CACCCATTAC GGTGCCTTCT CTAGTATCAT CACTTCCACC 1020

CGAAGCTTCA TACGTTGTTG GGTCAACCTG TAGTCCATGT ACATCTCCAA TATAAGCATC 1080

TGGTTTATGT TCCATTGCAT GTCCATGTGC AATCAATGCT AATATTGTAG ATTGTGAAAA 1140

TTGAGGCTCC CATTCAATGC GATTAGGATG GCTACTATAA ATTCTAGGTT CATCTATAGC 1200

CTGCTGAATA TCCATGCCAA ACACTAATAC ATTGATTAAT GTTTGCGCAA CACTAGCAAT 1260

GATACTTATG GCACCAGGTG CACCTACTGT TAATATTGGC TTCCCGTGAT ACATCACAAT 1320

CGTTGGAGCC ATGTTACTTA GTGGTCGTTT ATATGGTGCA ATTTCGTTAA TACCACCATC 1380

TACTACATCA AAGCCATCCA TTGTCGTATT CAATAACACA CCGTAGCCTG GAATCGTGAT 1440

ACCTGAACCA TAAATCATAC CAATTGATGT CGTAAATGAA GCAATATTAC CTTCCTTATC 1500

ATCAGACACA ACACCATGCT CTATATCAAT ATTTGCTTTA TTGCTATCAA TGAGCGTACT 1620

GCGTGCTTTT AAATAATCAT CATCAATTAA TGACTGTACA GGCACCTCAT GAAAATTATC 1680

ATCCGCCAAG TATTGCGCAC GATCACTATA TGCTAAATGC ATCGCTTGTA TCAAATGATG 1740

CAAGTAATCA ACAGATCTTG GACCCATAGA TGGTAAATCG ACATGTTCTA ATAACTTCAA 1800

TATTTGAATT ACCGTGATAC CGCCAGAACT AGATGGTCCC ATTGaATAAA TGTCATAGTC 1860

TTTAAATGTT GCACTGATTG GCGCTTTAAT CTGAATGTCA TATTTGGCTA GATCCTCTAA 1920

AGTGATTGTC CCACCACATG CTTTGACAAC ATTGACTAAT TGTTTCGCAA TGTCACCTTT 1980

ATAAAATGCA TTAAACCCTT GTTCTCTTAA TATTTGAAAT GTCTTACCTA ATTCGGGTTG 2040

TACAATCCAA TCACCTTCAC GCCAATATTG ATTTTCATGC GTAAATACTT GTGCCGTTTC 2100

ATGATACTTT GTCAATCGTG CGTGTTGCTG GCGCGAATAT TTTTCAGTAG CCCAATTGGC 2160

TGCATGACCT TCAATGGCTA GTTCAATTGC AGGATTAATT AAATCTTCCA ATGACAATTT 2220

AGCATAACGC TTGTGAATAT AATCAAACAG CTTTGGAATT GCTGGCACAG CGACAGTTTT 2280

ACCATGTGTA GTCATATCAA AAAATGATTT ATATTCGCCT GAATCATCTA GATAAAATTG 2340

TTTGTCTACA TGTTCAGGTG CTGTCTCACG TGCATCAAAC GCAGTTATAC TGCCAGTACT 2400

TTGCTCATAA TATAGCAAAT ACCCGCCACC ACCAATACCT GATGCAAATG GTTCTACCAC 2460

ATTCAATGCC AGTTGAATTG CAATCACTGC ATCCATGGCG TTGCCACCTT GATCTAATAC 2520

ATCCTTACCA ATTTTAGCCG CAAGAGGATG TGATACGGAA ATTAACCCTT CTTTAGATGT 2580

TTTTGTCTGT TTGTCATTTA AGTTAATGAC CATACTATAT CCTCCTACTT TCTGTTAAAT 2640

ATTTAAAACA TTATTGATTA ATGGCTTTTT CTACTTTTTC TAAATCTTGA CGTTGCTCGT 2700

TACCAGTATC GACAAGTGGT GTAATCGGTG ATGCAATTTT AAATTTATCG CCACGATAAA 2760

ACTTAATAAA TTGATCCTGA TCTATCGCAT TAACTACTGC TTGTCTCAAG TTTGGATGCG 2820

TCTTAAATAT ACCTTTTTTA ATATTTAGCA TTAAAAAGAC TGACTTGCGT CCATTTTTGC 2880

GAATAATGCT TAAATTTTTA TCCGACTTAA TTAAATCAAA ATGTTTTTGA TTCACATCTG 2940

CCAACATATC AATTGAATGA TTTCTAAGTT CTGACAATGC ATTATTCGGG TCACCATTAA 3000

ACTTCAATGT AATATTTTTA ATTTTAGCTG GTCCATAACT ACCTTTTTCT GTTTCGTTGA 3060

ATCCTGGATT ACGTTGAAAC GTTGCTTGAT ATGCATTTTT CTGTGTCATA ATGTATGCGC 3120

CACTTGCATA CAGCGCATTT TTCCCATCTG AATTTGCAGG AATTGTACTG CTATCCCCAT 3180

ATCCTTTTGG ATATTCTTGA TTTACTTGAT TAACAAATTT TTTAGATAAA ATGCCTGCCG 3240

AAGAGTGTGT TAAGTAATTT ACCTCTCGAG GCATCGATTG ATCTGTCGTA ATTTTAACAA 3300

TATAAGCTTT AATCAACTTA TCATAGATTG ATTTATCGTC CTTGTCTTTC TCTTTACGCA 3420

ACTGATCGAT GTCCTCATCT TTTAATATCT TGATGTCATT TATATGTTTG TGCATATTGT 3480

AAGTATTATT GTTAGGCACA GACTTTTTAT CACGTGCTCT ATCTAAAGAA AACTTAACAT 3540

CTTCAGCCGA TACACGCTCT CCAGTATTAC GTGCTTGTCC ATTGACCACT TTCGCAAAAT 3600

AATCATCATC TCTTAACAAG AAATAAAATG CTTTATTGTC CTTATTCACA GCATAATCAT 3660

GACTTAACGA ACCTTTCGTT GTTAAATGAT CATTTTCATC TAATAATAAT AACCTTGTGT 3720

ACATATTCAT ATTAATTGAA TATACTGACG GCGCAATTGA ACGTATTGGA TCCAATGTAG 3780

GAATTTCACC ATCTTGTTGT GTCATCACAA GTGGCCGCGT ATCTCGTTCT CTACTATTGT 3840

TGTAATCAAA TTGTTGCCAT ATTAATGCAC GTGAATTTGG CAATCCAACA CTATTTTTAT 3900

CTAACACTTT ATTGTCATAT ACTAAATTCT TTTTTGATCC ATATAAAGGC GCCATATACC 3960

CTTTATCAAA TACAACTTCA TCTTCAATTT GCTTATATGT TTGTTTAACA TCTGCTTCAT 4020

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ATCCTGTAGA ACTAAATAAT GCCGTCATAG CATAGTTCGG GTCACCAAAC ACTGTCATCC 4140

AGTCATCAAT TTGGATATCA TAATTGCCGG CTTGACGTTG TGTACGATAG CTACCATAAT 4200

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CTTCAACTTT CGATGACTTT TGAGCCACTT CTGATTTCGT AGGGACACCA CAACCACTTA 4380

ATACCAACGC TAAAACTATA ATTGCGATAC TAATGATTTT CTTCACATCT ATCCCTACCT 4440

TTTTAATGAA TTCTTGGATC TAGTGCATCA CGCACTGCAT CACCTATAAA ATTAAATGCT 4500

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CCTAGGAAAC TTAAACTACT TGTTGTTAAT ACAACCACAC CTATATTTAA TGAAAAACGT 4680

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CGCATTGTCC GTGCAAATGA TGGTATATTA CCGATACTTA AAGCAATAAT TAAATTTGGA 4860

ATACTTGCTC CAAATGATGC AATAATTGCC ACCGCTAACA ATAATGATGG AATTGCAAAC 4920

ACTACATCTA AAATTCGCAT TATTAAATTA TCAATATGAT TAAAATAACC TGCGATAGTG 4980

CCTAGTAACA CACCAAAAAT AACTGCAATA ACTACTGAAA TAATTGAAAT TGAAAATGTC 5040

AGCTTCGTTC CTACAACTAC GCGTGTAAAT AAGTCTCTAC CGAAATCATC AGTACCAAAC 5100

GTATCAAATG TAAATTGTGA CACAATTGAT AATGTCAGCA TGTAGACTAA AATAAGTAAC 5220

CCGATAATCG CAATACGATG TCTAGTAGTT TTTCGTATAA ACGATTCCCA CCCGTTATAA 5280

CTATGTATTT GCGATGTACG TTGGTAACGT CTAATACTTA CAAACATTAA TAATGTAAAT 5340

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TTGTTCCAAT GACAAGTACA GGTAAAATCA ACGATATTGG ATGTTCTGGC ATATAAGATG 6060

GTGGCAAAAT ATCCAATTTC AATGAGAACG CTAAAATGAA TAATAGCCCT TGCCAGAAAC 6120

TTGGAATAGA TAAACCAATT AATGCAATTA TCATTAACGT GATATCAAGC CAACTATTTC 6180

GCTTCATCGC ACTGATAATA CCAATTGGTA TTGCAATAAT TAATGCCACC ATTAGCGCTA 6240

ATACTGCGAC AATTATTGTA ATTGGAATTC TTTCGCCAAC TGCTTTAGTC ACAACCTCAT 6300

TCCCTTTGTA AGTCGTACCT AAGTCAAAGG TAAAAACACC CTTGATGGTA TCCCACAATT 6360

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TTGCATTTTG TCCCAGTATG CTATAAGCCG CATCAAGCGG TGAAAAATAC AGAATGGTAA 6480

ACACACTGAC AATAACACCA ATGATGACAA TCACAGCCAT GACAATTCGT TCAAAAATAT 6540

ATCTAACTAA TGGCTGTAAA TAAAAAGTCA ATAAGATGAA CATCGGCAAG GCCAATATCA 6600

CTTTGATCAT GATGAACTTA TGAAATAATA CATTTTCAAA GTATGTTGAA AAATGTGCTT 6660

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TATGTATTTG TGTGGATGAC TTTTGCTGCG ATAAATATTT ATATTTTTGA TGTAACGCCT 6780

GTTCAATTTC TGAAATTTCA GAATTATTAG CGTAAAAATT TTTCCTCTTA GCAGAAAAGA 6840

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TCACTCACGA TTTAGGCGCT GTGTATCAAT TTTGCGACGA TGTGATTGTA ATGAAAGATG 7740

GAAGTGTCGT TGAAAGTGGC ACGGTTGAAA GTATTTTTAA ATCGCCACAA CATACCTATA 7800

CAAAACGCTT AATAGATGCG ATTCCTGATA TTCATCAAAC GCGTCCGCCA AGACCGTTAA 7860

ACAATGATAT TTTATTAAAA TTCGATCGCG TGAGyGgGAT TACACATCAC CGAGTGGCAG 7920

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AGACTCCAAG TATCTATTCA TAATTTCTAG GTGATGCATG ATAGATAACC TTTTAATTAA 10080

ACCTAATCCT GGATaCTTAT TATTTTCATT TAATTCTTCA AATTGTCCCA AGCGCATAAG 10140

ATCTATTTTT AATATCTAAG TTTTTTGACC ATGTTACTAA TT 10182

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AACTCAGGCA ATTGAAACAG CATTAGGTGC TTCATTACAA CATGTCATTG TAGATTCAGA 60

AAAAGATGGA CGCCAGGCTA TTCAATTTTT AAAAGAACGT AATTTAGGTC GTGCGACGTT 120

TTTACCATTA AATGTTATAC AGAGTAGAGT GGTAGCGACT GATATTAAAT CTATTGCTAA 180

AGAGGCAAAC GGATTTATTA GTATCGCTTC GGAAGCAGTT AAAGTAGCAC CAGAATATCA 240

AAATATTATC GGGAATTTAT TAGGTAATAC GATTATCGTT GATCATTTAA AGCATGCAAA 300

TGAATTGGCA CGTGCGATTA AATATCGAAC TCGTATTGTT ACTTTGGAAG GTGATATTGT 360

AAATCCTGGT GGtTCTATGA CTGGTGGTGG CGCTCGTAAG TCAAAAAGTA TTCTGTCTCA 420

AAAAGACGAG TTGACAACAA TGAGACACCA ATTAGAAGAT TACTTGCGTC AAACAGAATC 480

ATTTGAACAA CAATTTAAAG AGTTGAAGAT AAAAAGTGAT CAATTAAGTG AACTGTATTT 540

TGAAAAAAGT CAAAAGCATA ATACACTTAA AGAGCAAGTG CATCATTTTG AAATGGAGCT 600

CGATAGATTA ACTACACAAG AAACACAAAT AAAAAATGAT CATGaAGAAT TCGAATTTGA 660

AAAAAATGAT GGTTATACGA GTGACAAAAG TCGACAAACT TTGAGTGAAA AAGAAACTTA 720

TCTAGAAAGT ATTAAAGCAT CTTTAAAACG ACTAGAAGAT GAAATTGAAC GCTACACAAA 780

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AAATAATCAA AATCAACAAA CTAAACATCA ATTAAAAGAT GTTAAAGAAA AAATTGCATT 960

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TGGTCAACAA GAAACGAGAA CACGCTTATC AGATGAATTA GATAAATTGA AACAACAACG 1080

TATTGAGTTG AATGAACAAA TCGATGCGCA AGAAGCTAAA CTACAAGTTT GTCACCAAGA 1140

TATTTTAGCT ATCGAAAATC ACTACCAAGA TATTAAAGCT GAACAATCAA AGCTAGATGT 1200

ATTAATTCAT CATGCGATAG ATCATTaAAT GATGrATATC AATTGACTGT TGAACGTGCG 1260

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TAAATGAACG TTATACATTT TTAAGTGAAC AACGTACAGA TCTTCGTAAA GCTAAAGAAA 1440

CATTAGAGCA AATTATAAGT GAAATGGATC AAGAGGTTAC TGAAAGATTT AAAGAAACTT 1500

TCCATGCTAT TCAAGGACAT TTTACAGCTG TGTTCAAACA ATTGTTTGGT GGAGGCGATG 1560

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AGATAAGTTT GCAACAAATA AAGAAAATGA AGAAGTTAAA TCCTTAACAG AAGAACAAGG 2040

TCAAGACAAA TTAGAAGATA CACATTCTGA AGGTTCAACG CAGGACGCAA ATGATTTAGC 2100

AGAAAATGCT GAAGTGAAAA AGAAGCCACG CAAGTTGAGT GAAGCGGATT TTGATGACGA 2160

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CATTTTAATG GTTGGTGTGA ATGGTGTTGG TAAAACAACA ACAATTGGAA AATTAGCTTA 2580

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AAAGGACGAT AATCATGGGT CAAAATGATT TAGTtAAAAC GTTACGAATG AATTATTTGT 3240

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TGAAGATTAT TCTTTAAGTG AAATCGCAGa TACTTTTAAT GTGAGTAGaC AAGCAGTTTA 3360

TGATAATATA AGAAGAACTG GCGATTTAGT TGAAGATTAT GAAAAGAAAT TGGAATTATA 3420

CCAGAAATTT GAGCAACGCC GAGAAATATA TGATGAAATG AAACCACATT TAAGTAATCC 3480

AGAACAAATA C 3491

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AGTACGTTTT ATAATTATAA GTACGTAATT AACATATTAA CATATCGCAA GTATGTATTT 60

AAATAAgATT GTTATAATTT CAAAGTTCAT CCAAGaTTAT GGCGTTTGCA TTTACCTATT 120

AAAAACGTTA TTATATCAAA GATGCGAAAG ATAATACGGG TTTATTTTAT GAAAGTGAGA 180

AGGATAAAAT GGATAATGAG CAACGCTTAA AAAGAAGAGA GAATATAAGG AATTTCTCGA 240

TTATAGCACA TATTGACCAC GGAAAATCTA CATTGGCTGA TAGAATTTTA GAAAATACCA 300

AATCAGTTGA AACAAGAGAT ATGCAAGATC AGTTACTAGA TTCAATGGAT TTAGAAAGAG 360

AACGTGGTAT TACAATCAAA TTAAACGCgT ACGTTTAAAG TACGAAGCTA AAGATGGAAA 420

TACTTATACA TTCCATTTAA TCGATACGCC TGGACACGTC GATTTTACAT ATGAAGTGTC 480

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TATTAACAAA ATTGATTTAC CTGCTGCAGA ACCTGAACGC GTGAAACAAG AAATTGAAGA 660

TATGATAGGT TTAGACCAAG ACGATGTTGT TTTAGCAAGT GCTAAATCTA ACATTGGAAT 720

TGAAGAGATA CTAGAGAAAA TAGTTGAAGT TGTGCCAGCT CCAGATGGTG ACCCAGAAGC 780

ACCACTAAAA GCGTTAATAT TTGATTCTGA GTATGATCCA TATAGAGGGG TAATTTCATC 840

GATAAGAATT GTGGACGGTG TTGTTAAAGC CGGAGATAAA ATTCGAATGA TGGCCACTGG 900

TAAAGAGTTC GAAGTAACAG AAGTTGGAAT TAATACACCT AAGCAGCTTC CAGTTGATGA 960

ATTAACAGTT GGTGATGTTG GTTATATTAT TGCAAGTATT AAAAATGTTG ATGATTCTAG 1020

GGTTGGTGAC ACCATCACAT TAGCTAGTAG ACCTGCATCA GAACCATTGC AAGGTTATAA 1080

GAAAATGAAT CCAATGGTAT ATTGCGGACT GTTCCCAATA GATAACAAAA ATTATAATGA 1140

TTTAAGAGAA GCATTAGAAA AATTACAATT GAATGATGCA TCATTAGAAT TTGAGCCTGA 1200

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ACAGGCTGCA ATAGGACAAA AAATTGTAGC GCGTACAAAT ATTAAATCAA TGGGTAAAAA 1860

CGTTTTAGCT AAATGTTATG GCGGTGACAT AAGCCGTAAA CGTAAATTAC TTGAAAAACA 1920

AAAAGCAGGT AAAGCTAAGA TGAAAGCAGT TGGTAATGTT GAAATTCCAC AAGATGCTTT 1980

CTTGGCTGTA TTGAAAATGG ATGATGAATA ATTTTAAAAA ATCAATTAAC AATTTACAAT 2040

GAATAAAGTT TAATAACTAA AAAGAGGGAG CCTAGGATAA ATTAACGTCC TGGGCTTTAC 2100

AATGTTATAT TGGCAGCCAT CGACAGAGTT AAAATGAGCT TATAACAATG GGGCCCCAAC 2160

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AGTGGTTCTT TATTATTTCT ATCTCACTCC CTCTAAACAA GAATAAATAT TAAAATGAAT 2460

CGATATATTA GACAATCATT GATTAAACGT TAAAGTTAAA AGTAAGAATA ATTGCAGATA 2520

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CAGGCGAGTA TACATTTGAA GCAAATCCTG ATGAGTTAAC TAAAGAGAAA GTCCAACTAT 2880

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TTGAAGATTT TGAACAAAGT TTAGATCTAG CTTTAGATAT GGATATTCAA CATATTTCGA 3120

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TAAATAAAGA AAGTAAAGCA ATTTTAGTAT CAAATAAACC TTCTTTGACT GAGAGAATGG 3480

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GTAATGAGGT TTTTGAAGCT TTCCTAATAA ATGATTAAAA AAAATTGAAA TTTCGAGTCT 3720

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TGCTAATGAG GTGAAAACAT GATTACAGAT AGGCAATTGA GTATATTAAA CGCAATTGTT 3840

GAGGATTATG TTGATTTTGG ACAACCCGTT GGTTCTAAAA CACTAATTGA GCGACATAAC 3900

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ATCGAGAAGA CACATAGTTC TTCAGGGCGT TCGCCATCAC AATTAGGTTT TAGGTATTAT 4020

GTCAATCGTT TACTTGAACA AACATCTCAT CAAAAAACAA ATAAATTAAG ACGATTAAAT 4080

CAATTGTTAG TTGAGAATCA ATATGATGTA TCATCAGCAT TGACATATTT TGCAGATGAA 4140

TTATCAAATA TATCTCAATA TACAACTTTA GTTGTTCATC CTAATCATAA ACAAGATATT 4200

ATCAATAATG TACACTTGAT TCGTGCTAAT CCTAATTTAG TTATAATGGT TAT 4253

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TCCCTAATCG AACAAAATTA TGCGCATAAA CAAAGTAGAT TGATATAAAA TTCTTAATTA 60

TCAGAATATA TTTACAAATC TGAATTTTAT TAGTATATTG GrTAGTrTTC ATAGAGGCAT 120

GACGGTaTTT GAGCAGGATT TTAAATCGGg ATTTTATAAT CGATTTAAGA GAGGCCACtT 180

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TTTTCTAACA ATTTTGCACA TTATATGTTT AAAATCAATT TCATGTTTAT GGTCTGATTG 3360

GCTAGTGTGT ATGAAATGTA AnTCTTTGAC TnnGA 3395

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13508 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

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ATTTATTTAT TATTACGTCT ACTCATGGTG AAGGAGAACC GCCTGATAAT GCATGGGATT 180

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AAGAAGACGC AGAAAAGTGG ATGGCAGACA TCATTAATAT TATTGATACC ACATCAGAAG 420

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CAAAATATGG TAGATAACGG TGTCGTCATA TGGAAAGAAA AAGAATTTGA ACCAAGCGAT 1860

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GTTGTATTTC CAAGTGCACT ACACCGCGAC AAGCTAACTA TCAGTGTATC AACTGATGGT 2040

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CTGCTAATAA TGTTACGAAT ATTGCCTTGG AACTTGGCGG TAAAAATCCA AACATTATCT 11640

TTGATGATGC TGATTTTGAA TTGGCAGTAG ACCAAGCGTT AAATGGTGGA TATTTCCATG 11700

CAGGTCAAGT TTGTTCAGCA GGATCAAGAA TATTAGTACA AAACAGTATT AAAGACAAAT 11760

TTGAGCAAGC ACTTATTGAT CGCGTGAAAA AAATCAAATT AGGTAATGGT TTTGATGCTG 11820

ATACTGAAAT GGGACCAGTG ATTTCAACAG AACATCGTAA TAAGATCGAA TCTTATATGG 11880

ATGTAGcTAA AGCAGAAGGC GCAACAATTG CTGTTGGTGG TAAACGTCCA GATAGAGATG 11940

ATTTAAAAGA TGGTCTATTC TTCGAGCCAA CAGTCATTAC AAATTGTGAT ACGTCAATGC 12000

GTATTGTACA AGAAGAGGTT TTCGGACCTG TCGTTACTGT AGAAGGCTTT GAAACTGAAC 12060

AAGAAGCGAT TCAATTAGCG AATGATTCTA TATATGGTTT AGCAGGTGCT GTATTTTCTA 12120

AAGATATTGG AAAAGCACAA CGCGTTGCTA ACAAGTTGAA ACTTGGAACG GTGTGGATTA 12180

ATGATTTCCA TCCATATTTT GCACAAGCGC CATGGGGTGG ATACAAACAA TCAGGTATCG 12240

GTAGAGAATT AGGCAAAGAA GGCTTAGAAG AGTACCTTGT TTCAAAACAC ATTTTAACAA 12300

ATACAAATCC ACAATTAGTG AATTGGTTTA GCAAATAAAA ATTAGATAAG GTGAGTGCCA 12360

TTGTAAGAAC ACAAGACACT CACTTTGTTT TGTATAAGTG GCGAAATGTT GATTGATAAT 12420

TTGGACTAAA CGCAAAATGA ATCATAGATT ATTTCATTAC TGTTAGTAAC AATCGTAAAA 12480

GGAAAAGCGA GTGTTTTGGT TAGCTAAGTT TAGCAATTCA ACGATAACCA ATCAGCCACT 12540

AACAAATATT TCATGCAATA CTCACTTTGA AATACAACAA ACTTTGGAGG TCATAACGAT 12600

GAGTAACAAA AACAAATCAT ATGATTATGT CATCATTGGA GGAGGCAGTG CAGGTTCTGT 12660

ACTAGGTAAT CGTCTGAGTG AAGATAAAGA TAAAGAAGTC TTAGTATTAG AAGCGGGTCG 12720

CAGTGATTAT TTTTGGGATT TATTTATCCA AATGCCTGCT GCGTTAATGT TCCCTTCAGG 12780

CAATAAATTT TACGATTGGA TTTATTCAAC AGATGAAGAA CCACATATGG GCGGTCGTAA 12840

TCAACGTGGT AATCCAATGG ACTATGAAGG CTGGGCAGAA CCAGAAGGTA TGGAAACTTG 12960

GGATTTTGCG CACTGTTTAC CGTATTTTAA AAAATTAGAA AAAACATACG GTGCAGCGCC 13020

TTATGATAAA TTTAGAGGCC ATGATGGACC AATTAAGTTA AAACGAGGGC CAGCAACGAA 13080

TCCTTTATTC CAGTCATTCT TTGATGCAGG TGTTGAAGCA GGCTATCATA AAACACCTGA 13140

TGTGAATGGA TTTAGACAAG AAGGTTTTGG ACCGTTCGAT AGTCAAGTAC ATCGTGGTCG 13200

CCGAATGTCA GCTTCAAGAG CATATTTACA TCCAGCGATG AAGCGTAAAA ACTTAACCGT 13260

TGAAACACGT GCCTTTGTAA CTGAAATTCA TTATGAAGGT AGAAGAGCAA CTGGTGTTAC 13320

GTATAAGAAA AATGGCAAAC TACATACCAT CGATGCTAAT GAAGTCATTT TGTCTGGTGG 13380

GGCATTCAAT ACGCCACAAT TACTACAATT ATCTGGTATC GGTGATTCAG AGTTCCTAAA 13440

ATCAAAAGGC ATTGAGCCAC GTGTTCATTT ACCTGGTGTG GGTGAAAACT TTGAAGATCA 13500

CTTAGAGG 13508

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7646 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

GTAAGTATTG TCTTGATTTC CTAATAAAGT TATATCTTGT AATTCATCTT GTTGACGGCC 60

ATGTGCCATA TAAAGCGCTC CTTTAAATTT ATTTTTTTAT TATTTTGGCG TCTCGGCGTG 120

CTTTTTCAAA CATGTAATAA CTTGCACCGA TAATAACGAC GTAACCTAAT GTTGCATAGA 180

AATCTGGAGA TTCTCCGAAT AGAATAAATC CAAGTATTGC TGTGAAAATT ATAGATGCAT 240

ACGTAAAAAT AGAAATATCT TTTGCTGCTG CAAAACTATA TGCTAAAGTA ACACCAATTT 300

GACCCACAGC GGCAgCTAAG CCAGCCCCTA ATAGATAAAG TATTTGCATC TGACTCATTG 360

GTTCATAAGT ATATGCAGTG AAAGGTATTA AAACGATGAC AGAAAATAAG GAGAAGTAAA 420

ATACTATAGT ATATGGTGCT TyTCTTGTAC TAAGTGCTCG AACACATGTA TATGCTGATG 480

CTGCAAAAAT ACCTGAGAAT AAGCCAGCTA ATGATGGAAT CATAGATGAT GAAAATTCAG 540

GTTTCACTAT TAAnAGCAaC CTAAAATAGC AATTATCATT GCTGTAATTT GaTACTTCCT 600

TACCTTTTCA TGtAAGAaaA CAATGCTTaA TAAAATCGTC CAGAAAGGAT TGAGTTTCAT 660

TAATGAATCG GCATCACTAA GTACCATATG ATCAATGGCA TAAATATTTA ACAATACACC 720

TGGCTGATGG TATTTATATA TAAAAAATAA TGGAATAAAC ATTGCTACTA AGTTTCGTGC 840

TAATGATTTT TGAAAAACAG GAAGGTCACC TGCAAGTCTG AAAAACACTG ACATAAAACT 900

GAAACCAATA GCCGAAATTA AAATGGCAAT GATACCTTTT ACTTTAGGAT TCAATTTTAT 960

CGCCTCTTTT ATATAAAATT AACGTATTTA TATTAGCATA AAACAACATG TTGTGCATAA 1020

ATAGTTGAAA TTTACTATAA AAAGACTATA ATAGACTGTA GCGAACAAAC GTTCTGTGTT 1080

TATTTGTCGG AATAATAGGG CATTACACTT TTATGAATGT TTGTGTTATT ACATAAAACA 1140

AATATCAATT CAGTATCAAG CTAATAAGCT TTTTCTTGAT TTCTGTTGAT ACAATTGAGA 1200

TTGACACAGA TTTAAAAAAA TCAAGTGATA TCTACTAAAA AATTTTTTTA AATTTGTTCA 1260

AGTTTTTCTA ATTTAGTATT GGTGCCTAGT TGGAACGTTT TACGAACATT CGATTAGAAA 1320

ATGGCACTTT AAATCATAGT GTGTCTTATG TATAATGAAA CACATAATAT AGTGTTGGTG 1380

AAACGAAAAA gACACAATAT CTTGTGTTTT GTATGCAAAT GCTTTATTTA TGAAGAAATT 1440

ACATTTAAAA GTAATTTAAC ACAGAAATTT AATAGTTATT ATCAATTAAT AGTCATATTT 1500

TTAGAAAATG TACTGAGCAA ATGGAAGATA TCCAATGATG TAAACACTAC ATATAGTGAT 1560

TTTTATACAT TCAACCCATA TAAGCTACTA TTTTCTCAAA TATAAATCTA TGCAATTGGT 1620

TTACATTTGA GAAAATAAGT AGCTTCATTA TAGTTAATAC AATGCTGAGA TAACCATAGT 1680

AACCATGTTG TTAAAGCATT TTTTAATTGG AATGACTACT TTATTTAAAA GGGTTGAAGA 1740

AAGAAGGTGA TCCAATGAAA ATAATATATT TTTCATTTAC TGGAAATGTC CGTCGTTTTA 1800

TTAAGAGAAC AGAACTTGAA AATACGCTTG AGATTACAGC AGAAAATTGT ATGGAACCAG 1860

TTCATGAACC GTTTATTATC GTTACTGGCA CTATTGGATT TGGAGAAGTA CCAGAACCCG 1920

TTCAATCTTT TTTAGAAGTT AATCATCAAT ACATCAGAGG TGTGGCAGCT AGCGGTAATC 1980

GAAATTGGGG ACTAAATTTC GCAAAAGCGG GTCGCACGAT ATCAGAAGAG TATAATGTCC 2040

CTTTATTAAT GAAGTTTGAG TTACATGGAA AAAACAAAGA CGTTATTGAA TTTAAGAACA 2100

AGGTGGGTAA TTTTAATGAA AACCATGGAA GAGAAAAAGT ACAATCATAT TGAATTAAAT 2160

AATGAGGTCA CTAAACGAaG AGAAGATGGA TTCTTTAGTT TAGAAAAAGA CCAAGAAGCT 2220

TTAGTAGCTT ATTTAGAAGA AGTAAAAGAC AAAACAATCT TCTTCGACAC TGAAATCGAG 2280

CGTTTACGTT ATTTAGTAGA CAACGATTTT TATTTCAATG TGTTTGATAT TTATAGTGAA 2340

GCGGATCTAA TTGAAATCAC TGATTATGCA AAATCAATCC CGTTTAATTT TGCAAGTTAT 2400

ATGTCAGCTA GTAAATTTTT CAAAGATTAC GCTTTGAAAA CAAATGATAA AAGTCAATAC 2460

TTAGAAGACT ATAATCAACA CGTTGCCATT GTTGCTTTAT ACCTAGCAAA TGGTAATAAA 2520

ACATTTTTAA ACGCAGGCCG TGCGCGTCGT GGTGAGCTAG TGTCATGTTT CTTATTAGAA 2640

GTGGATGACA GCTTAAATTC AATTAACTTT ATTGATTCAA CTGCAAAACA ATTAAGTAAA 2700

ATTGGGGGCG GCGTTGCAAT TAACTTATCT AAATTGCGTG CACGTGGTGA AGCAATTAAA 2760

GGAATTAAAG GCGTAgCGAA AGGCGTTTTA CCTATTGCTA AGTCACTTGA AGGTGGCTTT 2820

AGCTATGCAG ATCAACTTGG TCAACGCCCT GGTGCTGGTG CTGTGTACTT AAATATCTTC 2880

CATTATGATG TAGAAGAATT TTTAGATACT AAAAAAGTAA ATGCGGATGA AGATTTACGT 2940

TTATCTACAA TATCAACTGG TTTAATTGTT CCATCTAAAT TCTTCGATTT AGCTAAAGAA 3000

GGTAAGGACT TTTATATGTT TGCACCTCAT ACAGTTAAAG AAGAATATGG TGTGACATTA 3060

GACGATATCG ATTTAGAAAA ATATTATGAT GACATGGTTG CAAACCCAAA TGTTGAGAAA 3120

AAGAAAAAGA ATGCGCGTGA AATGTTGAAT TTAATTGCGC AAACACAATT ACAATCAGGT 3180

TATCCATATT TAATGTTTAA AGATAATGCT AACAGAGTGC ATCCGAATTC AAACATTGGA 3240

CAAATTAAAA TGAGTAACTT ATGTACGGAA ATTTTCCAAC TACAAGAAAC TTCAATTATT 3300

AATGACTATG GTATTGAAGA CGAAATTAAA CGTGATATTT CTTGTAACTT GGGCTCATTA 3360

AATATTGTTA ATGTAATGGA AAGCGGAAAA TTCAGAGATT CAGTTCACTC TGGTATGGAC 3420

GCATTAACTG TTGTGAGTGA TGTAGCAAAT ATTCAAAATG CACCAGGAGT TAGAAAAGCT 3480

AACAGTGAAT TACATTCAGT TGGTCTTGGT GTGATGAATT TACACGGTTA CCTAGCAAAA 3540

AATAAAATTG GTTATGAGTC AGAAGAAGCA AAAGATTTTG CAAATATCTT CTTTATGATG 3600

ATGAATTTCT ACTCAATCGA ACGTTCAATG GAAATCGCTA AAGAGCGTGG TATCAAATAT 3660

CAAGACTTTG AAAAGTCTGA TTATGCTAAT GGCAAATATT TCGAGTTCTA TACAACTCAA 3720

GAATTTGAAC CTCAATTCGA AAAAGTACGT GAATTATTCG ATGGTATGGC TATTCCTACT 3780

TCTGAGGATT GGAAGAAACT ACAACAAGAT GTTGAACAAT ATGGTTTATA TCATGCATAT 3840

AGATTAGCAA TTGCTCCAAC ACAAAGTATT TCTTATGTTC AAAATGCAAC AAGTTCTGTA 3900

ATGCCAATCG TTGACCAAAT TGAACGTCGT ACTTATGGTA ATGCGGAAAC ATTTTACCCT 3960

ATGCCATTCT TATCACCACA AACAATGTGG TACTACAAAT CAGCATTCAA TACTGATCAG 4020

ATGAAATTAA TCGATTTAAT TGCGACAATT CAAACGCATA TTGACCAAGG TATCTCAACG 4080

ATCCTTTATG TTAATTCTGA AATTTCTACA CGTGAGTTAG CAAGATTATA TGTATATGCG 4140

CACTATAAAG GATTAAAATC ACTTTACTAT ACTAGAAATA AATTATTAAG TGTAGAAGAA 4200

TGTACAAGTT GTTCTATCTA ACAATTAAAT GTTGAAAATG ACAAACAGCT AATCATCTGG 4260

TCTGAATTAG CAGATGATTA GACTGCTATG TCTGTATTTG TCAATTATTG AGTAACATTA 4320

ATGTTTTGGA GACAAAATAT ATCTCAAATG TGGGTTGAAA CAGAATTTAA AGTATCAAAA 4440

GACATTGCAA GTTGGAAGAC TTTATCTGAA GCTGAACAAG ACACATTTAA AAAAGCATTA 4500

GCTGGTTTAA CAGGCTTAGA TACACATCAA GCAGATGATG GCATGCCTTT AGTTATGCTA 4560

CATACGACTG ACTTAAGGAA AAAAGCAGTT TATTCATTTA TGGCGATGAT GGAGCAAATA 4620

CACGCGAAAA GCTATTCACA TATTTTCACA ACACTATTAC CATCTAGTGA AaCAAACTAC 4680

CTATTAGATG AATGGGTTTT AGAGGAACCC CATTTAAAAT ATAAATCTGA TAAAATTGTT 4740

GCTAATTATC ACAAACTTTG GGGTAAAGAA GCTTCGATAT ACGACCAATA TATGGCCAGA 4800

GTTACGAGTG TATTTTTAGA AACATTCTTA TTCTTCTCAG GTTTCTATTA TCCACTATAT 4860

CTTGCTGGTC AAGGGAAAAT GACGACATCA GGTGAAATCA TTCGTAAAAT TCTTTTAGAT 4920

GAATCTATTC ATGGTGTATT TACCGGTTTA GATGCACAGC ATTTACGAAA TGAACTATCT 4980

GAAAGTGAGA AACAAAAAGC AGATCAAGAA ATGTATAAAT TGCTAAATGA CTTGTATTTA 5040

AATGAAGAGT CATACACAAA AATGTTATAC GATGATCTTG GAATCACTGA AGATGTGCTA 5100

AACTATGTTA AATATAATGG AAACAAAGCA CTTTCAAACT TAGGCTTTGa ACCTTATTTT 5160

GAGGAACGTG AATTTAACCC AATCATTGAG AATGCCTTAG ATACAACAAC TAAAAACCAT 5220

GACTTCTTCT CAGTAAAAGG TGATGGTTAT GTATTAGCAT TAAACGTAGA AGCATTACAA 5280

GATGATGACT TTGTATTTGA CAACAAATAA CAATTAAATT AAAAGACCTT CACATGTAAA 5340

GGGAAATAGC GATTCGTTTC GTCTTGTCTC CTACATGTTG AAGGTCTTTT TTTATGTGTA 5400

TCTAACTCAT TATGAGTCTG AGTAAGAAAT CAATGCTCTA AGATGTACAA TGCTATTTAT 5460

ATTGGCAGTA GTTGGCGGGG CCCCAACACA GAAGCAGGCG GAAAGTCAGC TAACAATATT 5520

GTGCAAGTTG GCGGGGCCCC AACATAGAAG CAGGCGGAAA GTCAGCTAAC AATAATGTGC 5580

AAGTTGGCGG GGCCCCAACA TAAAAGCAGG CGGAAAGTCA GCTAACAATA TTGTGCAAGT 5640

TCGGgCGGGG CCCCAACATA AAGAAAAACT TTTTCCTTTA GAAATTATCA CTTCCaCaTG 5700

AGTTTTACTC ATGTATTCCT ATTTTTAAGT ACACATTAGC TGAGGCTAAT GTTAAGAACC 5760

ACTACTTAAT CAATCATTAG TAGTTTTTAT CATTTCCACT ATTCCCaGAC ATCaAAATCT 5820

TAAGTGTTCT ATTTTACTTT AAGTAAACAA AATACACATT CCGAAAAATT AAATTTCAGT 5880

TTAATTGCAA ATATCAATAA AATTGACACT AAATTATTTG AAAGGCTATT GAAATTATGG 5940

TCAAAAAACG CTACTATTAA TGAGAAATAT TATCAATGAT AATGATTATC ATTAATTTAA 6000

AGGGAGAAAA ATTTGTAATG AAGTATTTAT TAAAGGGAAA TATTTTGCTT CTATTACTAA 6060

TATTGTTGAC AATTATTTCG TTGTTCATAG GTGTGAGTGA ACTATCAATT AAAGATTTAC 6120

GTATTTTAAT TGCTGGAAGT TCGTTGGCTT TAGCAGGCTT GATAATGCAA CAAATGATGC 6240

AAAATAAGTT TGTTAGTCCG ACTACAGCTG GAACGATGGA ATGGGCTAAA CTAGGTATTT 6300

TAATTGCTTT ATTGTTCTTT CCAACCGGTC ATATTTTATT AAAACTAGTA TTTGCTGTTA 6360

TTTGCAGTAT TTGCGGTACG TTTTTATTTG TTAAAATCAT TGATTTTATA AAAGTGAAAG 6420

ATGTCATTTT TGTACCGCTT TTAGGAATTA TGATGGGTGG GATTGTTGCA AGTTcACAAC 6480

CTTCATCTCA TTGCGCACGA ATGCTGTTCA AAGCATTGGT AACTGGCTTA ACGGGAACTT 6540

TGCCATTATC ACAAGTGGAC GCTATGAAAT TTTATATTTA AGTATTCCTC TTTTAGCATT 6600

GACATATCTT TTTGCTAATC ATTTCACGAT TGTAGGAATG GGTAAAGACT TTACTAATAA 6660

TTTAGGTTTG AGTTACGAAA AATTAATTAA CATCGCATTG TTTATTACTG CAACTATTAC 6720

AGCATTGGTA GTGGTGACTG TTGGAACATT ACCGTTCTTA GGACTAGTAA TACCAAATAT 6780

TATTTCAATT TATCGAGGTG ATCATTTGAA AAATGCTATC CCTCATACGA TGATGTTAGG 6840

TGCCATCTTT GTATTATTTT CTGATATAGT TGGCAGAATT GTTGTTTATC CATATGAAAT 6900

AAATATTGGT TTAACAATAG GTGTATTTGG AACAATCATT TTCCTTATCT TGCTTATGAA 6960

AGGTAGGAAA AATTATGCGC aACAATAATA AAAAAATAAT GCTTTTAATT GCAGTAACGT 7020

TATTAATTAG TATGCTGTAC TTATTTGTAG GTATTGATTT TGAAATATTT GAATATCAAT 7080

TTTCAAGTCG TTTAAGAAAG TTCATATTAA TTATTTTAGT AGGTGCTGCC ATTGCAACTT 7140

CAGTGGTGAT TTTTCAAGCG ATTACAAATA ACCGTCTATT GACACCATCA ATAATGGGGT 7200

TAGATGCAGT TTATTTATTT ATCAAAGTAT TGCCAGTCTT TTTATTTGGA ATTCAATCGG 7260

TATGGGTTAC TAATGTATAT TTGAACTTTA TATTAACACT TATAACGATG GTGTTATTCG 7320

CACTAATCCT ATTCCAAGGT ATCTTTAAAA TCGGACATTT TTCAATTTAT TTTATCTTAC 7380

TTATTGGTGT CCTTTTAGGA ACATTTTTTA GAAGCATAAC AGGTTTTATT CAACTGATTA 7440

TGGATCCTGA GTCATTTTTA GCAATACAAA GTAGTATGTT TGCTAATTTT AATGCTTCTA 7500

ATTCGAATTT AGTTACTTTC TCAGCAGTGC TATTAGTAAT CTTATTAGTC ATTACAATTT 7560

TACTATTGCC TTATTTAGAT GTATTGCTTT TAGGTCGTGC TGAAGCAATT AATCTTGGGA 7620

TATCGTATGA AAAATTAACG CGAATT 7646

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

ATGAATATAT TTnnAAATAA ATTATTATGG ATTGCACCAA TnGCCACTAT GATTATCTTG 60

GTAATCTTTT CTTTAGCTTT TTATCCTGCA TATAATCCTA AACCAAAAGA TTTACCAATT 120

GGTATATTAA ACGAGGATAA AGGTACAACG ATTCAAGATA AAAATGTTAA CATTGGTAAA 180

AAATTAGAGG ATAAATTATT AGATAGTGAT TCTAATAAAA TTAAATGGGT TAAGGTTGAT 240

AGTGAAAAAG ACCTTGAAAA AGATTTGAAA GATCAAAAAA TCTTTGGAGT AGCTATTATT 300

GATAAAGACT TTTCAAAAGA TGCTATGAGT AAAACACAAA AAGTAGTTAT GGATAGTAAA 360

AAAGAAGAAA TGCAACAAAA AGTTGCTTCA GGTGAAATTC CGCCACAAGT GGTTCAACAA 420

ATGAAACAAA AAATGGGGAA TCAACAAGTA GAGGTTAAGC AGGCTAAATT TAAAACGATT 480

GTAAGTGAAG GATCAAGCTT ACAAGGTTCA CAAATTGCAT CAGCTGTGTT AACTGGTATG 540

GGTGATAATA TTAATGCTCA AATTACGAAG CAAAGTTTGG AAACATTAAC GAGTCAAAAT 600

GTTAAAGTCA ATGCCGCGGA CATCAATGGT TTGACGAATC CAGTAAAAGT GGATAATGAA 660

AAACTTAATA AAGTTAAAGA TCACCAAGCA GGTGGTAATG CACCATTCCT AATGTTTATG 720

CCAATTTGGA TAGGTTCAAT CGTAACGTCT ATCTTATTGT TCTTTGCATT TAGAACTAGT 780

AACAATATCG TCGTGCAACA TCGTATCaTT GCtTCAATTG GACAGATGAT ATTTGCAGTT 840

GTTGCAGCAT TTGCAGGTAG CTTTGTTTAT ATTTATTTCA TGCAAGGCGT TCAAAGATTT 900

GATTTTGACC ATCCAAATCG TATCGCAATT TTTGTAGCAT TTGCGATTCT TGGTTTCGTG 960

GGCCTTATTT TAGGTGTTAT GGTATGGCTA GGTATGAAGT CAGTTCCAAT TTTCTTCATT 1020

TTAATGTTCT TTAGTATGCA ACTTGTAACG TTACCTAAAC AAATGTTGCC TGAAAGTTAT 1080

CAAAAATATG TATATGATTG GAATCCATTC ACACACTATG CAACAAGTGT AAGAGAcTAT 1140

TATACTTGAA TCATCATATT GAATTAAATA GTACAATGTG GATGTTTATA GGGT 1194

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

GACCGACCTA TACATCCGTA TAAGTATTTC TTGATATAAG TCTTCTAAAT CATAATGATT 60

AAATCCAAAT GTTTTGATGC GTCGAATAAT TAATGGTTGT AGATCCATTA CTAACTTTTC 120

GTATTTCAAA TATTAAACTA ACCCCTTCTA TCTAAAATTT AAGGTTAGTT TAATATTGTT 240

ACATTCAAAA TTTCAAGATG ACGGAAATGT CATTTCTTAT GATGTCCTCT TCGTATTTTT 300

TCAAATTCTG CAAGGATTTC AGAAGATAAC GGAATTCGAG TTCTTGGCTT GTTTTCACTT 360

ATATCATCTA ATGATTTACT CACATCAATT TCATTTTCTT TTAAATCTCT CCACATTTCG 420

CGAGATGATA TTCTATATGC ACCTGATCCA AAGATAGCAT GTTGcTCACT CaTATCACTT 480

GTTACAACTG TAATATGcTT AGtATGCTTG tCaTAAAGtT CaTAAACCAT AACGGTTCTA 540

ATGGAAACCA ATCAGCTG 558

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

GCTTCAGACA TnTGATGATA TAATCTCTCA TCATCGATTA ATTCTTTTGC AGCTTGATAC 60

ACATnTTGCT TATTTGTTCC AATGACTTTT AATGTGCCAG CTTCAACACC TTCAGGACGT 120

TCTGTAACAC TTCGCCAAAA CTAAAACTGG CTTATTAAAT GATGGCGCTT CTTCCTGAAT 180

TCCACCTGAA TCTGTCAAAA TAAAATAAGA TTTTnTAGCA AAATTATGGA AATCTATACG 240

TCCAAAGGTT CAATCAATTC AATTCTGTCA TGACTACCTA AAATCTTTTG AGCCACCTCT 300

CGAACTTTCG GGTTTTTATG CATTGGATAT ACCAGTGCTA AATCAGTATA CTCATCTATT 360

AAGCGTCTAA CCGCTTTAAA TATATTTTCC aTGGGTTTCC CGATATTTTC TCGTCGGTGT 420

GCTGTCATrA GAATGAATTT kTtGTCATGG TATTTATCCA TGATGTTAGA TTTATAATTG 480

TCATCAACTG TATATTTCAT AGCATCAATC GCAGTATTAC CAGTGACAAC AACACTTTCT 540

GAATATTTCC CTTCACTTAA CAAATGCGAT GCAGCATTTT TAGTAGGTGC AAAATGTAAG 600

TCAGCTAATA CACCAACTAA TTGTCTATTC ACCTCTTCTG GAAAAGGTGA ATATTTATCA 660

TAACTTCTAA GCCCTGCTTC AACGTGTCCA ATCGGCACTT GGTTATAAAA TGCCGCTAAA 720

CCACCTGCAA ATGTCGTCAT CGTATCACCA TGTACAAGTA CCATGTCTGG TTTTTCTAAT 780

TGAATCACTT GTTCTAATTG AGTGATTGAT TTAGAAGTTA TCTCAGAAAG TGTCTGTCCT 840

GATTTCATAA TATTCAAATC GTATTTTGGT TTGATTTCAA AGGTACTTAA TACTGAATCA 900

AGCATTTCTC TATGCTGTGC TGTAACAACA ACAATTGGCT CGAGCATTTT TTCTTGTTCC 960

ATCTTTTTCA TCAAACTACT TATCTCCGAT TCTTCTATTT AGTACCAAAC AATCTATCTC 1080

CAGCGTCGCC TAACCCTGGT GTGATATATG CTTTGTCATT aGCTTTTCAT CAAGTGCAGC 1140

AATATAAATA TCTACATCTG GATGTGCTTC ATGCATCTTT TCTACGCCTT CTGGTGCTGC 1200

AATTAAACAC ATGAAGCGAA TATTTTTAGC GCCACGTTTC TTCAATGAAG TAATAGCTTC 1260

AATTGCTGAT GCGCCTGTTG CTAACATAGG ATCAACAACA ATGATTTGTC TTTCAGTAAT 1320

ATCTTGAGGT AACTTAGCAA AATACTCTAC AGCCTTTAAT GTTTCGGGAT CTCGATATAA 1380

ACCGATATGT CCAACTCTGG CTGCAGGTAC TAAACTTAAA ATACCATCAG TCATACCTAA 1440

ACCAGCTCTT AAAATTGGAA CGATAGCTAA TTTTTTACCA GCTAATCGTT TAGCCGTCAT 1500

TTTAGTTACA GGCGTTTCAA TATCAACATC CTGAAGCTCT AAGTCTCTAG TTACTTCATA 1560

TGCCATCAAC ATACCAACTT CGTCTACAAG TTCTCTAAAT TCTTTAGTAC CTGTATTTAC 1620

ATCTCTAATA TAGCTTAGTT TGTGTTGAAT TAATGGATGA TCGAAAACGT GTACTTTACT 1680

CATAAAAATT ACTCCTATCT TTGTGTATGT TTATTGATAT AGAGGATATT CAGCTGTTAA 1740

TTTCGCAACG CGTTCTTTAG CTTGTTGTAA TTTTTCTTCA TCTTTACTAT TTTTCAATGC 1800

TAAACTGATG ATTTTTGCAA CTTCCTCAAA AGCTTTTTCA TCAAATCCAC GCGTTGTTGC 1860

AGCAGGTGTA CCTAAACGTA TACCACTCGT TACAAAAGGT TTTTCTTGAT CGAACGGAAT 1920

GGTATTTTTG TTACATGTGA TACCAACTGA ATCTAAAGTC TCTTCAGCTT CTTTACCAGT 1980

AAGTCCTATA GACCCTTTTA CATCAACAGC TACTAAGTGA TTATCTGTAC CGCCAGAAAC 2040

AATTCTAAAT CCTTCATTAA TTAATGCTTC TGCAAGAACT TTTGCGTTTT TAACCACTTG 2100

TTGTTGATAC GTTTTGAAAT TATTTTCTAA CGCTTCTCCA AAAGCAACTG CTTTtGCTgC 2160

AATAACATGC TCAAGAGGTC CACCTTGAAT ACCAGGGAAA ATTGTTTTAT CTATGTCTTT 2220

TTTATATTCT TCCTTACATA AAATCATACC ACCACGtGGT CCGcGTAATG TTTTGTGTGT 2280

TGTAGTTGTT ACAAAATCAG CATATTCTAC TGGATTTGGA TGTAAACCTG CCGCTACTAA 2340

TCCTGCAATA TGTGCCATGT CTACCATTAA CTTAGCGTTT ACTTCATCTG CGATTTCTTT 2400

AAACTTTTTG AAGTCAATTG TTCTTGAATA TGCTGATGCT CCTGCCACAA TAAGCTTAGG 2460

CTTATGCTCT AACGCTAATT TACGAACTTC ATCATAATTG ATTCGTTCTG TGTCTTTATC 2520

TACTCCATAT TCAACGAAAT TGTAGAATTT ACCACTAAAA TTAACAGGCG CTCCATGTGT 2580

CAAGTGACCA CCATGACTCA AATTCATACC TAAAACTGTG TCGCCCATTT CTAATGCAAC 2640

TAAGTAAACA GCCATGTTCG CTTGTGAACC TGAATGTGGT TGAACATTGA CATGTTCAGC 2700

TCCAAACAAT GCTTTAGCAC GATCAATTGC GATGCTTTCA GTAACATCTA CAAACTCACA 2760

TTGTGCTTCC ATAACCGCTT CCGATACAAA ATTTTCCGAT GCGATTAACT CTATGTTGCT 2880

ATTTTGTCTC TGAAATTCTC TCTCGATTGC TTCTGCGATA ACTTTATCTT GCTTGGTGAT 2940

ATAAGACATA AAATCTCCCC TTCTTTCAAA AAAACTTATT GGTATTTAGC ACGTTCGCCA 3000

CCAATCTTTT TCGGCCTAGA TGTGGCAATA GTTACAATTG CCTGTCCTAC TTGCTTTACT 3060

GAGGTCCTTA CAGGTACACA TACATGTTTA ATATGCATGC CTATTAACGT TTGACCAATA 3120

TCAATTCCAC AAGGAACAGT AATATGTTCG ACCACGATCG GATCCTTCAT ATGCTGAAAA 3180

GCGTATGTTG CCAAACTCCC TCCAGCATGT ACATCTGGAA CGACGGAAAC TTCTTCCATT 3240

GTTAATGGAT TATACTGAGA TTTTTCTATT GTTATCGCTC TGTTGATATG TTCACATCCT 3300

TGAAAAGCAA AAGTAACGCC TGTCTCTTTA CTCACAACAT CTAATGCATT AAAAATAGTT 3360

TCTGCAACTT CCaTCGAACC GACAGTCCCT ATTTTTTCGC CAATGACTTC CGATGTTGAA 3420

CATCCAATTA AACATATATC TCCTTTATTA AAAAAGGACA TATCTTTTAA TTCGTCTAAT 3480

AACATTGTCA AATCTTTCAT AAAAGCCCAC CCTTCCTAAA AATAAAAAAG GAATATAGCA 3540

AAGTGCTACA CTCCTCTATT ATAACTTATT TAACTGTTAA CATATACTAA TTATACAGAA 3600

TTCCTACTAG CAAATAATAT CTTTTAATTT TAAAATTAAA CTTACAAGTT CTTCATAGGT 3660

ATGTACATAC ATTTCTTTTG TTCCACCGTA TGGATCTATA ACTTCTCCTG CTTCTTTtAC 3720

ATATTCATGC AATGTGAAAA CATGATTTTG CAAACCAAAG TGTGCCTCTA TTAATTCTTT 3780

GTGCGAATAC GACATCGTCA AAATAATATC TGCTTTCAAA TCTGCTTCAG TAAATTGTTG 3840

CGATAAGGTC GTTTCAGCTA AATGATGTTC TTCAACTAAG TCTTCAACAT AATTCGAAAC 3900

ACCTTGATTG TTCACAGCGA ATATACCTCT TGATTCAAAT TGATGATTTG GCATAACCTC 3960

TTTTGCAATA CTTTCCGCTA ATGGGCTACG ACATGTGTTA CCTGTACAAA CGAATAAAAT 4020

CTTCATAGTT CACATCCTTT AATAATGTGA TTACCTGCAG CTTTTAACAT GCGATTCATA 4080

ATTGCTTCTG TATTATCATT CAGCTCAAAG CCGTATATAT ACGCCGCTGA AATATTTTCA 4140

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AGCTTTAACG GCAATATAAA CGAAATAGGG CCCGGCCAGA ATGCCTGCAT TAACTTTTCT 4800

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TTTAAAACAA TGTCTTTTAT TTCATTAATT TTAGGATATT GCTGTAAATC TTCATTATAT 5040

TCTCTAACAT CCCAAATTTT AGTATCCAAC TTAATCACGC CTTTCTTATT TATCATAATA 5100

TAAAGCAAAA AGCTATGCAC TTAACTAATC ATAGCAAAGG CATAACTTCT AATTACCATT 5160

TAAATGAGAC GATTCGATCG TGGCCATTTA TATCTTTAAT AATGTCGATT TTTTTGTCAG 5220

GAAATTTATT TAAAATTATT GATTTAAGTG CCTCACCTTG ATTGTAACCA ATTTCAAAAA 5280

CAACTGGGCT GCCTTTTTCC ATAACGTGAG GTAAATCTTC AATGATTGAT TCATAAATAG 5340

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ACATCGTAAC CATATCTTTT TCATCTATAT ATGGTGGATT AGATATCAAG CCGTTCAACT 5460

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ACATCTTCAA CTTCTGGTAA AACTGCCACT GTAGCTGTTG AAGTATGAAT ACGTCCACCT 6480

GATTCTGTTT CAGGCACACG TTGAACGCGG TGCGCACCAT TTTCAAATTT CAATTTACTA 6540

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GCTTTAGAAA TATTAATCGC TTCAATGGCA TTACCATTAT GAGAGACCAC TTTTTCTTTA 7500

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TCTATCCAAC CGGAATGGTA AGTTTCATAC ATTGAGAGTn CCACCTTTTT CAAAACATAA 7680

TCGCTTTATT ATATCATATT TCAAATATTC ATAAATGTCT TTnTCATAAT TATATCGATA 7740

TTGTACATGA ACAATTATTT TA 7762

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

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TAAAAAAATT ATTATCAATG ATGAACTAGA ATTGACTGAA TTCCACCAAG AACTTACTTA   120
TATTTTAGAC AACATAnAAG GGAATAATAA TTATGGTAAG GAATTTGTTG CAACCGTTGA   180
AGAAACATTC GACATTGAAT AaAGCGGGGT GgaAGCACTA TGAATCAATG GGATCAGTTC   240
TTAACACCTT ATAAGCAAGC GGTTGATGAG TTGAAAGkGA AcTTaAAGGC ATGCGCAAAC   300
AATATGAAGT TGGTGAACAA GCGTCGCCAA TAGAATTTGT TACTGGTCGT GTTAAACCAA   360
TCGCTAGTAT TATAGATAAG GCAAACAAAC GACAAATACC ATTTGATAGG TTAAGAGAAG   420
AAATGTACGA TATCGCTGGT TTAAGAATGA TGTGCCAATT TGTTGAAGAT ATTGATGTTG   480
TCGTCAATAT TTTAAGACAA AGAmAAGATT TTAAAGTAAT TGAAGAACGA GATTATATTC   540
GTAACACTAA AGAAAGTGGT TACCGCTCGT ATCATGTCAT TATTGAATAT CCAATTGAAA   600
CATTACAAGG CCAAAAATTT ATATTGGCTG AGATTCAGAT TCGTACATTA GCAATGAATT   660
TCTGGGCAAC GATTGAACAT ACTTTACGAT ATAAATATGA TGGTGCTTAT CCGGATGAAA   720
TTCAACATCG TTTGGAAAGA GCGGCAGAAG CAGCGTATTT ACTTGATGAA GAGATGTCTG   780
AAATTAAAGA TGAAATTCAG GAAGCTCAAA AATATTACAC GCAAAAACGT TCTAAAAAAC   840
ATGAAAATGA TTAACGAGGT GTTATAAATC ATGCGTTATA CAATTTTAAC TAAAGGTGAC   900
TCCAAGTCTA ATGCCTTAAA GCATAAAATG ATGAACTATA TGAAAGrTTT TcGCATGaTT   960
GaGGATrGTG AAAaTCCTGA AATTGTTATT yCAGTTGGTG GTGACGGTAC ATTACTACAA  1020
GCATTCCATC AGTATAGCCA CATGTTATCA AAAGTGGCAT TTGTTGGAGT TCATACAGGT  1080
CATTTAGGAT TTTATGCGGA TTGGTTACCT CATGAAGTTG AAAAATTAAT CATCGAAATT  1140
AATAATTCAG AGTTTCAGGT CATTGAATAT CCATTGCTTG AAATTATTAT GAGATACAAC  1200
GACAACGGCT ATGAAACAAG GTATTTAGCA TTAAATGAAG CAACGATGAA AACTGAAAAT  1260
GGCTCAACAC TTGTTGTGGA TGTTAACTTA AGAGGGAAAC ACTTTGAGCG ATTTAGAGGC  1320
GATGGATTAT GTGTATCAAC ACCTTCGGGT TCAACGGCTT ATAACAAAGC GCTAGGTGGC  1380
GCACTGATAC ATCCTTCACT TGAAGCAATG CAAATTACAG AAATTGCCTC GATAAATAAT  1440
CGTGTGTTTA GAACGGTAGG ATCACCACTT GTATTACCAA AGCATCATAC ATGTTTAATA  1500
TCACCAGTTA ATCATGATAC CATTAGAATG ACGATAGATC ATGTTAGTAT CAAACATAAA  1560
AATGTTAATT CAATACAATA CCGTGTAGCA AATGAAAAAG TGAGGTTTGC ACGTTTTAGA  1620
CCATTCCCAT TCTGGAAACG TGTGCACGAT TCTTTCATAT CAAGTGATGA AGAACGATGA  1680
AATTTAAGTA TCATATATCA CAACAAGAAA CTGTTAAAAC TTTTTTAGCA CGACATGATT  1740
TTTCTAAGAA GACAGTGAGC GCCATTAAAA ATAATGGCGC TTTAATTGTT AATGATGAAC  1800
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AAATACCGAG TGTTAATTTA ATACCTTATG CTCGTAAGCT AGAAGTATTG TATGAAGATG 1920

CTTTTATCAT CATAGTTACT AAACCAAACA ATCAAAATTG TACGCCTTCG AGAGAACATC 1980

CTCATGAAAG TTTAATCGAA CAAGTACTAT ATCATTGTCA GGAACATGGT GAAAATATTA 2040

ACCCACATAT TGTTACGCGT CTAGATCGTA ATACAACTGG TATTGTGATA TTCGCTAAAT 2100

ATGGACATAT CCATCATTTA TTTTCTAAAG TAAACTTGAA AAAAATATAT ACTTGCCTTG 2160

TATATGGTAA AACCCATACA TCTGGTATTA TTGAAGCTAA TATTAGACGG TCAAAGGATA 2220

GGATTATAAC TAGAGAAGTT GCCTCGGATG GTAAATACGC TAAAACATCT TATGAAGTAA 2280

TAAATCAGAA TGATAAATAC AGTTTATGCA AAGTTCATTT GCATACGGGA CGTACACATC 2340

AAATTCGTGT ACATTTTCAA CATATTGGGC ATCCAATTGT GGGAGATTCT TTGTATGATG 2400

GTTTTCATGA CAAAATTCAT GGTCAAGTAC TGCAATGTAC GCAAATATAT TTTGTTCATC 2460

CAATCAATAA GAACAATATT TATATTACAA TTGATTATAA GCAATTACTT AAATTATnCA 2520

ATCAACTCTA ATnCACACAG GGGGTGTAAG TATGTCAATG AnCACAGATG AAAAAGAGCG 2580

TGT 2583

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1818 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

ATCAAGTGAT ACATTTAACT GGTAAAGGAT TAAnAGATGC TCAAGTTAAA AAATCnGGAT 60

ATATACAATA TGAATTTGTT AAAGAGGATT TnACAGATTT ATTnGCAATT ACGGATACAG 120

TAATAAGTAG AGCTGGATCA AATGCGATTT ATGAGTTCTT AACATTACGT ATACCAATGT 180

TATTAGTACC ATTAGGTTTA GATCAATCCC GAGGCGACCA AATTGACAAT GCAAATCATT 240

TTGCTGATAA AGGATATGCT AAAGCGATTG ATGAAGAACA ATTAACAGCA CAAATTTTAT 300

TACAAGAACT AAATGAAATG GAACAGGAAA GAACTCGAAT TATCAATAAT ATGAAATCGT 360

ATGAACAAAG TTATACGAAA GAAGCTTTAT TTGATAAGAT GATTAAAGAC GCATTGAATT 420

AATGGGGGGT AATGCTTTAT GAGTCAATGG AAACGTATCT CTTTGCTCAT CGTTTTTACA 480

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GAAGTTTATG AGTTTGTATA TTCATCAGAG AGCTTTATTA CGACATCTAT CATGCTTGGG 600

CTCATGTTAA AGCGCCACAA AATTGAAGCA TTATTTTTTG CATTAACAAT GGCATTATCT 720

GGAATTTTGA ATCCAGCATT AAAAAATATA TTCGATAGAG AAAGACCTAC ATTGCTGCGT 780

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TTTGGAAGTG GTATCTATCT ATTAAATCGA TTAAATCAAG GTAATTCAAA AGGTATTCTT 900

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CATTATCCAA CAGATATTAT TGCCGGCATT ATTGGTGGAT TATTTTGcAT TATTTTATCA 1020

ACGTTATTAC TTAGAAATAA ATTAATAAAT TAAATAGTAA AAAAACAAAA GCAGTAAACC 1080

TAAAGTGTCG TAAGGGTTTA CTGCTTTTAT AAAACGTTGT TATAACGTAT ATTGTCTTTT 1140

ACGGGCATAT AAnAGGGGAA TATTTGAnAA TGACCAATCC AACAAGAACG AAACGTTGTG 1200

GGGGGGATGT TCTATGTGGT ATTGATAATC ATTTTCAACT ACTATTATAC ATTAGTGAGA 1260

ATCATTGTCA ATTAGAAACT AAAACTTTTT TTGAATATTT TTTAAGAATA GTAAATAAAA 1320

CGCATGATTA CGCTATTTTA GAAAATAAAA AAATTTGTAT TTCTCATTAG AATTAGAATA 1380

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GTATATGACA ACAATTAATA TTGCGGTAAG GCCTTGTGTT ACAGTATTCT ATATTTAAGT 1620

ACTGCAATCA GAATTAACAG AATGCCATTA ACTGATTATT AAATATTTGA GTTAATAAAT 1680

AATTAATGAT TGTAGCTTGA AAAATTTAAA ACATGGTTAT TGATTTGTGA TAAAATTTAA 1740

ACGTAAACAA ACTAATTTAA AAAGCAACTA TTGTATAGAA AAATACAAAA TTTAAAATAT 1800

ATTACCTTAT TAGAAAAA 1818

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12658 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

TGTTTAAACA ATAGGGGGAA TCTTATGATT GAAAAATTAG TAACCTTTTT AAATGAGGTT 60

GTTTGGAGTA AGCCATTAGT TTATGGTTTG CTAATTACTG GTGTGCTATT TACATTGCGT 120

ATgCGATTTT TTCAAGTTAG ACATTTTAAA GAAATGATTC GATTAATGTT TCAAGGAGAG 180

GGTACAGGTA ATATTGTCGG TGTATCTACT GCAATATTTA TAGGAGGACC TGGTGCAGTA 300

TTTTGGATGT GGATTACTGC GTTTTTAGGT GCAAGTAGTG CTTTTATTGA ATCTACACTT 360

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GAATATGGTA TTGGTGGTAA ATTTGGTAAA ATTTACGGAA TTATCTTTGC TATTGTTACG 480

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CATAATGCGA TTCATGTTCC ACAATGGTTA ATGGGTGGTA TTGTTGTAGT TATTTTGGGA 600

TTAATTATTT TTGGTGGTGT ACGTATTATT GCCAATGTTG CAACAGCCGT TGTACCATTT 660

ATGGCAATTA TTTACATACT GATGGCTGTC ATTATCATTT GTATCAATAT ACAAGAAGTG 720

CCAGCGTTAT TTGCATTAAT TTTCAAATCA GCATTTGGAT TACAATCTGC TTTTGGTGGT 780

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CCGCATTTAA TTAAAGATGG CGGTATTTAT GTTgAAAATG CAACAGGTAA AGATTATTCA 1080

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GTCACGTTAA GTATTTATTT ACCAGAATCT TATAATCAAC TTGTTAAATA TAATGTCATT 1860

CTTTGCTTTG ACGGATTAGA TTTTTTACGT TTCGGGAGAA TACAACGTAC ATATGAATCG 1920

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GATAAGCTAA ATCAATGTGC AAATAAAGAA CAATTGACAA TTTGGCATGT CATTGGTCTA 2280

GATGAAAAAG ATTTTACTTT ACCAACAAAT GGTAAGCGTG CCGATTTCTT AACACCGAAT 2340

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GTAATTAATC CGCCAAATAA TGGCCCTATC ATTGAGCCGA ATCCTTGGAT ACTATTAAAA 3480

ACACCCCAAG TTTCTTCTTG TTCATCTGAT TTGATAAATC GTGCCATAAA GGTATTCCAT 3540

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ATAACACCAT ACATAAAGTT TCTGCTGCGG TTATCTATTA GTTTCGATAA AAATAGCATC 3720

GAAACTGCAC AGCCGATACC ACCAATAATG ATTGCAACAG TATATTCAAT TGTGCTTACG 3780

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AATTGAGCTT TAACTGGACG AGTATTATAA TTTGTTAACT TTACATCGAC AAAATAATAT   3960
AATATCCATG CAATTAAAAC GACTAAAGAC ATCATGAAGG CAAAGCGTGT TGGGTGCACT   4020
TTGATAAGTA GATTCATAAA AACCATACCT ACCAATAGGC CTAACAACCA TGAAAAATAA   4080
ACATAGCCCA TTTGTTTGCC ACGTTTATCT TCTTCAACAC TGGATAACAT AATGACCCAA   4140
ATAGGACTAA CTGCAATACC GAGCATCATA GCACTAAATA TGATTACAAA AGGTGATGCT   4200
GGAAACCAAA TAACTAAAAA TAAACTTGTA AATGCTAAAA TAAATCCAGT CGTTAAAACG   4260
ATTTTTGTGC CGAATTTTTT CAGTAAAAAT CCTATAACAA AGTTTGTAGA TGCATCAGCA   4320
ATAAAATGTA TTGAAAATGC TAGAGACGTT ATTGCTACAG CAATGGATGT AACTGTTGGC   4380
AAGAAATTAA TATAGCTTAG GATATACATG CCTCTCGCAA ATTCCATTAA AAATAAGATA   4440
ATAAGCaTTA AAATGAAATT TTTATGATTA GCGTAATTAT TTAACGAAGA ATCTTGCATA   4500
TAAAGGAACC TTTCCATAAA TCTCTTGTGG TTGTGATGAA TGACCGATTA AATCAAGTAA   4560
GTCTCGACAT ATTGTCTGTG TAGCATACTT AATTTTATCT TGTTCCATTG TACTAATCAT   4620
GTTAGTTAAT TGCTCATTAC CGTTAGTTAA ACTTGCTACA ATTTTTATTG CTTCTTCTGG   4680
AGTATCAGCG ATTTTACCAA AACCTTTTTC TTCAAAGTAA AGGGCATTTT CAAGCTCTTG   4740
ACCAGGTGCA GGATTTAGGA AAATCATTGG AATACAACGG GCGAAACCTT CAGTTATTGT   4800
GATACCACCA GGTTTCGTAA TCATAAGTTG ACTTGATGCC ATCCATTCAT TCATGTGTTT   4860
GGTATAACCT AGAATCAATA CATTCTCGTT AGATTTAAAC TTAGCTGTTA AAGAACGCTT   4920
TAGCTCTTTG CTCTTACCAC AAATCATAAC TACTTGTGCA TTTGCaCTTT tCGCTAATAT   4980
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AGTTTGCTTA TCTGGATCTA AGTTGTTGTC TATTAACCAC TGCTTTTGAT TAATAGGCGT   5100
TTCAAATTTG TTATCAATAG GAATACCTGT CaCTTTAACT GTTGAAGGAT CAATACCTAC   5160
GTCTATGAAG TCTTGTTTCG TTTCTTTTGT TGCCACATAA TATCTTGTTG AATACGGCGT   5220
AATCCAGTTT TTATGTAAGC GATAGTCTGT CATCACTGTA GCAACTGGAA TATTAATGTT   5280
AAATTGCTCA GTTAGTACCG ACATAACTGG TGTAGGAAAC GTTAATAATA TTAAATCTGG   5340
CTTTTCTTTT ATCAATAAAT TAATTAACTT ATTAAGTCCA TAGTATTTGT AAAAACATTT   5400
GTCTAGTTTA TCTGGGCGGC TGTAATAAAA CCCTTTGTAC ATATTTCTAA AATATTTAAA   5460
GCTATTGATA TACCATTTTT TACAAATAGA AGTCAAAATT GGATGAGCTT CCATAAATAA   5520
ATCGTGCTCA ATGACGCTTA AATGGTCTAG ATTCATATCA TTAAGTTGAT TAACGATACT   5580
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TTGAGTAACC ATTAATAGCC ACCCTCCGTT AGTTTGAAAA TTTTATTTAA GTGTAACTTA 5700

TTTTACGGCA TTATAAAAGA AATAAAGACG CAAAGTCGTT ACATTTATAG CAATTTTAAT 5760

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CCAGCTAACG TAACACAAGT GGTTGTGCCG GACACATTAA GAGTAGCTAG TATTCTAGCA 6360

CACACATTAT ATGATTATCC GAGTCATCAG TTAGTGACAT TTGGTGTAaC GGGTACAAAT 6420

GGTAAAACTT CTATTGCGAC GATGATTCAT TTAATTCAAA GAAAGTTACA AAAAAATAGT 6480

GCATATTTAG GAACTAATGG TTTCCAAATT AATGAAACAA AGACAAAAGG TGCAAATACG 6540

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GGAAGAGGCA GAATCGATTG CATCACAACT AACAGATTGG ATAGAAACAT ATAAAAAGGA 7800

GAAAGACTAA TGAACTTAAA GCAAGAAGTT GAGTCTAGAA AGACTTTTGC GATTATTTCA 7860

CATCCCGATG CAGGGAAAAC AACGTTAACT GAAAAACTAT TGTACTTCAG TGGTGCTATT 7920

CGTGAAGCGG GTACAGTTAA AGGGAAGAAG ACTGGTAAAT TTGCGACAAG TGACTGGATG 7980

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CCACAAACAT TGAAGTTATT TAAAGTTTGT AAAATGCGTG GTATTCCAAT CTTTACATTC 8220

ATTAATAAAT TAGACCGAGT AGGTAAAGAA CCATTTGAAT TATTAGATGA AATCGAAGAG 8280

ACATTAAATA TTGAAACATA CCCTATGAAT TGGCCAATTG GTATGGGACA AAGTTTCTTT 8340

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GGTGCGATTC AATACTATAA AACATTACAC ACAAACCAAA TTATTTTAGG TGCTGTTGGT 9120

CAGTTACAAT TTGAAGTTTT CGAACATAGA ATGAAAAACG AATATAATGT TGATGTTGTT 9180

AAGATGAACA CATCAAGATC GATTTTAGTG AAAGATAGAT ATGACGATTT AGTATTCTTA 9300

TTTGAAAATG AATTTGCAAC AAGATGGTTT GAAGAGAAAT TCCCTGAAAT TAAATTGTAT 9360

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TGAAGAGATT AAAGCAAGTA ACAAATCATT CTGGGGAACT GTGTTGAAAA TAGAATTTGC 10080

AGATATCGCA TTTGCCATTG ATTCTATGCT TGCTGCTTTA gCTATTGCTG TAACACTTCC 10140

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TGGAATGATT GGTGTTATTC TAATGCGTTA TGCAGCAACA TGGTTTGTAG AGCTATTAAA 10260

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AAGTTCAGAT AAAAACAAAG TTGGTCATGA AGAGCAACAT GTACTTTCTA AACCTTCAGA 11220

ACATGATAAA GAGACTAGAA TTGATTCTGA GTCTTCAAGA ACTGATTCAG ACAGCTCGAT 11280

GCAGACAGAG AAAATAAAAA AAGACAGTTC AGATGGAAAT AAAAGTAGTA ATCTGAAATC 11340

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TGTTCCTATT GATTTCGATA AAGATAATAA ATATGATATG TTGATGAAAG CTTTCCAAAT 12540

TGATGCATCA GTAAATCCAG GTAACTCGGG TGGTGCTGTC GTCAATAGAG AAGGAAAATT 12600

AATAGGTGTA GTTGCAGCTA AAATTAGTAT GCCAAACGTT GAAAnTATGT CATTTGCA 12658

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6048 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

TGAAATnGAA TAGTACTATT GCAAGTGTAA AGAGGTTAAT TTTTGCCnCA CGCGGGACTT 60
AAAAAGGCAA CCACTGGTTG TGACATATCC TTATTTACAT TTATAAATAT AAGGAGGAGG 120
TAGTAGTGAA AGACTTATTG CAAGCACAGC AAAAGCTTAT ACCGGATCTC ATAGATAAAA 180
TGTATAAACG TTTTTCTATT CTTACTACTA TCTCAAAAAA TCAGCCTGTC GGACGTCGAA 240
GTTTAAGCGA ACATATGGAT ATGACTGAAC GTGTACTGCG TTCTGAAACA GATATGCTTA 300
AGAAACAAGA TTTGATAAAA GTTAAGCCTA CCGGAATGGA AATTACAGCT GAAGGTGAGC 360
AACTGATTTC GCAATTGAAA GGTTACTTTG ATATCTATGC AGATGATAAT CGTCTGTCAG 420
AAGGTATTAA GAATAAATTT CAAATTAAGG AAGTTCATGT TGTTCCTGGT GATGCTGATA 480
ATAGTCAATC TGTTAAAACA GAATTAGGTA GACAAGCAGG TCAATTACTT GAAGGCATAT 540
TACAAGAAGA CGCGATAGTT GCTGTAACTG GCGGATCCAC GATGGCATGT GTTAGTGAAG 600
CAATTCATTT ATTACCATAT AATGTATTCT TCGTACCAGC CAGAGGTGGA CTAGGCGAAA 660
ATGTTGTCTT TCAGGCAAAC ACAATTGCAG CCAGTATGGc aCAACAAGCT GGCGGTTATT 720
ATACGACGAT GTATGTACCT GATAATGTCA GTGAAaCAAC ATATAATACA TTGTTGTTAG 780
AGCCATCAGT CATAAACACT TTAGACAAAA TTAAACAAGC AAACGTTATA TTACACGGCA 840
TTGGTGATGC GCTGAAGATG GCGCATCGAC GTCAATCACC TGAAAAGGTC ATTGAACAAC 900
TTCAACATCA TCAAGCTGTC GGAGAGGCAT TTGGTTATTA TTTTGATACA CAAGGTCAAA 960
TTGTCCATAA GGTTAAAACA ATTGGACTTC AATTAGAAGA CCTTGAATCA AAAGACTTTA 1020
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CACCCAAGAA TACAGTGTTA ATCACTGATG AAGCCGCAGC AAAGATAATA CTTGAATAAG 1140
AGATAAAAAG TTTAATACTT TTTAAATATC ATTTTAAAGG AGGCCATTAT AATGGCAGTA 1200
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GTAGAAGGTC TTGAAGTTGT AGCAGTAAAC GACTTAACAG ATGACGACAT GTTAGCGCAT 1320
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GGTTTCCGCG TAAATGGTAA AGAAGTTAAA TCATTCAGTG AACCAGATGC AAGCAAATTA 1440
CCTTGGAAAG ACTTAAATAT CGATGTAGTA TTAGAATGTA CTGGTTTCTA CACTGATAAA 1500
GATAAAGCAC AAGCTCATAT TGAAGCAGGC GCTAAAAAAG TATTAATCTC AGCACCAGCT 1560

ACAGTTGTTT CAGGTGCTTC ATGTACTACA AACTCATTAG CACCAGTTGC TAAAGTTTTA 1680

AACGATGACT TTGGTTTAGT TGAAGGTTTA ATGACTACAA TTCACGCTTA CACAGGTGAT 1740

CAAAATACAC AAGACGCACC TCACAGAAAA GGTGACAAAC GTCGTGCTCG TGCAGCGGCA 1800

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ACTCCAATTA TATGTGTTGG TGAAACAGAC GAAGAGCGTG AAAGTGGTAA AGCTAACGAT 4080

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TACATGGCAC AAACTGATAT TGATGGGGCA TTAGTAGGTG GCGCATCACT TAAAGTTGAA 4380

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AACGCCGTCG TTTAATTGAT TCACCTAAAG TTGCAACGTA TGACTTGAAA CCAGAAATGA 5520

GTGCTTATGA AGTTAAAGAT GCATTATTAG AAGAGTTAAA TAAAGGTGAC TTGGACTTAA 5580

TTATTTTAAA CTTTGCTAAC CCTGATATGG TTGGACATAG TGGTATGCTT GAGCCGACAA 5640

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AAAGATGTTA AGTAAACGCT TAATGACACT TATTTTTTGA AAATAATAGT AATATCnTTT 6000

TGTTAAATGA AAGAATAAAG CTATAATAAT TATAGAATAA CTATTTAn 6048

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

AAACAAGTGC AAGATATCAT CGCATTAATT AAGTCGTTAC AAAgTGTAAT TGTAGACaTC 60

GCTTCCAATA ATGTTGATAC AATTATGCCT GGTTATACTC ATTTACAGCG TGCACAGCCA 120

ATTTCATTTG CACATCATAT TATGACTTAT TTTTGGATGT TACAACGAGA CCAACAACGA 180

TTTGAAGATA GTTTAAAACG AATCGATATT AATCCTTTAG GTGCAGCAGC CTTAAGTGGT 240

ACCACATACC CTATCGATAG ACACGAGACA ACAGCATTGT TGAACTTTGG CAGTCTCTAT 300

GAGAATAGCC TAGATGCTGT TAGTGACAGA GACTATATTA TTGAAACATT GCATAATATT 360

TCTTTAACGA TGGTTCACTT ATCACGCTTT GCAGAGGAAA TTATTTTCTG GTCCACAGAC 420

GAAGCTAAAT TCATTACATT ATCAGATGCA TTTTCAACTG GCTCATCTAT TATGCCACAA 480

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GAAGGTATGA TTCAAACGAT GACAATTAAT AAAGAACGAC TCAATCAAAC TGTTAAAGAA 720

GATTTTTCAA ATGCAACGGA ACTAGCAGAT TATTTAGTAA CTAAAAATAT TCCATTTAGA 780

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TCTACCTACC CACAATGTCT ATTAAAATTA CATTGTGGGT ATTTTAATGC TCTCTTCGTC 1080

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TGGCTATGCA CCCGAGCATA CGTTTCAAGC ATATGATAAG AGTCATAATG AGTTAAAAGC 1500

ATCTTATATC GAAATTGATT TACAACGTAC CAAAGATGGC CATTTAGTTG CTATGCATGA 1560

TGAAACTGTT AACCGTACAA CAAATGGACA CGGTAAAGTT GAGGATTATA CCCTTGATGA 1620

ATTAAAAACAG TTAGATGCAG GAAGTTGGTT TAATAAAAAA TATCCAAAAT ACGCAAGAGC 1680

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TGCAAACTAT TATATTGAAA CAAAGTCACC TGATGTATAC CCAGGAATGG AAGAACAATT 1800

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AATGATTCAA TCATTTTCTG ACGAAAGTTT AAAGAAAATT CATCGTCAAA ATAAGCATGT 1920

GCCATTAGTA AAATTAGTTG ATAAAGGTGA ACTACAACAA TTTAACGACC AACGCTTAAA 1980

AGAGATACGC TCTTATGCGA TTGGATTAGG TCCTGATTAT ACAGATTTAA CTGAACAAAA 2040

TACCCATCAT TTAAAAGACT TAGGATTTAT AGTACATCCT TATACAGTGA ATGAAAAAGC 2100

TGATATGTTA CGATTAAATA AATATGGCGT TGATGGTGTC TTTACAAATT TCGCTGATAA 2160

ATATAAAGAA GTCATTAAGT AGTAATGTTA AACTAGAAAA CATAAATACA AAAATATAGC 2220

TATTACTATA AAAAACAGCA GTAAGATATT TCCAAATTGA AATTATCCTA CTGCTGTCTT 2280

TTTGGGAGTG GGACAGAAAT GATATTTTCG CAAAATTTAT TTCGTCGTCC CACCCCAACT 2340

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CTATTGTAAG CTGACTTTCC GCCAGCCTCT GTGTTGGGGC CCCGCCAACT TGCACACTAT 2520

TGTAAGCTGA CTTTCCACCA GCCTCTGTGT TGGGGCCCCG ACTATTTTTG AAAAGAGCGT 2580

GTTACACGGG CATTGTTTTA CAGTCAACTA CTGCTAAAAT AAAATTAACG AGCTTAGGGC 2640

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CGTTCAGTTA AAATACGTGT TGCTTCTGGT GTTGTAGGTC CATTAGCAGC TTCAACAACG 3000

ATACTAGCTT TAATATCATG TGCATTGTCT TCTGTAATTT GGTTTGAAAT AGCCGCTGGT 3060

ACTAAAATGT CACAATCTAA TTCAAACAAT TCTTTATTTG AGATTGTTTC TTCAAATAAA 3120

TTTGTTACCG TACCAAAACT ATCACGACGG TCTAATAAAT AATCTATATC TAAGCCATTT 3180

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GTTGATCTGT CGCGTCCATG AGAACCACCC AATACAATTG GTTTACCTGT GATGAAACCT 3420

GGTGAATTAA ATTTATCTAA TGCACTATAT TCATCCATCA TCCAAGCCAT AATTTGTGAG 3480

TTTGTAAATA CATCTGGTGC TGGAATATCT TTGTTCGGAC CTACGAATTG TGAAATTGCT 3540

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GAAGTTACTA AATTATTGTT CTCAGTCATG ATCCTTTTCG CCTCTTCTTT ACCTAATGAT 3960

TTCGCTTTCA AACATATTGT AACATAACGT ATTCCTTTTT AAAGCCCTTA CAAACTGATT 4020

GTTACAACTT TTTGACATTA TTGAAATACA TGTCTTATTT TTTCAAGTGC AAGGTCCAAT 4080

TCTTCTTTAG TAATAATTAA TGGTGGTGCA AAACGAATGA CAGTATCATG CGTTTCTTTA 4140

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AATTGTTCTT TAAAATAATC TCCTAATTCT AAAGAGCGGC CTGGTAAATC CTCATCAACG 4320

ATAACATCTA ATGCAGCAAT TGATGCAGCA CAAGCAAGTG GATTACCACC AAATGTTGAA 4380

CCATGTGAGC CAGGTGTAAA GACATCTAAT ACTTCTTTAT CTGCTAATAC AACAGAAATT 4440

GGGAAGACTC CACCACCTAG TGCTTTACCT AAAATATAGA CATCAGGTTT TACATTATCC 4500

CAATCCGTAG CAAATAATTT ACCCGAACGA CCTAATCCTG CTTGGATTTC GTCAGCAATA 4560

AATAAGACAT TATGTTCATC ACATAATTCT CTAATTGCTT TCAAATATCC TTCTGGCGGT 4620

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ATTGCAGCTT TCAATGCATC TACATCTCCA AAATCAACTT TTCTAAATCC ATCTAATAAC 4740

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ATGaTTACAA GCAAAAGAAT TGATAATTTT ACACTTAATC AAAAGTATAT TTTACTAAGA 5460

ATATTTTTAT TTATAAATAT TGAAAACCAC TAACAAATTG CATACACAAT ATCATTAGTG 5520

GTAACAGTTA AACACTTATT TATCTTTACG GGGTAATGGG TTAAAACCCT TnCATTAAAA 5580

TTGGATGnCC ATAAAATTAG GG 5602

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5924 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TAACCCCATT TTACCTGGAA AAATCgTTTG CGATGCaATm GCaTTtGaAT ATAaATACAT 60

TTTACGTATa GAATTATAAA AgGTTTCATT CaAATCTTAG GGTCAAAAAT GTTATAATAT 120

TTTTATGTCA AATTTAAAAC AGTAACACTT ATTTACAAGG TTGCAATATT TTGAAGTAAT 180

AAAGGAAGTG TCGCGTATTT TAACTTTTTC AGAGCAAAAT GCACTCGCGA AAATAGATGA 240

TTTAATGAAT ACTTATTGCA ATCAATGTCC AATCAAAACT CGTCTGCGTA AATTAGAGGG 300

GAAAACGAAG GCGCATCATT TTTGTATCAA TGAGTGTTCA ATAGGGAAAG AAATAAAACA 360

ATTAGGAAAT GAACTTCAAT AGGAGGAAGT CAAATGAAAA TTATATCTAT ATCAGAAACA 420

CCGAACCACA ACACAATGAA GATTACACTT AGTGAAAGCA GAGAAGGTAT GACATCAGAT 480

ACGTATACTA AAGTTGATGA TTCACAGCCA GCATTTATTA ATGACATCTT AAAGGTTGAA 540

GGCGTTAAAT CAATTTTCCA TGTTATGGAC TTTATTTCAG TAGATAAAGA AAATGACGCA 600

AATTGGGAAA CAGTATTGCC AAAAGTAGAG GCTGTATTCG AATAAATTTT TCATCAACTA 660

GTATTCGGGG GGAATAAAGT ATATGGAAAT TTTACGTATA GAGCCAACAC CAAGTCCAAA 720

TACAATGAAA GTTGTTTTGT CATATACAAG AGAAGACAAG TTATCTAATA CTTATAAAAA 780

AGTAGAAGAA ACACAACCAA GATTTATAAA TCAGTTGTTA TCTATAGATG GTATCACTTC 840

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CATATTACCT GATATTAAAG CTGCTTTTTC TGATGCGAAT AAGGTTTTAG AATCTGTAAA 960

TGAACCTCAA ATTGACAATC ATTTTGGTGA AATTAAAGCT GAATTATTAA CTTTTAAGGG 1020

TATACCGTAT CAAATTAAGC TAACTTCTGC TGACCAAGAA TTAAGAGAAC AATTACCACA 1080

AACATATGTT GACCATATGA CTCAAGCGCA AACAGCACAT GACAATATTG TTTTTATGCG 1140

TAAATGGCTA GATTTAGGAA ATCGCTATGG AAATATTCAA GAAGTAATGG ATGGTGTCCT 1200

AGAAGAAGTG CTAGCTACCT ATCCAGAATC ACAGTTACCC GTATTGGTAA AACATGCTTT 1260

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ACAAATGCGT GGCGAATTAA CTCAAAATGG TTTTACAAGT TTAGAAACGA GCGAACAGct 1920

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GGTTAACACA TTTTATAATA TTAAAAATGG TGTCTGTCAT TGAAAATAGA GAATATAGTT 2340

GTATTCTATT TGTTAAATAA AGTCCGTTTT TACCaACTAT ATTTTCTAGA AATTTAACTG 2400

TTTTAATAGG ACATCAAACA TAATATTCaA ATCaTGTGTT AACCTCTTTT TTAAAATTTT 2460

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CGATGGGGTA GGTACTTAAT CAGCATTTTA TAAATAAAGT AACGGAATTC ATGATATTAA 2580

TATCATATTC CTAAAATGAG TGATAACAAA ATGCTACATA AAGTTAAGTT ATATCAAACT 2640

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CGAATGGGCT TTTGAAAATT ATATCAAATC AGACGAGTAT AAAGGTCCAG ATATGACAGA 3000

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TCATATTGAT GCGATTCAAA CACAATTAGC ACGTGAAAGC TTCAATCCTC CAACATTAAA 3540

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AAATGATTGA TAAAGTGGAC GACATGTATA TTACTGTTAT TGAAGGTAAA TTCCGTGGTG 4200

ATACGTTCTT TCCACCTTAT mCATTkGAgr CTGGGAAGTT GCCTCTTCAG TTGAAGGTAA 4260

ACTAGATGAG AAAAATACAA TTCCACATAC CTTTCTACAT TTAATTCGTA AAAAATAAGG 4320

GGGAAAACGA CCATGACAAA ACAGATTATA GTAACAGACT CAACATCCGA TTTATCTAAA 4380

GAATACTTAG AAGCAAACAA CATTCATGTA ATTCCTTTAA GTTTAACTAT TGAAGGAGCT 4440

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TAAATTTATA ATTAGATAGA TAGAGGAGGT AATTCATATG ACAAAAGAAT ATGCAACATT 5280

AGCAGGAGGA TGTTTCTGGT GCATGGTTAA ACCATTTACA TCATATCCAG GCATCAAGTC 5340

GAATCAAACC GGCCATGTCG AAGCAGTACA AATTACGTTT GATCCAGAGG TTACTTCCTT 5460

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CAAAAAGAAC CCGGTACATT ATTACCAATA TCAACGTGGT TCAGGTAGAA AAGCGTTTAT 5760

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AATATATTGT TACACAAGAn AACGGCACTG AACCACCATT TATGAATGAA TATTGGAATC 5880

ATTTTGCTAA AGGATTTATG TAGATAAAnT TCnGGTAAAC CTTG 5924

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

GGCCGTTnAA AATCTCCAAA ATAnAAAAAC CCATCTTGTT CCAATGTTTT AAAATCGCCa 60

TCCaACACTT GaTCaATAGC TTGCAACAAC GTTGAACGTG TTTTaCCAAA AGCATCaAAC 120

GCTCCCACTA AAATCAGTGC TTCAAGTAAC TTTCTCGTTT TGACTCTCTT CGGTATACGT 180

CTAGCAAAAT CAAAGAAATC TTTAAATTTG CCGTTCTGAT AACGTTCATC AACAATCACT 240

TTCACACTTT GATAACCAAC ACCTTTAATT GTACCAATTG ATAAATAAAT GCCTTCTTGG 300

GAAGGTTTAT AAAACCAATG ACTTTCGTTA ATGTTCGGTG GCAATATAGT GATACCTTGT 360

TTTTTTGCTT CTTCTATCAT TTGAGCAGTT TTCTTCTCAC TTCCAATAAC ATTACTTAAA 420

ATATTTGCGT AAAAATAATT TGGATAATGG ACTTTTAAAA AGCTCATAAT GTATGCAATT 480

TTAGAATAGC TGACAGCATG TGCTCTAGGA AAACCATAAT CAGCAAATTT CAGAATCAAA 540

TCAAATATTT GCTTACTAAT GTCTTCGTGA TAACCATTTT GCTTTGCACC TTCTATAAAA 600

TGTTGACGCT CACTTTCAAG AACAGCTCTA TTTTTTTTAC TCATTGCTCT TCTTAAAATA 660

TCCGCTTCAC CATAACTGAA GTTTGCAAAT GTGCTCGCTA TTTGCATAAT TTGCTCTTGA 720

TAAATAATAA CACCGTAAGT ATTTTTTAAT ATAGGTTCTA AATGCGGATG TAAATATTGA 780

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TCTATTTTTA ATAACCCAAT ACGTTCGGCT TCAGTCATTG TCCATTGCGT TAATAATCCT 1140

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TCATATTGAG GAAGTAGAGA TTGATGATAT TTTAATTCTG CATCACACTT TTGAGCTATA 1920

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ATCGAAACAT GTTTTCTACC TTGAATCGAA ATACTAAGGT GGTCCATATA TGTGTCATTA 2160

TGGGTTTCAA ACACTTGTAC AATATCACGA TGTTGATCAC CGACTTTTTT AAAAATGATA 2220

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TGGCCCCTTT CTATTAGTTA AGTTTTGTGC GTAAAGCTGT AGCAAGTTGC TCAAATTCAT 2640

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CATCGACTGC AAATACCCAT ATTTTCAAGC CTTTGATGTC AGCAATTGTA TTAACAAACT 2820

GAGATGCTTC ATTTGGCTGA ATACCGAATT GCTCCAATAC ATCTTCAGTT ATTTTAACTT 2880

GGCAGAATCC ATCATCCATA AGTTCGAAAT GTTGTAAAAC ATAACCTTGA AACGGCAACA 2940

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TACTCCCTTT TTTAGAAAAG TTGCTTAATT TAAGCATTAG TCTATATCAA AATATCTAAA 3600

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CAAACAATGC aAGTTGGGGT GGGGCCCCAA CGTTTGTGCG AAATCTATCT TATGCCTATT 3780

TTCTCTGCTA AGTTCCTATA cTTCGTCAAA CATTTGGCAT ATCACGAGAG CGCTCGCTAC 3840

TTTGTCGTTT TGACTATGCA TGTTCACTTC TATTTTGGCG AAGTTTCTTC CGACGTCTAG 3900

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TAATATAGCC GTACCTCTTT TTAAAGCTTC AATCTGCACA TCTTCACGAT TTCCGACAAT 4740

CAATAATGTC TTTGGACCAA TATACTTTAA AATATCTTTG AGTTCCATTG CTCCAATTGC 4800

AAATTTAGAT ACCATCTTAG TGATACCTTT GTTGCCACCT AACACTTGGC CATCAATAAT 4860

ATTGACAATT TCATTAAAAG TTAAATGTTC AATTTCATTA CGATTACGTT TTTCGATTCG 4920

AACCGTACCA ACACGATCTA TCGTTGCGAC CATGCCCATT TTATCAGCAT CTTTmATTGc 4980

ACGATATGCT GTCCCytCaG ATACGTTTAA AAATTTAGCG ATTTTACGCA CCGAAATTTT 5040

AGAGCCTATA GATAACGATT CAATATAATC TAAAATTTGT TCATGTTTTG TCATTCTTTA 5100

CCTCTTCTTT TCGAACAGTA TTAACTACAT TATAACTTTA TTTTGGATAA AAAGCATTGA 5160

AGTGAAATGA AATAATGATC GTTtCACCTA TTTTATTTTT TGAAAATATA CAACAAACAC 5220

AAAGATCACA AAATCTTTAA TTTTAAATGG AAAAATCCAT TATTATTTAT TAGAATGTAA 5280

GTGAGGAGGG ATGTACTAAT GTATAAAAAT ATATTACTTG GTGTAGACAC TCAGTTAAAA 5340

AATGAAAAAG CACTAAAAGA AGTGTCTAAA TTAGCTGGCG AAGGTACAGT CGTAACAGTT 5400

TTAAACGCAA TCAGCGAACA AGaTGCTCAA GCATCAATTA AAGCAGGTGT TCATTTAAAC 5460

AAACTTACTG AAGAACGAAG CAAGCGATTG GAAAAAACAC GCAAAGCTTT AGAAGATTAT 5520

GGTATTGATT ATGACCAAAT AATTGTTCGT GGTAATGCAA AAGAAGAACT ATTAAAACAT 5580

GCTAATAGCG GTAAATATGA AATTGTTGTT TTAAGTAACC GTAAAGCAGA AGACAAAAAG 5640

AAATTTGTAC TTGGAAGTGT CAGCCACAAA GTAGCAAAAC GTGCGACTAT CCCTGTATTA 5700

ATCGTTAAAT AAAATTTTTA TCCAGAATCA CAAATAATCT TTCAATCATG ATGCAGTCTC 5760

AAACGACTGA GTAAATACAA GAAACGATTA TGACTGTGGT TCTGGATTTT TTATATCGTA 5820

GTAAATTTAT AATCAATGTC TAATTGTATA AAACTAAAAT TACGAGAGTA GGTCAGAAAT 5880

GATAAAGAAC CACTGATGTC CCCCGTCCAC GTCGTAACTG AATCAGTAGA ATATAAAAAC 5940

ACCCACTAAA AATATGCAGA CGATAACTTC CACATAGATT AGCGAGGTGT TTTTTAGTGT 6000

AAAATCTATA TTCTATTTAA AACTGAACAG ATTCACCTGG TTTTAAAATT TGCACGTCCC 6060

CTACATTAAC AGCATCTTTA AATTGTTGTG GATCTTGTTC GATTAATGGG AATGTATCAT 6120

AATGAATCGG TACAGAAATT TTTGGTTTAA TAAATTCATT AATAGCATAA CTTGCATCAT 6180

CAATACCCAT CGTAAAATTA TCTCCAATTG GTACAAAACA TACATCAACT GGATGACGTT 6240

TTCAACTTCA AACACGATAC CCATTGGCAT ACCTAAATAA ACTGGgAATA CCATTTTCAT 6360

GTGTAAAACT TGAACTATGA AATGCTTGAA CAAATTTAAC GCTTCCGAAA TCAAaGTTTG 6420

CTTTACCACC AaTATTCATA CCATGAACAT TTTCAACACC GTGATATGAA GAAAGATAGT 6480

CAGCCATTTC TGCACTTCCA ATTACTGTTG CTCCTGTTTT CTTTGCTAGT TCCACAACAT 6540

CACCAAAATG ATCAAAATGA CCGTGCGTTA AAACGATATA GTCTACCTGC ACTGTTTCAA 6600

TATTCAAATC ACACTTAGGG TTATTTGAAA TAAACGGATC TACGATAACC TTTTTGTTGT 6660

TCCCTTCTAA ATAAATCGTT GATTGACCAT GAAATGATAA CTTCATTTGA GCATCCTCCT 6720

ATCAATTACT ATATAAATTT AGTACCCTTT TGCCACTTAA TTATAACAAA TTCTCAAATT 6780

TTAAAAATTG AAAATCTAGT TAATGTATTA GCTCGATTTT GAAATCTAAT AATAATTGGC 6840

ATAAAATGGA AGTAATATTA TGTTGAGGAG TGTTTATAAA ATGACAAAAA TATCAAAAAT 6900

AATAGACGAA TTGAACAATC AACAAGCTGA TGCAGCATGG ATTACAACAC CGTTGAATGT 6960

ATATTATTTT ACTGGATACC GTAGCGAACC CCATGAAAGA TTATTTGCAT TATTGATTAA 7020

GAAAGATGGT AAACAAGTAC TATTTTGTCC AAAAATGGAA GTCGAAGAAG TCAAAGCATC 7080

ACCTTTCACA GGTGAAATCG TTGGATATTT AGACACTGAA AACCCTTTTT CACTTTATCC 7140

TCAAACAATC AATAAATTAC TAATTGAAAG CGAGCACTTA ACAGTAGCAC GCCAAAAACA 7200

ATTAATCTCT GGTTTCAATG TCAATTCATT CGGAGATGTT GATTTAACAA TCAAACAATT 7260

GAGAAATATT AAATCCGAAG ATGAAATTAG CAAAATACGT AAAGCTGCTG AGTTAGCAGA 7320

TAAGTGTATC GAAATAGGTG TTTCTTATTT AAAAGAAGGT GTGACTGAAT GTGAAGTAGT 7380

CAACCATATT GAGCAAACTA TCAAACAATA TGGCGTCAAT GAAATGAGTT TTGATACGAT 7440

GGTTTTATTT GGAGATCATG CCGCATCACC TCATGGCACA CCAGGAGATC GCAGATTAAA 7500

AAGCAATGAA TATGTACTAT TTGATTTAGG TGTAATTTAT GAGCATTATT GTAGCGATAT 7560

GACACGTACT ATTAAATTTG GTGAACCTAG CAAAGAAGCA CAAGAAATTT ATAATATTGT 7620

ATTAGAAGCA GAAACATCTG CAATCCAAGC AATTAAACCT GGAATACCAT TAAAAGATAT 7680

CGATCATATC GCTAGAAATA TTATTTCAGA AAAAGGTTAT GGTGAATATT TCCCTCATCG 7740

CTTAGGTCAT GGCCTAGGAT TACAAGAACA TGAATATCAA GATGTTTCAA GTACTAATTC 7800

TAATTTGTTA GAAGCTGGCA TGGTTATTAC AATCGAACCA GGTATTTATG TACCTGGTGT 7860

TGCAGGTGTA AGAATTGAAG ATGACATACT TGTCACTAAT GAAGGATATG AAGTATTAAC 7920

ACATTACGAA AAATAAGGAG TGGGATAAAA ATGAAAAGCT TGTTACAAGC GCATTCTCAT 7980

TCAGTCAAAC ACTGCCAATA TAACATTGTA GCGCCTAAGA CATAAATTTT TATCCAAGTC 8040

TGTAATGAAT CAAATCAATA TCATTCATGT TCGATGATTT CTTCGCATTG TTTCTAGCTT 8160

TAATTTATCA TTATTTAATT TTAATAACCA AGGAGATGAT AACGTCATTC TTTAGTACGC 8220

TGTAATCCAT TCCCTTTTCA TCAAATTCAA ATTATAATTG TAATGCTTCT TCTACAGATT 8280

TATATTCCAT TTCAAATGCC TCTGCAACGC CTTTATTGGT TACGTGACCT TTGTAAGTAT 8340

TTAAACCTAA TGATAATGGT TGATTTGATT TAAATGCTTC TCTATACCCT TTATTAGCTA 8400

GCATGAGCGC ATAAGGTAGC GTAgCATTAT TTAAAGCTAA CGTCGAAGTA CGCGGTACTG 8460

CACCTGGCAT ATTTGCAACT GCATAATGAA CCACACCATG CTTAATATAT GTAGGATCAT 8520

CATGTGTCGT AATTTTATCA GTTGtTTCAA AAATACCGCC TTGATCAATA GCAATGTCAA 8580

TAATAACTGA CCCATTTTTC ATTTGTTTAA TCATGTCTTC TGTTACAAGT CTTGGCGCTT 8640

TAGCACCTGG AATTAAAACT GCACCTATTA CTAAATCACT TTGTTTAACA TACAACTCAA 8700

TATTCAACGG ATTTGACATA ATTGTATGTA CACGTCCACC GAATAAATCA TCTAATTGTT 8760

GTAAACGCTT TGGATTAACA TCTAAAATCG TAACATCTGC ACCTAGTCCT AGTGCAATTT 8820

TAGCTGCATT TGTTCCTGCT TGACCACCAC CGATAATAGT TACTTTACCC TTAGGTACTC 8880

CTGGGACACC ACCTAGTAGA ATTCCCATAC CACCATTAAG TTTTTGTAGG AACTCTGCGC 8940

CAACTTGAGC TGACATTCTT CCTGCTACCT CACTCATTGG TGATAACAAT GGTAAAGATC 9000

GGTCTGGTAA CTGCACAGTC TCATATGCAA TACTAATTAC TTTTCTATCT ATCAAAGCTT 9060

GTGTTAATTT TTCTTCATTT GCTAAATGAa gatAaGTGAA TAATACAAGC CCTTCTTTAA 9120

AATATGGATA TTCAGATTCA AGTGGTTCTT TAACTTTAAT AACCATATCC ACATCCCAAA 9180

CTTTTGCTTG TTCAGCAACA ATCTCAGCAC CTGCTTCTTT GTAATCTACA TCTTCAAAGA 9240

ATGATCCTGA ACCCGcATTT GTTTCCACTA AAACAGTATG 9280

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4669 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

CTGATTAATC TCTTGTTGTC GTGTATTTAC TAATTGAATC GTTGGTGTCT GAACACGTCC 60

CAGGGATAGC TGTGCATCAT ACTTTGTTGT TAGTGCACGC GTTGCATTAA TCCCAACAAT 120

CCAATCTGCC TCACTTCTCG CTAACGCTGC ATAATACAAA TCGTTATATT GACGACCGTC 180

ACGGATTGGC TTTTTGTTAC CAACTTTATC CAAAATCAAT CTTGCAACTA GTTCACCTTC 300

TCGTCCaGCA TCTGTTGCAA TAATAATATC TTTCACTTTA TTATCTAAAA TTAACGCTTT 360

TACTGTTTTA AATTGTTTGC TTGTTTTACC AATAACAACA GTTTTCATAT ATTTAGGTAT 420

AATTGGAAGG TCTTCTAATC GCCATTCCTT TAAATTTTTA TCGTATTGTT CAGGTGTCGC 480

ATTTGTCACT AGATGACCTA ACGCCCACGT GACAATATAT TGGTTATTTT CAAAGTAACC 540

ATTACGCTTC TGATTTATTT GTAAAGCATC AGCAATATCT CTTGCGACTG ATGGTTTTTC 600

AGCTAATATT AAAGATTTCA TAAATTATCC TTTCTCATAC GTTCTTTTAT TTCGAACGTG 660

CTTCATCTAT TCCACTAATC TTTGATTTAA ATTCAATGAT TGCAAATGAT GTGTTAAATG 720

TATTGTAACA TGTTAATATC ACTATTAACT TTCATTTCAG TTGAAATACT ATATAATAAA 780

AGTAACAAAA AGTACGGAGG TAATGACATG AGCATAGTTC AGTTATATGA TATTACACAA 840

ATAAAATCGT TCATTGAACA TTCGAATTAT GAATCAGCAT CATACTTATA TAAACTTCCT 900

CAACAGTACA ATGAAATAGA TGTATTAATA ACCGATGCGA TTGAATCACC TGGTGTATTT 960

TCGATTAAAG AAAACGATTC AATCAAAGCA ATCATATTGT CTTTTGCATA CGATAAAAAT 1020

AAATTCAAAG TCATAGGCCC TTTCGTGGCT GACAATTATG TATTATCTGT CGATACGTTT 1080

GAAACGCTAT TTAAAGCAAT GACTTCGAAC CAACCTGACG ATGCCGTCTT TAACTTTTCT 1140

TTTGAAGAAG GCATTCAACA ATACAAACCA TTAATGAAAG TTATTCAAGC AAGTTATAAC 1200

TTCACTGACT ATTACATAGA AGCCCGTACA AGATTAGAAG AAGATATGCA CCAACCAAAT 1260

ATCATTCCTT ATCACAAAGG GTTTTATCGT GCTTTCAGCA AATTACACAC AACTACATTT 1320

AAATATCAGG CACAGTCACC ACAAGATATC ATTGATAGTT TAGACGACCA TCATCATTTG 1380

TTTTTATTTG TTAGCGAAGG TTTACTTAAA GGTTATTTAT ACCTTGAAAT TGATTCACAA 1440

CAGTCAATCG CCGAGATTAA ATACTTCAGT TCTCATGTAG ATTACCGTTT GAAAGGTATC 1500

GCTTTCGAGT TGCTTGCGTA TGCATTGCAA TATGCTTTTG ATAATTTTGA TATTAGAAAA 1560

GTTTATTTTA AAATTCGTAA TAAAAATAAT AAACTCATCG AACGATTTAA TGGTCTAGGT 1620

TTCCATATCA ACTATGAGTA CATTAAATTC AAATTCGAAT CACGTAACGT AAAAGATCAA 1680

ACAATCCCTG AATAAAACAC CAAGCAAATA CCCTACAGTA CATCATTAGC ATGTATTGTG 1740

GGTTTTTCTA CTTTTTGTAA ATATTGAAAA TTATAAGTAG TTGTTTTTTA CTATTAGGGC 1800

AGAATGCTTT ACAATAACAT GCAAGTGTCA ATTAAGGGGA GCACTTGCAT AAATAGTATA 1860

GGAGAGTGAG TAGTCTTGCA ATTTCTTGAT TTCTTAATCG CACTTTTACC TGCTTTATTC 1920

TGGGGAAGTG TCGTTCTTAT TAATGTGTTC GTCGGCGGTG GACCTTACAA CCAAATTCGT 1980

TTCAATAATC CTACTGTAAT TATTGTCGGT CTTATTTCTG GTGCATTATG GGCGTTTGGA 2100

CAAGCGAATC AGCTTAAATC TATTAGTTTA ATCGGTGTAT CAAATACTAT GCCAGTTTCT 2160

ACAGGTATGC AATTAGTTGG TACAACATTA TTCAGCGTTA TCTTTTTAGG TGAATGGTCT 2220

TCAATGACTC AAATTATCTT TGGTTTAATC GCCATGATAT TATTAGTTAC TGGTGTAGCA 2280

CTTACTTCAC TTAAAGCTAA AAATGAACGT CAATCAGATA ATCCTGAATT TAAAAAAGCA 2340

ATGGGTATTT TAATTGTATC TACAGTTGGA TATGTAGGTT TCGTTGTACT TGGTGACATC 2400

TTTGGTGTTG GTGGAACTGA TGCATTGTTC TTCCAATCTG TCGGTATGGC AATTGGTGGC 2460

TTTATCCTAT CCATGAATCA TAAAACATCA CTTAAATCAA CAGCACTTAA TCTATTGCCA 2520

GGTGTGATTT GGGGAATTGG TAACTTGTTC ATGTTCTATT CTCAACCAAA AGTTGGTGTA 2580

GCTACAAGTT TCTCATTATC ACAGTTACTT GTTATCGTTT CAACCTTAGG CGGTATTTTC 2640

ATTTTAGGAG AAAGAAAAGA TCGTCGTCAG ATGACGGGTA TTTGGGCAGG TATTATTATT 2700

ATCGTGATAG CTGCTATAAT TCTAGGTAAT TTGAAATAGA AAGTTAAATA CTCATGTAAC 2760

GTAAAAATGT AATCACTTCT GAAAATAACC ATTCACTTAT AGAATGATTA AAATTAATTT 2820

TCGGGAATTT TACGTTGAAT GTTCCTCTAT ATGTCCTAGG AAATACGTGG CTCTAAAAAC 2880

AAAACGCAAT AACACATCAT GACATTAATC ATGCGTTTTA AGACTTTAAA ATTAGCGATA 2940

CTTTTAAAAT CTTGATGATA TTCATATATC AAGTATGCGC CATACATATG AAGTGGATAG 3000

CTGCATAACG CACTGCATTA TCAACTTGAA TGTATGAGTT GAACAACTAT GTCATAAATA 3060

AAAGCCCCCT TTTCACAATA TACATTTACA TATTGTGGTA AAGGGGGCTC TCATTTTCTA 3120

CGAATACTAA AATGGATTTT ATTTTCAAAT GTGTAAACTA GACAAACACT GCCTGATACA 3180

CGTACAAAAT AATGATACTA ATAATGATTG TCAAATTGGT CGTCATACCT ATAAATGGCA 3240

GTGTTCGATA TTTAAACTGA ATACCATAAG AAATAATTGC AACACCTACC GGGAACATCC 3300

AAGTGACCAA CAATGTCGTC TTAATCATAT CATCTGATAC TGGTAACAAG ACATATACTA 3360

ACAATCCCGC AACTAATGCT AATCCATAAT GCAAACATAA ATATTTAATA GTAGCAGGTA 3420

TATACTTTCT TTCCAGAGTA AAATTCAACA TGACACCTAG CAAAATCATT GATAACGGCA 3480

TATTTGCATG GGAAAGTATG CTAAAGAAAT CGATTGCCAC ATGTGGTAAA TGGATGTGAC 3540

TTATATTCAA TATAAACATT ACAATGTATG TAACGAGTGG CACTGATTGT AATAATTTCT 3600

TACCTAAATA TTTAAAATCG AATTGATCAC TACCTTCACT AAAGTAGCTA CCTACAAAGT 3660

AAGTAATTCC AAACATCACA AAGGCACCAC CTATATCAGC CATAACAAAA TAAATAAGTC 3720

CCGTTTTAGG CCATATCACT TCAATTAGTG GATATGCAAA CAATCCAATA TTCATAGCAC 3780

CAATCATTTT CGCCACAATA CCATATATAA TCATTAAAAT TGGTAAAATG GAGAATGACA 3900

ATTTTAATTC TGCACTGTTT AAATTCACAA TAACTAAAGA TGGGAGTGTG ACATTAAGAA 3960

CTAATGTAGC AATGACTTGA CTATCTGTTG CTTTTATAAA ATTAATGCGC TTCAAAAAGT 4020

AACCAAGCGC AATTAATAAA ATAATCATAG TAAATTGTTC TGTCACTGTT ATCCCTTCTT 4080

TCAATAATCT TCATAATTTA TAACTTTAAC ATACTCCACA GATATTTTAG AAGTCTACTG 4140

TTTCATGCTA TAATCTACAT TAAATGCACT TAATTATATT TCAAAGGAGT GTTATAGTAT 4200

GTCTTTAGAA AACCAACTAG CCGAACTTAA ATATGATTAT GTTCGTCTTC AAGGTGACAT 4260

AGAAAAACGG GAATCTTTGA ATTTAGATAC TTCCGCACTT GTTCGTCAAC TTAAAGATAT 4320

TGAAAATGAA ATTAGAAACG TTCGTGCTCA AATGCAAGAT TAATAATCTA TCATTCAAGC 4380

AATAAATGCT TTTTGTTACA TAAATTTGAC TAGCATTGCT CTGAATACGT TATATTGATG 4440

AATTGCTTCA TTTTTCGCTC AATTACATCT AGAATCACAA GATGTTGTCG TGTTATGATT 4500

TAGTGTTTCA TTAACAACAT ACACGCATAT CTATCCCAAC ACTGCTATTT ATGTTTTCTA 4560

CGCTGnTGTA CTACATGAAC CCTTTGAAAC GGAGAGGAAG TTATCATATG CAATTTTAnC 4620

TGATTTTACT AGCAATACTT TAACnAATTG nTAGTTTAAT AGAATTTTA 4669

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2785 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

TTTGCACCCA TCTGaTACAA TGCACCATGC GGTTTAACAT GATTAATTTT AACTTGATGA 60

ATGCGACAAA ACCCTTGTAA TGCACCTAAT TGATAAATCA TCAAATTATA AATCTCGTCG 120

TTAGAGATAT CTATATTTCG TCTGCCAAAG CCTTTCAAAT CAGGTAAACC AGGATGTGCA 180

CCTACTGCAA CATTATGTGC TTTGGCAAGT TTTACCGTTT CATTCATTAC ATTTTCATCA 240

CCAGCGTGAA AACCACAAGC AACATTCGCA CTTGTAATTA ACGGAATAAT TTGATGATCA 300

CCACCAAAGG AATAATTTCC AAATGCTTCG CCTAAATCAC AATTCAAATC AACTCGCATT 360

ATAATTCCAC CCCTTTAACA ATTTGATGTT TTTCTAAAAA TTTAATATCA ACATCTTTTG 420

CATCTCCATC ACGATATAGT GGATAATTTA AAACTGCATA TAAAAAATCG GCAGTTGTAG 480

AAAATCCATC TATCACCATT TCATCTAAGG TGACTTTCAA CTTATCAATT GCTGAAGCTC 540

AACCGTGATA TAGTAAAGAA TCGACTCGCA CATTAAAGCC TTGAGGTAAA TGTAACGCTG 660

TCACTTTACC TGGTGTTGGT TGAAATTTCT TTTCaGGATT TTCGGCATTT ATTCTCGCTT 720

CTATCACATG ACCATTAAAT TGAATATCGC TTTGTGAAAA AGGTAAATGA TTATGTTCCA 780

ATAAATACAG TTGTGCTGCA ACCAAATCAC GTTCTGCTCG CATCTCTGTA ACAGTATGTT 840

CAACTTGTAT TCGAGCATTC ATTTCAATAA AGTAATGTGC GGTATCAGTT ACTAAAAATT 900

CAATCGTACC TGCACTTCTA TAATTTGCTG CACGTGCAAC TTTAACAGCA TCGTTACATA 960

TTTGTTGTCG TCTTTCTTCA GTTAATGCTG CACAAGGAGA TTCTTCGATT AATTTTTGAT 1020

TTTTACGTTG TACAGAACAA TCACGTTCCC CTAAATGTAC ATAATTATCC TGCCCATCTC 1080

CCaTAACTTG AACTTCAACA TGTTTTGcAA CAGGTATAAA AGCCTCAACA TAAACACGAT 1140

CATCATCAAA GTATTTTTTT CCTTCACTTT TAGCTTCTTT AAATGCCTTT TCTAAATCTT 1200

CAGCTTTCTT TACAATACGT ATACCTTTAC CACCACCGCC ACTGGCAGCT TTGATAACAA 1260

CTGGATAACC GATGTCTTTG GCAAGATTCT CAATTTCAGA CACATGATTC ACAGCACCAT 1320

TTGATCCTGG AATCACAGGA ACACCTGCAT GATGAACTGT TTGTCTTGCT GTTATTTTAT 1380

CCCCCATCAT TTCCATCGTT TTTTTAGTAG GCCCTATAAA CGCTATGCCT TGTTCCTCAA 1440

CGGTTTGAGC AAATTTTGTT GATTCTGATA AAAAGCCATA TCCTGGGTGA ATTGCATTAG 1500

CACCAGTGAT TTGTGCAGCA GATATGATGC GGTCAATATT TAAATAACTA TCTAAAgCAT 1560

TArcwTCCCC AATACATATA GCTTGATCTG CTAAATGTAC ATGCAAGCTT TGCTCGTCCC 1620

CTTTTGCATA AACTGCTACA GTTTCAATCC CATATTCTCT GCAAGCTCTT ATAATCCTTA 1680

CAGCAATTTC ACCTCTGTTC GCAATTAAAC AACGAAGCAT TTACTTACCC CCTTTACTTA 1740

ATACGTACCA AAACTTGGTC GTATTCAACA TTTGTGCCAT GATCAGCTAC TATTTCAGTA 1800

ATTTCTCCAG CAACATCTGT TGTTACCTCG TTTAATACTT TCATCGCTTC AACATATCCT 1860

ATAATATCTC CCTTGTTAAC TTTGTCACCG ACATTCACAA TTGGTTCAGT TAATTCTTTA 1920

CTATCTTGTA AAAAGAATGT ACCTATCATT GGTGATTTAA TGTCATGATA ATCATTTGTC 1980

GAAACATCGG AGTTATCATT CGCTTTTGAA GCTGTCAAAT CATTATTGTT CATACTTTGA 2040

TTTGATTGAT TACTGTGTGC AGCCAAATGA TTCGAGTCAG TGAAGTCAAT TTCTATTTCA 2100

TCTTCAAAAT TTTTATATTT AAATTTCTTA ACATCATTTT CCTTCACTAA TTTGATTATT 2160

TGTTCGATTT nTTCAATATT CATTTTACAA ATCCCCTTTT AAAATTGTTG CTAATTTTTT 2220

CGAAGTATGT CGCAAGCTAG ATGTATCAAA AATTGGAGTC TTTTGATGAC TCTTAAGAAT 2280

TTCATTAAAC AGAGACATTT GTTCCCGATT CTTATCTACA GCTTCTTGGA ATGATATCCA 2340

TACAGTTGCA ATTTTGGTAT AACCACCTAT CGTTTGTTTA TCATTAAGCA GAATAATAGG 2460

TTGACCATCA TTTGGTACCT GAACACTACC AAGAGCAACC GGTTCAGAAA TGATATCTGC 2520

TTGATTAAtT GGTGCAACGC TGTCACCTTC CAAACGATAG CCCATACGGT CTGATTGTTC 2580

AGTAATTAAA TATGGATGAT TTACAATTTT CGCTCTAGCC TCTTCAGAAA ATGCCTCGAA 2640

TTGAGGTCCT TGAAGAATGT GTATAATATT ATTTTCTGGC AATAAATCGT CCTGTAAATG 2700

AATCGTCTTT CCAATGTTTT CTTTAAAGTC ATTATTTATT TTCACTGTTA TTACATCATC 2760

AGCTAATAAC TTTCTACCTT TGAAT 2785

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1010 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

AATGGAAACG GTTGAAACAG CAATTATTAC TATTTCTATG GGTGAAGGTA TTTCAGAGAT 60

ATTTAAATCA ATGGGTGCCA CACATATCAT TAGTGGTGGA CAAACGATGA ATCCTTCTAC 120

AGAAGATATC GTTAAAGTCA TTGAACAATC AAAATGTAAA CGTGCAATTA TTTTACCGAA 180

TAATAAAAAT ATCTTAATGG CAAGTGAACA AGCAGCGAGT ATTGTTGATG CAGAAGCTGT 240

TGTTATTCCA ACGAAATCTA TTCCTCAAGG TATAAGCGCA CTATTCCAAT ATGATGTGGA 300

CGCAACACTT GAAGaAAATA AAGCGCAAAT GGCTGATTCA GTAAATAACG TTAAATCTGG 360

TTCATTAACG TACGCTGTTC GTGATACGAA AATTGATGGC GTTGAGATTA AAAAAGACGC 420

GTTTATGGGC TTGATTGAAG ATAAGATTGT AAGCAGCCAA AGTGATCAAT TAACAACGGT 480

TACTGAGTTG TTAAATGAGA TGTTAGCAGA AGATAGTGAA ATATTGACTG TGATTATTGG 540

TCAAGATGCA GAGCAAGCAG TTACAGATAA CATGATAAAC TGGATCGAAG AGCAATATCC 600

AGATGTAGAA GTGGAAGTTC ATGAAGGTGG ACAACCAATT TATCAATATT TCTTTTCAGT 660

AGAATAAAAA TTTAAAATAA AAAACTACCA ATGATAAATC ATCAGTTGGT AGTTTTTTAT 720

TTTGCTATTT TAGTGATATT GCGGGTTAAA AGTATCGTTC TCGAGTTGCT AACAATGTCA 780

TGTTCAACTT AGTCATGATA AAATAAATAA CATACTAAAT GATACGTAAA ATCAAATAAA 840

ACATAGGTGA TTTATTTTGG CTAAAGTAAA CTTAATAGAA AGTCCATATT CTCTTTTACA 900

ATTAAAAGGT ATAGGTCCTA AGAAAATAGA AGTATTGCAA CAACTAAATA TTCATACAGT 960

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1540 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

TGTAGTTGAA CATGAACAAC AAAAGAAAGA AAAGACAAAA AAGCAATACA AGCCATTTTG 60

GATTGTCATG AGTTTTATAA TACTTATAGT TGTACTATTA CTCCCGGCAC CTTCAAGTCT 120

GCCGATAATG GCTAAGGCAG TACTAGCTAT TTwAGCTTTT GCAGTTATTA TGTGGGTAAC 180

GGAAGCTGTA TCATATCCGG TGTCAGCAAC TTTAATTATT GGCTTAATGA TATTACTTTT 240

AGGATTTAGC CCTGTTCAAA ATTTAGGGGA GAAGCTAGGT AATCCGAAAA GTGGCAGTGC 300

TATTTTAGCT GGAAGTGACC TTCTAGGAAC TAATCATGCA TTATCATTAG CGTTTAGTGG 360

ATTTGCAACT TCAGCTGTAG CTCTCGTTGC AGCTGCATTA TTTTTGGCTG CTGCTATGCA 420

AGAAACGAAT TTGCATAAAA GACTAGCTCT TTTAGTGTTA TCAATTGTTG GTAATAAAAC 480

TAGAAATATA GTTATTGGAG CAATTATCGT TTCAATTGTA CTTGCATTTT TCGTTCCTTC 540

TGCAACAGCT AGAGCAGGGG CAGTTGTACC AATCTTGCTG GGTATGATTG CGGCATTTAA 600

AGTTTCCAAA GATAGCAAGT TAGCGTCTTT ATTAATAATT ACTTCAGTAC AAGCTGTGTC 660

AATTTGGAAT ATTGGTATCA AAACGGCGGC AGCACAAAAT ATCGTAGCGA TTAATTTTAT 720

AAACCATCAA TTAGGATTTG ATGTTTCATG GGGCGAGTGG TTCTTATATG CAGCGCCTTG 780

GTCCATAGTT ATGTCCGTAG CTTTATATTT CATCATGATT AAAGTGATGC CTCCAGAAAT 840

TAATACAATA GAAGGTGGTA AAGATTTAAT AAAAGAAGAA TTGCATAAAC TTGGCCCCGT 900

TAGCCCACGT GAATGGCGTT TAATTGTTAT ATCGATGTTA TTATTACTGT TTTGGTCAAC 960

TGAAAAAGTA TTACATCCGA TTGACTCTGC ATCCATTACT ATTATTGCTT TAGGTGTTAT 1020

GTTAATGCCG AAAATTGGTG TCATGACATG GAAACATGTT GAAAATAAAA TACCATGGGG 1080

AACAATTATC GTGTTTGGTG TAGGTATTTC ACTAGGTAAC GTTCTTTTGA AAACAGGTGC 1140

AGCTCAATGG TTAAGTGATC AAACTTTTGG TGTTTTAGGT TTAAAACATT TACCTATTAT 1200

CGCGACAATT GCACTTATCA CGCTTTTTAA TATATTGATT CATTTGGGCT TTGCGAGTGC 1260

AACAAGTTTA TCATCAGCGT TAATACCTGT TTTTATTTCG CTAACCTCTA CGTTACACTT 1320

AGGAGACCAG TCTATAGGAT TTGTTTTAAT TCAACAATTT GTTATTAGTT TTGGTTTCTT 1380

AGATTTCTTG AAGGCAGGTA TACCATTGAC AATTGTAGGG aATAtctAgT GaTAGTTTTT 1500

AGCATGACTT ATTGGAAATG GGTAAGGTTG CnTTAATTAA 1540

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11823 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

ACTTCTCACA ATAAGAAATA TGAAATTGTT ATGTGTTAGT TGAGATTCAG TGATGAATTA 60

CTTTTATCAT TTAAAATGTT GTTATCATTG TCATGCGTTA CCAAATCGCT TACGTATACA 120

CGATTCCCAA TCTTAACATA GACGATTTGT ATATCAGAAT TTTCTGATTA CTAACAGTTT 180

ACCTAAGTTT AAATATCTGT TCAATGATTT TCAGTTATTT TTAAAAGAAA AATCGTAATG 240

CTGCCATGAT AACAATCCCA CTAATAATTG TAATAGTTAA AtACGCGTGA TTATAGATAA 300

AATAACCGTC GGAATGAGCG CGATAATGTA AGGGATGTTT AATGTATACC CCTCACCATG 360

AGGCGTCTGT TGAATAATGC TGTCAATGAC AAGTGCCGTA AATAGTGTGA TTGGGATAAA 420

TGATAGCCAT CGAACCACGA CATCAGGCAA TTGCACTTTT GAAATCATGA TAAAAGGTAT 480

AATTCGAATT AATAGCGTTA CGATACCACA CAATAAAATA AGTATTAACA TGTTCATATG 540

AGTTATCATT GTTCCATCAT CACTCCTAAC GCTGCTGAAA TTGTGGCTGC AATTAATATT 600

GCTAGATATG AAGGCATAAA CATACTTAGC GATAACATCA TTACTATGAC GGCAATAATG 660

AGTACTATGT AAATTCTTAA TCGCGATTTA GTAATTGATT CAAATTGCGC AATGGCCAAA 720

AAGATAAACA TAGCCGTGAT AGCAAAATCT AACCCTAGCG TTTGCGGATT TGAGATATAT 780

TCGCCAAATA AAGCCCCAGC TACACATGAA ATTGCCCAAA ATAAATATGC TGTGATGTTA 840

AGACCATGCA TCCAACGATC ATTGATAGCT TCTCCTTTTA AATAAGGTGT AATGGCGACG 900

CCAAACGTTT CGTCAGTTAC TAATGAACCT AATCCAACAC GGTTCCAAAA CCCATATGTC 960

TTGAAGTTTG GTGCAAGCGA CATACTTAAA AGGAACATTC TTGAATTTAC GATAAATACA 1020

GTTAGTACAA TCGCTGATAT AGGTGTACCT GCTATAAACA ACGCGCACAT AATAAATTGC 1080

GCAgcaCCGG CATATATAAC AAGACATAAC AAGACAATTT CTAAAATACT AAAGTTTTGA 1140

GACGAAGCCA CAATACCAAA TGAAATACCA ACACCGGCAT AACCCAATAA TGTTGGGATA 1200

CACTCTTGCA CGCCTTGTCT AAAACTTAAA TGTGTTGTCA TCTCAATTAC CTCCTTTGCC 1260

TAAGCAATAA CATTAGACAT CAGTTTGTCT GAGGTTAGAC ATTCCGGAGT CTTTAGTCAG 1380

CTTCATATTA ACTTTTTATT TTTGAGAATT TTCAATTTTT TATTTAAGAC TACCTCCATA 1440

TTTTCTATGG aTTTGTAGTT GTTTTTAAGT ATCAATTTTA TAAATTTTTA TATCTGATGA 1500

TGAGTCTGGG aTATTGaTTC ATGTACCACT CCCTTaTaAT CATCCCCTCC CCCTaCCCTA 1560

CTCCATCGAT ATAACTCATA CTACATATCA ACGAAATCAG TATTTTATCG CTTCCTTTCC 1620

TATATTAGTG ATGCTCAAAC TTGTTACGTT TTAGATTGTT TTAGTTCATC ATAATTATCC 1680

CGTATTGTTG CTATAATGAA ATGCGTTCAC CCCATTAAAC CACAAACTTA ATTTATTGTT 1740

GTTATGTGCA TTGGCTCACT ATTATATTTT TACAGCACAA AAAAAGTGGC GACAGTTCGT 1800

CACCACTTTT TAAAATATTA TTTAAAGTAT CTTGCCCTTG CTTTAAGTAT ACGTAGATAT 1860

ATACTTTTTA AAGCTTGTAG CTAAAGCCTT TATTTAACTG GTTTTGAAAT TTGTGTTTTA 1920

CCACCCATAA ATGGTACTAA TGCTTCTGGA ATTGTTACTG TTCCATCTTC ATTTTGGTAA 1980

TTTTCAACAA TAGCAGCAAA TGTACGTCCA ACTGCTAAAC CACTACCATT TAATGTATGT 2040

GCTAATTCTG GTTTAGCTGC TTTGTCACGC TTGAAGCGGA TGTTAGCACG ACGCGCTTGG 2100

AAATCCGTAC AGTTTGAGCA TGAACTAATT TCTTTATAAT CATTGTAGCT TGGTAACCAA 2160

ACTTCTAAAT CATATGTTTT GCTTGCACTA AATCCAATAT CACCTGTACA TAAAATAACA 2220

CGACGGTATG GTAAACCTAA CTCTTCTAGA ATTGCTTCTG CGTTTGTTGT CATTTCTTCT 2280

AAAGCATTCC ATGAATCTTC AGGTTGTTCA AAACGTACCA TTTCCACTTT ATCGAATTGA 2340

TGTAAACGAA TTAATCCTCT TGTATCTCTA CCTGCTGATC CTGCTTCACT ACGGAAACAT 2400

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TCATCAGATT CACCTTGAGG TACATCATCA CTTATTAAAT TTGGAATACG ACAAAGGATA 2880

CCTGTCATTT TATTATCAAT TTCATTTAAT TGACTATCTT TTTCTTTAAT ATCGTCACCT 2940

AATGTGCGCA TTTCAGCAAT CACATCATCA GCATTTTCTT TATTACGTTT TTTTAATGCG 3000

ATTTCTTCGC TTACTTTATT ACGACGTGCT TTCATTTCTT CTGTTGCACT AATTAATTTA 3060

TCAATTTTGC TCTTAACTGT GTCAGGCTCA TTTCTGAATA ATCTAATGTC TAACATTAAC 3180

CTTCATCCTT TCCCAAATAA TTATCATTTA TTATGGAATG ACGTACGTCT TTATTTTTTA 3240

GAAAATAAAA AAAGACCACA TCCCTACAAG GGACGTGGTC TACGCGTTGC CACCCTATTT 3300

AACAATTTAA GTTATAAAGA TACACTAAAC CTAAATTGCA CTTCACTAAA ATAACGGTTA 3360

TCACCGATTG TTCTTTTAAA TTAAGTAGGT AGATTCATAT ATATGTTGAT TCTTGTTCAC 3420

ACTAACCACA AGCTCTCTGA TATCGAACAC TATATATTAC TTGTCCTACG AACAATGTCT 3480

TATTAAGTTA TTTTTAATAT AGCAAACTAT ATTTGCTTTT TCAAGTAACG ATTTCAAACA 3540

TCACTCATGT CGATTTAGTG ACATGCAGTC GTTTGATAAA TTGATTGCTT TAAATACTGT 3600

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TGATAACCAT GTCTAGCAGC TGTAGTTCCC ATAGATACGT GATCTTCTTG GTTCGCAGAT 3840

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GCAGCAGCAT ATTGCATAAT CATCGCGCCA CTTTGCAATC CTGGCTCTGG ACTAAGAAAT 3960

GCTGGTAAAT CACCATTTAA TTGAGGATTT ACTAGTCGCT CTAGACGACG TTCCGATACG 4020

TTTGCTAATT CACTTACACC TAATTTAAGA TGATCTAATG CAAAAGCAAT AGGTTGTCCA 4080

TGGAAGTTAC CACCTGAAAT AACAAACGTT TCATTTGCTT CCTCAAATAT AAGTGGATTA 4140

TCATTAGCCG CATTCATTTC AAATTCTAAT TGCTGTTTAA CATAATTGAA TACTTGAAAA 4200

CTCGCGCCAT GGATTTGTGG TATACAACGC AACGTATATG CATCTTGTAC ACGTATTTCT 4260

GATTGTCGCG TCGTTAATGT TGATCCTTCT AACCAATCAC GCATACGCGC TGCCACATTA 4320

ATCTGTTCTT GAAAATTACG AACTGCGTGC ACATCATGTC GATATGCATC TATAATGCCA 4380

TTAAGAGACT GATGCGTTAA TGCAGCAATC CATTCAGATT GGTAACCTAA ATCTTCTGCT 4440

TCTATATAAC TAATGACACC TTGAGCTGTC ATAGCTTGCG TACCATTAAT CAATGCTAAA 4500

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ACGTTAAATT CTATTAACAT TCCTAAGCGT AAAGAAGATT CACATAAAGG TGATTATGGC 5460

AAAATTTTAT TAATTGGTGG ATCTGCTAAC TTAGGTGGTG CCATTATGTT AGCGGCTCGT 5520

GCATGTGTAT TTAGCGGTAG TGGTTTAATC ACTGTAGCTA CACATCCAAC AAATCATTCA 5580

GCATTACATT CTCGTTGCCC AGAAGCGATG GTTATTGATA TTAATGATAC GAAAATGTTG 5640

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CGTTTAACGA CACCACGTTT AGTTGCAAAC ACTAAGAAGT TGTCTTCACT TTCAAGGTCT 7140

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CGTCTTCTAA CAACTGTCTT TTGATGCTCT AAATAATGTA CCAACGCTTC TTTTAAATTA 7920

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GGTGTTTGTT TGTATAAGTT ATTTAAAATG ACACTAGCAT TTGCATCCTT ACGCACATCA 8040

ATAACGACAC GCACACCAGT ACGTAAACTT GTTTCATCAC GTAAATCAGT GATACCGTCA 8100

ATTTTCTTGT CACGAACGAG CTCTGCAATT TTTTCAATCA TACGAGCCTT ATTCACTTGG 8160

AAAGGAATTT CAGTGACAAC AATACGTTGA CGTCCGCCTC CACGTTCTTC AATAACTGCA 8220

CGAGAACGCA TTTGAATTGA ACCACGACCT GTTTCATATG CACGTCTAAT ACCACTCTTA 8280

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ATAGATGAGT CACCATGAGG GTGATATTTA CCCATTACGT CACCAACGAT ACGTGCTGAT 8760

TTTTTATATG ATTTATCCGG TGTCATACCT TGTTCATTTA ATCCATATAG TATACGACGA 8820

TGTACTGGTT TTAAACCGTC ACGAACATCT GGCAATGCAC GAGCAACGAT AACACTCATC 8880

GCATAATCTA AAAATGATTC ACGCATTTCA CTGGTAATAT TTCGTTCATT TATTCTTGAT 8940

TGAGGTAATT CAGCCATCAA GAGTTCCTCC TTCAAAAGTT CAGTTCACAG CGCTTAGAAG 9000

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GTAGACCCCC CGGCAGAGTC CCCTTCGACT AAGAAAATCT CACATTCTTC AGGACTTTTA 9660

CTAGAGCAAT CGGCTAATTT ACCTGGAAGG CTTGCTACAT CTAACGCTGA TTTACGACGT 9720

GTTACTTCAC GCGCTTTTTT CGCAGCAACA CGTGCACGTG CCGCCATAAT ACCTTTTTCA 9780

ACCACTGTAC GTGCGACTTG TGGATTTTCA TATAAAAATC GTTCAAAGTG CTCTGAGAAT 9840

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GCAAGCTCTC TAATACGCTG CTGTAATGTT TCATAGTTGT ATACAGTTGT CTCTGTGAAG 10380

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GCAAATAGAA CCACATTGAG GTGTCCAATA TATTGAGTTA GACGACTTTG CTCTAAGTGn 11760

ATTCACTTTG GACTTGTTTA CCTTTnTTAG TTATAAACAT TGTTAATGGG CATCGTGCCG 11820

TGT 11823

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 692 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

ATAATTATTA ACATGGTGTG TTTAGAAGTT ATCCACGGCT GTTATTTTTG TGTATAACTT 60

AAAAATTTAA GAAAGATGGA GTAAATTTAT GTCGGAAAAA GAAATTTGGG AAAAAGTGCT 120

TGAAATTGCT CAAGAAAAAT TATCAGCTGT AAGTTACTCA ACTTTCCTAA AAGATACTGA 180

GCTTTACACG ATTAAAGATG GTGAAGCTAT CGTATTATCG AGTATTCCTT TTAATGCAAA 240

TTGGTTAAAT CAACAATATG CTGAAATTAT CCAAGCAATC TTATTTGATG TTGTAGGCTA 300

TGAAGTTAAA CCTCACTTTA TTACTACTGA AGAATTAGCA AATTATAGTA ATAATGAAAC 360

TGCTACTCCA AAAGAAACAA CAAAACCTTC TACTGAAACA ACTGAGGATA ATCATGTGCT 420

TGGTAGAGAG CAATTCAATG CCCATAACAC ATTTGACACT TTTGTAATCG GACCCGGTAA 480

CCGCTTTCCA CATGCAGCGA GTTTAGCTGT GGCCGAAGCA CCAGCCAAAG CGTACAATCC 540

mTTATTTATC TATGGAGGTG TTGGtTTAGG aAAAACCCAT TTAATGCATG CCATTGGTCA 600

TCATGTTTTA GATAATAATC CAGATGCCAA AGTGATTTAC ACATCAAGTG AAAAATTCAC 660

AAATGAATTT ATTAAATCAA TTCGTGATAA nA 692

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7900 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

ATACTGTAGC GCAAATTTCA CAATGGCATG TTATAGAAGA TTTAGTTACG AATGAATTAG 60

GTATTAGTAT TTTACCAACA TCAATTTCAG AgCAACTAAA TGGAGATGTG AAGCTGtACG 120

CATTGAAGAT GCTCATGTAC ATTGGGAATT AGGTGTTGTT TGGAAGAAGG ATAAACAATT 180

AAGTCATGCC ACAACGAAAT GGATAGAATT TTTGAAAGAC CGTTTAGGCT AACATATTAA 240

TAAAGCACTC ATTATTTAAG GCGCATCATT ACGTGGGTCA TTGAAATAAT GAGTGTTTTT 300

TTGTGAAAAT GAAGTGAAAT TTAGAGAGCG TTTCCATAGA AAATAGTAAT ACAAACTATA 360

AAAAAAGAGT ATTTTTATAT TGTGTACGCC ATCTTTATAA TAGTTATTGT AACAATTTAG 420

ACATATTTAG AAAGGGATGG CGCCATGCAC AAAGTCCAAT TAATAATCAA ACTACTACTA 480

CAACTAGGAA TCATCATTGT GATTACTTAT ATTGGCACAG AAATTCAAAA GATTTTTCAT 540

ATTGTACCGC TAACTTGGGT AGAAGACGGT GCAAACTTTT TATTAAAGAC GATGGTCTTT 660

TTCTTCATAC CGTCAGTTGT AGGtATTATG GaTGtgCTTC CGAAATTACG CTAAATTATA 720

TACTCTTTTT CGCAGTCATT ATCATAGGAA CATGTATCGT TGCATTATCT TCAGGTTATA 780

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TACGTGCAAG CCTTATTAAT GATTTTGTTG ACTGTCGTTT TATATTATTT CGCTAAAAGG 900

TTACAACAAA AATATCCGAA CCCATTTTTG AATCCAGCAT TAATTGCATC TTTAGGAATT 960

ATTTTTGTCT TACTTATCTT TGGAATTAGT TATAACGGGT ATATGAAAGG TGGCAGTTGG 1020

ATCAACCATA TTTTAAACGC AACGGTCGTA TGTTTAGCGT ACCCACTTTA TAAAAATAGA 1080

GAGAAAATTA AAGACAATGT CTCTATCATT TTTGCAAGTG TATTAAcTGG CGTCATGCTG 1140

AATTTCATGT TAGTGTTCTT AACACTTAAA GCATTTGGCT ATTCTAAAGA CGTCATTGTA 1200

ACGTTATTGC CCCGATCTAT AACAGCCGCA GTAGGTATCG AAGTGTCACA TGAACTAGGT 1260

GGTACAGATA CGATGACCGT ACTTTTTATT ATCACAACGG GTTTAATCGG TAGTATTTTA 1320

GGTTCGATGT TATTAAGATT TGGAAGATTT GAATCTTCTA TCGCCAAAGG ATTAACGTAT 1380

GGGAATGCGT CACATGCATT TGGCACAGCT AAAGCACTAG AAATGGATAT TGAATCCGGT 1440

GCATTTAGTT CAATTGGGAT GATTTTAACT GCAGTTATTA GTTCAGTGTT AATACCTGTT 1500

CTAATTTTAT TATTCTATTA ATTTAGATAT TTAAAATGAT AGACAGAAAG GGAGGCTATT 1560

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GCTGCTGGTT ACACAAAATT AACTGGTAAA ATCGGTGTGG CATTAAGTAT CGGTGGCCCT 1800

GGTTTAATTC ATTTATTAAA TGGTATGTAT GATGCCAAAA TGGATAATGT ACCGCAATTA 1860

ATATTATCTG GACAAACGAA TAGTACAGCA CTTGGAACGA AAGCATTCCA AGAAACAAAT 1920

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GATACATCAA GACCAACAGT AGTATCACCA AAATATAAAG ACATCAAAAA AGCGGTTAAA 2160

CTAATTAATA AAAGTAAAAA GCCTGTCATG TTAATTGGTG TAGGTGCGAA ACATGCGAAA 2220

GATGAGCTAC GTGAATTTAT TGAAATGGCT AAAATTCCTG TCATTCATTC ATTACCAGCT 2280

AAAACAATCT TGCCGGATGA TCATCCATAT AGTATCGGtA ACTTAGGTAA AATCGGTACC 2340

CCATATGTGG ATTACTTACC TAAGAAAAAT ATTAAAGCCA TTCAAATTGA CACAAATCCT 2460

AAAAATATCG GACATCGTTT CAATATTAAT GTAGGAATTG TTGGAGATAG TAAAATTGCG 2520

TTGCATCAGT TAACTGAAAA TATTAAACAT GTTGCTGAAA GACCATTCTT AAACAAAACG 2580

TTAGAACGTA AAGCGGTTTG GGATAAATGG ATGGAACAAG ATAAAAATAA TAATAGTAAA 2640

CCATTACGTC CAGAACGATT AATGGCATCA ATCAATAAAT TTATTAAAGA TGATGCAGTG 2700

ATTTCAGCAG ATGTAGGTAC AGCAACAGTT TGGTCAACTC GATACTTAAA CCTTGGTGTA 2760

AATAACAAGT TCATCATTTC AAGTTGGTTA GGTACAATGG GTTGCGGTCT TCCAGGTGCA 2820

ATTGCATCAA AAATTGCATA TCCAAATAGA CAAGCCATCG CAATTGCTGG TGACGGTGCA 2880

TTCCAAATGG TAATGCAAGA CTTCGCTACA GCAGTACAAT ATGATTTACC TTTAACTGTA 2940

TTTGTACTTA ATAACAAACA GTTAGCATTT ATTAAATATG AACAACAAGC AGCTGGTGAA 3000

TTAGAATATG CAGTTGATTT TTCTGATATG GATCATGCAA AATTTGCTGA GGCAGCAGGT 3060

GGTAAAGGTT ATACAATTAA GAGTGCTAGC GAAGTAGATG CTATAGTCGA AGAGGCATTA 3120

GCACAAGATG TACCAACGAT TGTAGATGTA TATGTTGATC CTAATGCTGC GCCATTACCA 3180

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TTATAACTGA TTTAAAGGTT ATCACAATTG AATTGAACTA TAAAAACGGT AATTTCTATT 3360

TCAACAAAAT GGGAATTGCC GTTTTGTTTA TTTATCACAA ATGATCGTAC TGAATTGATG 3420

ATAAAATTGT GAAAAAGTTG TTGAAAACGC TTTTACAAAT ATGTATAATA GCTATGAATT 3480

AGATATCACT TGCGTGTTAC TGGTAATGCA GGCATGAGCA AACAACCGCA CTATGAGAAT 3540

AGTCTTGTTT GTTCATGCCT GCTTTTTTTG TACATGGAAG CGGAAATTGA GATAGGGGAT 3600

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CCTGTTGCGA TTTTACCAGC AGCTGGTATT TTATTAGCGT TTGGTAACGC AATGCACAAC 3720

GAACAATTAG TAGAAATTGC ACCATGGTTA AAAAACGATA TCATTGTAAT GATTTCGTCG 3780

GTCATGGAAG CAGCAGGACA AGTTGTATTT GATAACTTGC CATTATTATT TGCAGTTGGT 3840

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AAAAATTTAA CATTAACAAC GTTTATATTC GGTATTATTG AACGCTCATT AATTCCATTT 4320

GGTTTACATC ATATTTTCTA TTCACCGTTC TGGTTTGAAT TCGGAAGTTA TACAAATCAC 4380

GCAGGTGAAT TGGTTCGTGG TGACCAACGT ATTTGGATGG CACAATTGAA AGATGGCGTA 4440

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GTCGGTATTG TATATGCTAT CGTGTATTAC TTCTTATTCG ACTTTGCAAT TCGTAAGTTT 4860

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AAATTACCAT TTGATGTCTT AGATGCAATG GGTGGAAAAG AAAACATTAA ACATTTAGAT 4980

GCATGTATTA CACGTCTACG CGTAGAAGTG GTTGATAAAT CAAAAGTAGA TGTAGCAGGT 5040

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GGTCCAAAAT CAGATCAAAT TAAACATGAT ATGGCCAAGA TTATGAGTGG TGAAATTACG 5160

AAACCAAGTG AAACGACAGT GACTGAAGAA ATGTCAGATG AACCAGTTCA CGTAGAAGCA 5220

CTTGGAACAA CAGACATCTA TGCACCAGGT ATCGGTCAAA TCATTCCATT ATCAGAAGTA 5280

CCTGATCAAG TATTCGCTGG TAAAATGATG GGTGATGGTG TTGGCTTTAT CCCTGAAAAA 5340

GGTGAAATTG TAGCACCGTT TGATGGTACA GTGAAAACAA TCTTCCCTAC GAAACATGCG 5400

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CAACCATTAA TGAAAGTGAA TTTAGCATAC TTGAAAGCAC ACGCACCAAG CATCGTTACA 5580

CCAATGATTA TTACAAATCT TGAAAATAAA GAACTTGTCA TTGAAGATGT ACAAGATGCT 5640

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TGAATGAACT TTTAGTCATT CGTAGTGCGT ATGCGAAGTA GCGAGTTGAA AGAGAATACG 5760

TTACAAAAGG CAGTAGCTTA AAATGAAGCT ACTGCCTTTT TAGTGCGCAA TGATGTATAG 5820

CAGGTGTGTT GATGrTAATA AGTTAAATAT TAGTGTTAGA TATAGAAAAC ATTGCTTATG 5880

TTTTTGTCAC ATTTTAGAAA AATGCATCTT CGCGACTAGC CAAATTAATA GTCTCATTGA 5940

AATAAATTAA CATGATTTTA AATCTATTTG TAAGATAAGG AGATTTGTCA TTATGACAAC 6060

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GGGTGTCGTT AGTAATATCG TTTATATTAG ATGGTTCGAA GATTTGAGAA CAGCGTTTAT 6180

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AACGGAAGCA GAGTATAAAG TACCTGTCAC AATACATGAC AAACCAGTAG GTCGTATTTA 6300

CTTAGTTAAA GCAAGCAAGA TGAAATGGGT GTTTCAGTTT GAAATTGTGT CCGCACATGG 6360

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GAATTTATTC ATCAATATCC GTTAGCAGTT GTACATGTCA TGCGCGATCA GTGTAGCGTG 6600

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GCTGTGATTA ATCAAAGTCA GGTGGAAGCT ATTGCTGGAG AATTAAATAT TTTCaCTGTA 6720

CCTGTGGATT TAATTTTTAT GAATGGAAAA GAAATGCATC GTCAAGGGCG TTTTATCGAT 6780

ATGCAACGTT TTGAACATCA TCTTAAGCAA ATGAATGATA GTGTAAATAA CGATGTCGAT 6840

GAGCATTAAT ATCGCAAATG ATTAGCATTG CTAAGATTAT GTAGACATCA TAACTTATTT 6900

CCCAGTAAAT ATTGGTAGTA ATTAGAATCA GCATGGTACA GTAGAACTAT AGTAGAAATC 6960

ATCAAAGAGG AGTGACGACA AATGCGTAAA AAATGGTCTA CACTTGCGTT TGGATTTTTA 7020

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AAACAAGATA AGCATCAACG CGTTGTATTA TATGCACATG GAGGCGCATG GTTCCAAGAC 7320

CCACTCAAAA TTCATTTCGA ATTTATTGAT GAACTTGCAG AAACACTCAA TGCTAAAGTC 7380

ATCATGCCAG TATATCCGAA GATTCCGCAT CAAGATTATC AAGCGACGTA TGTGCTTTTT 7440

GAAAAGTTGT ACCATGATTT ATTGAATCAA GTAGCAGATT CTAAACAAAT CGTTGTAATG 7500

GGTGACTCTG CGGGCGGTCA AATTGCTTTA TCATTTGCTC AATTGTTAAA AGAAAAACAT 7560

ATTGTGCAAC CAGGACATAT TGTATTAATT TCACCAGTTT TAGATGCAAC GATGCAGCAT 7620

CCTGAAATTC CTGACTACTT AAAGAAAGAC CCAATGGTAG GTGTGGATGG CaGTGTGTTC 7680

TTAGCTGAAC AATGGGCAGG GGACACACCT TTAGATAACT ACAAAGTATC ACCAATTAAT 7740

CCAGATGCTT TGAACTTATC GCAATTGTTG AGTGCGAAAG GTATCGAACA TGACTTTATA 7860

CCTGGATATT ACCAATTCCA TATTTATCCA GTATTTCCGA 7900

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1984 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

GTCTAAATAA ACAAAATTAT CATTGATTaC TGAACTGGCA TTTCGAAGTA ATGCTTCAAT 60

ATCATTCGAA TATTTCTTCA ATTTATGATT GTGAAATAAT TCTTGCATCA AAAATGGTCT 120

TTGGTCACAT GAATGTGCAT CTGAAGCTAC AAAATGAGCC AAATTACATT CTATAAATTG 180

TAATGATAAC TTTTGAATGT TTTTACCAAA TCCACCAACT AAAGAACTCG ATGTTAATTG 240

ACTCAGTGCC CCATTTGCAA CCAATTCATA TAATATTTCC GGATTTTTGG CGATACTTCT 300

ATTTCTTTCA GGATGTGCAA TGATTGGTAT GTAACCTCTC GATTGTATTT CAAAAAACAA 360

TTGTTTTGTA TAATGTGGTA CTTCGCCCGT TGGAAATTCA ATTAATAAAT ATTTCGAACG 420

ATTAATACCT TGAATACTAC CATTATCTAA GCCTTTCAGA ATCGAATCTG TAATTCTAAT 480

TTCTTGCCCG GGAAATAATT TAATATCCAA TGCTTGAACT TCTGGATGCG TTCTTAACTC 540

CGCCAATTTC ACAAGCACTT GTTGAAATGT ATTATCATAT CTCGGATGCA AATGATGAGG 600

TGTCGCTACA ATACTTGTTA CACCTTCATC CTTAGCTTGC TTTAATAGTG CAATACTCTT 660

TTCAATTGTT TTAGGACCAT CATCTATATC AACTAATATA TGGTTATGAA TATCAATCAT 720

GATTCATCAG TCCCATAATA TGCATAGTAA CTAGCACTTT TATCTTTAGG CATTCTATTT 780

AAGACTACAC CTAATAATTT AGCACCTGTT GCTTCAATAA GTTCTTTTCC TTTTTTAACT 840

TCATCTCTAT TATTATTTTC CGAATTAACT ACGTAGACAA CATTGCCGGT AAACTTTGAA 900

AATAATTGCG CATCTGTAAC TGTGTTCACT GGTGGCGTAT CGATAATTAC AAAGTTATAA 960

TTCATCAATA ATGTGTCATA CAAATTTGCA AATGCCCTTG ATGTAATTAA CTCTGACGGA 1020

TTCGGTGGGA TTGGCCCAGA CGTCAAGACG TCTAAATCTT GAATTTCAGT TGAGATAATA 1080

CTGTCTTGAT AAGTTGACCA ATTTAGCAAT AAACTTGATA GGCCTTCATT GTTTGGCAAA 1140

TTAAAAATAT AATGCTGCGT AGGTTTACGC ATATCCCCGT CTACGATTAG TGTTTTATAA 1200

CCTGCTTGCG CATATGCAAC TGCTAAATTT GCTGCAATTG TAGACTTACC TGCGCCTGGT 1260

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TGAACCTAAA ATAGGTAATC CTAGTTGCGA TTCAACATCT TCTTCTGTCT TAATACGCTT 1500

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GATAACTAAG TTGACAGATA CTATTGGAGA TACTTTTACA GCATTATCAT GTGCTGAGGA 1620

AAGTATCGTA ACATTATCAA CACTCATAAT TTTAGGCATG TCATGAGCAA AAACTTTAGA 1680

TATTTTATTA ACAATTTTGT CAGATTCAGA TTTATTCCCA GTGGTAACTG ATACAGTAAT 1740

AATTTGAGAG TTTGTTTGAT TGGTTACTTT TAAAAATGAA TTCAACTCAG CTGTTGAATA 1800

CTGACCATCA AnTTCTCTAG ATACTTTATC TAGAATTCTA GGACTTTTGA TAATTTCCGT 1860

ATATGTATTA ACAGACTGCA AACTACTTTG AACATTTTGG AAAGCTAAAT CACTTGAGGA 1920

CTTTTTCATG TTCACTAATA TTTGAGTAGA AGCAGTATAT TTGTCAGGCA TAACAAAAAA 1980

GGTT 1984

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CAAATCCCTT GGTGATGAtA AAtGtATTGC TGTGTAGCCA AATAATCTTC GTATATATGA 60

CTGACGTTCA ACAACAGCTT GCAATCGTTT CGTTGGTACA GTTACTTTCT TCTTGTTAAA 120

GAGACCATAT TCAATTTTAA GTTGCTCATT TTCAAGCATC ACCGAAAAGC CATAAAATCT 180

TATCATTGTT ATAATCGTTC CAATAATATA TGCCACTATT AATACTAGTA AAATGATGAT 240

TAATACTGAA ATACTTACAA TTTGAACCCA TTGACTAATT TCATGATTTA GCTTCGACCA 300

TGGGATCAAC TCTCTTACAG CCCCGTAAAT CGGTACTAAA GCTGCTAACG TTACACCAAT 360

GGCGCCACTG GTCATTGCCA TAAATAGTGA TTCTTTAAAA TTCATCTGAT ATATAGGAAT 420

GCGTTTATTT TTCTGATTAA GCATACTATC AGTGTTCTGC ACTTCATCTA AGCGACCTTC 480

TGCGATGTCT TCCACATTAC CTTCAATGTC ATGATTACAG TTGTCATTCT TCTCAGCACT 540

AGACTTTTGC GCCACTTCTG TCTTCAACTC TGTTTGCAAT TGATCAATAT ATCGTTCAAG 600

ATATTCACCT TGTTTTTTCG AAATAACACT TAAGACAATA CCATCACTTG GTGTTTTGAT 660

AATACGTTTT ATATTTAATT CTTTACGCTT TTTATTAAAA ATACCTGTTG TTAAAATGAA 780

ATAATTATCC tCAATCCAAT ATCGCGTGTT CATAATTCCG ACAATTTGAG AAATGTATGA 840

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AAAATCTTTC AATTGAAAGA TAATGAAAAT AAAAAAGACG ACTATGTTTT GTTTGATAGC 960

ATTGATTATG CCATTAAAAT ATGAAATCGG ATGTAATTTT TGAGGTTCAG ACATCACTTT 1020

CAACCCCTCT CAAATTCGAC ATAGTTCTCT CTTCGATTAT TTTAACATCG TCATGAGACA 1080

TCATCGGTAA ATAAATAGTA TGACCTGCAG TCATAAATCC AACTTTATAC AAATTAAGCA 1140

CTTTACTAAT TGGATTAGAT TTAATCGACA AGTATTGTAA ACGTTCAATT CGACTCGTTT 1200

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ACAATGCTGA CTTAGGACTC TTAGTCAACT TAGTATAATC TGACATATAC CCCTCTCCCC 1500

AAATAAAAAA TTATACGGAT TTATAATCTA TTTCATTTTA TTTTTATATG ATGATAATTA 1560

TAGCATATGG AATATTTCAT GCTAATTTAT TCTTCCTAAA GGTACATCTA AAAATTTAAT 1620

TAAGCAGAAA GTGCTTGAAT TGCTAAAAAG ACACCATGTT ATAATTTTAT CAACATGATG 1680

CCTTTCATCT ATAATCAATC TTTCATCTTA TCAAGAGCGA TATTTAGTTC AAGCACATTC 1740

ACATAATCAT TTGTTAACAC ACCACGCTGC TTACGATGTT GAATCAAGTC GGCCACTCTT 1800

GAAGTAGATA CATGACGAGC ATCAGCAATA CGAGGTGCTT GCTTCAATGC ATTTTCGACC 1860

GTAATATGCG GATCTAAGCC CGACCCAGAA CTTGTTGCAG CATCTATTGT TACATTTGAA 1920

TTCCCAAATT TAACATGATG TTTCATGCGT GCTATTAATT CGGTGTTTCC ATTCGATTCA 1980

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GATCCAACTA TACGATTGTC ATACGTAATT AAACTGCCAT TTGCTTGTTG ATAAAAAAAT 2160

ATTTGACCAA TTAACGTGAT AGCTAACGGG AATAAAAATC CACATAATAC CATAGTTATT 2220

ATCGTTAAAC AAATACTATT TCTTATCGTA TTCATGGTAC AGGCTCCTTC CTCTTTACAC 2280

AAAAAATTGT ACAATCATAT CTATTAATTT AATGCCTAAA AACGGGACGA TTAATCCACC 2340

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TACACCTTTC ATGGCAATTG GAATTAAGGC AACAATGATT AATGCATTGA ATATCAAAGC 2460

AATTGTTGAC ATCATTAGTG CAGGTAAAAT TGCAAAGTAT TTTGCTACGT CATTAGCCAA 2580

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TAGCTGCTGT TAAAGCATTA TCACCTGTAC ACATAACTGT TTCAATCCCC ATTTTTCTCA 2940

ATTCAGTAAA TCGTTCTACA AGACCATCTT TAATCACATC TTTTAAATAA ATCACGCCAA 3000

GCATGACATT GTTTTCAATG ACTATTAAtG GnGTGCCACC TTTACTCGAT ACATCCATAC 3060

AGAGAGACTC AATATTAAGA GGAATATTGC CTTGTTGTTG TTTGACAAGA TTTATCATAC 3120

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GcttCGCTAA TCGTACAATA CTTTTTCCTT CTGGCGTATC ATCGTAGATT GATGACATAT 3300

AAGCAGCGAC TATCAATTTT TCAAGCATTT GTTGATTCAC TGGTAAAAAT TCACTAGCGA 3360

TTCGATTGCC ATAAGTGATT GTGCCTGTCT TGTCTAAAAT CATTACATCG ACATCTCCAC 3420

ATACTTCTAC AGCACGCCCA CTTTTCGCTA ATACATTGAA TTGAGTAACA CGATCCATGC 3480

CTGCAATACC AATCGCCGAT AACAAACCAC CGATTGTCGT TGGTATTAAA CATACTGTTA 3540

ACGCAATGAG CATCGCAATA GGTAAAATTA AATGCAGGTA AGATGCTATT GGATATAACG 3600

TTACAATAAC GACTAAAAAT ATAATTGTTA ACGTTGTTAA TAATGTAAAA AGTGCAATTT 3660

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CAATGACTCC ATCAAAATCG CCACCTGATT CTTTTATCAC AGGTGCAGAC TCACCAGTAA 3840

TTGCAGATTC ATCAACGGTT GCTAATCCAT TTATTACAAC GCCATCAGCA GGGATTGTTT 3900

CTCCATTTTC TACCCGAATA TTTTGTCCGG CTTTTAACTC TGTGGCGTTC ACTATCCGAT 3960

ACGCACCATT TTCTTCTATC AATCGAGCAG TTAAATTTGA TTGTGCTTGT CTTAAACTAT 4020

CAGCTTGCGC TTTTCCACGA CCTTCAGCAA AGGCTTCTGA AAAATTAGCA AACAATATAG 4080

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AACCACTTAG TAAAACGATA AATACGATTA GTGATACGCC AAAATAAGGT TTATCAATCG 4440

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GACGATGTAC TCGTTTACCA TGTCTACTTA ACATGCGACC AAATAAGAAC AACATTGACA 5220

TAGGAAGTAA CATCATACTG CCCATTTCTA TAAAATTGCT CCAAATATTT GGATTTTCAA 5280

AAGGTGTTGC AGAATTTCCT GCTAAAAATC CTCCACCATT CGTACCAAGA TGTTTTATTG 5340

ATTCAAGTGA TGCAATAGGT CCAAATGCAA TATGTTGAAT ATGTCCGCTT AAAGTCCGAA 5400

TCATTAAATT AGCATGCAAC GTTTGTGGTA CaCCTTGAGT CATCAATAAA ATACTAATTA 5460

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CTGaTTCACC GTTATAGTGT TGtAAATTAC TATTTGTTAA AAAAGATATT GCTGTATTAA 5700

ACGCTAAATC TATCGATTGG TTTAAATTAT GATTTGGATT TAAAAAAAGC CATTGCTGAA 5760

CTATTAGCAA TACAAATGTT ATAAACCCCA TAAATCCATT AAATGCCAGA AAATGTTTGA 5820

CATATGTTTT AGCTGACATG TGTTCTAAAT CTGTGCCGAT AATTTTAAAA CACATATTTT 5880

CAAATCTAGT AAATATTAAA TCTACTCTTG ACGATTGCAC CAATGCTACG CGATATAGAT 5940

ATCCACTAAA AACATACGTA ATCATAACCA TCATTGTTAG AAACAAAATT ATTTCCATGA 6000

TAACCCTCAC TTAATATATT TCTAAAATTT TTCACTACGA ATTAAGGCAT AAAATAAATA 6060

ACACAACAAC ATCGTAACAA CTTGTTTATG AGAGAAATnT TAATTTTCAA ACTTAGTTAT 6180

TAAGAAAnCA TTAAGATGTG TATGCAGAAA TAAATTTTAT AGCATTTAAT TGTGAAGAAT 6240

ATTATGATAT TGCTATCGAG GTGAAGGTTA TG 6272

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1978 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

AAATGATGTT TTACAATAAA TATAnAAACG TATCAACATA TATCATCATA TTTTTAGTTT 60

CAAGTGCAGC CTTTGCAATA TTCTTGTTAA GTGCGnACAT TAGTGCTCAC TCGGAACAAG 120

TGTACGAAAT GACTGACCAT CAAATTAAGA ACAATACGAT AAATAAAGCA TACGAACATA 180

AAGACCCTAC AAACAATAGC GAACAAAGAG ATGGGAAAGT GTTCGCTTTA ATAAATTGAT 240

ACATTGTCAC AACGTTATTT TGCCTATTTT TGCGmAATAG CGTTTTTTAT TACwTTTTTG 300

CTGATsTTAA ATTTGTTATA TTTTGTTAAA GTATTATAAT GATTGAATAA ACAAATTGAA 360

GGTAGGTTTT TTAATTGAGT AATTCTGATT TGAATATCGA AAGAATTAAC GAGTTAGCTA 420

AAAAGAAAAA AGAAGTAGGA TTAACTCAAG AAGAAGCAAA GGAGCAAACA GCCTTAAGaA 480

AAGCTTATCT TGAGAGTTTT AGAAAAGGGT TTAAACAACA AATTGaAAAT ACTAAAGTAA 540

TTGATCCAGr AGGTAATGAT GTAACACCTG AAAAAATTAA AGAGATACAA CAAAAAAGAG 600

ATAATAAAAA TTAAATCACA AATCTGTAAA GAATTTTCTG ACATTATAAC TTGAAATAAG 660

TATTTTACTT ATCTTTTTAT TTTAAAATAA GTTATAATGT ATTTGATAAA ATTGAAGAAG 720

GGAAGATACA CAAGATGTTT AATGAAAAAG ATCAATTAGC TGTTGATACG CTACGTGCAC 780

TAAGTATCGA CACAATCGAA AAAGCGAATT CTGGTCATCC AGGATTACCT ATGGGAGCTG 840

CCCCAATGGC TTACACTTTG TGGACACGTC ATCTGAATTT TAATCCACAA TCTAAAGATT 900

ACTTCAATAG AGACCGTTTC GTATTATCTG CAGGGCATGG TTCAGCATTA TTGTATAGCT 960

TGTTACATGT TTCTGGTAGT TTAGAATTAG AAGAATTAAA GCAATTTAGA CAATGGGGTT 1020

CTAAAACACC AGGTCATCCT GAATACAGAC ATACAGATGG TGTAGAAGTT ACTACCGGAC 1080

CACTTGGACA AGGTTTTGCT ATGTCAGTAG GATTAGCTTT ACAGAAGATC ACCTAGCAGG 1140

gAAATTTAAT AAAGAAGGAT ATAATGTTGT AGATCATTAC ACATATGTAT TAGCTtCTGA 1200

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TAAAGATGGT AATGATTTAG AAGAAATTGA TAAAGCGATT ACTACAGCTA AATCTCAAGA 1440

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TGAAACACCT GAAGGtAAAA ATGTGTGGTT TGGTGTACGT GAATTTGCTA TGGGTGCT 1978

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7588 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

TAGTAGTATT TATTAAATTA TACGAAGGGA CCcAACACAG AAAATTCATT TTATTGAATT 60

TTACATTTAT GTGCCAAGTT GGGAAAAATG TCTTATTTTT TCaAAGTATT TAAAAGTAAA 120

ATTACATGTT AATACGTAGT ATTAATGGCG AGACTCCTGA GGGAGCAGTG CCAGTCGAAG 180

ACCGAGGCTG AGACGGCACC CTAGGAAAGC GAAGCCATTC AATACGAAGT ATTGTATAAA 240

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AGCCCATTGT ATTGACGCTG TTATTTAAGA AAGTCAGAAT ATAACGCATT ACTTCATCAC 420

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GTGTTTGATA TTTTTCTTTA AACTCATCAA TTGCCCTAGT ATCAACAATT AAATCCTTCG 540

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TTTGAAAGTT TTCAATTTGT CCTTTATTAG CTCTTGAAGT TTGACCTTGA CCAGGCAAAT 1020

CTCCCATAAT CACATGATAG CCATTTCTTC TTAACATCGT AATAACATAT GCATATCTTC 1080

CCGTATGTTC TAATATATTA TGAGCAATAA CAACGACGCC TTTCGCATCA TTTTCAGCTT 1140

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GCAGAAGAAA TCGCAAATGA AGGCTATAAT TTCACTATTT ATGTACCTTA TGGCGATGAT 2220

TGGTTTGCGT ATTTTATGAG AAGATTAGCA GAACGCCCAC AAAACCTATC TCTTGCTGTA 2280

AAAGAATTTG TGAAACCTGC TGGCTTAAAA CGTGTTGGCA TAATTGCAGC TTTAGGAGCT 2340

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CTTCAAGTAA TCTTCCAGTG ATAAAATCAT TAAATCGACT AACTACGATT GCAACTTTCA 2940

AATCTTTTCC AATTAATTTA CCTTCAAAAT TCATGTTAAA ATCCTCCTAT ATTAAATGAC 3000

CCATTTTTAT TTTTTTCGTT TCCATATAAT CATGATTATG TACCGTTTCT GGTACGATAA 3060

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CAATACTCAC TGTAAATTGC GTACCAAAGA TGTCGGAGTT ATCATCAACC ATTTGTACCA 3960

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TCGCCATAAA ATTAATGGTA TTATCGTTCA TCCATTCAGT AACCGCTACT AAATCACCTT 4080

CATTTTCACG ATTCTCATCA TCTACTACAA TAATTGGTTC TCCATTTTTT AAAGCCATTA 4140

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TTAACACTGA TGGAATCACC AATATGCATA TCTGCCGTAA TCTTATGTGC TTCAATTTCA 4740

ATCGTCCTGA CTGATTGACG AATTTGAACA CTTTTAACGA CACCTATTTC TTCAACGATG 4800

CCAGTAAACA TGCATCATCA CTTCTTTCGT AAAGTTAATT TAACATTTTG ATTTAATAAC 4860

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ACATTATATA TGTCTACTGA TTCTTGGTTT TTGTATGAAA AATAATACAA CTTGCCATaC 6720

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ATTAGTTCAG CAGTTCTTGG AGGCATTGGA TTTGAATTTA ATTGAATCAT CTTTGAGTAT 6840

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TTAGTTGATA TATTTGGATA TTTTTTCGTG AACATAGATA AATAAGATTT CATATAATGT 7560

CCGAATACAA ATCTCGGTAA ATATGCAG 7588

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

nCTAGGTATT TTAAACCTAA TCTAGATAAA CTAGCTTCGT AAGCAGCTGC TACATTTTCA 60

CGACCGAAAT CCTCAAAATA TAATTTTGAA GTAATAAATA AGTCTTCTCT AGCAATACCA 120

GTTGACTCCA ATCCGGCACG AATGCCAGCA CCTACTTGTT CTTCATTCCC ATAAACTTTT 180

GCGGTATCAA TACTACGATA TCCTTGTTCA ATGGCATACT TAACACTTTC CATGCAATTT 240

TCATCATTTT CCACACGAAA TGTCCCTAAA CCAATTTGTG GCATCGTGTT TCCATTATAA 300

AATGTTTTAA CCTCCATAAA TATCGCCTCA CCTTTTTGAT GTATTATACC CTGTTATCAT 360

AACAAATCTG AGTTGAATAC ATGAGAAAAA ACACTTAGAG CAATCAACCA CTAAAATTCT 420

AGTAATATCT CTCAAATATT AATCAAATTG TAAAAGTAAT TCTGTTTAAT TTATGACAAA 480

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TTCAATTTTA TCCATCATTT GTTGTAAGTC TTCCACGTTG TATTGAATAC GACCATGGAA 600

TACAAATTTG TTAAAGAACT CGTCTAATTG TTCAGCACCG ACAAGCACTT TGACAGCACT 660

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TGAAGTTGGT GTATATTTGG CACCTAATTC TTTTTGTAAG TCTTCAGCCA ATTGTTTAAT 780

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CATCACAATA GTTTGCGGTC TAGATTTATC TAAATCCAAT GTATCAAATA CTTGTTCCAT 900

TGGTGGTAAA TCTTTAAATT GACCGCCACT AATACCATTA TAAACATGAC CTTTTAACAA 960

TTGAGAATCA ATAATATAAA GACCAGTTCT TGTTAATACT AAATGACTAA TTCGTTCAAT 1020

ATTATTAAAG CCATCCTTTG GTAAAAAGAT ATTTGCCATA ATGTGCATAT CTTCTGGTCG 1080

AATTCGTTTT TCTTTAACTA ATCTTTCACG AATACCAATT AATCTCATGT CCGTTACATA 1140

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ACGACAATCG TATCAATACG TACTGGGTTA TCATTTTCAT CATATTCAAC AGTGACCTGA 2220

ACTTTACCGT CTGGTCGTAA ATAATTTAAC GTACCATCTT TACGCACATC TGATAAACGT 2280

TTTGCCAATT GATGTGATAA ATAAATTGCT AGAGGCATAT ACGTCTCTGT TTCATTCGTT 2340

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TTTGTCTGCA AAcGGTTTGG CACCTTTCTT TTATAAAAAA GAGGTTGCTG GGTTTCATTG 2940

GGTCCATGTC CCTCCACCAC TCAGGATAAG AGAATCCGTT AAAAATAATA GTACCTAATT 3000

AATGAATTAA TGTCAATTTT TCACAAATAA ATTTACAGTA AAATATTGTA GATTAATTAT 3060

GTTAATGTGT TATACTAATT AAATGTAAAG GCTTACATTT AAATTATCGC TTTGGAGGGA 3120

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GGCACTGGTA AAACAACCTT ATCGGCTGAC CCACACCGTA AACTAATCGG TGATGATGAA 3900

CACGGCTGGA ATAAAAACGG GGTCTTTAAT ATCGAAGGTG GCTGCTATGC AAAAGCAATT 3960

AATCTTTCCA AAGAAAAAGA ACCACAGATT TTTGACGCAA TCAAATATGG TGCAATTTTA 4020

GAGAACACTG TAGTTGCAGA AGATGGTTCA GTGGACTTTG AAGACAATCG TTATACAGAA 4080

AACACGCGTG CCGCTTATCC AATTAATCAC ATTGACAATA TTGTAGTACC ATCTAAAGCA 4140

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CATGCGTGGC ACCTTTTAAC TCTAGTTGGT CCGCTAAATA ATACGCATGA TGAATACCAA 5880

CTTGCTGGTC TTTCCCTCCA TGTACAATTA ATATTGGCGG ACTGTTTTCA TTAATGTTTG 5940

GAATCGCTTG GCGTGCCTCA TATGCCGCTC GATCTTTTTT CGGATGACCA ATCATTCTTC 6000

GTAGCATGCC TCTTAAATCG ACACGTTCTT CATACATTAA ATCAATATCT GAGACACCAC 6060

CCCAGATTGT ATAACTTGTT ACTGGTAAGT CTTGAAATGT CAACAATCCT TGTAAACCAC 6120

CTCGCGAAAA ACCAACCATG TGGATAAATG CATGTGGATA TTTATCATGT AGCAACCTTA 6180

ATAATTGCGT CACATCATTT AAATCGCCAC GGTAAAATTC GTCTTTGCCT TCACTCCCAT 6240

TGTTACCTCG GTAGTATGGC CCAATCACTA AAGTTTGACT ATCTGAAAAT TGCATTAATC 6300

TACCTGCGCG CACACGTCCT ACTTGACCTT TGCCACCTCG CAAATAAACT ACAATGCGAT 6360

TTACTTCATG ATGTGGTGTC ATCATTAAAG CTTTTACTTG TAAGTCATCT GACAAATATG 6420

TAATTTCTTC GAATTGATGC GTAAAATATT CAATTGGCAT TCGTTTACGT TTGATAAAAC 6480

CCAAGTGATT GCACCCTCTC TACGCATTTT AAAATGGTAC TATCTTGCAG TAAGAAACTC 6540

CGTTGTGCGA GTTCAATATC ATTGATACAG TTAAACAACA CTGGCCCTGC TGTTTCTAAA 6600

TAATCGTTCT TGCTTACCAA TGATTCAACT TCGATAAAAT ATACATCTTT TACAAAATCA 6660

GTTTGATCAT GTGTTTCAAT GGTATATTGT GCTATGTAAT AAATATTTTT AACTTTGGCG 6720

CCTGTTTCTT CATATAATTC aCGTGTAACT GCTTCAGCAC TACTTTCCCC GCGTTCCCTT 6780

TTACCACCAG GAAATTCAAT CCCCCGTAAA TTATGTTTGG TAAAAAGCAA TTGATTTTTA 6840

AACGTTGGAA TAGCTAGCAC ATGATTGCCA TCTGCTATCT CATTATCCTT TTTAAATGTC 6900

AAATTAACTT GACGATTATC TTTATCCCTA AACTTCACGC GCATCACATC CCTACATTGT 6960

ATGTTAATAT AATAGTTAAT TACTATCGTT GGAGGCATTA ATTATGAAAA AGATATTCTT 7020

GGCGATGATT CATTTTTATC AACGTTTCAT TTCGCCACTC ACTCCACCAA CTTGTCGTTT 7080

CCTTTATTTA GGTATCCGTC GTATTTTAAA ATGTCATCCG CTTCATAAAG GCGGCTTTGA 7200

CCCTGTTCCG TTAAAAAAAG ACAAGTCAGC AAGCAAGCAT TCACATAAAC ATAACCATTA 7260

ATATGGTTGT AATTGAGTTA TATCCACTAA AGGGGGGCGA AATTCGAGTC GCCCCTCTTT 7320

TAATATGCCT GAATGCGCCA CCACATCTTG TTCAAAATAA TAACCTGCTG GTGTAACATC 7380

TCCTGGATAA TCACCTTTAC GAGCAAGCAT CGCTGTAAAA TAGCGGCTTA AACCATATTC 7440

GTACATGCCG CCAATAACCA CTTTTGCACC ATGACTTTTC AAAGTATCAA TTGCCGTTTG 7500

CACTTTATCA ATGCCACCTA GACGAAATGG TTTTAATACA ACAACTTTCA CATTGTATAA 7560

TTCTATCAAA TTAATTATGT CCaACAACGA TGTTGCCTTT TCATCAAGGG CTATTGGAGG 7620

TATTGTTCCA TCCGCTACTT CATCAAGCAT GGAGATATCT TTAAATGGCT CTTCGATATA 7680

AAGAACCTGT TCACGCGCTA ATAACTGTAA CTGTGTGAAA TCTTGACGAT CCAAGGACTC 7740

ATTTGCATCT ATAACCAATT GAAAGTGAAA GTCTAATTCC CGTAACACTC TAATTTGATG 7800

CATGATTTGA GGCGTCCATT TTAATTTAAT TCTGGTCGGC TTTGTTGCTT TTAATGACTC 7860

TAGTTGTTTA TTTGATAAGC CGCTCGcTGT CGCTCCATAT GCTACTGAAA ATGAAGGCAG 7920

TACATGAAAC ATTTGATACA ATGCCATGAC AATAGTTGCC CTTGCAGCAG GCGTATTTTC 7980

CAATGAATCT ACTAATTTTA GTGCTGCTTC ATACGTTTCA AATGATTTAT TTCTATTATC 8040

TTCGAACCAT TGCTCAATTA CATGTTTCAC TGAGGCAATT GTTTCATGAT CATACCAATC 8100

TGTTTGAAAA GCGTTACATT CCCCGAAATA TGCATTTCCT TTGTCATCAA TCAATTCGAT 8160

AAACAAACAA TCACGATGCG TTAAAGTGAC TTTCGGTGTT ACAATTTGTG ACTTAAATGG 8220

CTCACTATAT TTATAAAAAT GCAAAGCTGT CAACTTCATC AAATCATCCT CTATACAACT 8280

TATTTCTTTG TAATTTACCT GTTGATGTAT AAGGTAAAGT ATCAACCTTT TCAAAGTGTT 8340

TCGGTACTTT ATATTTCGCT AAATGTTGTG ATAAATATGC AATCAATTGT GCCTTTGAAA 8400

TGTCACTTTC ACTGACAAAA TATAATTTAG GCACTTGGCC CCAAGTATCA TCAGGATGCC 8460

CTACACATAC TGCGTCACTG ATACCTGGAA ATTGctTCGC TACCGTTTCA ATTTGATATG 8520

GATAAATATT TTCACCGCCA CTAATAATTA AATCTTTACG TCGGTCATAA ATCATGACAT 8580

AACCTTCATG ATCTATTTCA GCAATGTCAC CCGTATTAAA ATAACCATTT TCAAACGTAC 8640

CCGTTAAATC TGTTGGATAC AAATATACAT TCATCACATT GGCGCCTTTA ATCATTAATT 8700

CTCCATGACC TTCTTTATTA GGATTTTTAA TTTTTACGTC AACATTGGCA CTTGGCATCC 8760

CTACAGTGTC AGGACGTGCA TGCAACATTT CCGGTGTTGC TGTTAAAAAT TGCGAACATG 8820

TCTCAGTCAT ACCAAATGAA TTATAAATTG GCAGGTTATA TTGTAATGCC GTCTCTATCA 8880

AACCTTGTTG CATAAGCCAA TTTAAAGTTT GTGGCACAAG CGAAATGTGC GTGATTCGTT 9000

CATTTTTAAT CATCGTTAAA ATTTGTTCGG CATTGAATTT ATCAACAATG CGCACAGTAA 9060

AACCTTCAAT AACAGCTCTT AAAAGTACAC TGAGACCCGA AATATGATAA ATCGGCAAGA 9120

CAGATAGCCA ATTAGTGTCA CGATCAAATC CCAAGCTCTC TTTACATCCG ATTGCACTGG 9180

CATAATGATT ACGAAACGTT TGTGGCACCG CTTTTTGAGG GCCCGTTGTC CCTGATGTAA 9240

ACATAATCGA TGCAATGTCA TCTAAATTAA ATGATGTATT TAATATGTTG GACGGCGACT 9300

CTTTCGGCAC CACAGTTTCA TTCGATGTTT CATATTGGAT ACCCATTGTG TTGTCCAACA 9360

AACTGTTCGT TGTAATATCC CTTCCAGCGA ATTCAATATC ATCCAGCGAT ACAATTTGAA 9420

ACCCTCGTAA TTCCAGTGGC AAGGTACAAA AAATCAATTG TACATCGATT GACTTCATCT 9480

GATTCGTCAT CTCATTAGGT GTCAACCTTG TATTAATCAT CGCAATTTCA ATATTTGCCA 9540

ACCAACATGC ATGTATTAAA ATGATCGATT GAATCGAATT ATCTATGTAT AGCCCAACAC 9600

GAGATTGTTG ATAAGCCTTG AGTCTTTTAG CCAATAGACT CGCTTCACAG TATAAATTTT 9660

GATAAGTATA AGATTCTTGA CCGTCTGTTA TCGCAATATG ATGTCCATTT TGTTGTGCTT 9720

GTTTATATAA CCAAAAGTCC ATGCGTTATT CCTCCAAAAT CATTTACATT ATAATTATAA 9780

CGATTTTATG ACATTCTAGC AGTGGTTATG TTTAAAAATA TAAAAAAGTA GACGAATTGA 9840

TGCATTGATA TGATTGTTAT AATGCTCAAT ACATATCGTT ATATCATTCG TCTACTATTA 9900

TCAGTTATTT TTATTTAATT TTAGTGTCAT TCTGTCATTT TGATGTGGTG ATTTACCCAT 9960

TGTTGCCACA TCATCTGCAA TGTCAATTGG TATACGGTTC ATGTCTTGTA ATGCACTTAA 10020

ATGGAATACT TCATCATCTA AATTTTCAAT GAGATATACA TAATATGTTA CCTTGTCCTT 10080

TTTATATTTT AACGTTTTCC AAAAGTCCGG CTTGCAATTC AATACATTAT CCGGAATATA 10140

TTCAATAAAT AAGTAACGTT TGCTGCCTAC TTTGTCTATG AAATATTTTG CAGTGCCTTT 10200

TTCTATACCT CTTATATGTG CATAGTCTGC TGAAAAGTAA ATACTACCTA TTGTTTCATT 10260

ATGTTGTTGT ATTTCAAATC GTTGGCCTAC TATTTTATTA TTTGTGCTAC nGGGGACTTA 10320

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

GTGTGGATTG GATTTTAAAA TCACCCTCAT AAATACTGTC ATCAATATGA TAAGTTACAA 120

TTTCACCTAT TATTAAATCA GCCCCATCTA ATACATCTCC AAGCAATATC ATTTGCGmTA 180

GTTTACATTC GAATCTCATT TTCGCATCTT TAATTCCTGG CGTCTTAATC GTTGTAGATG 240

TTAAAAGTGA TAATTCTGTA CGACTCAACT CACTGTCACC ATATGCTAAC GGCGCTGCAG 300

TCTCATTAAT ATCTTGAACA TTATCTTCGT CTGTAATATG CACAACAAAG TCTCCAGTCC 360

GTTCTATATT TAATGCAGTA TCTTTTCTCT TACCTCCTGC ACGTTGAACT GCAATAGCAA 420

TCATTGGCGG ATGATTATTA ACAATATTAA AAAAGCTAAA TGGTGCTGCA TTTACTGATG 480

CATCTTGATT TAATGTTGTA ACAAAAGCTA TAGGTCGTGG AATAATTGAA CCAATTAATA 540

ATTTATAGTT TTCTCTAGCA GTTAATGATT GTGCATCAAA CGTATACATA ATACCTACCT 600

CTTTTCTAAG TATATCTAGG TATTTCTCCG ATTTTGGTTA ATTTAAACAT CTATTCTCCT 660

CTGAAAATCA CTTGTATTTA TTTAGCAAAT CTTTTGAAAT ATGACACATA TGCATATCTT 720

CTGGATATTT TTCTAAATGT TGCTGATGTT CTTCAGCACT TTTAATGTAG TTAGACAGCG 780

GTAAGACTTC CACTGCAATT TGATCTCTGT CTTTACGTCG TTCAATGAAC TGACGCGCTT 840

CAATTAAGTG GTCATCTACA CAACTATATA AACCCGTTCG ATACTTTTGT CCAATATCAT 900

TTCCTTGTTG ATTCACACTG TAAGGATCAA TGATTTCAAA TAAATAATTC ATAATGTCTG 960

TAATTGTTAA CATACGATCA TCGAAATGAA GTTTGACACA TTCAGCATAA CCATCATACG 1020

GACCGTCTAA TTTAGAGCTT CTTCCATTTG CTCTTCCTGC TTCTGTATGT ATAATTCCAG 1080

GTATTGTTGC AAAAAATGCT TCAACACCCC ATAAACATCC TCCTGCTACA TAAACAACTG 1140

CCATATTTAC ACCTCATCAT CCTTTTTTAT ATTTTTAACA AGGTTATACC ATTTAATACC 1200

GCCATGACAT GATTCTGATA CACCTTCATT ACGATACCCA TATTTTTCAT AAAATGAAAT 1260

TAATGATTCT CGACATGTTA ACGTTACACC ATGTCGATGA TGATTCTTAG CAAGAGTTTC 1320

AAAATAGTTT AGTAAGCGAC CTGCAATACC CTGACCTTGA TAATTTGGTG CTACAACAAG 1380

ACCTAACACA CTAATATAGC CACCTTCACT ATTATTTGTG GAGACATTTT TAAATAAATC 1440

ATCGCTAATG TAACGCTCTT TTATGACTGG ACCGTTG 1477

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3976 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AGGTGATTAT CCTAAAAATG CTCATGAGGT CGCTATTAAT GATAAGTTAG CTGCAGACAA 60

CATTAGAGTC GGGGATAGAT TACATTTTAA AAATAATTCA ACTAGTTATA GAGTTTCTGG 120

TATTTTAAAC GACACAATGT ATGCGCATAG TTCCATTGTG CTATTGAACG ATAACGGATT 180

TAATGCATTG AATAAGGTTA ATACGGCATT TTATCCAGTG AAAAATTTAA CACAACAACA 240

ACGTGATGAG CTTAATAAAA TAAATGACGT TCAAGTTGTG AGTGAAAAAG ATTTAACAGG 300

TAATATTGCG AGTTATCAAG CAGAGCAAGC ACCGTTAAAT ATGATGATTG TTAGTTTGTT 360

TGCTATTACA GCAATCGTTC TAAGTGCATT TTTCTATGTT ATGACGATTC AAAAAATATC 420

ACAAATTGGC ATTTTGAAAG CAATTGGTAT TAAGACAAGA CATTTATTGA GTGCGTTAGT 480

TTTACAAATT TTAACACTAA CAATAATTGG GGTAGGTATT GCTGTGATCA TCATAGTAGG 540

ACTATCATTT ATGATGCCGG TAACGATGCC TTTTTACTTA ACAACGCAAA ATATTTTATT 600

AATGGTGGGG ATATTTATAT TAGTAGCGAT TTTAGGTGCC TCACTATCAT TTATCAAATT 660

ATTTAAAGTG GATCCTATCG AAGCAATTGG AGGTGCAGAA TAATGGCATT AGTCGTTGAA 720

GATATCGTCA AAAATTTCGG AGAAGGTTTG TCTGAAACAA AAGTTTTAAA AGGTATTAAT 780

TTTGAAGTGG AACAAGGGGA ATTTGTCATT TTAAATGGTG CCTCTGGTTC TGGGAAAACA 840

ACATTGCTAA CGATATTAGG CGGATTGTTA AGTCAAACGA GTGGTACAGT GCTTTACAAT 900

GATGCGCCAT TGTTTGATAA ACAGCATCGT CCTAGTGATT TACGATTGGA AGATATTGGT 960

TTTATTTTTC AATCTTCACA TTTAGTTCCT TATTTAAAAG TGATAGAGCA ATTGACACTC 1020

GTAGGTCAAG AAGCGGGAAT GACCAAACAA CAAAGTTCAA CAAGAGCAAT ACAACTTTTG 1080

AAAAATATTG GTTTAGAAGA TCGCTTGAAT GTATATCCGC ATCAGTTATC TGGCGGTGAA 1140

AAGCAACGTG TTGCGATTAT GAGAGCATTT ATGAATAATC CGAAAATCAT TTTAGCAGAT 1200

GAGCCACAG CAAGTTTAGA TGCCGATAGA GCAACAAAAG TTGTTGAGAT GATACGTCAA 1260

CAAATTAAAG AACAACAAAT GATTGGTATT ATGATTACAC ACGATCGAAG ATTATTTGAA 1320

TATGCAGATC GAGTGATTGA ATTAGAAGAT GGCAAAATAA CTGATTAGTG GCTTGTAAAG 1380

ACGCTAAATG TTAATGATTT AAGACATAGT AGTATAAAAG TTAGATAACA GAATACGATT 1440

TGGGTTTACA AAAAACAGGC TGGGACATTA AGTTCTTAGG CAATGTAAAA AAGCTGATTT 1500

CTATTAATTA TTTGATAGAA ATCAGCTTTT TTGATATGTA TTTTATAATG TACAGCTCGT 1560

TGCATTCATA TAGCTTGAAG TCACGTTTAA AACCATATCT ATCATTATGG TATGCATATC 1620

TTTTAAAACC TATTCTTTTG TTATTAGGAC ATATAAATTC ATCATTAAGT TCGTCATATT 1680

TCCAATTTTG AGTGTTAAAA ATGTCACTTT TAAACTTTCT AGTTTTATCT TTAATAAACA 1740

CACTATCATA ACATGCATCA GCTACAATAT ACTCCGGTAA ATAACCGAAG nTATTTTgAA 1860

TCATTGTTAA AAATGGAATT AAAGTTCTAG TATCTGTTGG GTTTTGAAAT AGGTCATAGG 1920

ATAAAACAAA TTGAGAATTT GTCGCTATTT GTAAATTGTA TCCTGGCTTA AGTTGGCCAA 1980

AGTGTCTTAT TTTTTTAAAG TATTTAAAAG TAAAATTACA TGTTAATACG TAGTATTAAT 2040

GGCGAGACTC CTGAGGGAGC AGTGCCAGTC GAAGaCAGGG GCCCCAACAC AGAArcTGAC 2100

ATATAGTCAG CTTACAACAA TGTGCCGGTT GGGGTGGCTG AGACGGCACC CTAGGAAGGG 2160

ACCCGTCATC AAAAATTCTA TTTATAGAAT TTTACAGTAA TGTGCCAGAT GGGCATAGCG 2220

AAgcCATTCA ATACGAAGTA TTGTATAAAT AGAGAACAGC AGTAAGATAT TTTCTAATTG 2280

AAAATTATTT TACTGCTGTT TTTTTTAGGG ATTAATGTCC CAGACTCTTT AGTTTATTTA 2340

TTTTCAATAT AACAATTGTC TAATCAAGGA TTAACGAATA TTTAAAGATA GTTTGACGCA 2400

ATATTAGAAA CAACCTATAA TAATAGTTTG TTTGTGGATT AACTATTATA AATAAAAGCG 2460

GCGTAAAGAC ATATAAACCA ACTACTTGAA CAATATAACG TTAATAACAA TCTATACTGA 2520

TACATTACGC CTAGATAATC TTTGATGAGC ACATGTAAGA AAAAGTGATA TGGTGTATGA 2580

CTTCCGACAC CATCGATAGA TAAACCTAAT TTTTGGGCTA GTCGTAAGGC GCGCAATACA 2640

TGAAACTGAC TTGTtACACA AACAATTTTA ACTGCTTCAT GATACAAATT GTTGATGATT 2700

TGTTTAGAAT ATAAAAAGTT TGTGTATGTA TTTATAGAGT GAGATTCCAT TAGTATATCT 2760

GTTTTATCAA CACCATGTGC AATCAAATAA CGTTGCATAG CTAAAGCTTC AGAAATTGGT 2820

TCGTCTGGTC CTTGTCCGCC AGATACAATG ATCTTTGTTG CTGATGCTTG TTGTTGATAG 2880

ATATCAAGTG CACGATCTAA ACGCGCTGCA AGCATTGGTG TGACAAATTC GGTAAAAATA 2940

CCAGCACCTA ACACAATTAT GATATCAACT TCTTTGTTGT ATGATCTATG TCTATATGAT 3000

ACTGTCCAAA CGAGATAACA AATAAAGGTT AGTAACAGGG AAAGACATAA TATAGCTAAC 3060

CACATAGACA AACCTTTCAC AATAGGTGAC TGAATCGTAC TTATAAATAG AAGTGCTGAT 3120

GTGTAGAGTA CAAATTTATA TGAAAAAGAT AATAATTTTT TAATAAATAA GCGACTAGAA 3180

GTATGAGAAA ATAAATATCT ATGTTTGAAT AGCATGATAA TACTGATTAT TATAAATGTT 3240

ACAAACATAG ACCAAGGGAA AGTATAGGTC ATGATGCTAT AGATGAGTGA CAAAAATATC 3300

GATATGACAA CTAAGATGTA GCATGTTAAA TTTAACGTCA GAGTATAGTT GAAAATTAAC 3360

GGACAAATAA CGATAAGTAT AAATATTAAT AATAAATTCA ATAACATACT GACACCTCGC 3420

TTATAATAAA TATTAAATAT AAATGTAGAT GATTTAATTT ATTAAAGCAA GGAGAAAGCA 3480

GCAACATGTA AATCTTAATT TGTTATATTA TATATGGGTC AATATTTTTG TGTTTTTTAG 3540

TATGGTAAAA CATTTACAAG ACCATATTCA ATTTTTAGAG CAGTTTATAA ATAACGTTAA 3660

CGCATTAACT GCAAAAATGT TGAAAGATTT ACAAAATGAA TATGAAATTT CATTAGAGCA 3720

GTCTAACGTA TTAGGTATGT TAAATAAAGA ACCTTTGACA ATTAGTGAAA TCACGCAAAG 3780

ACAAGGTGTA AATAAGGCCG CAGTAAGCCG ACGAATTAAA AAGTTAATCG ATGCTTAATT 3840

AGTTAAGTTA GATAAACCAA ATTTAAATAT TGATCAACGT TTGAAATTCA TAACCTTAAC 3900

TGACAAAGGT AgAGCATATT TGAAAGAACG TAATGCGATT ATGACAGATA TTGCGCAAGA 3960

TATTACTAAT GATTTA 3976

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

GCTACCTAGG CATTTAAGAG ATCAAAAAAT GTATGAATAT GAACGTTATT TTTATGAGCA 60

AGAACTTAAT GGCGTTGATG aAGGGGAAAT TTTAAAGAAG TTAAAAGACC CACAAGATGT 120

TGCAGCTGAA ACAAAAGCTA GAAGTGTTAT TGATTATGCT GAATCTAAAC CAACATTTGA 180

AAATATTTCA AGAGCTGTTG CTGCTTCATT AAGTTTAGGC ATTCTATCTA TTTTTGTCAT 240

CCTTATACCA GTATCTATAG TTGGATTATT TGTATTAGCA TTATTTTTAA TATCACTTTT 300

GCTGCTGTTT TGTCCAATTA TTTTATTAGC ATCAGCAATA TCCAGAGGAA TTGTGGACTC 360

AATTAGTAAT GTATTTTTTG CCATATCATA TTCAGGATTA GGATTAGTAT TTATCATTGT 420

CATATTTAAG ATTTTAGAAT ACATTTATCG TTTAATCTTA AAATATTTAC TTTGGTATAT 480

TAAAACTGTC AAAGGAAGCG TTAGAAAATG AAGAAATTCT TTTTTATTGG GCTTTTAGTG 540

TTTGTTGTCT TTTTTACAGC AGCAACCATT ATTTGGTTCA GCTATGATAA AAACAAATAT 600

GGTACTAAAC AATATGATAA AACATTCAAA gACGATGCTT TTGACAATGT ATCTATAAAT 660

TTGGATAGTA CAGAACTTCG TATAAAACGG GGGAATCAAT TTAGAGTTAA ATATGATGGT 720

GACAATGATA TATTAATTAA TATAGTAGAT AAGACGTTGA AGATTAGTGA TAAAAGGTCT 780

AAGACAAGAG GATATGCAAT TGATATGAAT CCTTTTCATG AGAATAAGAA AACGTTAACG 840

ATTGAAATGC CTGATAAAAT GATTAAACGT TTAAATCTAT CATCTGGAGC AGGAAGTGTT 900

AGAATCAGTG ATGTTGATTT AGAGAACACA AGTATTCAAA GCATTAACGG TGAAGTAGTT 960

AGTAAAAGTA ACATTAAAAA TAGCAATATT AAAGTTGTTA TTGGTACGCT ACAAATCGAC 1080

AAGAGTCAAA TTAAACAATC CATATTTTTA AACGATCATG GTGACATTGA ATTTAAAAAC 1140

ATGCCATCAA AAGTAGATGC AAAAGCTTCT ACTAAACAAG GAGATATTCG TTTTAAGTAT 1200

GATAGTAAAC CTGAAGACAC TATACTAAAG CTAAATCCGG GAACGGGTGA TAGCGTAGTT 1260

AAAAATAAAA CATTTACTAA TGGtAAAGTT GGGAAAAGCG ACAATGTTTT AGAATTTTAT 1320

ACGATTGATG GTAATATCAA AGTTGAATAA ATAAAGGATG TAAGCACCGA TATTAGGAAG 1380

CATAATTTCT CTAATATCGG TGTTATTTAT TTGTTGGCAA AAGTTAAGTC GGTATCTATA 1440

TTGCCAGTAA AGTGAGTGAT ATTAAGGTCT TGACCATCTA ACCATGATTT GAAATCTATT 1500

ATTTCTGGTG GCGCATTTTC TCCCAATGTA AAATATGCAG TTAATGTTTC AGGTTGATAC 1560

ATTGATGTAT GGATGGTGCC AGACCAGCTT TTGAATAGTT TACTGTAAAT TTCATACTGA 1620

GGATTATTGA ATAACTTAAA TGCTGTAGTC ATATCTAAAT TATCATTAGT TTGTGAAATG 1680

GTACGCGCCA GTCTTTCTTT AGATTCTTTT GTATAATTAC GATTTTCATG TGTTAATATT 1740

TCAAAATGAT TTGTACATAT ATTATCATAA CGAACATCTA TTGATCTCGG TGTCACTTCA 1800

ACAATTGCAT GGTTCAATGA TTTGTCCATC AGTATGTAGC TAAATGAGCT TCTGTGTGGT 1860

ATTTCTTTCA ATAATTGGAT TGCTTCTGTT ACATTTCGGC AATTTTCAAG AATTAGACGA 1920

CCAATCATAT AACATACAAA ACCATTTGCT GGTTTCTTCC GGTGCATAAA GTTATAGCCC 1980

ATAGTTAATC CTGACTCATT CATACCATCC ATTCTTCCAG TTACCCTTGA TACAGGACCA 2040

ATTTGAGCTA AACCGCTATC TGTAGGTTGA TAAAGTAAGT AGCGACCATC ATAAGTTGCA 2100

GGGTGGTAAT CATAATTTCT AACCATGAAG TCTTTGCCTT GAAAGACCGT GCAaCCACTT 2160

TCTTTTAAAT CGGTAAAACG ATAATGTCCA AAGTTTAAAA TAATTTGGCG TGTTGGCATT 2220

TTGAGTATAC TTTGTAGTCC CATTAATTCT TCCCATATTT GAGGTGCGTA TGTTTGGAAT 2280

ATTTGATAAG TTTCATTTAC ATCTATATCG AAACGTGGGA CaCnTTTTTT CCATTCTTTT 2340

TCTCGATTTT TTAGAAGAGG TGTTTGTTGA AGCCATTTAC CAGTTTTAAC ACCTAACTCG 2400

AAATGTGAAC CTCTAAAAGT CATGATATCT GATGTCACTT GTTGCATATC ATCGGCCCCT 2460

TTCTTTTTAG TTGTAATATA TTGTAAATAA ATAGTAATCG TATGTATATT GAATGTCATG 2520

TTAAATAAAG TTATATTTTA CTAAATGAAA TATAAAATTG TTTGAGGTGA TTTCTCGGTG 2580

TATAAGACTT ATCAATCAGT TAAAACATAT TTTTATAGAT GGTGGGGATA TTGAGTTAAA 2640

AACTTAAAAT CATCTTATCA TAAATATCAA TCTTAAGTTA GCATTCACGA TAATAGTCAT 2700

TGTTAACATT AGCATATAAG GTCATGTCAC GTTGAAACAG AGGTTCCTCG GCATTTTTGA 2760

TTATTTAATG ATTATTCTAT ATATGATAGT ATAATGAAAT GTAGATAGGT ATTTAATTTA 2880

ACAGAGGTGA AATTGAGATG TGGAATTTTA TTAAATGtGT GkTTAAATTC GTATTTAGCT 2940

TAGTTGCTAT TACAACATTA GTTGCTGGTG TTGGTGTAGT AGCATTTGCT TATATCTTTA 3000

AAAAAGATTT TGAAGATATT GAAAGAAAAA CTAAAGAAAT TATTTCTGAT ATTGAAAGTA 3060

AAAATAACTA ATAACATTTA GAGGCTGGGA CATAAATCCC TAAAAAACAG CAGTAAGATA 3120

ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTn ATcAmTACTt CGTATTGAAT 3180

GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTTGGTCTTC GACTGGCACT GCTCCCTCAG 3240

GAGTCTCGCC ATTAATACTA CGTATTAACA TGTAATTTTA CTTTGGAAAT ACTTTTAAAA 3300

AATAAGACAC TTTGGCCCAA CTTGGCACAT AAATGTAAAA TTCAAT 3346

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2375 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

GTTGAAGAAA GAAATATAAC AGTCAATTAT AATTATAACC TTGTTGAAAT CGACGGTGAC 60

AAAAAAGTGG CTACATTCGA ACATATCAAA GCATACGATA GAAAAACAAT AAGTTATGAT 120

ATGTTACATG TAACACCACC TATGGGTCCC TTAGATGTAG TAAAAGAAAG TACACTTTCA 180

GATAGTGAGG GTTGGGTAGA TGTTAACCCA ACCACATTAC AGCATAAAAG CTACTCTAAT 240

GTATTTGCAC TTGGTGATGC TTCAAATGTA CCTACTTCAA AAACAGGCGC ACTATTcGTA 300

AGCAAGCACC TATCGTCGCT AATAATTTAT TGCAAGTGAT GAATAATCAA ATGTTAACGC 360

ATCATTATGA TGGTTATACT TCATGCCCTA TTGTTACTGG ATATAATAGG TTAATACTTG 420

CAGAGTTTGA TTATAATAAA AATACTAAAG AAACAATGCC GTTTAATCAG GCCAAAGAAC 480

GTaGAAGTAT GTATATATTT AAGAAAGATT TATTACCTAA AATGTATTGG TACGGCATGC 540

TAAAAGGATT AATATAATAA AGTACAGAAA ACAATAAATT TTTAATGAAA AATCTTTTAC 600

TATAAAAGAT TAAGTATTTA AATGACGTGT CAGTGTTGTG TTTATATGTC GTGAATTTTT 660

AGCTCTAAAT AGTATAAGAT TGAAAAAGTT GTTACTGTTT TAAATGATCA CGATGAAGTC 720

ATTCAATAAG AATGATTATG AAAATAGAAA CAGCAGTAAG ATATTTTCTA ATTGAAAATC 780

ATCTCACTGC TGTTTTTTAA AGGTTTATAC CTCATCCTCT AAATTATTTA AAAATAATTA 840

AGATATTCAA ACCACGTGTA CTCAAAATGA TAGCTTGGTA TGTACCTCCA ATAGTAATTT 960

CAATAACTTT GTCTGTTGAA CACTAAGAGC AATTTTAATT TCATAATGTG TTGTAAACAT 1020

TTTTTTTGAT TGGAGTTTTT TTCTGAGTTA AACGATATCC TGATGTATTT TTAATTTTGC 1080

ACCATTTCCA AAAGGATAAG TGACATAAGT AAAAAGGCAT CATCGGGAGT TATCCTATCA 1140

GGAAAACCAA GATAATACCT AAGTAGAAAG TGTTCAATCC GTGTTAAATT GGGAAATATC 1200

ATCCATAAAC TTTATTACTC ATACTATAAT TCAATTTTAA CGTCTTCGTC CATTTGGGCT 1260

TCAAATTCAT CGAGTAGTGC TCGTGCTTCT GCAATTGATT GTGTGTTCAT CAATTGATGT 1320

CGAAGTTCGC TAGCGCCTCT TATGCCACGC ACATAGATTT TAAAGAATCT ACGCAArCTC 1380

TTGAATTGTC GTATTTCATC TTTyTCATAT TTGTTAAACA ATGATArATG CAATCTCAAy 1440

ArATCTAATA GTTCyTTGCT TGTGTGTTCG CGTGGTTCTT TTTCAAAAGT GAATGGATTG 1500

TGGAAAATGC CTCTACCAAT CATGATGCCA TCAATACCAT ATTTTTCTGC AAGTTCAAGT 1560

CCTGTTTTTC TATCGGGAAT ATCATCGTTA ATTGTTAACA ATGTGTTTGG TGCAATTTCG 1620

TCACGTAAAT TTTTAATAGC TTCGATTAAT TCCCAATGTG CATCTACTTT ACTCATGCGT 1680

TTGATAAAAA CTTAAATAAT ATTAATTCGG TCATCAGTGG CGTTAAATCT TTTATCATTT 1740

TTAGTTATAG TTGATAAATT TATATTTATA AGCATATATG GATATTTCAT CAAAAATTTT 1800

TATTTATATA AATCCGAACT GCATACATAT TTGTTTAAAT AAGAGGTATT ATTTTTCGGG 1860

AAATTGCTGT CTGAGTTAAA AGGATTAGTT TTATAAAATG AGTTGAACTA TAGCCAAAAA 1920

CGATTAAAAT ACTGATAATC CATTTTTGtA TTATGTTAGG GACTTTTTTA CTTAATTTTA 1980

ACCCTATTGG aGCmAATATA ATACTCCCTA TTATAAGGAA TAAGGCGTCA TATAAaGGGA 2040

TATAACCTTG AATAAGTTTG ATGACAAAAG CACCAATTGA AGATATAAAA GCAATTACTA 2100

TACTATTAGC GACTACAGTA TTCATTGGTA ATTTGAATAA AACCAATAAT ATAGGAATAA 2160

TAATGAAGGC ACCACCTGCA CCTACTATAC CTGAAATAAT ACCAATGAAA AGGCCAATGA 2220

TAACTAATAA ATATTTATTA AATGAAGACT TTTCGGAACT AGGTTTcCACT TTAATAAACA 2280

TTAATGTTAA TGCAAGTAAA GCAATAATGA TATATACCGT ATTTACAAAT GTAGCATCAA 2340

ATAAATTTGC TAGAAATGCA CCTAACATAC TCCCT 2375

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

GAGGTTTCTA GACAAGCTTT TAATAACTTA CCAAACTCAT TAAgrTGGTT gTGtTGGACT 60

GCCtATTATC mAAGtATTAT GaGTTGTTTA ATATTAGtGC TAArACATAC GAAGAGTGGT 120

TTAAACAATT TAGTAGTAAG AAAGCACAAT TCAGTATTAA TCTCACGGAT AAATGGATAA 180

TTCAAATCGC ATATGGTAAA TTAATAATAA TGGCTAAAAA TAATGGCGAT ACATATTTTA 240

GAGTTCAAAC AATTAAAAAG CCAGGTAATT ATATTTTTAA CAAATATCGA TTAGAGATAC 300

ATTCTAATTT ACCAAAATGT TTATTTCCGC TTACAGTGAG AACACGACAA AGTGGCGATA 360

CATTTAAACT GAATGGGCGC GATGGTTATA AGAAAGTGAA TCGCCTGTTT ATAGATTGTA 420

AAGTGCCACA GTGGGTTCGG GATCAAATGC CAATCGTATT GGATAAACAA CAGCGCATTA 480

TTGCGGTAGG AGATTTATAT CAACAACAAA CAATAAAAAA ATGGATTATA ATTAGTAAAA 540

ATGGAGATGA ATAGCGTTAT GCATAATGAT TTGAAAGAAG TATTGTTAAC TGAAGAAGAT 600

ATTCAAAATA TCTGTAAGGA ATTGGGAGCA CAATTAACAA AGGATTATCA AGGTAAACCA 660

TTAGTATGCG TGGGTATCTT AAAAGGCTCA GCAATGTTTA TGTCAGATTT AATTAAACGA 720

ATTGATACCC ATTTATCAAT TGATTTCATG GATGTTTCTA GTTATCACGG AGGCACTGAG 780

TCAACTGGTG AAGTTCAAAT CATTAAAGAT TTAGGTTCTT CTATTGAAAA TAAAGACGTA 840

TTAATTATTG AAGATATCTT AGAGACTGGT ACTACACTTA AGTCAATTAC TGAATTATTA 900

CAATCTAGAA AAGTTAATTC ATTAGAAATA GTTACTTTAT TAGATAAACC AAACCGTCGT 960

AAAGCGGACA TTGAAGCTAA GTATGTAGGT AAAAAAATAC CAGATGaATT TGTTGTTGGt 1020

TACGGTTTAG ATTATCGTGA ATTATACCGA AACTTACCAT ATATCGGTAC GTTAAAACCT 1080

GAAGTGTATT CAAATTAATT TTTTAATCAA TTTCAGTTAT TATTACTATG CGTTTGAGAA 1140

ATAATAGTGT AGACTCAAAA ATATGAAAAA TGTATTTCAT ATATATTTAA TTTTAGACAA 1200

GACATATGTC TTGAAAAGTT GAAAAATATA GAGATTGATA AAACTAATAC GGGTGTGAAT 1260

GACATTGATG TTAAGCTCAA TTACTAGCTT ATAAAACATG TCATATGTTA CAATTTTTGT 1320

TAGTTTTATT ATGGGAAGTA GGAGGAAATG ACGCATGCAG AAAGCTTTTC GCAATGTGCT 1380

AGTTATCGTA ATAATAGGCG TTATTATTTT TGGTCTATTT TCATATTTAA ACGGTAATGG 1440

AAATATGCCG AAACAGCTTA CATATAATCA ATTTACTGAG AAGTTGGAAA AAGGTGACCT 1500

TAAAACTTTA GAAATCCAAC CACAACAAAA TGTCTATATG GTAAGTGGTA AAACGAAAAA 1560

TGATGAAGAC TATTCATCAA CTATTTTATA TAACAACGAA AAAGAATTAC AAAAAATTAC 1620

TGATGCTGCT AAAAAGCAAA ACGGTGTAAA ATTAACGATT AAAGAAGAAG AAAAACAAAG 1680

TTTCTTCCTA AGCCAAGCAC AAGGTGGCGG TAGTGGCGGT CGTATGATGA ACTTTGGTAA 1800

ATCTAAAGCA AAAATGTACG ATAATAATAA ACGTCGTGTT CGTTTCTCTG ATGTAGCAGG 1860

GGCAGATGAA GAAAAACAAG AATTAATTGA AATTGTTGAT TTCTTGAAAG ATAATAAAAA 1920

ATTCAAAGAA ATGGGATCTA GGATTCCTAA AGGTGTCTTA CTTGTTGGAC CTCCAGGTAC 1980

TGGTAAAACA TTACTTGCTA GAGCGGTTGC AGGTGAAGCT GGCGCACCAT TCTTCTCTAT 2040

TAGTGGTTCA GACTTTGTAG AGATGTTTGT TGGTGTTGGT GCGAGCCGTG TTCGTGACTT 2100

ATTCGATAAT GCTAAGAAAA ACGCGCCTTG TATCATCTTT ATCGATGAGA TTGATGCTGT 2160

TGGTCGTCAA CGTGGTGCAG GTGTTGGTGG CGGTCATGAT GAACGTGAAC AAACCCTAAA 2220

CCAATTATTA GTTGAAATGG ATGGTTTCGG TGAAAATGAA GGTATCATTA TGATAGCTGC 2280

TACAAACCGT CCTGATATCC TTGACCCAGC CTTATTACGT CCAGGTCGTT TTGATAGACA 2340

AATTCAAGTT GGTCGTCCAG ATGTGAAAGG CCGTGAAGCA ATTCTTCATG TTCATGCTAA 2400

AAACAAACCA CTTGATGAAA CGGTTGATTT AAAAGCAATT TCACAACGTA CACCTGGTTT 2460

CTCAGGTGCT GATTTAGAGA ACTTATTAAA TGAAGCATCT TTAATTGCTG TACGTGAAGG 2520

TAAAAAGAAA ATTGACATGA GAGATATCGA AGAGGCAACG GATAGAGTTA TAGCCGGACC 2580

TGCTAAGAAA TCTCGAGTTA TTTCTAAGAA AGAACGTAAT ATTGTTGCTC ATCACGAAGC 2640

TGGTCATACA ATTATCGGTA TGGTACTTGA TGAGGCAGAA GTAGTGCATA AAGTTACTAT 2700

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CGGTCATAGC AATGGTCAAG TATTCTTAGG TAAAGATATG CAAGGTGAGC CTAATTATTC 3000

AAGCCAAATC GCATATGAAA TTGATAAAGA AGTTCAACGA ATCGTTAAAG AACAATACGA 3060

ACGTTGTAAA CAAATTTTAT TAGAGCACAA AGAACAATTA ATTTTAATTG CTGAAACATT 3120

ATTAACAGAA GAAACATTAG TTGCTGAACA AATTCAATCA TTATTCTACG AAGGTAAATT 3180

ACCTGAAATT GATTATGATG CAGCTAAAGT TGTTAAAGAT GAAGATTCTG AATTTAATGA 3240

TGGTAAATTC GGTAAATCTT ATGAAGAGAT TCGTAAAGAG CAATTAGAAG ATGGACAACG 3300

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CGATCCAAAT CACCCAGACA ATAAATAATC GATTATATTC AGTACCTCTT TCTATGATAA 3480

AATTGTTATA GCAGAAAATA ATTGTAAAAC AAGTTACTTC ATTATTTAGA ATGATGGGTG 3600

TAGAATAAGT ACAATTGTTG CATTTTATGA AGTAAAGTAA TTTTTTAAAT ATAGAGTAAT 3660

AGAGGAGATT GAAATAATGA CACACGATTA TATTGTTAAA GCATTAGCAT TTGATGGAGA 3720

GATTAGGGCT TATGCTGCTT TGACAACTGA AACTGTTCAA GAAGCACAAA CGAGACATTA 3780

TACATGGCCG ACAGCATCTG CTGCAATGGG AAGAACAATG caCAGCAACA GCTATGATGG 3840

GCGCAATGTT GAAAGGTGAT CAAAAATTAA CTGTCACTGT AGATGGCCAA GGACCTATTG 3900

GACGAATTAT TGCCGATGCA AATGCTAAAG GCGAGGTGCG TGCTTATGTA GACCATCCAC 3960

AAACTCATTT TCCATTAAAT GAGCAAGGTA AACTTGATGT AAGACGAGCG GTAGGGACAA 4020

ATGGATCTAT TATGGTTGTT AAAGACGTTG GAATGAAAGA CTATTTCtCT GGAGCAAGTC 4080

CaATTGTTTC AGGAGAACTT GGTGAAGATT TTACTTATTA TTATGCTACA AGTGAACAAA 4140

CACCTTCATC GGTAGGTCTT GGTGTATTGG TAAATCCTGA TAATACGATT AAAGCAGCAG 4200

GAGGATTTAT CATTCAAGTT ATGCCAGGTG CCAAAGATGA AACAATTTCA AAATTAGAAA 4260

AAGCAATTAG TGAAATGACA CCAGTTTCTA AATTAATTGA ACAAGGATTA ACGCCAGAAG 4320

GATTACTAAA CGAAATCTTA GGTGAAGACC ATGTGCAAAT TTTAGAGAAA ATGCCTGTTC 4380

AATTTGAATG TAATTGTAGT CATGAGAAAT TTTTAAATGC TATTAAAGGA TTGGGCGAGG 4440

CTGAGATTCA AAATATGATT AAAGAAGATC ATGGTGCTGA AGCAGTATGT CATTTCTGTG 4500

GAAATAAATA TAAATATACT GAAGAAGAAT TAAACGTGTT GCTAGAAAGT TTAGCGTAAT 4560

TTAATTTAAA TCAATACGCT AAAATGTTTA TTTTTAGCGG TTTAGTGAAA TGTAGAACTA 4620

AATAGTTGTA TAATCCTTAG TGATTTTGTT TGCTTTCTAG AATTTATTTG ATAAAATAAT 4680

TCTATATCCG ATAAATAAAC TAAGATTTCA ACAACTAACT AAAAAGGAGT GTTCTTAATG 4740

GCACAAAAAC CAGTAGATAA TATTACTCAA ATTATTGGCG GTACACCGGT AGTCAAATTG 4800

AGAAATGTAG TAGATGACAA TGCAGCAGAT GTTTATGTAA AATTGGAATA TCAAAATCCA 4860

GGTGGTTCTG TAAAGGATAG AATTGCTTTA GCAATGATTG AAAAAGCAGA GCGAGAAGGC 4920

AAAATTAAAC CTGGCGATAC AATTGTAGAA CCAACAAGTG GTAATACAGG TATCGGTTTA 4980

GCATTTGTAT GTGCTGCTAA AGGATATAAA GCAGTATTTA CTATGCCCGA AACAATGAGC 5040

CAAGAGCGTC GTAATTTATT AAAAGCATAC GGTGCGGAAT TAGTTTTAAC GCCTGGATCA 5100

GAAGCGATGA AAGGTGCAAT TAAAAAAGCT AAAGAATTGA AAGAAGAACA TGGTTACTTC 5160

GAGCCACAAC AATTTGAAAA CCCTGCGAAC CCTGAAGTTC ATGAGTTAAC TACAGGTCCT 5220

GAGTTATTAC AACAATTTGA AGGGAAAACT ATCGATGCGT TCCTAGCTGG TGTTGGTACT 5280

GTTGCTATAG AGCCTGAGGC TTCTCCAGTA TTGAGCGGTG GTGAGCCAGG TCCACATAAA 5400

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GGTATTTTAG CAGGTATTTC ATCAGGTGCT GCGATTTATG CTGCCATTCA AAAAGCAAAA 5580

GAATTAGGAA AAGGTAAAAC AGTAGTAACA GTATTGCCGA GTAATGGTGA ACGCTACTTA 5640

TCAACACCTT TATATTCATT CGATGACTAA TTAATGTCAT TTAAAAGAGT GAGTTATCTT 5700

TTTGAGATAA CTTGCTCTTT TTTTCTACCA TGTATATTTT TAAAAATATG AGCGTTAAAT 5760

TAAACATTTT TCTGATAAAA ATATCCAGTG AATGATAAGA TAATAAACGT ACATACTAAT 5820

AACTAGTAAA TAGCAGGAGT AAATTTTATT AGAGTTAAAC AATACATAAT TAAAGGGTGG 5880

TTAACATGAC TAAAACAAAA ATTATGGGcA TATTAAACGT CACACCTGAT TcATTCTcAG 5940

ATGGTGGAAA ATTTAATAAT GTTGAATCAG CTATAAATAG aGTGAAAGCC ATGATAGATG 6000

AAGGTGCTGA CATTATAGAT GTTGGAGGTG TTTCAACGAG ACCCGGTCAT GAAATGGTTT 6060

CATTAGAAGA TGAGATGAAC AGAGTATTAC CTGTTGTTGA AGCTATTGTC GGTTT 6115

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

TAGATACTGG GnTAAAcaTc AAAAATAtyT GCtTaTTCaC GTGTTTAcGc TCCCtCAAAC 60

GCAACGTTAA TTGCGTGTAA TCATTTAGTG TGAATTcAGA CGCTTCTTCC ATGACTATGT 120

CTGATATGCC TTTTATCGAC TTTATTTTCT CTGGGTTATC TAATCCTTTA AACAAAAAAA 180

CTGCGCCGTT TGGCAATTCA ACTTTGTTAT CAGTCTTATT CCAAAGGCAC ATGTCCCAAA 240

TACCAAAGTT TATCAAACAA TCTTTAACAT CTTCGAACAA ACTATCTTTA ATTGTTGATT 300

GTACTTTTCT AAGCCACAGT ATACGCCTAG GATATTTCCA ATCTTGCAAT GCTTTGAGTA 360

CAACTTTTTG TATAACGCCG TGAGACTTAC CGCTCGAACC TCCACCGTAA TGkACTTCAG 420

TGAAGTtATC GTAATTGGTT AGTATTTCGA ATATGTTTCT ATTGAAAACA TTAGACGGTT 480

TGTTAAAGTT TAATTTAACT TTCGTCATCG TACTCACCAA TATTAATCTC AATATTCTTC 540

TGAGTAATTT CTTTTTTATC GATATACGCA CCATGTACTT TTAGTATGTG GTCAATAGAT 600

TTTAAATGGT CATATTTCTT ACTGTAAGCC TCTTGAGGTT CTCCTCTAGC AATAGAAGCA 720

GATAACGCTA AAGCTTCTGT AATACTCATT AAACGCTCTT CTTGTATCTG TTCTAATCGT 780

TCTTTAATAT ATTCCGAAAC ATTAACATTT CTTAACAATC GACTTGCTAA AGACTCTGCT 840

GTTTTCTTAC TATAACCTGC TGTAATTGCT GCTTTTTTAC CATTACATCC ATTCATTATA 900

TATTCATCTG CGAATCTCTT TTGTTTTTCG TTCATTTCAT TTACCACCAA CTCTCGCGCT 960

ATACGCTTTT TAAAATTAAA AAAGGATTGG CTATAATCAG CCAACCCACA TAGATCCTTT 1020

ATTCCTAATT GCGATAAGGG AAACGCAGTA CGATAGTCAA TATCCTACAC TATCATAATA 1080

TCTCATTTAA GGTATCAAAA ACTGCCACTT TACTGCCAAT TTCAGTCTTC CCCTAACTCT 1140

TCCGCCAATC TAGATATGAT TTTTCTTTTG ATTCTATGAG CAGTTCTATC AGAAATGTGT 1200

ATGTCAACAC AAACTTTCAC TAATTCCTTT TTATTAAAAT AATACTCTTG AATGAATTCG 1260

CGTTCTTTCC TGCTTGATGT GTTGATTATA CGTTCAATAG CGCTCTTAAA CTCAAGGATT 1320

TTACCTCTTC GTATACTACA AAGATAATTA GTTACTGCCA TTTCTGTTTT CGATGTATTA 1380

GACGGTACAA ACTCCCCGCC TATATTTGTA TCTGTTGGAA TCCACGGTGT CATTATTTCA 1440

CTTCTTAAAT CTTCAAGTTG TTTATGATAA TTAGGATAAT CACACAACTC ATCTTCTAAC 1500

TTTCGAACTG TTGATAATTT TAATCCGTAT TTCTTTTTAG TCATGAATAC CCTCCGTACA 1560

AATATGTTTA ATCTTCAAAG TGTCTCAATC TACTTCTTAA TATCTCTATC TCTCGCTCTT 1620

TAACTTTTAC ATCACCTTTT AACTGTTCCG CTTGTAACAT CACACCAAAC AATAAGATGA 1680

CTAGTAATAT AATTGCTATG ATTAACCACA TCATCTACTC CGACACCTCC GCCCTCATCA 1740

AATCAGACTG ATCACTCAAC TTTGCGAAGT CACTTGGCGC CTCTACATCA TCATTAGCCG 1800

TCATCATAAT ATATACTTGC TCAGTTACAT ACTTACCTAA CTCATACATC GCTAGTAAGA 1860

ATAATAGTCT CAAAATTTCT TTAACCACCA CTAAACACCC CATGTTAATT TATCGATAAT 1920

TTGTATAGCT TGTTTTAATG CGTCTCTTTT TTCTTTGATA TCTCTATTAT CGCCATCTTC 1980

ATCAGCTGAC ATTAACTCAC TGTCATATTC ATATAATAGT TCTGATATTT CATTACTAGC 2040

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TCCTTATCTT AACTTGTGCC TCGTATTTGC GCTCAGCTTC TTCTTTACTC TCTGCCTCAA 2160

CAACTGTAAA CGTCTGATTA TCTCTAGCAG TAGTAAAATG TTCATGTGGT TGTCCTGTTG 2220

AATCTTTGAA TGTTGTGACT AAGTATTGCG TCACTTCTTA TCACTCCTTT GAATGATTCT 2280

AAGTTTTTCT ACGAATAAAA GTATTAGTAC AACACTCAAT GTAGCCAACA TATTTTTTTG 2340

CTTTGCAAAA TCTACTATAA CGATTAAGAC TAATAACATT CCAATTCTGC ATGTAAATAA 2400

TACAAGTATT GGAACTAATG TAATGATGTA ACTCACTTCC CCAAAACCTC CTTGACTCGA 2520

TCTAAGATGT CTTTACACTC CGCTACTTCC GAAGCCTTTT TCTCCACGTT CTGAAACACT 2580

TTCGAATTCC TCCACTTGCT TTAGTTCAGG TGTCCATATA GGCACGATAA CCAATTGAGC 2640

TAGTTTGTCT CCTTCGTTGA TTTGATAAGT TCCGTATTGT CTTATGGCGT CACTCAAATC 2700

GATTTCTCCT TTAATATCAA AAACACCTGG TGTGATATAA CCATTCGATG CAATAGCGTC 2760

ATTCTTGATA TTAATCCCTA AATTGCCGTG ATATCCCGCG TCTATCTTGC CTGTTTCAAT 2820

CACTAAATGC GTTTTACTAC TTACACCACT ACGGCTAGTT AATAGTCCGA CATAGCCCTC 2880

TGGTATGCTT ACAGCTACAT CTGTTTTAAT CACTGCCTTT TCTTGTGGCT CAAGTACGAC 2940

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AGCATTTTCT GATAATAGCC TTACTTGTAA TGTGTTAGTC ATTTTCCTGC TCCTCCCTAG 3060

CTGTAGCAAA CGCTATTCTC AATTTCAATC TTTCAACAAT ATGAATTAGT GCGGTATTGA 3120

GGAATATTTC AAATTCTTCA ATGTTCTCAT CTATAAAATC AAGTATTTCT TCCTCTTGTT 3180

CACTGTCAAA CTCGCTTAGT ACATCCCAAA TATTTATGTC GCTTTTGCTC GTTTCTAATA 3240

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ATAGACAACT TGACCTGCCA TAATCCCTAC TGCTTCATCA AGTTCAATAC CTTCTTTAAC 3360

TGAATGTTGA ATAGCATTTG TCATTCCCTC AAGTATTTCA TCAAACGCTT GTGCTCTCTT 3420

ATACACGTCC TCAATCTCTT TTAGTAATCC CTCTGTGTCA TTACCGTTAT ACGCACTAGC 3480

ACTGATCACT GATTGTTCAA TTTGTTCGCG GTTATTCATC ATTTCCATCT CCTCTAAAAT 3540

AAAGTTAGTT GCTTCTGCTC CTCGTATTCC AAACCATGTT GCTTTATATA TGTTTCGAGC 3600

TCTTCCGCTG TATCAAATGT CTTTTTCACG CCTTGCCAAC CTGGCACGAT ATGCCCATGa 3660

AAGTAATAAG TGCCGTTCAC TACATGGATA TGTGCCACTC GTTCGTTATC CTGATACAGA 3720

TATCTCTTAG ATCCGAAAAA TTGGTTTAAG TATTCTTTAC ATGCGCTATC GGTTTTAGGC 3780

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TCTTTACGTC GTTGCCTAGC CATTTCACGC TCTTTGCTCT CTCGCTCCAT GATTTTGGAT 3960

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AACGCCCAGC CACCTCGTAC TCTTTTTGCA ACCATTCCTG GAGTTAAACC GTTCTTTTTT 4080

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ACGCCAGTTT CATTGTGCAA ATCTTGGACA CTTACGTTAT CTCTAGCCAT GATTACCCTT 4380

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TCTTTTACGT CTGACTTTCA CTAAGTCCTC ATATACCATC CATTCTTGAC CTGTGTATTT 4680

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TTGTAATTCA AATTTCGGTT GTATTTCGAT ACGATCATAG TTAGTGCCAT TCATATTACT 4920

TTCTAAATAT TGGTAATATT CGCACTCTAC TTTGCTATCA AATACAATTC CTTTGTACTC 4980

AACTTTCTTA GCATTGTATT TACTCATTGT GCCACCTCTA AATATCAAAT ATCGTTGCTT 5040

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TTACGTTGTC TTTATACTTG ATGACCTTAA TATCTTCCGT GCCATCTTCT CGGTATAAGT 5220

AATATTTTTC TTTCGGCATT TTTTAACACT CCTTAATGTG TGTTTTCTTC CAGTTGATTT 5280

CATTCATGAT TTTCTTTTCA ACTCTGTCGT AATCATCGAA AGGCGATAAC TCGTTATTGT 5340

CCAACAATCT ATTGACCGCC CAACCAGTCT CGATATATAC ATTTGCTACA ATCGGGTCGC 5400

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GAAAÃACCTC TGAGTCTTCT TGTAATACTC AAATTCAATT ATTCCGGTTT CGCCGTCTTT 5520

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GTTATAATAA TCATCACGGT AAAGTAGCAT CGCTAAACTC GCATCTGCTT CTATTCCGCC 5640

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CTGTATAACT CTTCGACAAA CTCCTCAACA AACTTCTTGG TTCCATCTTC TTTTTTGTTA 6300

GTAATTGTTT TTAAATCCTT GAGTTCATCA ATCAAGTTGT TAAAGTTTTG GTTCGTAGGT 6360

TGTTGTTTGA ACTCAGTTAC CAATTCGTTA GCTTTGTTGA GCTGATAACT TTCCAATAAT 6420

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TCTATCTTTC CGACGTCCAT TACATAATTG AAAAAGGTTT TAAACTTTTC GTTCGTAAAC 6600

ATGTAATCTT TAACTCTTAT CTTTTCTAAT ACGTCCGGTT GTTTAAGTAG CGTAGCGATT 6660

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ACTTATTCAT GAACTTATCT AGCGCTATTT TTCTTTGTCT GACATATTCG GGGTCATTCT 6780

GCATTTTCCA TTGGTGTGTA GCGGTTTCGT TATCTACTGG CTCGATAGAT ACTTTTTTAG 6840

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CATCTACCGC TTTTACAGTT GGTTGATAAT CTCCATTTTG ACTTAATACA TCAATCCACA 6960

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TTTGACATTC TCTTTAGCCC AGTTGTTTAA AACTTTAATT AAATAGCCAC CATGCGCACT 7200

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TTCTTCTTCT TTTTCTTCTT CTCTTTCTTC TTCTTCTTCT GTATCGTTAC GTAACGTTAC 7440

GGTAACGTTA CGTTTTGCTT CTAGTAACTT TTTCTGTTTC TCACGATAGC GTTGTTGTCG 7500

CAATTTATTT TTTTCTTTAT GCTTAGCTTT GCTATCTAAG CTTTGATGCT TCTCCCAGTT 7560

TGTCACTTTT ATGACACCAT TAACTTTTTC AATCATGCCC AATGTCTCAA AAGTTTGAAT 7620

TGCTAACCTT ATTGAGTTAA TAGGTCTATT AAATTCATTT GCTAACATTT CTTCGTTGTA 7680

CGGCAAGTTT TCGGATAGCA TAATATAACC TTGTTCATTG TACTTTCCTG ATAAAGTTAG 7740

TAACTTAACC CAAATAGTTA TGATCGTATC TCTTTCGGGT AAAGCTTCGA TATATTTGAT 7800

CTCCTTTCAG CATTTTGTTG AGCCTCTCAT CAACTTTTAT CCACGAGTCA TGCAAGTGAT 7920

ATTTATCATC AAACGACTTA ACGCCAATTG CGTGCTGTTC ATTATGATGT TGTCTACACA 7980

GTGCTAACAC ATGTTTGTCG TAGTGATTCA TTTTGTTTCT GTTCATGCCT CTGCCGACTG 8040

CTTCATAATG TGCCAGGTCT GCGTGAGGCT TTCCGCATAT TACACAGTTG CGGTTGATTG 8100

TAGCCCAATA TAATAACGCT TTATCTTCGC TTAACAACTT ACTCGTTTCT ACACTCATAG 8160

GTATTTGATG ATGAAACATA AACGCTATAA TCAGTTCTAT TAACTCCCTT GCAACTTTCA 8220

TAGAACAGTC GCGCAGACTG ATTTCTTCAT AACCTTTCAT AATTTCCAAT TCTGTTTGTA 8280

ATAATTTTCT AGTTGATTCT ACTGGTTCGC CCCAGTGAAG TTCTATATCT CTACACATTG 8340

CGAATATTTT TTTGCGTTGT TCTATAGATA GTTTTTTATT GTCCGGAACC TCTACTTCTG 8400

CTTTTAGTGG ATATCCGTTT TCTAGTAAGT CAATGTGACT TTGTTCAAGT TCAACACCAG 8460

TAGCAACGAC GGAATAAGTA CCGTCATTGT CTTTCTGGTA TCTTGTAATG TATTGCATTT 8520

AAACCACGTC CTAGAACGGT AAATCATCAT CATTGATTTC TATTGGACCA TTAGCATTAG 8580

CGAATGGGTT TGATTGTTGA CTCATTGGCG TCTGTTTCCC ATTTGCTTGC TGTTCTTTTT 8640

GTTTCATCTC ATCAGTTTTA GGTTCTGGTT TATTAACTAC TTCATCGTCT TTATTCCAAA 8700

CTTTTACATA TGAGAGTCTT ACAAAATACT TGCCTTGTTC CTCGTTAAAT TTATTTTTAA 8760

GTACAATAGT TCCGATTTTG TTAATTAATT GATCTGTGTC AAAAGTTAAA TCTGGTAAGT 8820

TCAATTTAAT TCCTAATCTA CTAAGTAACT CGATATATTG TTTTTCTTGA TAATCTTGTT 8880

GGAATGGTGG GACGAATTGG TTGTGTTTGT ATTGTTTACC TTCGTTGTTT TCAAAAACAA 8940

TCGTGAAGTA TCTGTTTTCT CTGTCGTTAA ACTCGACATT TGCAACTTTT ACTGTAAATT 9000

CTCCAGCTCC TAAAAAGTCC CCACCTTTCA TGAATGCCTC TTGATTAGTT TCTTGAATGT 9060

ATTGTGTTCT ACCAGTGATT TTCATAATTT TTATACCGTC CTTTTAATTA ATTTTTAATT 9120

ACCATTTCTA ATTGCTTGTA CAACATCGTT AATACTTGGA TTAATGAAAC GTTTGTTGTT 9180

AATTTTGATG TTGCTTGAGT GTCTTATCTT TGTCTCGAAT AAATTTGATG GTTCAGCGTT 9240

AAGTACATAT TGATAAGTTT TTTCGCCGTC TTGCTCATGT TCTTCTATTG TCATTCTTGC 9300

TAACACGTCA GATTGACTGA TGACTGCTTT TTTTATTTGG TCTTGTGCCT CTATCGTGAT 9360

TGTTGGATTG ATAGTACTTC CCTCATCATC TTTGTCTTTG TTAATGCCCT CGTGTCCGCT 9420

TATAGCAAGA TGAAATTGAT AATGTTCTTG TAATTTAGAA ATATAACGAT AAATACTTAC 9480

AATGCGTGTA GCACACTCGC CCCAATCATT AAATGTCGGT TTCTTTGATT TACCGTCCAT 9540

GATGTCGTCC ATAGTGATAT CACGTAACTT TTGGATTGTT TCAATCACTA CAACATCAAT 9600

AAAATGCTTA TAATTCTTAA TCTGCACAAC TGCCCCATCT TCTGTTACCG TTGTTCCGTC 9720

CTCATTTATA TCTAGTACTA AGGCATTGTT ATCTTTTGTT AAAAACGTAG TTTTACCAGT 9780

ACCGAACTTG CCGTATATCG CAAATTTATA AAACTTGTTT GCATTTTGTT TGCTGATGTC 9840

TTTTACACCT AGTTGCGTTA AAATATCGAC ATCTTGATTA GTTTTTTCAG TCATCTATTC 9900

TCCCACCTTT ACCGTGTATG ACGTTGGTTT CTCCACAATG CTAGCACCCT CTAAAACTTC 9960

GCCGTTTGCG TCAATCAATG TGCCGTTTTC AGTTACATTG AAATCTTTCT TAATGTCTGA 10020

TTGGCTAAGT TTTTTAGTTA CTTTTACATA GTTGTCAAAA CCTCGTTGCT CAAGTTGTnT 10080

AATGACTTCT TGCTCATTGC TAACTTGAAT GACTTTTGAA CCTTTTCTGG CTGTCACTTT 10140

TCCGTAAGtG TATTCAACTT GAATTTGCTA TCTTGTTCTT TTTGTATTCT GTAATATTCA 10200

ATTACAAGGC TTTGTAAATA TTCTTTGCCA CTCTGTAATT TTTCTACTTC TTTATCTTTC 10260

CATTCGTTTA TGCGTTCAAT TTCTTTATTT GCTAAATCGT TGATTTCATT CTCTTTAGTT 10320

GTGATTGCAT CCAGTTTCTn AAAAACCCAG TTAGCACTGT CTAGATCAGT nACTTTGAAT 10380

CGGTCGTCTT GTTCGAATGT n 10401

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2989 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

TTTCTCTCTA TTATTCTCGA TGCGTAGATA ATTGTTTAAA TTTAAGTTTA TAGTAATGTT 60

GAGTTTATAA TTTCATATAT CTAAAAACAG GTGTTGTATA TATAATCATT CATCTAGTTA 120

TACTTACTTT AAAAATAATA TAATTTCATG CGATGCAATT CATTGATGGA TGTTTTTAAT 180

CTTAATCAAA TCCAaATAAA GCATATATTT TTAAATTCAC TTTCTTTCGA ATCGATTTTT 240

ATCTCTTGnA TTAAACTTTT CCATTGTTTC ATTAAAGCTC TCTGTCATAT CTATTCCCAT 300

TGAATTCGCT AAACATAACA ACACAAATAA ATTATCACCT AATTCTGCTT TAATCGTATT 360

TGCTTCCTCT GAATCTTTCT TCTTTTTTTC ACCATAGGTA TGATTTATTT CACGTGCAAG 420

TTCGCCCACT TCTTCAGTCA ATCTAGCTAA GTTAGCTAAT GGTGAAAAAT ATCCTGTTTT 480

AAATTGTCCA ATATATTCAT CAACTTCACG TTGCATTTCT ACCATTGATT TCATTTCTAC 540

GTTCTCCTTA TATTGCATTT CTAATATAGT ATATATCAAT TTGAAGTCTC ATGCATGTTT 600

AATTCAGTTT ATATAAATGT AATGCATTCC TAACTAAATT AAATCAATTG AAATTGGGAT 720

TATAACTTTA TGATACGTAC CACTACAATA AAATAATATA GTGAATAATC TACCATTAGA 780

AAAATAAGCA CAAAAAAACT AGCAACCACA CAAAAATGTG ATTAGCTAGT TAATAAGTGT 840

CTAATTTAAG TTAATTGTTA ATCTATAAGA TTAATCACTT GAACGCGCAA TCAAAATAAT 900

ACGTACAAGC TCTGCTACAG CGACTGCAGT TGCTGCAACA TAAGTCATTG CTGCTGCAGA 960

TAATACTTTA CGCGCATGCT TGTATTCTTT TTCATTTACA ATGTTCAATG CCGTAATTTG 1020

TTTCATCGCT CTTGAACTCG CATCAAACTC AACTGGTAAC GTAACAATTG AGAATAATAC 1080

CGCTAATGAC ATTAAACCAG CACCAATCCA TAAAGCAGTT GAACCaAATG CACTACCTAT 1140

CGCTGTTAAG ATAATACCTA ACATGATGAT CATATAACTT AATGAACTCC CTAGGTTTGC 1200

AACAGGTACT AATGCTGCTC TGAATCTTAA GAACCAATAT CCTTGGTGAT CTTGAATGGC 1260

ATGACCAACT TCGTGGGCTG CAATTGCAGT TCCAGCAACT GATGGTCTGT CATAGTTTGC 1320

AGGAGATAGT GAAACAACTT TCTTTTTAGG ATCGTAATGA TCTGTTAAGA ATCCTTCACC 1380

TTTAACAACT TCGACATCAT AAATACCGTT TGCATGTAAA ATTTCTAATG CAACTTCACG 1440

ACCCGTTTTA CCACTAGTTG ATCTAACTTG TGAATATTTC TCATAGTTAG ATTTAACTTT 1500

GTGTTGTGCC CATAAAGGAA GCACCATTAA TATTACGAAA TAAATTATCA TAGTAAAAAT 1560

TGAAGACAAT AAACTCACTC TCCTTTATAA ATATTTTACT GTCATTTGCC GTTTTTATCA 1620

AATCATTTAC ACTTTAATAA TTTGTTTAAT TCAATATAAA GCAAAAGTCC AAAAACACTT 1680

AGACAACATG ATAATACACC AATTTGCCAC ACATGTGTAG TTATAAAATC ATAATATGGA 1740

AATTGAAGGT GAAAATAGTC AATATAATCA TTCAAAAACA CCCAAATCAT yGCTACACTG 1800

ATTCCAATCA TAGAACGTTT AAACCTAGGA TAGAAGTAAA TTGCCTGAAC AGCCATTATA 1860

CTGTGGGAAA ACATTAATAC CAAACCATTT ACTGTAATAT CACCTTGTTC AATAATAAAT 1920

AATATATTCA TTATAACTGC CCAAATCCCA TATTTGAATA ATGTTACAAA TGCCAGTGCA 1980

TCGATAATAC TATTTTGTTT TTGAATTAAT ATCAATGAGA TAGAAATAAC TAAGTATAAT 2040

ATTGCAGTTG GGCTATCTGG AACAAAAATC TTAAAATGCC AGGGCGTATG ACTTAATTGT 2100

TCACCATACC ATATATAACC ATAAATCATC CCTAATATAT TACAAATGAG TAGCATCATT 2160

AACCAAGAAC GTTGATAAAG TGTATATTGC CAAAATGCTT TAATTGTCAT CTGCTAAGTC 2220

CTCAAATTGA TTATGTTTAT TTACTAGCTT GAGTGTATTT AAAATTTGCG TTAGTTGATA 2280

AAAACGTTGC TTTTCATTCA TCTGTAAACT TAAATCAATA TTGTGTAACA AGTAATCTAT 2340

TAATAACGCA TGTTTATGCC GATCTATAGC CATACTATTT AAGTCATGAA GATAAGTTTG 2400

TGACACGTTT GCGAAGTGAA TTTGAATATC AAAAGCACAG TTATGATTAG CGATATAATC 2520

AAATATTTCA TTTGTATTCA TTAACTTTAT ATTACGCTTA GTAAATTGAA TTGCAGAAGC 2580

GTGACTTCCC ACTTCTGCAA TTTCTAATGT TTCATGATGA TTAATTTTTG TATCTACAAA 2640

ATGAATGTTT GCCAATTTCG CCTCATTCAC TTTTATATAG TTAAGCACCC AAACTGCAAT 2700

ACGCGACTTA AATCGATATT GAAAAAGTAA ATATTCAATA AAACTTTCTT TAATTTGATT 2760

GAGTGTCTCT GACATCAAAT ACCCCATTTT AAGATTGCAA TCTTGaTAAT TCGTCATGCC 2820

AATTTTCGTT ACTTGGcTCT AGTTCCAACA ATTGATTTAA AATAGTAATT GCTTGTTCCT 2880

TTTGACCAAT TTCAATTAAA TAGAAATAAT AATCACTCAT AAAATCAATA TTTGTTTTCA 2940

TCGTTGGATA TGCTAATTCA AAGAAATGTT GAGCTTCTTT ATCTCGCTC 2989

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

CATCAACTCC TTAATTACAC TGTAAATGAT ATGCGTCTTT TTGACAACTA TATTTGTCAA 60

ATCTACACCA AAAAATATGA TTATCCACCT ATGTATGACA TTTTGAAACA AACACCTCAA 120

CGCCTACAAG TCATAATTGT TTACTTTCGT TACACCTTCC TGCATAATTA ACAGCATTCT 180

AATTTTAGTA TGATGCACGC ATTTTCACTA AATCAAACCA TTCAAAGGAG ACTATTATGG 240

CATTTACATT ATCTGCAATT CAACAAGCAC ATCAACAATT TACTGGTGTT GACTTTCCAA 300

AACTATTCAA AGCTTTTAAA GATATGGGGA TGACTTACAA TATCGTCAAC ATTCAAGATG 360

GCACTGCAAC ATACGTACAT CAATCAGAAG ATGATATCGT TACGTCATCT GTAAAAAGTA 420

ATCATCCTGT TGCTCAAAAA TCAAACAAAA CAATAGTTCA AGACGTCTTA ACTAGACATC 480

AACAAGGGCA AACAGATTTT GAAACATTTT GTGATGAAAT GGCTGAAGCT GGCATTTATA 540

AATGGCATAT CGATATTCmA GCGGGCACTT GTACTTATAT CGACTTGCAA GACCAAGCTG 600

TTATTTCAGA ATTAATCCCT CAATAAACTA TATTTATAGC AACATTTTAA TTATTTCATA 660

AAATTTTATT GATAATCATT ATCGTTCGGT ATAAAGTAAA TACTATATAC TACTTATGAG 720

TGAGGTTGAT TATCATGATA ACTAACACTT TTATTTTAGG CATCACAGGC CCAACAAGTC 780

TTGTCGTCAT TAGCATTATC GCTTTAATTA TTTTTGGTCC GAAAAAATTA CCACAATTTG 840

AGTCTCACGA TACACCCAGT AAGGAATCGA AACAACAGCG AGAGCAATAG CACTGACCAC 960

ACCTTACTGG TTCACTTTAG CGAACTACGC CATCGGTTAG TAAAAATTTT ATTGTCGTTC 1020

GTCATTACGG TCATCGTCGT ATATGTyTCA TCATTTTGGT GGATGACACC ATTCATAACG 1080

TATATyACCC GgCACATGTG TcCTTACATG CATTTcATTC ACAGAAATGA TACAAATAAC 1140

GTG 1143

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7953 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

CAACGCCTGA ACGTAAACCA TATCGTTTCG CGATTTCCTC ATCTTGACTA TTTACTAAAA 60

ACTCTCTCAT GGCGATTAAT GTTTCTTTTT CTTCTTTAGT TAATGGTAAT TCTAACTCAG 120

CTGCTTTTTG ACGCAAAGTT GGATGACCAT CTCTAATGAT GTCTTTCATT GTTAACATAT 180

ATTGCACCTT CCTTATTTTA ATTTGTTTTA GTTGAATGAC AGTAAAAAGG TTGTTAAGAT 240

ACTCATACAT TTTTATGTGT AAATATCTAC AAAGTTAACC AACTACTGCC AATGTTTATT 300

TTAGATAGTA TATGTAAATT TTCAaGAtAT GCgTAATTGC gTTAAAAAAT GaTTAAAGTG 360

TTGGTTTCAA GCAATGaTAC TTTAGAAATT TATTTATCAT CTTGACTTTA AAAATTATAT 420

TATAAATGAC GTAACTGTCA ACAGATATAC TTAGTArTGA AGATGTGTAA TGTAATTGTT 480

TAAAATTGAT TTCCAAGCAG ATTTTATTTA TCATTTAATT TAAATAGCAA GTGGAGGTAC 540

AAGTAATGAA ATTTGGAAAA ACAATCGCAG TAGTATTAGC ATCTAGTGTC TTGCTTGCAG 600

GATGTACTAC GGATAAAAAA GAAATTAAGG CATATTTAAA GCAAGTGGAT AAAATTAAAG 660

ATGATGAAGA ACCAATTAAA ACTGTTGGTA AGAAAATTGC TGAATTAGAT GAGAAAAAGA 720

AAAAATTAAC TGAAGATGTC AATAGTAAAG ATACAGCAGT TCGCGGTAAA GCAGTAAAGG 780

ATTTAATTAA AAATGCCGAT GATCGTCTAA AGGAATTTGA AAAAGAAGAA GACGCAATTA 840

AGAAGTCTGA ACAAGACTTT AAGAAAGCAA AAAGTCACGT TGATAACATT GATAATGATG 900

TTAAACGTAA AGAAGTAAAA CAATTAGATG ATGTATTAAA AGAAAAATAT AAGTTACACA 960

GTGATTACGC GAAAGCATaT AAAAAGGCTG TAAACTCAGA GAAAACATTA TTTAAATATT 1020

TAAATCAAAA TGACGCGACA CAACAAGGTG TTAACGAAAA ATCAwAAGCA ATAGAACAGA 1080

AAGAAAAGCA AGACGTTGAT CAATTTAAAT AATTAATATA ATACAGATGG TAGGAAACAA 1200

CTAATACAGT TCCTATTATC TGTATCTTTT TTTATTAAAA CAGAACTTTT TCAAATGGTT 1260

TAACAGTCCC ATTTATTTGT GGTACAATTA GTAAGGATAA AATGAATTTC TATACAATTA 1320

TGGGAAAGGT ATTGTGAATT GAATGGCTCC TAAGTTACAA GCCCAATTCG ATGCAGTAAA 1380

AGTTTTAAAT GATACTCAAT CGAAATTTGA AATGGTTCAA ATTTTGGATG AGAATGGTAA 1440

CGTCGTAAAT GAAGACTTAG TACCTGATCT TACGGATGAA CAATTAGTGG AATTAATGGA 1500

AAGAATGGTA TGGACTCGTA TCCTTGATCA ACGTTCTATC TCATTAAACA GACAAGGACG 1560

TTTAGGTTTC TATGCACCAA CTGCTGGTCA AGAAGCATCA CAATTAGCGT CACAATACGC 1620

TTTAGAAAAA GAAGATTACA TTTTACCGGG ATACAGAGAT GTTCCTCAAA TTATTTGGCA 1680

TGGTTTACCA TTAACTGAAG CTTTCTTATT CTCAAGAGGT CACTTCAAAG GAAATCAATT 1740

CCCTGAAGGC GTTAATGCAT TAAGCCCACA AATTATTATC GGTGCACAAT ACATTCAAGC 1800

TGCTGGTGTT GCATTTGCAC TTAAAAAACG TGGTAAAAAT GCAGTTGCAA TCACTTACAC 1860

TGGTGACGGT GGTTCTTCAC AAGGTGATTT CTACGAaGGT ATTAACTTTG CAGCAGCTTA 1920

TAAAGCACCT GCAATTTTCG TTATTCAAAA CAATAACTAT GCAATTTCAA CACCAAGAAG 1980

CAAGCAAACT GCTGCTGAAA CATTAGCTCA AAAAGCAATT GCTGTAGGTA TTCCTGGTAT 2040

CCAAGTTGAT GGTATGGATG CGTTAgcTGT nATATCAAGC AACTAAAGAA GCACGTGACC 2100

GCGCAgTTGC AGGTGAAGGT CCAACATTAA TTGAAACTAT GACATATCGT TATGGTCCTC 2160

ATACAATGGC TGGTGACGAT CCAACTCGTT ACAGAACTTC AGACGAAGAT GCTGAATGGG 2220

AGAAAAAAGA CCCATTAGTA CGTTTCCGTA AATTCCTTGA AAACAAAGGT TTATGGAATG 2280

AAGACAAAGA AAATGAAGTT ATTGAACGTG CAAAAGCTGA TATTAAAGCA GCAATTAAAG 2340

AGGCTGATAA CACTGAAAAA CAAACTGTTA CTTCTCTAAT GGAAATTATG TATGAAGATA 2400

TGCCTCAAAA CTTAGCAGAA CAATATGAAA TTTACAAAGA GAAGGAGTCG AAGTAAGCCA 2460

TGGCACAAAT GACAATGGTT CAAGCGATTA ATGATGCGCT TAAAACTGAA CTTAAAAATG 2520

ACCAAGATGT TTTAATTTTT GGTGAAGACG TTGGTGTTAA CGGCGGTGTT TTCCGTGTTA 2580

CTGAAGGACT ACAAAAAGAA TTTGGTGAAG ATAGAGTATT CGATACACCT TTAGCTGAAT 2640

CAGGTATTGG TGGTTTAGCG ATGGGTCTTG CAGTTGAAGG ATTCCGTCCG GTTATGGAAG 2700

TACAATTCTT AGGTTTCGTA TTCGAAGTAT TTGATGCGAT TGCTGGACAA ATTGCACGTA 2760

CTCGTTTCCG TTCAGGCGGT ACTAAAACTG CACCTGTAAC AATTCGTAGC CCATTTGGTG 2820

GTGGCGTACA CACACCAGAA TTACACGCAG ATAACTTAGA AGGTATTTTA GCTCAATCTC 2880

CTATTAGAAG TAATGACCCA GTCGTATACT TAGAGCATAT GAAATTGTAT CGTTCATTCC 3000

GTGAAGAAGT ACCTGAAGAA GAATATACAA TTGACATTGG TAAGGCTAAT GTGAAAAAAG 3060

AAGGTAATGA CATTTCAATC ATCACATACG GTGCAATGGT TCAAGAATCA ATGAAAGCTG 3120

CAGAAGAACT TGAAAAAGAT GGTTATTCTG TTGAAGTAAT TGACTTACGT ACTGTTCAAC 3180

CAATCGATGT TGACACAATT GTAGCTTCAG TTGAAAAAAC TGGTCGTGCA GTTGTAGTTC 3240

AAGAAGCACA ACGTCAAGCT GGTGTTGGTG CAGCAGTTGT AGCTGAATTA AGTGAACGTG 3300

CAATCCTTTC ATTAGAAGCA CCTATTGGAA GAGTTGCAGC AGCAGATACA ATTTATCCAT 3360

TCACTCAAGC TGAAAATGTT TGGTTACCAA ACAAAAATGA CATCATCGAA AAAGCAAAAG 3420

AAACTTTAGA ATTTTAATAC ATTTTAAAAG TTAACGAAGT TAGCGTATTT TAGTCTCATT 3480

GATTAAAATG AAATGTTTAA TTTACGAAAT CTTAGGAGGG CAAAAACGTG GCATTTGAAT 3540

TTAGATTACC CGATATCGGG GAAGGTATCC ACGAAGGTGA AATTGTAAAA TGGTTTGTTA 3600

AAGCTGGAGA TACTATTGAA GAAGACGATG TTTTAGCTGA GGTACAAAAC GATAAATCAG 3660

TAGTAGAAAT CCCATCACCA GCATCTGGTA CTGTAGAAGA AGTTATGGTA GAAGAAGGTA 3720

CAGTAGCTGT AGTTGGTGAC GTTATTGTTA AAATCGATGC ACCTGATGCA GAAGATATGC 3780

AATTTAAAGG TCATGATGAT GATTCATCAT CTAAAGAAGA ACCTGCGAAA GAGGAAGCGC 3840

CAgcAGaGCA AGCACCTGTA GCTACTCAAA CTGAAGAAGT AGATGAAAAC AGAACTGTTA 3900

AAGCAATGCC TTCAGTACGT AAATACGCAC GTGAAAAAGG TGTTAACATT AAAGCAGTTT 3960

CTGGATCTGG TAAAAATGGT CGTATTACAA AAGAAGATGT AGATGCATAC TTAAATGGTG 4020

GTGCACCAAC AGCTTCAAAT GAATCAGCTG CTTCAGCTAC AAGTGAAGAA GTTGCTGAAA 4080

CTCCTGCAGC ACCTGCAGCA GTAACATTAG AAGGCGACTT CCCAGAAACA ACTGAAAAAA 4140

TCCCTGCTAT GCGTAGAGCA ATTGCGAAAG CAATGGTTAA CTCTAAGCAT ACTGCACCTC 4200

ATGTAACATT AATGGATGAA ATTGATGTTC AAGCATTATG GGATCACCGT AAGAAATTTA 4260

AAGAAATCGC AGCTGAACAA GGTACTAAGT TAACATTCTT ACCTTATGTT GTTAAAGCAC 4320

TTGTTTCTGC ATTGAAAAAA TACCCAGCAC TTAACACTTC ATTCAATGAA GAAGCTGGTG 4380

AAATCGTTCA TAAACATTAC TGGAATATCG GTATTGCAGC AGACACTGAT AGAGGATTAT 4440

TAGTACCTGT TGTTAAACAT GCTGATCGTA AGTCTATTTT CCAAATTTCA GATGAAATTA 4500

ATGAATTAGC TGTTAAAGCA CGTGATGGTA AATTAACAGC CGATGAAATG AAAGGTGCTA 4560

CATGCACAAT CAGTAATATC GGTTCAGCTG GTGGACAATG GTTCACTCCA GTTATCAATC 4620

ACCCAGAAGT AGCAATCTTA GGAATTGGCC GTATTGCTCA AAAACCTATC GTTAAAGATG 4680

ATGGTGCAAC TGGCCAAAAT GCAATGAATC ACATTAAACG TTTATTAAAT AATCCAGAAT 4800

TATTATTAAT GGAGGGGTAA AACATGGTAG TTGGAGATTT CCCAATTGAA ACAGATACTA 4860

TAGTAATCGG AGCAGGTCCT GGTGGATACG TTGCAGCAAT TCGTGCAGCT CAATTAGGAC 4920

AAAAAGTAAC AATCGTTGAG AAAGGTAATC TTGGTGGTGT TTGCTTAAAC GTAGGATGTA 4980

TTCCTTCAAA AGCATTACTA CATGCTTCTC ACCGTTTTGT TGAAGCACAA CATTCTGAAA 5040

ACTTAGGTGT TATTGCTGAA AGTGTTTCTT TAAACTTCCA AAAAGTTCAA GAATTCAAAT 5100

CATCAGTTGT TAATAAATTA ACTGGTGGTG TTGAAAGCTT ACTTAAAGGT AACAAAGTTA 5160

ACATCGTTAA AGGTGAAGCA TATTTCGTAG ATAACAATAG CTTACGTGTT ATGGACGAAA 5220

AGAGCGCACA AACATACAAC TTTAAAAATG CAATCATTGC AACAGGTTCA AGACCAATTG 5280

AAATTCCTAA TTTCAAATTC GGTAAACGTG TTATCGACTC AACAGGTGCT TTAAACTTAC 5340

AAGAAGTACC aGGTAAATTA GTTGTAGTTG GTGGAGGATA CATTGGATCA GAATTAGGTA 5400

CAGCATTTGC TAACTTTGGT TCAGAAGTAA CCATCCTTGA AGGTGCTAAA GATATCTTAG 5460

GTGGCTTCGA AAAACAAATG ACACAACCTG TTAAAAAAGG TATGAAAGAA AAAGGTGTTG 5520

AAATCGTTAC TGAAGCTATG GCTAAATCAG CTGAAGAAAC AGATAACGGA GTTAAAGTTA 5580

CTTATGAAGC TAAAGGCGAA GAGAAAACAA TCGAAGCTGA TTATGTATTA GTAACTGTAG 5640

GTCGTCGTCC AAACACAGAC GAATTAGGCC TAGAAGAATT AGGTGTTAAA TTCGCTGACC 5700

GTGGATTATT AGAAGTTGAT AAACAAAGCC GTACGTCTAT CAGCAATATC TATGCAATTG 5760

GTGATATCGT TCCAGGTTTA CCACTTGCTC ACAAAGCTAG CTATGAAGCT AAAGTTGCTG 5820

CTGAAGCAAT TGATGGTCAA GCTGCTGAAG TTGATTACAT TGGTATGCCA GCAGTATGCT 5880

TTACTGAACC AGAATTAGCT ACAGTTGGTT ATTCAGAAGC GCAAGCTAAA GAAGAAGGTT 5940

TAGCAATTAA AGCTTCTAAA TTCCCATATG CAGCAAATGG TCGTGCATTA TCATTAGATG 6000

ATACTAACGG ATTTGTTAAA CTTATTACAC TTAAAGAAGA TGATACTTTA ATCGGTGCTC 6060

AAGTAGTTGG TACTGGTGCA TCAGATATTA TCTCTGAATT AGGTTTAGCA ATTGAAGCTG 6120

GTATGAATGC TGAAGATATC GCATTAACAA TCCATGCACA TCCAACATTA GGTGAGATGA 6180

CTATGGAAGC AGCAGAAAAA GCTATCGGAT ACCCAATCCA TACAATGTAA TAACTGATTA 6240

TCTATAAAGA TTCAGTCATT AAAAGCTGTA GCATATGCTA CGGCTTTTTT GTTTTAGGTA 6300

AAGTAATGTA AGGAAATTGA TTTGAGATAT CGTTAACATG TGACATGCAT GTTATACTAG 6360

CGATGCTAAT AAAAGAATTG AAATGGAGGG TTCAACAATG GAATATGAGT ATCCAATTGA 6420

TTTAGACTGG AGTAATGAAG AGATGATTTC AGTGATAAAT TTCTTTAATC ATGTAGAGAA 6480

AATTGTGCCT GCTAAAGCAG AGGAAAAACA AATTTTTAAT ACTTTCGAAA AAAGTAGTGG 6600

CTATAATAGT TACAAAGCAG TTCAAGATGT AAAAACTCAC TCTGAAGAAC AAAGAGTAAC 6660

AGCTAAAnAA TAATTCGTTC GAAATTAACA CAATTTAATA GGAATTTTTC TTTAAAACTA 6720

TTGCTAATAA AGCTATATTT TGATACCTTT ATCAAGTGTT AAACAAAATG TTTGATAAAA 6780

GTAAACTTAA TATAGCTTTT TTAGGTGGAA AAATAAATGA ACATAGGTAA TAAAATTAAA 6840

AATCTTAGAA GAATTAAAAA TTTAACGCAA GAAGAACTTG CTGAACGTAC AGACTTATCG 6900

AAAGGCTACA TTTCACAAAT AGAAAGTGAA CATGCCTCAC CAAGTATGGA AACTTTCTTA 6960

AATATTATAG AGGTGTTAGG AACGACGCCA AGTGAATTTT TTAAAGACAG TGAAAATGAA 7020

AAAGTATTAT ACAAGAAGGA AGAACAAGTT ATTTATGATG AGTATGATGA AGGTTATATA 7080

TTAAATTGGT TAGTTTCAAA GTCAAATGAA TATGATATGG AGCCATTAAT ATTAACTTTA 7140

AAGCCTGGAG CATCATATAA AAATTTTAAT CCATCAGAGT CTGATACGTT TATTTATTGT 7200

ATGTCAGGTC AGATAACACT TAATTTAGGC AAAGAGATAT ATCAAGCACA AGAAGAAGAC 7260

GTTTTGTATT TTAAAGCACG AGATAATCAT CGTTTGTCAA ACGAATCAAA CAATGAAACA 7320

CGAATACTTA TTGTAGCGAC AGCTTCATAT TTATAGGGGG GATCTTATTT GGAACCGTTA 7380

TTATCATTAA AATCAGTTAG TAAAAGCTAT GATGATCTTA ATATCTTAGA TGACATAGAT 7440

ATTGATATTG AATCAGGATA CTTTTATACA TTATTAGGTC CTTCAGGTTG TGGTAAAACA 7500

ACAATTTTAA AATTAATTGC AGGGTTTGAA TATCCTGACA GTGGTGAAGT GATTTATCAA 7560

AACAAACCAA TTGGTAATTT ACCACCAAAT AAACGTAAAG TGAATACAGT CTTTCAAGAT 7620

TATGCATTAT TTCCACACTT AAACGTCTAT GATAATATCG CTTTTGGTTT GAAATTAAAA 7680

AAATTATCAA AAACCGAAAT TGATCAAAAA GTAACTGAGG CATTAAAATT AGTAAAACTT 7740

TCAGGTTATG AAAAAAGAAA TATTAATGAA ATGAGTGGCG GACAAAAGCA ACGTGTTGCA 7800

ATTGCACGTG CTATCGTAAA TGAACCAGAA ATATTATTGT TAGATGAATC TTTATCCGCA 7860

TTAGATTTGA AATTGCGTAC TGAAATGCAA TATGAATTAC GAGAATTGCa ATCTAGATTA 7920

GGtATTACAT TTATATTTGT aACACATGAT CCA 7953

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGCGTGATCA TACGACCGTC ATTCATGCTC ATGAAAAAAT ATCTAAAGAT TTAAAAGAAG 60

ATCCTATTTT TAAACAAGAA GTAGAGAATC TTGAAAAAGA AATAAGAAAT GTATAAGTAG 120

GAAACTTTGG GAAATGTAAT CTGTTATATA ACAGCACTAA TGATnACAAT CATTTTTTAC 180

ATTTCTATAT GCTAATGTGG CAAGATGAGC AAAACTCATT TTGTGGATaA TGTTTaAAAG 240

TCATACACAC CATACACAAG TTATCAACAT GTGTATAAyT cGcCAAATCT ATGTTTTTAA 300

GACTTATCCA CCAATCCACA GCACCTACTA CTATTACTAA GAACTTAAAA CCTATATAAT 360

TATATATAAA CGACTGGAAG GAGTTTTAAT TAATGATGGA ATTcACTATT AAAAGAGATT 420

ATTTTATTAC ACAATTaAAT GACACATTAA AAGCTATTTC ACCAAGaACA ACATTACCTA 480

TATTAACTGG TATCAAAATC GATGCGAAAG AACATGAAGT TATATTaACT GGTTCAGACT 540

CTGAAATTTC AATAGAAATC ACTATTCCTA AAACTGTAGA TGGCGAAGAT ATTGTCAATA 600

TTTCAGAAAC AGGCTCAGTA GTACTTCCTG GACGATTCTT TGTTGATATT ATAAAAAAAT 660

TACCTGGTAA AGATGTTAAA TTATCTACAA ATGAACAATT CCAGACATTA ATTACATCAG 720

GTCATTCTGA ATTTAATTTA AGTGGCTTAG ATCCAGATCA ATATCCTTTA TTACCTCAAG 780

TTTCTAGAGA TGACGCAATT CAATTGTCGG TAAAAGTGCT TAAAAACGTG ATTGCACAAA 840

CAAATTTTGC AGTGTCCAcC TCAGAAACAC GCCCAGTACT AACTGGTGTG AACTGGCTTA 900

TACAAGAAAA TGAATTAATA TGCACAGCGA CTGACTCACA CCGCTTGGCT GTAAGAAAGT 960

TGCAGTTAGA AGATGTTTCT GAAAACAAAA ATGTCATCAT TCCAGGTAAG GCTTTAGCTG 1020

AATTAAATAA AATTATGTCT GACAATGAAG AAGACATTGA TATCTTCTTT GCTTCAAACC 1080

AAGTTTTATT TAAAGTTGGA AATGTGAACT TTATTTCTCG ATTATTAGAA GGACATTATC 1140

CTGATACAAC ACGTTTATTC CCTGAAAACT ATGAAATTAA ATTAAGTATA GACAATGGGG 1200

AGTTTTATCA TGCGATTGAT CGTGCCTCTT TATTAGCGCG TGAAGGTGGT AATAACGTTA 1260

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ATTTAATAAG TGTGCTTATA TGCCCTTTAA ATTTAAAATT TTAATAGTCA ATAACAAGTT 1740

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GTGACAAAAA AAGGTATAAT ATATTAATGA CATACAAAGA AATGGAGTGA TTATTTTGGT 1920

TCAAGAAGTT GTAGTAGAAG GAGACATTAA TTTAGGTCAA TTTCTAAAAA CAGAAGGGAT 1980

TATTGAATCT GGTGGTCAAG CAAAATGGTT CTTGCAAGAC GTTGAAGTAT TAATTAATGG 2040

AGTGCGTGAA ACACGTCGCG GTAAAAAGTT AGAACATCAA GATCGTATAG ATATCCCAGA 2100

ATTACCTGAA GATGCTGGTT CTTTCTTAAT CATTCATCAA GGTGAACAAT GAAGTTAAAT 2160

ACACTCCAAT TAGAAAATTA TCGTAACTAT GATGAGGTTA CGTTGAAATG TCATCCTGAC 2220

GTGAATATCC TCATTGGAGA AAATGCACAA GGGAAAGACA AATTTACTTG GAATCAATTT 2280

ATACCTTAGC TTTAGCAAAA AGTCATAGAA CGAGTAATGG ATAAGGGACT CCATACCGTT 2340

TTAATGC 2347

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

ACAAGACGTn TCTATAACTT ATCTGAAATC GCTCGTCAAG ATAAAGATTA TGCAACTATC 60

TCATTCTTAA ACTGGTTCTT AGATGAACAA GTCGAAGAAG AATCAATGTT TGAAACTCAC 120

ATCAATTATT TAACTCGTAT CGGCGATGAC AGCAATGCAT TATATCTTTA CGAAAAAGAA 180

CTTGGCGCTC GTACATTCGA CGAAGAATAA TTAAACATCA CTACAATAGA CAGATAAATA 240

TCATACGACA TGATAGGCAT TTGGGTCACT TACAATAACC CAATGTCTAT ATTATTTTGC 300

TTTACGGAGA TCACTAGATT CATTTTCTGA ATCATTGATC TGCGTTTTTT CATTTTCAAG 360

GCTAATTATT GTATTTTTAG TCATTTATTT TTTAAACTAC TAATGTTAAT AACTCTAAAT 420

TTGATGTTGA ATTAATTTGA CGATTTTAAA GCATATCATC ATTTACTTTT TAATCAGAGT 480

TACATCCAAA TGATAGATTT CACGTTATAC CTTCACGTAT AATATTATGT ATCGTTTGTA 540

AGCAAATGAC TAAAAGTCTA TTAATATATA CATTTAATTA ATTGAAAGGA TTGACTACAT 600

GATACAAGAT GCGTTTGTTG CACTTGATTT TGAAACAGCA AATGGTAAAC GTACAAGTAT 660

TTGTTCTGTC GGAATGGTTA AAGTCATTGA TAGTCAAATA ACAGAAACAT TTCATACTCT 720

TGTGAATCCG CAAGACTATT TTTCACAACA AAATATTAAA ATTCATGGCA TACAACCAGA 780

aGATTTACCT GTTGTCGCAC ATAACGCGGC ATTTGATATG AACGTCTTAC ATCAAAGCAT 900

TCAAAATATT GGTTTACCAA CTCCAAATTT AACTTACTTT TGTAGTTATC AACTTGCTAA 960

AAGAACCGTT GATTCGTATC GATACGGTTT AAAACATATG ATGGAGTTTT ATCAATTAGA 1020

TTTTCATGGT CATCATGATG CATTGAATGA TGCCAAAGCA TGCGCAATGA TTACTTTTAG 1080

GCTACTGAAA AATTATGAAA ATTTAACATA TGTAACTAAT ATTTATGGTA AAAATCTAAA 1140

AGATAAAGGC TAGGACTAAA TAAAATACTC CCTTCAAAAG TAAGCATTGT AAAAATGTAA 1200

ACTTTGCAGG GAGCTTTATT TTATATAAAG TCATATATCG TCATATTTTT ATAAGTTGAT 1260

TGTTCTAAAT TACCTACAGT GACACCAATA AGTCGAATTG GTACATCAGG GTCTTTTAAA 1320

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TAAACCCCGA CCTCTTTTTC CAAACAAACG TATTAATTCA AATTCCGTTT TCTCATATAA 1680

ATCTCTACCG TTAAAAATAC CATTATCATG CATTACTTTT TTGGAAGCTT TACCTACGCC 1740

TGGaAAATCT CCAATATCCA ATGTCATCAA AATATCATGG aCATTTTGAT AATCAATCAC 1800

AGTCATACCA TCAGGTTTAT TCATACCACT CGCTAATTTA GCTAAAAATT TGTTATAAGA 1860

AACACCTGCA GATGCTGTTA AATGTGTCTG CTCTAGAATA TCTTTTCTAA TATACTGAGC 1920

AATTTTCGAA GCAGGAAGGT CTGGTCTCAC TAATTCTGTA ATATCTAAAT ACGCTTCATC 1980

CAATGACATC GGTTCTACCT TATCTGTATA ACTTCGGAAA ATAGACATAA TCTGCGCAGA 2040

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CGCTTGTGAC ATAGGCATTG CTGAATGGAC GCCGTATTTT CGTGCTTCAT AGGATGCCGT 2160

AGAGACAACA CCCCTACTGC TTGCTTTACC ACCAACAATG ACTGGTTTCC CTTTCAATTT 2220

GGGGTTATCT CTCATTTCGA CTTGTGCAAA AAAATAGTCC ATATCTATAT GAATAATTCG 2280

TCTCTCAGTC AAGTGCTCAC CTCCCTACTA ATTTTTACTT TTATAACGCA CAAAAATATC 2340

TCAACATAAT TATACGCTGT GTACGATTTT TTTACATAAA TCTTGCACTT AGCGATAACT 2400

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CGATTGAGTA AGAAAACATA GGTAATCTGA AATAATTCAA GCAAATTCAT TTTGTTGGTA 2520

TCATCATATT AAAATTTATT ATTGAGTCGG CTTTTGATGA TACAAATAAA TACTATCTTC 2580

AAAGCAATAA GCGGTATGCA TACTAAACAT AAAAATAAGT GATGAATAAC CAAATACCTT 2700

AATTAAAATA AGCAAGCCAG TACTTAATAG GATTAGTGGT GACAGCATAA TAATTGAGAA 2760

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AAACATAGGT TTGCTATCTT TTTTAAATAA AAGAAATAAT GCTCTATGGA TAAGTTCATG 2880

TAAAATCAAT AAAATAATGA ATCCAGCAAA CCCATATACA AGATTGATGA TGATATTTTG 2940

ATCGACAACC GCTGTGACAC CTAACGCCCA CTTATACGTA AATAAAATCA CGAATAACGC 3000

AATAACAAGT TGCAAGATAA TAAACCTTCG CATTTGAAAA TTATTTGTCG TTAAATCAAT 3060

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GTGCTTTCCA TTGTAAAATA ACTTCTTCAG CTTTCCCACA GACAAAAGTT GTATTATTGC 3540

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CGTATACATG TTTTGCAAGT GGTGCCATAT ATAGCCCTAT TGTTCCAATA CCACAATAGG 3660

TATCTAATAC AACTTCATTA CCTGTCAATT GCGCATACTC AATTGCTTTA TTATATAATT 3720

TCTCTGTTTG TTCAGAATTA ATTTGGTAGA ATGACTGATC ACTTATTTTA AATGTACTAT 3780

CTGTTAATTG ATCAATAATT GTATCTTTAC CATATAGCGT TATAGATTGA CGTCCCATAA 3840

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CTAATATCTT CTCAACAACA GCATTTTTTT GTGGCCACTT TTTACCATTA GTTACAAAAA 3960

TAATCATCAT TTCGTCTGTA TGATATCCTG TTCTTACAAC CAAATGTCTC ATTAAACCTT 4020

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TCATCACTTC TTGATGTTGT GAATCTTGTA TTAAACAACT TTCCATGTCA ATAATGTCAT 4140

GGCTTCTTTG ACGATAAAAG CCCATAATAA CTTCATTCTG TTCATTCTTA CCAACTGGAA 4200

TCTGGGACTT GTTTCGATAT CTCCAAGGAT CTGTCATGCC AACTGTATCG TTAATCTTAG 4260

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GTTGTGCTTC GTATGATAAG TGTTGAAGTT GGCACCCACC ACAACGTTCA TAATATATAC 4380

AGTTCTTTTT TACTTTGATA ATTTTATATT CAATTTGTTC ATTAATTAAA GCTTGTGGTA 4500

TGAAAATAGG AAAGCGATCT ATTTTTACGA CACCATGGCC TTCATGCGTT AAATCAACAA 4560

CTGTTCCCGT TTTTATGTCA TTTTTAGCTA TTGCTTGCAA AATTTTACCT CCAAAATGAA 4620

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ATCATTAGGT GCAAAGACAT CTATATGACG TTCTAGATTT AAGAAATTCG CTGGTAATTT 4800

ACCACCATAT TCTCCATCTA CATTTAGTTG TAAGTCTGTG AATGATGAAA TATTAATTGC 4860

CTTTGCTTTT TCATAAATAA CTTTAGGATG CTTAGTATGT TCTCCTCTTG AAGCTAAAGT 4920

CATAATATGA CCAAGTTCTG CAAGGTTTGA TTTTTCAACT ATAATTAACG TAAAATAGCC 4980

GTCATCTAAC TTAGCGTCCG GCACTAATTT TTCAAATCCT GCCATTGAAT TTGTTAAACC 5040

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TACTTAAAAT TCATATATTT TAACTTCATC TTTGTTTCGT CTAATAGGGA GTGGGACAGA 5700

AATAATATTT AACAAAATTT ATTTCGTTCT ACCCCAACTT GCATTGTCTG TAGAATTTCC 5760

TTTCGAAATT CTCTATGTTG GGGCCCCACC CCAACTTGCA CATTATTGtA AGcTGACAGA 5820

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AATAGTTGAT TTACTAATTG TGGATTAGCT TGACCTTTAG ACGCTTTCAT AATTTGACCA 6480

ACTAAGAAGC CCATAGCTTT GCCTTTACCA TTTTTGTAAT CTTCAACTGA TTGTTCGTTA 6540

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CCATTATCTT CCATAATCTG TTTAGCATTA CCACCTTTAG CTGCTAACTC TGGGAAGACT 6660

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AATCGACGTG TTTCTTGTCC GATTTCTCCA CCATTTAACA ATTCTTCTTC TTGGCGTTTT 7140

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GGATCAGTCT CTTCAATTGC ATCATATATA TCTTTAACAA CATCAGATGG TTTGATTTTT 9240

TTGTCTTTTA TTAAAGTTAA TAAATTCTCA ACCGATTCGT AGCGAATGCT CATCTTACGC 9300

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ATTATGATTG CCGTCTACTT CTTGATACTA ATCGTTATTG GCTTTTACGG TTACAAGCAA 10080

GCAACTGGTA ACCTAAGCGA GTACATGTTA GGTGGACGTA tATTGGACCG TATATTACTG 10140

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TTTTTCATTG ATATTATGCC ATTCATTAAG CTTTGTTTGA CTCTTTTCTG CAGTCGCTTG 12000

AGTGATAAAT TCACCTGGTG TGATTGAATC TTCACTTGAT TGCTTATAAA TTGCAAAATG 12060

AATTGGTATA TCTTTTAAAT CATCATTTTC ACGTAACCTT GATAATATCT CACTAGCCAT 12120

TTGTTTACCT TGCTTTTTAA CTcGCTATCA TCTAGTTTTT TACTAAAAGT CGATCCATCT 12180

TTTTCTTTTT TATAGTAATA AACACTATTC ATAGCTAAAC CAATCGTCAT ACCTTTAATA 12240

TTCTTACCTT TTGTATCTCC ACCACCATAA AAATCTTGCT CTAAAATGTT AGATAAATAG 12300

GCTGGTGATT TTTCTGCAAT CTTTTCAGGA TCTGTTTCAC CTtCGTGTGA TGGATTAAGT 12360

CCTAAATTTT CATTCGCTTT CTTGTCTTTT TTATCTTTTT CAGACATTTT ATCGATTTCA 12420

CGTTTTGTAT ACTTAGGATT TAAATAGGCA TTAATTGTTT TCTTGTCCAA AAATTGACCA 12480

TCTTGATACA AATATTTATC TGTTGGAAAT ACTTCTTTAC TTAAGTTCAA TAAACCATCT 12540

TCAAAGTCGC CGCCATTATA ACTATTTGCC ATGTTATCTT GTAAAAGTCC TCTTGCCTGG 12600

CTTTCTTTAA ATGGTAACAA TGTACGATAG TTATCACCTT GTACATTTTT ATCCGTTGCA 12660

ATTTCTTTTA CTTGATTTGA ACTATTGTTA TGTTTTTGAT TATCTTTTCC AGCCTGGTCA 12720

TCCTTATGGT TACCACAAGC AGCGAGTATA AAGATAGCTG TAATCAATAA TACTAATGTA 12780

CGCTTCATCG ACATACCCCT CTAACTATTT AATTCATTTT GCTTATCTAC AAATTGTTGC 12840

TCTGTCCAAA TTTCAATACC TAAACTTTGT GCTTTTGTTA ATTTTGAACC TGCATCTTCA 12900

CCAGCAATAA CGACATCTGT ATTTTTAGTA ACGCTACTTG TAACTTTAGC ACCTTGTGAT 12960

GCAAGCCATT TAGATGCTTC ATTGCGTGTC ATTTGATGTA GCTTACCAGT CAGTACTATC 13020

GTTTTACCAC TAAATTCAGG ATGTCCTTCA ATATCTGATG TTTTGATACC TTTATAAATC 13080

ATATTAACAT GTTTATCTTT TAATTTTTGA ATTAAAGCAC GAATATCTTC ATTTTCTAAA 13140

TAAGTAACTA CAGATTGTGC TACTTTATCA CCTATATCAT GAATTTCTAC TAATTCCGCT 13200

TCAGTTACCG TTAGTAATCG ATCTATCGTT TCATATTTTT CTGCTAACAC TTGGCTCGCT 13260

TTAACACCTA AATGCCTAAT ACCTAGACCA AATAATAAAT TTTCTAAAGA GTTGTCCTTA 13320

GCTTGTTGAA TGGCAGCTAA TAAATTATCA ACTTTTTTCT GCCCCATTCT GTCTAAAGGT 13380

TAAAGCTGTT GAATAATTTT AGTGCCTAAA CCATCAATAT TcATGGCTTG TCTTGaTACA 13500

AAGTGnATCa ATCCtTcAAC AAGTTGTGCT TGGTCATTTT GG 13542

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1893 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

CAGTAAACAC CTCTGATTAC GAATATTTAT ACATTTATTT TAACACATGC ACTGATTTAC 60

GACTACTAAA CACCTTTACG TAAAAAGGGT AAACATGGTT TATCTATCTT GGTTATCTAT 120

TTATAAATAT TTnTCATATT ACGCATAACA ATTGCTTAAA ATATGTATAA AAATGAATAT 180

ATGTGTAATA AACTTGCTAA TTATTAGATT TAATAAGCGT CAATTGTTTG AACATATTtA 240

ATTAAAATCA CATTGATATC ACAGATACGA ATATTGTCGT ATAGAAATTG AAAATTCTAT 300

TTTTTAAATG AAAGTCTTCA ACATAATTTT AAGTTTCAAC ATGAGAAAAA TCGATTAACA 360

AACAACGTCA GTTGAATATG CCTTTTGAGA CATTTCAAAC TTTACAATTG TTGCTAATCG 420

ATATATTTGC TTTTAGTGAT CCCTGCTATA AAATAAATCA ACGATTTCTA ATAAGTGTTT 480

TGTATTGAAT TGTTCATCAA TTTGCGTTAG TTCATCCACT GCTGCGTCTC TATGATAAGT 540

CAATTTATCT TCTGCGCCAT CTTTCCCTAA TAAACTCACG TACGTACTTT TATTATTTTC 600

AAGATCGCTG CCCACTTTTT TACCTAACTT TGCTTCATCA CCATAGCAGT CTAATAAATC 660

ATCTTTAATC TGGAACATCA TACCTAAATG ATAACTATAA CTTTCTAAAT GTTCTTTAGT 720

TGTATCATCG ACATTAGCGA TATCTGCTGC ACTCATAACC GCAAAAGTTA ATAATGCTCC 780

TGTTTTTGTT TTGTGTATCA TTTCCAAAGT TTCAAGATCA ATTGGTTGGC CTTCGCTTTG 840

CATATCTAAC ATTTGACCGC CGACCATTCC AACATGACCA CTTGCTATTG ACAGCCGTTG 900

TAGAACTTTT ATTTTTACTT CATCAGTTAA TCTATCATCA CTTGAAATAA GTTCAAATGC 960

TTTAGTTAAT AAAGCATCAC CTGCTAATAT CGCAGTCCAC TCACCATATA CTTTATGATT 1020

TGTTAATTTT CCTCGTCGAT AATCATCATT ATCCATCGCT GGTAGGTCAT CATGAATAAG 1080

TGAATATGTA TGAATCATTT CTAGTGCAAT TGCGCTCTTC ATACCTAACT CATACTCGGT 1140

ATTTAGTGAA TCTAAAGTGA GTAATAACAG AACTGGTCGG ATGCGTTTAC CTCCAGCATT 1200

TAATGAATAC AACATACTTT CTTCTAGCTG AGTATCCATT ACTGATTTAT TTATCGCAAC 1260

CATCCTCAGC TTCTTCTTTT ATTAAGTCAT TCACCTTTTT TTCGGCATTT TTTAAAGTTG 1380

TGTCACAAGC TGCTGATAGT TTCATACCAC GTTGATATAA ATCTAATGAT TCCTCTAAAG 1440

ATACTGTTTC ATTATCTAAT TTTTGAACAA TTTGCTCTAA TTCTTGCATC ATTTCTTCAA 1500

AACTTTGCGT TTCTTTAGTC ATTATTACAC CTTACTTTCG TAACTTTTGC ATCTACTAAG 1560

CCATCTTTCA TTGTTAACGT CAATTGATCA TTTTCTGTTA AATCTTTAGT ACTCGTAATG 1620

ACTTCGTCTT TTTTATTAAC AATTGCATAT CCACGCAACA TTGTATTAGT TGGACTTAAA 1680

TTGTTTAAGT TTTCTACTTT ATTTTTCAAA TCATTTTTAT AACTTAATAT CTTAGAATTC 1740

AATAATTTAA CAAGTTGGTT TGTCAATTGA AGATTATnTT GTTGTTCTTG ATTAACACTA 1800

CTTAGTAATG CTTTTAAATn ATAACGTTGG TGCAACAGCA TTAAATCGAG GCCCCGGTGG 1860

TCCAAAGTTG CCCGAATTnG TGGTTTCAGG CCC 1893

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 821 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

AAAATATATT CCTTCACTTA ATATTCAATT AGAGAAAAAC ATGGTGATTG TAATATGTTG 60

TGCAATATTT CTGGGTGTTT TAATACTTTT TTTATTTCTG AATCGTAAGC TAAGGTTGGA 120

AATTTATAAT AATAACTCTA GTAAAGGGAA AATAATTTTA TTTCCTTCAT TAAAAAACTT 180

TTGTTTCACA ATATTTTATT ATTTTTTATT TGGCGGTCTT TCAATAATGG CTCTAAGTAT 240

GTTATTAACT TTAAATCCTC AAAATATAAT AGGCTTTATT GGTTGGTTGG TAATGACTGC 300

AGGTTTCTTT CTGTTAAACA TGTCATCGAT TATTGACAAA AAAATTTATG TATTATCTAA 360

AACTAACACG GTGGAAAAAT GATGGTTTAG CTGGATTTAC TGCAGGTTCT ATTTCGGCAA 420

TACTTGTATA TTGGACCAAT CAAAAAAATG AATTTGGAAT AAAAGATAAA AACGATTGGA 480

TAGGACATAA ACTAGACGTT GGTATAGATG CTGTAGAAAA ATCTGCAGAA AAAACAGTAG 540

ATGGTGTTGA AAATGTCATG GTGAAGCTTC AAAAAGTATT TCTAATCATA TAAGCCCTAA 600

GAAATGGAGC TGGTAAATGT TGCTATGCGA ATCTAAAATC ATCAATAAAA ACCCAAAATA 660

TAGAATTATT AAATATAATG ATGAATACTT AATGGTCGAT ATAATAAGCA CTTGGATTAG 720

TTTATTTTTT CCTTTTATTA ATTGGTTCAT CCCaAAAGaA TACGTCAAAA TTAGTAGAGA 780

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

AGTAAGATAA TTTTCAATTA GAAAATATCT TACTGCTGTT CTCTATTTAT ACAATACTTC 60

GTATTGAATG GcTTCGCTTT CCTAGGGTGC CGTCTCAGCC TTGGTCTTCG ACTGGCACTG 120

CTCCCTCAGG AGTCTCGCCA TTAATACTAC GTATTAACAT GTAATTTTAC TTTGAAATAC 180

TTTTAAAAAA TAAGACACTT TGCCCAACTT GCACATAAAT GTAAAATTCA ATAAAATGAA 240

TTTTCTGTGT TGGGTCCCTT CTTATAATTT AATAAATACC ACTAAACTAA ATTAACGAGG 300

TGCCTTATGT ATAAAAATTA TAACATGCCC CAACTACACT ACCAATAGAA ACTTCTGTTA 360

GAATCCCTCA AAATGATATT TCACGATATG TTAATGAAAT TGTTGAAACr ATACCTGATA 420

GCGAATTCGA TGAATTCAGA CATCATCGTG GCGCAACATC CTATCATCCA AAAATGATGT 480

TAAAAATCAT CTTATATGCA TATACTCAAT CTGTTTAATT ATGTTCAAAG CATTAAGGTA 540

ACAAGACAAT ATCTAAGATA TCAAAGATAG AAATTTTTTG ACGTTGTTGC TGATTGTAAA 600

CATAACCATC AATTTCATAA TTAATAGCAT CAATACGATA AATGGTTAAG CGTACTGAAT 660

CTACAAAGCC ATTATTATAA AATTTAACTT CTACAGGTTG GGCATATTGT AGCGCCTCGT 720

GTAGCCGAAT GTTTAGCTCA GCCAATTGAT CATCTGATAA TACAGGACGT GTAATTTTGT 780

TTTGGTCGAT AATGTATTGT TGAATCGTTT CGAATTGTTC GGGTAATGTT GCAAAAGGAG 840

CCCATTTAAT CATGCCTCTT CCCATAGGTA TATTGTTATC TAGTAATTCT CTTGGAACGT 900

TACGATAATC AGTTTCTTCT TCATAACTTG TCATCCTTAA TTCACCCCAA TCTGATAATT 960

ACATTATACG AACATGTGTT CTATTTTGCA ACAAAAATTT TGTGGaAGCA TAAACGCGTT 1020

AATAATTAAT GCTCGTGtAA GTAAAAAAGA GGGATTAATT AAAATCGAAT AATGaCATAT 1080

CACaGCAAAT AGTTCTTTTA AAGTAGTTAA ATAGTTTTAG CTTTAAGGAA aTGATAAaTG 1140

ATTGTwAATT CTAGCTAAAA TTTAATAAAA TGAAAATAAG ACTAACATGG AGGGGTAAAA 1200

GTAATGACAA ATGGATATAT TGGTTCTTAC ACTAAAAAGA ATGGTAAAGG GATTTATCGT 1260

TTTGAATTAA ACGAAAAATCA GTCACGTATT GATTTATTAG AAACAGGATT TGAATTAGAA 1320

GCGTCTACAT ATTTGGTGCG TAATAATGAA GTTTTATATG GAATCAACAA AGAAGGAGAA 1380

TGTTTGTCTT CAAAAGCTGG TACAGGTTGT TATGTATCGA TTTCAGAAGA TAAACGATAT 1500

TTATTTGAAG CGGTATATGG TGCTGGCATC ATACGTATGT ATGAATTAAA TACGCACACA 1560

GGTGAAATTA TACGTCTAAT TCAAGAACTT GCACATGATT TTCCAACAGG TACACATGAA 1620

AGACAAGATC ATCCACACGC ACATTATATT AATCAAACTC CAGATGGTAA GTACGTTGCA 1680

GTAACAGATT TAGGTGCTGA TCGTATCGTT ACTTATAAAT TTGATGACAA CGGGTTTGAA 1740

TTTTATAAAG AATCTTTATT TAAAGATAGT GATGGGACAA GACATATTGA ATTTCATGAT 1800

AATGGAAAAT TTGCTTATGT CGTACACGAA TTATCAAATA CTGTGAGTGT TGCAGAATAT 1860

AATGACGGTA AATTTGAAGA GCTCGAGCGT CATTTAACAA TTCCTGAAAA CTTTGATGGA 1920

GATACTAAAC TTGcAGCAGT GCGTTTATCT CATGaTCAAC AATTCTTATA TGTATCTAAT 1980

AGAGGGCATG ATAGCATTGC AATTTTTAAA GTTCTTGATA ATGGTCAACA CTTAGAACTA 2040

GTAACAaTTA CTGAAaGTGG TGGTCAATTC CCAAGAGATT TTAATATTGC CTCATCAGAT 2100

GACCyTTTAG TTTgTGCTCA kGaGCaAGGA GATTCAGTTG TAACTGTTTT CGAAAGAAAT 2160

AAAGAAACAG GTAAAATTAC GCTATGTGAT AACACTCGTG TAGCATCTGA AGGTGTATGT 2220

GTCATATTTT AATCTTTAAT TAATCATGAT AAAAAGAAAA CCATGTTTCC AAAAAATTTG 2280

TGTATACCTT GAAATTTATT GnTTTCCAGn ACATCAATTA TGGGAAGCAT GGnTTATTTT 2340

TGT 2343

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4837 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

AAATTGCCAG TTGGTATCGC TTCTGGTGCA GTAGTCGAAG GTTTCTTCCA AGGTATCATT 60

CCGATTGGCT ATATCGTTAT GATGGCAGTA TTGTTATACA AAATTACTGT TGAATCTGGA 120

CAATTTTTAA CAATTCAAGA TAGTATTACA AATATTTCAC AAGACCAACG TATTCAAGTT 180

TTACTTATTG GATTTGCATT CAACGCATTT TTAGAAGGTG CAGCAGGATT TGGTGTACCA 240

ATTGCAATTT GTGCACTTTT ATTAACACAA TTAGGATTTA ATCCATTAAA AGCTGCGATG 300

TTATGTTTAG TCGCAAATGC AGCGTCTGGT GCTTTTGGTG CGATTGGTAT CCCTGTAGGT 360

GTTGTAGAAA CGTTGAAATT ACCTGGAGAT GTTTCAGTAT TAGGTGTTTC TCAATCAGCA 420

GGTTTTAGAG GTGTTAAAGA AACATTACCA GCAATTTTAG TAGTTTCAAT CACTTATACA 540

CTTACTCAAG GATTATTAAC TGTATTCAGT GGACCTGAAT TAGCAGATAT TATTCCACCG 600

TTATTAACAA TGTTAGCATT AGCAGTATTT TCTAAAAAAT TCCAACCAAA ACACATTTAT 660

CGTGTTAATA AAGATGAAGA AATTGAACCT GCAAAAGCAC ATTCTGCAAA AGCAGTATTA 720

CATGCATGGA GCCCATTCAT TGTATTAACA GTCATTGTAA TGATTTGGAG TGCGCCATTC 780

TTTAAAAACT TATTCTTACC AAATGGTGCT TTATCATCAT TAGTATTTAA ATTCAACTTA 840

CCTGGaACAA TCAGCGAAGT TACGCATAAA CCATTAGTAT TGACTTTAAA TATTATTGGA 900

CAAACAGGTA CAGCTATTTT ATTAACTATT ATTATTACAA TTTTAATGTC TAAAAAGGTT 960

AACTTTAAAG ATGCAGGTAG ATTATTCGGC GTTACATTTA AAGAGTTGTG GTTACCAGTT 1020

CTTACAATTT GTTTCATCTT AGCAATTTCT AAAATCACAA CTTATGGTGG TTTAAGTGCA 1080

GCAATGGGTC AAGGTATTGC TAAAGCAGGT AATGTCTTCC CAGTTCTATC ACCAATTTTA 1140

GGTTGGATAG GTGTGTTTAT GACAGGATCA GTTGTAAATA ACAACTCATT ATTTGCACCA 1200

ATTCAAGCTT CTGTTGCACA ACAAATTGGA ACAAGTGGTT CACTTCTTGT ATCTGCTAAT 1260

ACAGTTGGTG GTGTAGCGGC AAAATTGATT TCACCACAAT CAATTGCAAT TGCAACTGCA 1320

GCAGTAAAAC AAGTTGGTAA GGAATCAGAA TTATTAAAAA TGACATTGAA ATACAGTGTA 1380

TGTTTACTAA TATTCATCTG TATTTGGACT TTCATCTTGT CATTATTATA AAAAAACGTA 1440

TTTCAAAATA TAAATATACA GAAGGTGAGA TGTTTTCTAA CATCTCATCT TTTTTTTATG 1500

GATCATTAAT GAAAGAAGTT TGACATTATA ATAATGGTAG CGCTTTATGT TAAAATGAAT 1560

AGTGAGTAAT CAGCAATCAA ATTAAATTGG TTGATAGCTG TTAAGGTTTG TGGTTTTGTC 1620

TTTGTGCTAT CGCnCATAAA GTATATAATT AAAGTAGTTT CGTTATTATA AAATATTAAT 1680

ATACATAGTA GATAGTAATA GAGCATCACC ATGGGAACCT ATTGAGACAC TTATTGATTT 1740

AAAGTGGTAT TAATATGTCG TATTTCTCGA ACGTTCCATT ATTCATTTTA AAAAGGGGGA 1800

CTGTATTTGT TATGACAACA CAACATAGCA AAACAGATGT CATCTTAATT GGTGGCGGTA 1860

TTATGAGTGC aCATTAGGAA CATTACTTAA AGAATTATCA CCTGAGAAAA ATATTAAAGT 1920

GTTTGAAAAA TTAGCACAAC CTGGCGAAGA GAGTTCAAAT GTATGGAATA ATGCCGGTAC 1980

AGGGCATTCA GCACTTTGCG AGTTGAACTA TACAAAAGAA GGTAAGGATG GCACAGTTGA 2040

TTGTAGTAAA GCAATTAAGA TAAATGAGCA GTACCAAATT TCAAAACAGT TTTGGGCATA 2100

TTTAGTTAAA ACAGGACAAT TAGATAACCC AGATCGCTTT ATTCAAGCGG TGCCACACAT 2160

GAGTTTTGTC ATTGGCGAAG ATAATGTAGC TTTTATAAAA AGTCGTGTTG CAACGTTAAA 2220

GGTACCGTTA ATGATTGAAG GTCGTAAGTC TGATGAACCA ATTGCTTTAA CTTATGATGA 2340

AACTGGTACa gATGTTAACT TTGGTGCGTT AACTGCAAAG TTATTTGATA ATTTAGAGCA 2400

ACGTGGTGTG GGAATTCAAT ATAAGCAGAA TGTATTAGAC ATCAAGAAAC AGAAATCTGG 2460

GGTATGGCTA GTTAAAGTTA AAGATTTAGA AACTAATGAA ACGACAACAT ATGAATCTGA 2520

TTTTGTATTT ATTGGTGCTG GCGGTGCGAG TTTACCATTA CTCCAAAAGA CTGGGATTAA 2580

ACAATCAAAA CATATTGGTG GTTTCCCGGT AAGTGGATTA TTCCTGCGCT GTACAAATCA 2640

AGAAGTGATT GATCGTCATC ATGCTAAAGT GTACGGAAAA GCAGCAGTGG GTGCGCCACC 2700

AATGTCAGTG CCGCACTTAG ATACACGTTT TGTAGACGGC AAGCGTTCAT TGTTATTTGG 2760

TCCATTTGCA GGTTTCTCAC CTAAATTTTT AAAAACAGGT TCACATATGG ATTTAATTAA 2820

ATCGGTTAAA CCAAATAATA TCGTGACGAT GTTATCTGCA GGTATCAAAG AAATGAGTCT 2880

TACGAAGTAT TTAGTGTCAC AATTGATGTT ATCTAATGAT GAGCGTATGG ATGATTTAAG 2940

AGTCTTTTTC CCAAATGCTA AAAATGAAGA TTGGGAAGTG ATTACAGCAG GGCAACGTGT 3000

CCAAGTAATC AAGGATACTG AGGATTCTAA AGGTAACTTA CAATTTGGTA CTGAAGTTAT 3060

TACGTCAGAT GATGGCACAT TAGCTGCATT ACTTGGTGCA TCACCTGGTG CGTCAACAGC 3120

TGTAGATATT ATGTTTGATG TTTTACAGAG ATGCTATCGT GATGAATTCA AAGGATGGGA 3180

ACCAAAGATT AAAGAAATGG TGCCGTCATT TGGTTATCGC tTAACAGATC ATGAGGATTT 3240

ATATCATAAA ATTAATGAAG AAGTAACTAA GTATTTACAA GTTAAATAAT AAACGAAACG 3300

GTAATGTCTT TTTTAATGTG ATAGACATTA CCGTTTTTTA GTGGTTAATA AAAATCATTT 3360

TAATTGTTTC AGTTGCTTGT TAATAGTGTC TACGTAGTTC TTGTTTTTAA AGAATTGAAT 3420

TATCCAAATT AATACATAAA CCACAATGAA GATAATTGTG AATATGATTA GATAATGCAC 3480

TGTTAGTGGA AACCAACCGG CAAGCATTGC TAAAGGCAAG AATCCGACAT ACGTTGTTAT 3540

GAAATGCATT ATAGTTGCTT TAGTAATGCT CCAATCTGTG TATTTAAAGA TAAAATCTCC 3600

AAGGAAAAAG ACGACGCCTA TGAGTAACCA TAAAATGATA GAAATCAACA TTACGGTAGT 3660

TTCTGTGAAA TGCGTATAAT ACAATATGCC AATAGTTGAT TGTGGGTTCA GTGGATAATA 3720

TTTGCCGTCT GCAAATAACA TACTAAAGAA CAGTGAAAGG GACAAACCAA TGATTAAGCT 3780

AATAAATAAT GAGTTTTTCA AATTTTTCAT ATTGATAAGC GCTCCTTTAT AGATTTTAAA 3840

TAACGTCTAG AAGAATAGGT GTAGTGTGCA TCTTTAAGAT ACATACGTAT AAGTCCATTT 3900

GGCTCTAATA ATAATTTTTC AATGTAATAC TTGTTGACGA TTTCTGATTT GGAAATGCGA 3960

ATGAAATGTT GTGGTAACTG TTTTTCTAGT TCATAAAGTC GTAATTTTAG TTTGAATTTT 4020

ACATTAATGA TATGGATTTC TTTGTCTATG TATCCGACTA ATGTATGTGA TTTGTCTAAA 4140

TCATTGACTG CATTAATAAT ACTTTGAACG TTATCATTCA TTTTAGGTGC ATGTATATCA 4200

ATATAAGATT CCGTCTCATT TGCATTGATA AATAAATTGA GTTTCATCAT AGGTTAATGC 4260

CTCCTTCAAA ATTATTAAAC CATAAATGAC CATCGATATA TTTAAATTTT GTTGAATGGT 4320

AGAAATTAAA TGTTAAGTGG CTAGAAAGCG CTAATCAATA TAAAAGATAC CTCCTGAAAT 4380

AAAAACAGAA ATGTTTTTTC AGGAGGTAGA GATTAAAGTG AATTATTTGG CAGTGTAATA 4440

GTAAAGGTGG TTACATACTC GTTACTTTGT GTGAATTGGA TTGTACCATG ATGCAATTCA 4500

ATGATGGATT TTGTAATTGC AAGACCTAAA CCATTGCTAT TATCATGTTT GCTCACTTTA 4560

TAAAAACGTT CAAATAAACG TGCTTCAGCT TGTGGACTAA TTGGTGAACC ATCATTACTT 4620

ATTGTGAAAA TGATATTGTT GTGACTATGT TGCAAAGCGA TGTCAATGGC ACCACCAACA 4680

TCTGTATACT TAATAGCATT TATTAATAAA TTACTCAATG CTTGATGTAA CAAACGTTGA 4740

TTTCCTAGGA AATTGATGAT TCTAGGTCAG CTAAnATGAT TAACGACTTT TCATCAGCAG 4800

CAnATTGTTC ATGTCGAATG ATATCnTTAA TGAGCTG 4837

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1600 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

ACAATTATTG GATTATTATC AAGCAACGTT AATGGATGAC TTCCACTTAC AACAGAAATG 60

CCCATAGATT CTAAATCTtT TGCATGAGCA TCTTGTGATA AGTCTTTTCC ATCATTGACA 120

GTTACATTCG CACCTAATTT ACTTAATAAT TTAGCTGCTT CATAACCACT TTTTGCCAAA 180

CCGACAACTA ATACATTTTT ATTTTCTAAC CCTGTATAAT TAAGCATCTT AATGCACTCC 240

AATCCATAAA CCGATTAAAC CTGAAATCAG ACCAACAGCC CAAAATACTG TAACTACTTT 300

CCATTCGCTC CATCCTATCA ATTCAAAATG ATGATGAATC GGACTCATTT TAAATATACG 360

CTTTCCAGTC AATTTAAAGC TAGCGACTTG TAACATAACA GATAATGTTT CAATTACGAA 420

TACTAAACCT ATAAAAATTA ATGATAATTC CTGATTAAGC ATGATTGAAA TGGTAGCAAA 480

TATACCACCT AAAGCTAAGC TACCTGTATC TCCCATAAAC ACTTTAGCAG GGTTAATGTT 540

ATATGGTAAA AATCCTAAAA GTGCAAACAA CATAATGATA CAGAAAATAC CAATTGCCGT 600

TGCTAATCCA TCTAAACCAT CTGTTAAATT TACTGCATTA GAAAAACCTA CTTGCCAAAA 720

AACAATGAAA ATAACATATG CAAATGATAG TGGGATTGCT ACATTCGTAA ATGGAATATG 780

TATGCTCGTA GAAAAATTCA CCAAATGAAA CACATTACTT AAAACAAAGA ATATAATCGC 840

AATACCAATT TGCGCCAAAA ACTTCTGTTT ACTTGTTAAA CCTTGGTTAT TCTTTTTAAC 900

AACAATAATA TAATCATCTA TAAAACCAAT TAACCCAAAA CCAATCGTCA CAAATAATAA 960

CAGTATGATT GGATTAGCTT GATCTACAAA TATAATAGCC ACCAAAGACG TTATCACAAT 1020

ACTTAATAGA AATGTTAGTC CACCCATCGT TGGTGTACCA GTCTTCTTCA TATGGCTTTG 1080

TGGACCTTCT TCTCGAATAC TTTGACCAAA TTTCATCCTT TTTAATGTAG GTATTAAAAC 1140

AGGTACCAAA ACAAATGTAA TCACTAGCGC TAATAACGCA TATACAAAAA TCATAACTAT 1200

CTCCTCTTCT TAATCCAGAC TTTTTTAACC ACTAATATAT TATCAATTTT TCAATTAAAT 1260

AAACAAAGTT GTAATCAAAA TTTATAATTT TTCTTTTTTA CGGCATAAGA GGCCAGTATA 1320

AAAAGTTTGC CTATAACAAA CAAGTTAATC TGACCTCGTC TACCTTAAAA TTCTCTATCA 1380

ACACTTATTT ATAAAGATTA AATGAAGATG TTGTTTTCTA TCACAGCATT ACTTTAGTAA 1440

AAACAAATAG TGACAATACA TCCTAATTTA ATGTAGCCAT TCTTGTTAGT CCGACTTATC 1500

CTTGTCAGTT TTACTGTCAG ATTTCnTCTT ATCATCTGAA TTTGAATCAG AATTATTCGT 1560

CGAATTGCTG TCTACATTCT CTGGATGGAA AATTCTACGT 1600

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

ATTGCCTTTG TTTTAATTTT AAATCAAAAT mGCCTATGAA AGATTTAAAT CAATTAATTT 60

CTATAATATT ATCATTTTTA AAGCATATCA TTGTTTAGTT TTTTTATAAT TGGATAAATA 120

CTAATAGTTA CTTTATAAAA CATTACATAG AGAAAGGTTA AGGAGTGCAC ATGTCGAAAA 180

AGGATCACTC TTCTTCAAAA TACCTTAATT CTGTTAAGGA AGCGCAAGAG GAGTCAAAAA 240

AGAAAAATAA AAGTAATCCC AAAATTGATG TTGATCGTAC ATATATTGAA CCTCAACAAT 300

TCCAATCTAA GAAACCTAAA AAAGATGATC AGGTTTTCTT CTTATCAAGA TTAAATAAAC 360

CTGCAAAATA TAAGAAAGAC TCTAATTTCT TATCATATCT CATCTATCGC ATAGGAAAAG 420

TGTTGCTTTT CCTATTAACA TTATTACCAT TTTTCAATAT TAAGCAGAGT CAAATTACTA 540

ATATGTTAAG CAATGCACCC GCTGAAACAT CTACTCTAAT TAAGAGTGTA ATTGGTGATA 600

TAACTCAAAA CTCCAGTGGT GGCTTATTAT CTATCGGTTT GATTTTAGCA ATTTGGTCAG 660

CTTCAAATGG AATGACTGCA ATTATGAATT CTTTCAATGT TGCTTACGAT GTAGAAGATA 720

GCCGTAATGG AATCGTATTA AAACTACTAA GTGTTGTCTT CACTGTAGTT ATGGGCGTTG 780

TGTTTGTAGT TGCTCTAGCA TTACCAACGC TTGGTTCTGT AATTAGTCAT TTCCTATTCG 840

GTCCACTTGG aTTTGACGAA CAAGTGAAAT GGATTTTTAA CCTTATTAGA ATTGTGTTAC 900

CAATCATTAT TATATTTATC ATATTTATCG TGTTATATTC GGTTGCACCT AACGTTAAAA 960

CGAAGCTTAA GTCAGTATTA CCAGGTGCAG TATTTACTTC AATTATTTGG TTAGCTGGTT 1020

CATTTGGTTT TGGTTGGTAT ATTTCAAATT TTGGTAACTA TTCTAAAACA TATGGCAGTA 1080

TCGCGGGTAT CATCATTTTG TTACTATGGT TATATATCAC AAGTTTTATT ATAATTGTCG 1140

GnGCTGAAAT CAATGCAATC ATTCATCAGC GTAGTGTAAT TAAAGG 1186

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7872 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

TCTTGAGCCA TCTTTTGAGC TAACTGACTA GATTGATACC CAAAAATCAT AGTTACCAAC 60

ATAAACTTTA ATTTTACCGA AGTCTAAATC AGCGATATGA GTACATACAT TATTTAAGAA 120

ATGACGGTCA TGCGATACTA CGATAACAGT ATTATCAAAG TTAATTAAGA AATCTTCTAA 180

CCAACTGATT GCTGGAATAT CGAGACCGTT AGTAGGCTCA TCCAGTAATA GTACGTCTGG 240

TTCACCGAAT AAACTTTGCG CTAATAATAC TTTAATTTTT TGGTTGTTTT CTAATTCAGC 300

CATTTTTTTA TCGTGTAAAG TTGGATCGAT ACCTAAACCA GATAAAAGGT TAGCAGCATC 360

AGCTTCAGCA TTCCAACCAT TCATTTCTGC AAATTCACCT TCAAGTTCAG CAGCACGGAT 420

ACCATCTTCA TCACTGAAAT CTGGCTTCAT ATAGATTTCA TCTTTTTCTT TCATAACCTC 480

ATAAAGACGT TCGTGACCTT TAATTACAAC ATCAAGCACG CGTTCATCTT CATAAGCATA 540

GTGGTCCTGT TTTAAAACAG CTAGACGTTC ATTTTTCCCT AATGAAACAT GTCCTGTTTG 600

AGAATCTAAT TCACCAGATA ATATTTTTAA GAATGTTGAT TTACCTGCAC CATTCGCACC 660

ATCTCCAAAA CGTAAACTCA CATCAGTTAC TTGTAACATG CATTTTCTCC TTTTTTTCAT 780

TCGATATTCT AACGGAAGAA TTATATCATA TTATCGTCAC AGTTTCGACC TCATATAAGT 840

TGTAATGATA GAATGACTCA CACATGTTAT AATAATAAAG AATACAAGAA TCGAAGGAGA 900

ATAACATGGC ATTAGACAAA GATATAGTAG GTTCTATAGA ATTCCTTGAA GTAGTAGGGT 960

TACAAGGTTC AACTTACCTT TTAAAAGGAC CAAACGGTGA AAACGTAAAG TTAAACCAAT 1020

CAGAAATGAA CGATGATGAT GAATTAGAAG TAGGTGAAGA ATATAGTTTC TTCATTTATC 1080

CAAACCGTTC AGGTGAATTA TTTGCAACTC AAAATATGCC TGATATTACG AAAGATAAAT 1140

ATGACTTTGC TAAAGTACTT AAAACGGATC GCGATGGGGC ACGTATAGAT GTTGGATTAC 1200

CCCGTGAAGT GTTAGTACCA TGGGAAGATT TACCAAAAGT GAAATCACTA TGGCCACAAC 1260

CTGGTGATTA TTTGCTAGTT ACATTACGAA TTGACCGTGA GAATCATATG TATGGACGTT 1320

TAGCGAGTGA ATCTGTTGTA GAAAATATGT TTACACCTGT ACACGACGAT AATTTAAAAA 1380

ACGAaGTCAT TGAAGCCAAA CCTTACCGCG TATTACGAAT TGGTAGCTTT TTATTAAGCG 1440

AATCAGGTTA CAAAATTTTC GTACATGAAT CAGAACGTAA AGCTGAACCA AGATTAGGTG 1500

AATCTGTTCA AGTTAGAATT ATCGGGCATA ATGATAAAGG TGAGTTAAAT GGTTCATTTT 1560

TACCACTTGC ACATGAACGT TTAGACGATG ACGGCCAAGT CATCTTTGAT TTACTAGTTG 1620

AATATGATGG TGAATTACCA TTCTGGGACA AATCAAGCCC TGAAGCGATT AAAGAAGTAT 1680

TCAATATGAG TAAAGGTTCA TTCAAACGTG CAATCGGTCA CTTATATAAA CAGAAGATTA 1740

TTAATATAGA AACAGGTAAA ATCGCTTTAA CTAAAAAAGG TTGGAGTCGA ATGGACTCAA 1800

AAGAATAATC ATTTTTACAC GTGTCGTAGG ATGCGTGTTT TTTTTATTCA ATATTAAATC 1860

GGACAGATGA AGTAGTTTTT TAAACATTCC TTTCAAAGTA AAAAATTAAA TAATTCAAAC 1920

GAATAGGCTG GGaCATTAAG TTCTTAGGCA ATGTAAAAAA GCTGATTTCT ATTAATTATT 1980

TGATGGAAAT CAGCTTTTTT GATATGTATT TTATAATGTA CAGCTCGTTG AGCTGCTATT 2040

TTCCTTATAT TAAGTGCCAT TAATACAAAA CCTAGCTCTC GTTTAACTTT ATTTATTCCT 2100

CGAACTGACA TTCGAGTGAA aCCCAAAATA GCCTTCATAA ATCCAAAAAC AGGCTCTACA 2160

TAAATTTTTC TATGACTATA GATTTTTTTC GTTTCTGGTT CAGAAAGCTT TTGaTTAATT 2220

TGGGCTTTAA TGTATTTCAA AGTAAAATTA CATGTTAATA CGTAGTATTA ATGGCGAGAC 2280

TCCTGAGGGA GCAGTGCCAG TCGAAGACAG GGGCCCCAAC ACAGAAGcTG ACATATAGTC 2340

AGCTTACAAC AATGTGCCGG TTGGGGTGGC TGAGACGGCA CCCTAGGAAG GGACCCGTCA 2400

TCAAAAATTC TATTTATAGA ATTTTACAGT AATGTGACAG ACGGGCAAAG CGAAgCCATT 2460

CTTACTGCTG TTTTTTTAGG GATTTATGTC CCAGCCATTT TTGTATTCAT ATTTAAATTT 2580

CGATAATTTT TCAGGAAGCA TTTTAATTTT ACTAATGAAG CAATATTTTT TAGATTAACA 2640

AAAATTAATA TTTACATTTT CTTAACAATT TTTTATGTAA CATTTACAGT TTCTAAAAAT 2700

GAGGTTAATA ATTCAAGGTT AAGATAAAGA TGTAATCAAT ACAAATACTA TTTGTTGTTC 2760

ATACAGGGAG GATATTTCAA TGAAAAAATG GCAATTTGTT GGTACTACAG CTTTAGGTGC 2820

AACACTATTA TTAGGTGCTT GTGGTGGCGG TAATGGTGGC AGTGGTAATA GTGATTTAAA 2880

AGGGGAAGCT AAAGGTGATG GCTCATCAAC AGTAGCACCA ATTGTGGAGA AATTAAATGA 2940

AAAATGGGCT CAAGATCACT CGGATGCTAA AATCTCAGCA GGACAAGCTG GTACAGGTGC 3000

TGGTTTCCAA AAATTCATTG CAGGAGATAT CGACTTCGCT GATGCTTCTA GACCAATTAA 3060

AGATGAAGAG AAGCAAAAAT TACAAGATAA GAATATCAAA TACAAAGAAT TCAAAATTGC 3120

GCAAGATGGT GTAACGGTTG CTGTAAATAA AGAAAATGAT TTTGTAGATG AATTAGACAA 3180

ACAGCAATTA AAAGCAATTT ATTCTGGAAA AGCTAAAACA TGGAAAGATG TTAATAGTAA 3240

ATGGCCAGAT AAAAAAATAA ATGCTGTATC ACCAAACTCA AGTCATGGTA CTTATGACTT 3300

CTTTGAAAAT GAAGTAATGA ATAAAGAAGA TATTAAAGCA GAAAAAAATG CTGATACAAA 3360

TGCTATCGTT TCTTCTGTAA CGAAAAACAA AGAGGGAATC GGATACTTTG GATATAACTT 3420

CTACGTACAA AATAAAGATA AATTAAAAGA AGTTAAAATC AAAGATGAAA ATGGTAAAGC 3480

AACAGAGCCT ACGAAAAAAA CAATTcAAGA TAACTCTTAT GCATTAAGTA GACCATTATT 3540

CATTTATGTA AATGAAAAAG CATTGAAAGA TAATAAAGTA ATGTCAGAAT TTATCAAATT 3600

CGTCTTAGAA GATAAAGGTA AAGCAGCTGA AGAAGCTGGA TATGTAGCAG CACCAGAGAA 3660

AACATACAAA TCACAATTAG ATGATTTAAA AGCATTTATT GATAAAAATC AAAAATCAGA 3720

CGACAAGAAA TCTGATGATA AAAAGTCTGA AGACAAAAAA TAATAAGACG CAATTTCAAA 3780

TGTGTCTTGA AACATGATTT TGATGGTGAA TCATTATTTA GAGTACAAAG CTTGATTTAT 3840

CGAGACGCTG ATTTTGACAT TCAGTTAGTC TAcAAGCTTA TCAACTTAAA ATAGTGGTTC 3900

ATCATTATTT TACAAATCTA ATTATTTTGG GAGTAATAGA AAGAGGTTTG ATTATGACTT 3960

CATCTACTAA TGTTAAAGCT TTAATCGAAA AAAATAATAA TAAAAAAGGA AAGCATAATG 4020

ACAAAATTAT ACCAGTTATT TTAGCCGCAA TTTCAGCGAT TTCCATTTTA ACAACACTAG 4080

GTATATTAAT CACATTGCTT TTAGAAACCA TCACTTTTTT CACCAGAATT CCAATAACTG 4140

AATTTCTATT TTCTACTACT TGGAATCCTA CCGGTTCAGA CCCTAAGTTT GGTATCTGGG 4200

CATTGATAAT AGGGACTTTA AAAATCACAG TTATTGCGAC TATATTTGCA GTTCCAGTCG 4260

AACCGATATT AGAAATTTTA GCAGGAATAC CAACAATTGT GTTTGGTTTC TTTGCATTAA 4380

CCTTTGTTAC ACCAGTATTA AGATCTTTCA TACCAGGTCT TGGAGAGTTT AATGCTATAA 4440

GTCCCGGCTT AGTTGTCGGT ATTATGATTG TCCCTCTCAT CACAAGTTTG AGTGAGGaTG 4500

CAATGGCATC TGTACCAAAT AAAATTCGAG AAGGTGCCTA TGGACTTGGA GCAACTAAAT 4560

TAGAAGTAGC AACTAAAGTC GTACTTCCCG CAGCAACATC AGGTATTGTA GCTTCAATCG 4620

TTCTCGCGAT TTCAAGAGCA ATTGGAGAAA CGATGATTGT ATCATTAGCG GCAGGTAGTT 4680

CGCCAACAGC TTCATTAAGT TTAACAAGTT CGATTCAAAC AATGACTGGA TATATTGTTG 4740

AGATAGCGAC AGGTGATGCA ACATTTGGAT CAAATATTTA TTACAGTATT TATGCTGTAG 4800

GGTTCACACT ATTTATCTTT ACCTTAATCA TGAATTTACT TTCTCAGTGG ATTTCTAAGC 4860

GTTTTAGGGA GGAGTATTAA TATGGAAACG ACAGATAATA ATAGACAATC ACTCGTCGAT 4920

CAACAACTTG TCCAAAAACA TTTATCATCC AGAACGGTTA AAAATAAAGT GTTCAAACTC 4980

ATATTTTTAG CATGTACATT ATTAGGACTT GTCGTACTTA TTGCGTTGTT AACTCAAACA 5040

TTGATTAAAG GGGTAAGTCA TTTAAATTTA CAGTTTTTCA CTAATTTTTC TTCTTCAACA 5100

CCATCTATGG cTGGCGTTAA AGGCGCGTTA ATCGGTTCAC TTTGGTTAAT GTTAAGTATC 5160

ATTCCATTAT CAATCATCCT AGGAATAGGT ACAGCTATAT ACTTAGAAGA ATATGCGAAA 5220

AACAACAAAT TTACTCAGTT TGTTAAAATC AGTATTTCCA ATTTAGCTGG TGTACCATCA 5280

GTTGTATTTG GGTTATTAGG TTATACTTTG TTCGTTGGTG GTGCAGGGAT TGAAGCCTTG 5340

AAAATGGGTA ACAGTATATT GGCAGCAGCG CTAACAATGA CCTTACTGAT ATTACCAATT 5400

ATTATTGTTT CAAGTCAGGA AGCAATTAGA GCTGTACCTA ACTCAGTACG CGAACTTcTT 5460

ACGGCTTAGG TGCTAATAAA TGGCAAACGA TAAGACGTGT TGTCTTACCA GCAGCGTTAC 5520

CTGGTATTTT AACTGGATTC ATTTTGTCTC TTTCAAGAGC ACTGGGAGAA ACAGCGCCAC 5580

TTGTGCTAAT CGGTATACCG ACTATATTAT TGGCAACACC TAGAAGTATA TTGGATCAAT 5640

TTTCAGCATT ACCTATCCAA ATATTTACTT GGGCGAAAAT GCCTCAAGAA GAATTCCAGA 5700

ATGTTGCATC GGCAGGCATT ATCGTTTTAC TAGTTATCTT AATCTTAATG AATGGCGTTG 5760

CGATTATTTT ACGTAACAAA TTTAGTAAAA AATTCTAATT TAAACAATCA ATCTCATTTA 5820

TCTATTAAAA AGGGAGTTTT AAATATGGCG CAAACACTTG CACAAACTAA ACAAATATCT 5880

CAAAGTCATA CGTTTGATGT CTCACAAAGT CATCATAAAA CACCAGATGA TACAAACTCA 5940

CATTCTGTTA TATATTCAAC ACAAAATTTA GACTTATGGT ATGGCGAAAA TCATGCATTA 6000

CAAAATATTA ATTTAGATAT TTATGAAAAC CAAATTACTG CCATTATAGG TCCATCTGGT 6060

AAAACAGCTG GTAAAATATT ATATCGAGAT CAAGACATTT TTGATCAAAA ATATTCTAAA 6180

GAACAATTAC GTACAAATGT GGGCATGGTC TTTCAACAAC CTAATCCATT TCCAAAATCA 6240

ATATACGATA ATATTACTTA CGGTCCAAAG ATTCACGGTA TTAAAAATAA AAAAGTTCTT 6300

GATGAAATCG TTGAGAAATC ATTACGTGGC GCTGCAATTT GGGATGAATT AAAGGATAGG 6360

TtGCACACAA ATGCATATAG TTTATCCGGT GGGCAACAAC AACGTGTTTG TATCGCGCGT 6420

TGTTTAGCAA TTGAACCTGA AGTCATTTTA ATGGATGAAC CGACATCAGC ATTAGATCCA 6480

ATCTCAACAT TAAGAGTAGA AGAGTTGGTT CAAGAACTAA AAGAAAAGTA TACAATTATT 6540

ATGGTtACAC ATAATATGCA ACAAGCAGCT CGTGTATCAG ATAAAACTGC ATTTTTCTTA 6600

AATGGTTATG TCAATGAATA TGATGATACT GATAAAATTT TCTCTAACCC ATCAAACAAG 6660

AAAACAGAAG ATTATATTTC AGGAAGGTTT GGTTGATATA TAATGGCAAT AATTAGACAA 6720

CGATATCAGG AGCAACTTGA TGATTTAATA AAAGAATTAC GTCGGTTAGG TGCaAATGTC 6780

TATGTGAGTA TTGaAAATGG TATAAAAtCA TTAAGTATTG aCGATAGAGG cTTTGCACGA 6840

CAAACAGTTA AAAACGATAA ACATATCAAT CAATTAAATT ATGATATTAA TGAGCGAGTT 6900

ATCATGTTAA TTACAAAGCA ACAGCCCATT GCGAGTGATT TGCGTATGAT GATTTCTTCA 6960

TTAAAAATCG CCTCCGATTT AGAAAGAATA GGAGATAATG CCTCGAGTAT TGCCAATATT 7020

CGATTGCGTA CAAAGATTAC AGATGATTAT GTGTTAACCC GTTTAAAGAC AATGGGTAAA 7080

TTAGCTATGT TAATGTTAAA GGACTTAGAT CAAGCATTTA AAAAGAAAGA TACCGTATTA 7140

ATAAGAGAAA TAATTGAGCG TGATGAAGAT ATCGATGACT TATATAGTCA TATTATTAAC 7200

GCAACGTATC TTATTGATAA CGtCCATTTG TCGCTGCACA AGCTCATTTA GCAGCAAGAC 7260

ATTTAGAACG TATTGGTGAT CATATTATTA ACATCGCTGA AAGTGTTTAT TTTTATTTAA 7320

CAGGTACACA TTACGAACAA TAACTTAAAG TTATTACTAT AAAATCCCTT ACGATAAATA 7380

TATATTTCTA TTATTCATAA ACCCTCAAAA AAACCAAGAT TCTCACAATT AGTAATGTGA 7440

AAATCTTGGT TTATATTGTT CTACTATAAA TTGTCTCGCA TCTTAGTTAT TTGCTTGCTC 7500

AATTTCATCT GTTAATTTTT CAACTTCATC GACTAAATCA GAAATATATT GAATTGTAGA 7560

TTTAAGTGGC TGTTCTGTAG TAATGTCTAC ACCTGCAATG TTTGCAAGTT CGACAGGTGA 7620

TACACTACCA CCTTTTTTCA ATGTTTCTAA CCAAGCATCA ACAGCTGGTT GGCCTTCATT 7680

TTTAATCTTT TGAGAAACGA CAGTTCCGAT TGTTAAGCCA GCAGAATACG TATACGAATA 7740

TAATCCCATA TAGTAATGAG GTTGACGCAT CCATGTTAAT TCAGCACCCT CAGTCATGTC 7800

TACTGCATCT CCAAAAAATT GTTTATAAAC ATTTAGCATT ATTTCATTTA ATGTnCGGCG 7860

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 798 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

TTTTTTCTTT TCTTCATTTG AAAATTGATC ATTCAGCAAT ATAAGCGTAT TTGTTAATGA 60

TTTAGGTGTT CCAATTTCAT AATCCCACCA ATTTAAGTTG GTATTCTTGC CAGTTGTTTT 120

AGTAAAATTC TCACTTAATT CTTTTACTTT TTTATCTGGT TCTTTTCCAT ATGCATTTTT 180

ATGCAGCCAC TCAAGGGCAT CTTTCACTTT CTTCTTATTT TCGTCAGTAT TTAAAGTGGT 240

TTTAGGATTC CTCATCGCTT CTGCGATTTT CTCAATATTA CGATAGGTAC GAGTCATATG 300

AGAAGAATTA GTTTCAAGGG TTTCCGCTCC TGACCACAAG TATTTCCTAC CACTTTCAGT 360

TTTCATTTCC TTGAGTAAAT TCGTCGCCTC TTTCTCTGTA GCATCAAACT TCTTCTTCAT 420

ATCTGGATTA TTCTCATCAT ACTTATCATA ACCATAGTTA ACGTCCAGCC ATGTGTTCCT 480

CAATTTTTCA TAATCTGGCG TTTGAACATT CGTATCAGCC ACAGCGATTT GATGTTTATC 540

AACACTTCTG AATTCACCAC CATTCAAAGT AATCACACCA GCCATTAATA ACGTAATGGT 600

GGATAATTTT TGCCATTTCT TTATTCTATA TGTCATTGaC ATGTCTCCTT TTTGTGTTGC 660

GCGTGCGCAA TGAATATTAT GATTAAATAA TGATTCAATT TTTCAAAATT CGTTAACGTA 720

TACAAATGAC TGTCTACTGT CAAACAATCC ACAAAGAATG TTGATGtCAT ATaAACAATC 780

GATCACCCAA ATTTTCCG 798

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

TACAGGTTTT ACTATAATGG ATGGTATTTT GGCTAAACGA CATTGGTTTA GTCTTCTTTT 60

TTTnACTTCC TAnATTTACA ATGGTATAAA TAATAATGCT ATATTTAGAA TGATGAGTAT 120

ACTTACTGAA ACTAAATTAA AAGTGTCTGG TTCTTTACTA AAGATAGCTG CTATCCTTGC 180

AATACAAGTT CCAATGAGCG CAATTAAAAG TACTAACCCA ACGATGAAAC TCTGTTTGTC 300

ACTTAACTCA AAGAAACTAT AGATAGGATA TTTTTTAATA ATCAAGCCAC CTAAAATCAT 360

CCATAAAAAT ACGATAATTC CATAAGTCAC ATTTATAACA TACGTTATTT TTTGGTCACC 420

AAATCGGACT AATGTATTTC GTAGAATCAG CATACCAATG ACAACACCTA AAATAACGAT 480

ACTAGCTATA TAAAGTAAAA ATGCAATTGT CACATCAAAT GTACCCAAAT CTAAAAACCT 540

AGGAATTAyA AyGACTGCTA AAATAAAAGC GAAGyACAAA GTAATATAkT TATACAAACC 600

GGTAGTAAGA CTTATCTCAG GTGATAATTG ATCAGCCATT GACTTAATCG GTGTATTAAT 660

AATTGAACTT GTATCTTCGT TATTTTTTTC AGCCATAGTT AAATGATCTT CGAGCTCTTC 720

CAATAACTCT TCTACTTCTG CTTCAGTCTT ACCTCTAAAT AACAATTCAA CACGTAATTT 780

TTCTAAAAAA TCTTGAGATT GTTTACTTAA CATCGTTTTC CCCTCCAAAC AAGTTAATCA 840

TCCCTTTATT CAAAACTTGC CATTTCGATT TAAATACTTT TAGTTCCTTT AAACCTGAAT 900

CGGTAATCGT ATAGTATTTC CGCCTCGGGC CGCCATTACT AGATTTTTTT ATTGTCGTAT 960

CAACGTATCC TTTTTTGTTT AAACGCATTA AAACTGGATA AATACTACCC TCACTTATCT 1020

CTGGAAACTC TTGATTCTTA AGTTTCGTCA TAATTTCATA TCCATACGTT TCGCCTTGGG 1080

CAATGAGACC TAATATCGCC CCATCTAAGA GACCTTTCAT AATCTGATCT GACACTGACA 1140

TTTTAATCAC CTACTATCTT ACATAATAAG ATAGTACATT GAGAACTTTT CGTCAACTAT 1200

CTTTTATTGT AAGGTAGTTG TTGTACACAT TCCTTAAATG ACTAACAACT TTGTTAATAG 1260

GGTAATACTT ACGGAAGTAT ATTTTATTTA TGGGGGAGGA ATTAATAATG ACTACAAAAA 1320

CAGTATTTGA TGTCATTGAT ATGGGGTTAG GATATTTAGT AAATGTGTAT GATGCTTGGA 1380

AAGTTGAAAA GGTACTTGAT GATTATCATA AGCCTTTTTC TAATACCATT CATTGGCAAT 1440

TTGGtCATGT ATTAACAATT TTTGAATCGG CCTTAGCTGT TGCTGGTAAA GAGAATATTG 1500

ATTTAAATAT CTATAGACCT TTATTCGGAA ATGGTTCGTC TCCAGATGAA TGGAAGGATG 1560

AAGTACCGAG TATTGAAAGG ATTTTAGAAG GTCTCCAAAC TTTACCTGAA CGTGCACGAA 1620

ATCTAACTGA AGATGATTTA GCAATTGAAT TGAAACAGCC AATTGTCGGT TGTAATAACT 1680

TAGAAGAGTT ATTAGTATTA AATGCCATTC ACATCCCACT TCATGCTGGT AAAATTGAAG 1740

AGATGTCTCG TATATTAAAA AATTTAAAAT AAATATGTGC TTATTAACCG TTAACAACAC 1800

GTTAACGGgT TTTTTATTTG TTTAAAAGGT CACTTTTTTG AATTTAATAA ACACCATCTA 1860

TACCAGTTCT TCACCGATTC TCGAAAAATA ATTATATTAA TGATTTCGTT AATTTAATTT 1920

TATATTTAAT TATTACTGTA CATCTTTTGT AGTTAGCTTT ATTCTTAAAT TGAAATATGT 1980

TACTCCCTAT CGTTGTAGGT CTCCTTATTT GGGCACTTAC ACCTTTTAAA CCGGATGCTG 2100

TGGATCCAAC AGCATGGTAT ATGTTCGCAA TATTCGTCGC GACAATCATT GCTTGTATTA 2160

CACAACCGAT GCCAATTGGG GCCGTCTCTA TAATTGGATT TACAATCATG GTACTCGTTG 2220

GCATTGTTGA CATGAAAACG GCTGTCGCTG GTTTTGGTAA TAATAGCATT TGGTTAATTG 2280

CTATGGCATT TTTCATTTCG AGAGGATTTG TGAAAACAGG TCTTGGTAGA CGTATCGCAC 2340

TTCATTTCGT CAAATTATTT GGTAAAAAAA CATTAGGATT AGCATATTCT ATCGTCGGTG 2400

TAGATTTAAT TCTAGCGCCT GCTACACCAA GTAATACCGC GCGTGCTGGT GGAATCATGT 2460

TCCCAATTAT CAAATCACTT TCTGAATCAT TTGGTTCGAA ACCGAAAGAC GGATCAGCAC 2520

GCAAAATGGG TGCATTTCTT GTTTTCACAG AATTCCAAGG TAATTTAATT ACTGCGGCTA 2580

TGTTTTTAAC TGCAATGGCC GGTAACCCCC TTGCACAAAA TTTAGCATCT AGCACATCTA 2640

ATGTTCACAT TACATGGATG AATTGGTTTC TAGCTGCTTT AGTTCCTGGA CTTGTTTCCT 2700

TAATTGTTGT ACCTTTTATT ATTTATAAAA TTTATCCACC AACTGTTAAA GAAACACCAA 2760

ATGCTAAGAG TTGGGCTGAA AATGAATTAG CGACTATGGG TAAAATCGCT TTAGCTGAAA 2820

AATTTATGAT TGGTATTTTT GTCGTTGCGT TAACACTATG GATTGTCGGA AGTTTCATTC 2880

ATATTGATGC AACTTTAACG GCCTTTATTG CGCTAgcATT gTTATTATTG ACAGGCGTCT 2940

TAACATGGCA AGACATTTTA AACGAAACAG GTGCTTGGAA CACATTAGTA TGGTTCTCAG 3000

TATTAGTGTT AATGGCCGAC CAATTAAACA AGCTTGGATT TATTCCTTGG TTAAGTAAAT 3060

CCATTGCTAC AAGTCTTGGT GGCTTAAGCT GGCCTATAGT CCTGGTCATT TTAATATTGT 3120

TCTACTTCTA TTCACATTAC TTATTTGCAA GTTCTACAGC ACATATCAGT GCGATGTATG 3180

CAGCATTACT AGgCGTTGCC ATCGCAGCCG GTGCACCACC ATTATTCAGT GCATTAATGT 3240

TAGGTTTCTT CGGTAACCTA TTAGCTTCAA CAACACACTA TAGTAGTGGT CCAGCGCCGA 3300

TTCTATTCTC TTCAGGTTAC GTGACTCAAA AACGTTGGTG GACAATGAAC TTAATATTAG 3360

GTTTCGTCTA CTTTATTATC TGGATTGGTT TAGGATCACT TTGGATGAAA GTAATTGGTA 3420

TATTTTAAAA TATTTAAATT AGCGCTCGAA TCTCATTGAT TTGGGCGCTT TTTAATTTGT 3480

ATTTAAAATC AACCTTTGCT AAATCAAGAC TCCCTTTTTA AAATACGTTT ATCCTTTAAA 3540

TCATTGCGTG CTTCACTGAA AATTTGTATA AAGATTTAAG TCATTACGTA ACATCACATA 3600

AAATACATTT CTATACTATT CCGCTTCATT GATTAACATT ACGTATGCCC TCATAAATCA 3660

TCATACAAAA AACACCTTCG TTTAAATTCA TTTTAATTGC GAATTCAACG AAAGTGCCTT 3720

ATTTCATATT TAATGTTTCA AATTTATACG TCTGTCACTG TTACTGCACA CATACCTCAG 3780

TTATAGGGTT TTTGCGACCG GATGTTTCTT CAATTTAATG TATTGAGAAA GACTATATAA 3900

CACAATACCT GTCCAAATAA ATATAAACGT AATTAATTGA TCTATACTAA AAGGCTCTTT 3960

GAAAACAAAT ATGCCGAGTA CAAACATTAT TGTTGGTCCA ACGTATTGAA TAAATCCTAT 4020

TAGCGAAAGT GGAATACGTT TTGCCCCGGC TGAGAATAGG ATTAGTGGTA TTGCCGTAAT 4080

AGCACCAGAA AATAACAACC AAAATGATGA CATGTTCAAT CCAAATGACA TCTGATGTTG 4140

CTGCCATAAA TAAATAACGT ATATTAGTCC AGCAGGTGCG GTAACAATAC ATTCAATCGT 4200

AATACTGCTG ATGGCATCAA TATGTACTAC TTTTTTCAAT AATCCGTATG TACCAAAGGA 4260

TAACGCTAAT ATAATAGAGA CGATTGGGAA TTCTCCAATC TTGAGCGTCA TATATAATAC 4320

ACCGATGAAT GCGAATAAAA TGGCTAGCCA TTCAAATTTA TTGAATCTTT CTTTTAAAAA 4380

GATAAGTGCG AGCAAAATGC TAACAAGTGG ATTTATATAA TAACCTAAAC TTGTTTGTAG 4440

GACGTGACCG TTCGTTACAG CCCAAATAAA TGTACCCCAA TTTAATGTAA TGACATAGCC 4500

TGCTACGACA ATCGCTAATA GCTGAATGGG CTTGCCTAAC AATTGATTCA TATCTCGTTG 4560

AAATGCATTG CGTTGTTTTT GTCCAACCGC GAGTATGAAA ATCATGAATA TTGCTGAAAA 4620

TATAATACGA AAGGCTAAAA TTTCAAATGC GCCTATTGCA TCAACGAACT GCCAATATAT 4680

AGGTAGTATT CCCCACAGAA TGTATGCACT GAGTGCTAAA AATATGCCTT TTTTATACTC 4740

TGAATTCACC TTCAAACCTC CTTACTTTCC TAATTTTTAA TTTACTGCAT ACGCTCACTT 4800

GGTTATGCTA ATATAACGAT TTTACTAATA ATATTTCGAT AAAGATATCA TTTTGTTTAT 4860

ATTTCCCACA TTTATTCACC AACCACTAAA CAATATTAAT TTTATAAATA ATTCTGTACA 4920

AATCAGGGTA TATTGCCAGA AAGACTACCA TACAACATAA AGGATGGATA CAAATGACTT 4980

TACCTAAAAT TGGAAAGCCT GCAACACGCG CGCTAAATTC ACAAGGTATA TACACATTAG 5040

AAGCAGTATC ACAATATACG AAGTCATCTC TAATGGAGAT GCATGGCGTT GGTCCTAAAG 5100

CTATATCAAT ATTGGAACAA GCTTTATTTC AG 5132

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

AAGTAAATTA TATTATGAAT TTGCCTGTCA ATTTCTTAAA GACATTCTTA CCGGAACTAA 60

TAGAAGCAAT TAATAATGCy mAAGAAAAGA CAGCTAATAA TACCGGCTTA AAATTAATAT 180

TTGCAATTAA TTATGGTGGC AGAGCAGAAC TTGTTCATAG TATTAAAAAT ATGTTTGACG 240

AGCTTCATCA ACAAGGTTTA AATAGTGATA TCATAGATGA AACATATATA AACAATCATT 300

TAATGACAAA AGACTATCCT GATCCAGAGT TGTTAATTCG TACTTCAGGA GAACAAAGAA 360

TAAGTAATTT CTTGATTTGG CAAGTTTCGT ATAGTGAATT TATCTTTAAT CAAAAATTAT 420

GGCCTGACTT TGACGAAGAT GAATTAATTA AATGTATAAA AATTTATCAG TCACGTCAAA 480

GACGCTTTGG CGGATTGAGT GAGGAGTAGT ATAGTATGAA AGTTAGAACG CTGACAGCTA 540

TTATTGCCTT AATCGTATTC TTGCCTATCT TGTTAAAAGG CGGCCTTGTG TTAATGATAT 600

TTGCTAATAT ATTAGCATTG ATTGCATTAA AAGAATTGTT GAATATGAAT ATGATTAAAT 660

TTGTTTCAGT TCCTGGTTTA ATTAGTGCAG TTGGTCTTAT CATCATTATG TTGCCACAAC 720

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TATTAAGTTA TACTGTCTTA TCTAAAAACA GATTTAGTTT TATGGATGCT GCATTTTGCT 840

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GAATCCTAAA AGAAAACGAA CAACGTATTT AACGCCACTT TCAGATAAAA TCGAAAAAAT 15900

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TCCTGAGATT AAATTTGATG GTATCGACCC ATTAGTTAAA CAAATGAACG ATGATAAATC 16560

GCGTGCTAAA TATTTATTAG CAGTTGATTT TGGTGATGAA GTAGCTTATA ATATCTAGAG 16620

TTGCGTATAG tTATATAAAC AATCTATACC ACACCTTTTT CTTAGTAGGT CGAATCTCCA 16680

ACGCCTAACT CGGATTAAGG AGTATTCAAA CATTTTAAGG AGGAAATTGA TTATGGCAAT 16740

TTCACAAGAA CGTAAAAACG AAATCATTAA AGAATACCGT GTACACGAAA CTGATACTGG 16800

TTCACCAGAA GTACAAATCG CTGTACTTAC TGCAGAAATC AACGCaGTAA ACGAACACTT 16860

ACGTACACAC AAAAAAGACC ACCATTCACG TCGTGGATTA TTAAAAATGG TAGGTCGTCG 16920

TAGcATTTaT TAAACTACTT ACGTaGTAAA GATATTCAAC GTTACCGTGA ATTAATTAAA 16980

TCACTTGGTA TCCGTCGTTA ATCTTAATAT AACGTCTTTG AGGTTGGGGC ATATTTATGT 17040

TCCAACCTTA ATTTATATTA AAAAAGCTTT TTACAAATAT TAACATTTAT TATATGTTAA 17100

GCTAATATTG AGTGAATAAT AAGGTTACAA TGAGATAAAG ATGATATAAG TACACCTAGA 17160

GTAATAATCA AGATATTAAA AATAAAGTAT GTTTTTTTAA AAAATATAAC TTATATTTAT 17220

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CAGACTCAAG CACTTTCAGT TTTAACATTA GGTGCTTTAG GCGATTATCA ATTAATTGAT 18480

GGTTTAGGAC CTGAAGAAGA AAAAAGATTC ATGCATCATT ACAACTTCCC GAATTTTTCA 18540

GTAGGTGAAA CTGGTCCAGT ACGTGCGCCA GGTCGTCGTG AAATTGGACA TGGTGCGTTA 18600

GGTGAAAGAG CATTAAAATA TATTATTCCT GATACTGCTG ATTTCCCATA TACAATTCGT 18660

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GAATTAAGTG cTTACGCGCC AAAAGTTGTA ACTATGACAA TTAAACCAGA TAAGATTAGA 19080

GATGTTATCG GACCTGGTGG TAAAAAAATT AACGAAATTA TTGATGAAAC AGGTGTTAAA 19140

TTAGATATTG AACAAGATGG TACTATCTTT ATTGGTGCTG TTGATCAAGC TATGATAAAT 19200

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GnCTGGCGCA CATATTATTC CAAATAACAA AAAGATTCAT GCTTCAAGTC ATGGTTGCAT 20820

GGAAGAATTA AAAATGATGA TTAATATTAT GAAACCTGAA TACTTTATTC CTGTACAAGG 20880

TGAATTTAAA ATGCAGATAG CACATGCGAA GCTAGCAGCT GAAGCAGGTG TTGCACCAGA 20940

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TAmaACTAGA CGAACGGCTG GTTCGATTGT ATTGCAAATT GCATTGCTAT TTGTATCACA 21960

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ATTATTATGC TCAAGTGTTA TTTTATTAAC AAACCATCAA CATCGTGAAG TTGCAAAAGT 22200

TGCACTGGAA AATATAAAAG CTTGGTTTGG TTCATTTAAT GAA 22243

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

TTATTAATnA TTAATATTTT TATTTTTAAA AATAAAGCGA GGAGCTATCA ATGGAACAAA 60

TTACTTCTGC ACAAAATAAT AGAATTAAAC AAGCGAACAA GCTAAAAmAG AAACGTGAGA 120

GGGATAAAAC TGGATTAGCT TTAATTGAAG GTGTGCATTT AATTGAAGAA GCTTATCAAA 180

GTGGAATTGT AATTACACAA TTATTTGCAA TTGAACCGGC AAGATTAGAT CAGCAAATTA 240

wCGCATACGC GCAAGAAGTT TTTgAAATAA ACATGAAAGT TGCTGAATCT TTATCAGGTA 300

CAGTGACACC ACAAGGGTTT TTCGCAATCA TTGAGAAGCC GCATTATGAT ATTTCTAAAG 360

CACAACAAGT ATTGCTCATC GATCGTGTTC AAGATCCTGG AAATTTAGGC ACATTAATTA 420

GAACTGCGGA TGCTGCTGGA ATGGATGCTG TAATAATGGA GAAGGGTACG ACAGATCCTT 480

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AAGATCTCGA TACGTTTATT ACTCAATTTA ATGGTCCTGT TTATGGTACA GCACTTGAAA 600

ACGCAGTGgC ATACAAAGAA GTTACTTCAA GTGATTCTTT TGCATTACTA TTAGGTAATG 660

AGGGAGAAGG TGTTAATCCT GAATTATTAG CACATACTAC ACAAAATTTA ATCATACCTA 720

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ATAAATAATT GTTTTAGGGA GAATAATCGT GACTGCAAGT TATTCCAATT ATTTAAAGTC 960

TTTTCACCTT TTTGGTTACT TAAAGAGATT TAAGTCGGAA AGACAATCCG TTATCAATAT 1020

TAAACAAGTG TATGCTTAGG CATAAATTTG GGTGGTACCA CGGAAATGAC TTTCGTCCCT 1080

TATTTTTTAA GAGGATGAAA GTCTTTTTTT AGTTAAACAA CAAATATGAT AAATAGAAAA 1140

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GTACGCATAC ATCACCAGTG CAGGCACGTa CGATGGAATC ACGTCATGGT CAAGGTCCAG 1740

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ATCAATTTAC ACAAATCGAA GGATTAGTTG TTGATAAAAA CGTTAAAATG AGTGATTTGA 1860

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GTAAAGGAAA AGGTTGTAAT GTGTGTAAAC ACACAGGATG GATTGAAATT TTAGGTGCTG 2040

GAATGGTACA TCCTAATGTA TTAGAAATGG CTGGTTTTGA TTCTTCAGAG TACTCTGGAT 2100

TTGCATTTGG TATGGGACCA GACCGTATTG CAATGTTGAA ATATGGTATA GAAGATATTC 2160

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CGTTTGTGGT GCACCGAACG TTGaTGCAGG ACAATATGTC ATTGTTGCTA AAGTAGGTGG 2520

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TATGATTTGT TCGTTACAAG AAATTGGTAT TTCAAGTAAC TATATACCGA AAAGTTTTGA 2640

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TCAAACAATT GATTTATTGA TGCCAATGAG TGAAGCGCAT GCGTCATTAC GTCAAAGTTT 3900

ATTACCACAT TTAATCGAAG CGGCATCATA TAATGTGGCA CGCAAAAATA AAGATGTAAA 3960

ATTATTTGAA ATCGGCAATG TCTTCTTTGC TAATGGAGAA GGTGAACTAC CAGATCAAGT 4020

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TGATAATGAT TTAAAACGTA CGTATGTTTT TGAGTTGAAT TTTGATGCAT TAATGGCTGT 4320

GTCGGTAGGT TACATTAATT ACCAGCCAAT TCCGAGATTC CCAGGCATGT CTCGTGACAT 4380

TGCATTAGAA GTAGATCAAA ATATTCCAGC AGCTGATTTA TTATCAACGA TTCATGCACA 4440

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CACAGTCAAC GGACCAAAGT AATCGCCACT TCCAGCCTCA TCACTACCAA TACAGTTAAA 5460

TTGrTCATAC ATTAaAGTTg TcCAgAAAAG AATTAGCCAT ATTTnCCTTT 5510

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9623 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

GnTTATACTT ATAAATTTTA CGGGGGTAAT ATAATACTtA TTTACCTGTA ATATATGATA 60

ATTCTTCAGC GGCAGCTGCG TTGATAGTTC TATGAGAAAT GATACCTAAT CCTTTAACAT 120

TGGATTCTGA AATAACGATA GAACCATCAC TGTTAACTTT TTCAACAAAT GCTACATGAC 180

CGTAATGTTG ATCTGCACCA AATTGTCCAG CCTCAAATAC AACAGCAGCA TGACGTTTTG 240

GTGTATGACT TACTTGATAA TCACGGTATT GAGCTCGATT ATTCCAATTA TGTGCATCAC 300

CTAAATCACC TGAGATAGAT GTACCAAATT GTTTCATACG GTTATATACG TACCAAGTAC 360

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CGTCAAACTG AGTTAATTGA TAGTGTTTAA TAATACTGTT TAATTTCTTA GCATAGTTTG 540

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ATTTCCATGT TGGTTTATAA ATTGTTCGAT TGCCATCAAT ACCATTTTTA ATAAGGTCAG 660

AGTAATCTTT TAGTGATTCT TTCGTGCTTG GATATTTTCG GAATCCAGCA TTAATACTAT 720

ACAATTGATT ACCATCAGCT TCTAATGTGT TAAAAGGAAC AGAATTCCCT TCaAAAGCAC 780

CTTTGATACC GAATAAATTA TGGTTTGGTG ACwTAGCTAA AGCACTACGA CCTGAGTCAG 840

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TATAATAATT AAGTGTGATA ATAAACTATG ATTTGTTATA ATTTATCGTA TGCTGAAAAT 1980

AGTTGATAGG TATCAATCGA CTAAATATCT TCCAGTAAAT TGATTATACT AATTCACAAC 2040

GCAAAAATAA ATTAATTTAC AAAAAATATA TAAAAAATAT GAATAATTCC TACATAGGAG 2100

TGTGACAATG AAGAACGCAT TTAAATTATT TAAAATGGAT CTGAAGAAAG TAGCTAAGAC 2160

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TTCAGCAGAT AAAGCTTTAC CTAAGATTAA TGACTTTGCG AATAAAATTG TATATTTGAA 2760

TAACCACCAA GCGGATTTAG ATAAATATGC CAATGATTTT AGAAAACTAG GAAATTATAA 2820

AGGTGATATT TTAGATGCTC AGAAAAAATT AAACGAaGTC AATGGTGCTA TTCCGCAACT 2880

TAATGAAAAG GCTAAGTTGA TATTAGCTTT AAATAATTAT ATGCCGAAAA TTGAAAAAGC 2940

GTTAAATTTT GCAGCTGATG ACGTGCCAGC GCAGTTCCCT AAAATTAATC AAGGACTTAA 3000

CATTGCGAGT CAAGGTATTG ATCAAGCTAA TGGACAGTTA AATGATGCCA AAGGCTTCGT 3060

CACACAAGTT AGAAGTAGAG TCGGTGATTA TCAAGATGCA ATTCGACGCG CGCAAGATTT 3120

AAATCGAAGA AACCAGCAAC AGATTCCTCA AAATAGCGCG GCGAACAACG AAACATCAAA 3180

TAGTGCACCT GCAGCTGGTA ATGGTGTAGC ATCAACGCCA CCAAGTGCAC CAAGTGGCGA 3240

TACTGCACCA AATAATAATG TTACGCAAAA TACCGCACCA AATAGTAATA ATGCGCCTGT 3300

ATCGACTACA CCACAAAGTA CAAGCGGGAA AAAAGATGGT CAAAGTTTTG TAGATATAAC 3360

AACAACACAA GTCAGCACAG CTAACGAGAA CACACAAAAC ATTACAGATA AAGATGTTAA 3420

ATCAATGGAA GCGGCATTAA CGGGCTCTTT ATTATCATTA TCAAATAATT TAGATACCCA 3480

AGCGAAAGCC GCACAAAAAG ATAGTCAGGC ATTACGTAAT ATTTCGTATG GGATTTTAGC 3540

ATCGGACAAG CCTTCTGATT TTAGAGAGTC TTTAGATAAT GTTAAGTCCG GTTTAGAATA 3600

CACAACGCAA TATAATCAAC AATTTATCGA TACATTAAAA GAGATTGAGA AGAATGAAAA 3660

TGTTGATTTA TCAAAAGAAA TTGATAAGGT AAAAGCAGCT AATAATCGAA TTAATGAATC 3720

ATTAAGGTTA GTTAATCAAT TAAGCAATGC ATTAAAGAAT GGTAGTTCAG GAACTGCTGA 3780

AGCTACTAAA TTACTAGATC AACTTTCAAA ACTAGATTCA TCATTATCAT CATTTAGAGA 3840

TTATGTTAAA AAAGATCTTA ACAGCTCTTT AGTATCAATA TCACAACGTA TTATGGATGA 3900

ATTGAACAAA GGGCAAACTG CATTATCCAA TGTTCAGTCT AAATTAAATA CAATTGATCA 3960

AACAGTATTA CCAAGTATTG AACAACAATA CATTAGTGCT GTTAAAAATG CTCAAGCAAA 4080

CTTCTCGAAA GTGAAAAGTG ATGTAGcTAA AGCTGCTAAC TTTGTGCGCA ATGACTTACC 4140

ACAGTTAGAA CAGCGATTAA CTAATGCGAC AGCAAGTGTG AATAAAAATT TACCAACGTT 4200

ATTAAATGGT TATGATCAAG CGGTAGGATT ACTAAATAAA AATCAGCCAC AAGCGAAAAA 4260

GGCTTTATCA GATTTAGCTG ATTTTTCTCA AAATAAATTG CCTGATGTTG AAAAAGATTT 4320

GAAAAAAGCG AATAAAATTT TCAAGAAATT AGACAAAGAT GATGCAGTCG ACAAATTAAT 4380

CGACACACTT AAGAATGATT TGAAAAAGCA AGCGGGTATT ATTGCAAATC CTATTAATAA 4440

GAAGACTGTT GATGTTTTCC CAGTTAAGGA TTATGGTTCA GGTATGACAC CATTCTATAC 4500

TGCACTGTCA GTATGGGTAG GTGCACTCTT GATGGTAAGT TTATTAACGG TTGATAATAA 4560

ACATAAGAGT CTAGAGTCAG TCTTAACGAC AAGACAAGTG TTCTTAGGTA AGGCAGGATT 4620

CTTTATAATG CTTGGTATGT TGCAAGCACT CATTGTATCG GTTGGAGATT TGTTAATCCT 4680

AAAAGCAGGA GTTGAGTCAC CTGTATTATT TGTACTTATA ACGATTTTCT GTTCGATTAT 4740

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AATCGTATTG CTTGTATTAC AAATTGCAGG TGGTGGGGGA ACATTCCCAA TTCAAACTAC 4860

GCCACAATTT TTCCAAAACA TTTCGCCATA CTTACCATTT ACGTATGCAA TTGATTCATT 4920

ACGTGAAACA GTAGGCGGTA TTGTTCCGGA AATCCTAATT ACAAAATTAA TTATATTAAC 4980

GTTATTTGGT ATAGGATTCT TCGTTGTAGG TTTAATTTTA AAACCTGTAA CAGATCCATT 5040

GATGAAGCGC GTATCTGAAA AAGTTGACCA AAGTAACGTT ACAGAATAAA AATTAAATCC 5100

ACACATTAGG GTTATAGCTC CTTAATGTGT GGATTTTTAT GTTTTTAGAC AGAAGAGATA 5160

GTAATTTCTG TCTTTTATGG GACGGTTGTT ATCATTGCTA TTATCCAGGA TGACTTACTA 5220

TAGGACTAAT ATTACCGACA AAGTGAATAT CCTCGTCTTC CGTAGTTAAA ATAAAGCTAG 5280

AACCTTTTTG GATGTCATAG TGCTTATCGT TTACTGTTAA AGTACCAGTA CCATCGATAA 5340

TTGTAACTAA GCAATAAGCA TGTGGTTTAT TGAATTTTAA ATCTCCATGA ATATCCCATT 5400

TATATACTGC AAAATATTGA TTATCTACAA ATTGAGTTAC AGTGTGTGTG TCGATGTGAG 5460

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CTAAGTGCAA ATCACGCAAT TGACCATTTT GATCTCGTCT ATCATAGTCA TAAATACGGT 5580

ATGTCGTATC GGAGGATTGT TGTGTCTCTA AAATTAAAAT ACCCGAACCA ATGGCATGGA 5640

CAGTGCCAGC AGGAACATAA TAAAAGTCAC CGGGCTTAAC AGGTATACGT TTGAAAAGAC 5700

TGTCAAATTC ATGATTATCA ATCATGTCTA TTAACGTCTG TTTATTATGT GCATGTACGC 5760

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CATTGGCATC TAATACTTTA GTTAGCAGAG GGAAACTATC TCGTGAATCA TTATCGAATA 5940

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AATATCAATT GAGGTAGACT ACCATCTAGA CTGTCCCATT TAACACCATG ATTATTTTTC 6360

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GAGACATGTC GTGATCAGTA ATTATCATAG TTTGTTGATC AAAAACATGA GAAGGTTTAT 6600

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CAAATAGTCC CATAGTGAAG GAAGCCTTAC CCATTTCTCT TTCGGAATGA TTGAATTTAT 7020

ACTTTTGAAC AAACGTTGCT AAACCTAAAC CGATTGGTGG TGTACATACA GCAACTGCGA 7080

CCATACCCAT AACGGCGTAA TTACCTTCAG CAATAAGTGC TGAGCCAAAT AAAAATGCTA 7140

CCTTGTTTAC TGGACCGCCC ATATCGAAGG CAATCATCGC ACCTATAATC ATCGCAAGTA 7200

TAATAATATT AGCACCTTGC ATACTTTTTA ACCAGGTTGT TAATGCCTCA AAAATATTAG 7260

AAATTGGTGC ACCGATTAAA AATATAAATA TCAATCCTAC AACGACCGAT GAAATAATGG 7320

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CATCACTGCC ATAAAAACTA CCGTCAGCAG CGATAGCGCC GCCAATCATA CCAGGAACAA 7500

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GCGCATCTTG ATTAATGATA CGTTGAATTA GACCTCTCGG ATTATGAATC CCTTCGCGAA 7860

CATTTTCATT AATCAACCGT TTACCAACAA ATCGGGACAG ATCAACTTGT TTATCAGCTG 7920

CAATTATGAC ACCGTCAGCT TCTTCGATGT CTTGCGTAGT TAAAACATTT TCAGCACCAA 7980

CACCGCCCTG TGTCTCTACT TTAATATCCA CACCCATTTC TTTTGCTACC TGCTCAAGCT 8040

TTTCTTGAGC CATATATGTA TGTGCAATGC CATTTGGGCA TGAGGTAATA GCTACAATTT 8100

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ACATCGTGTT GTCGCCAAGG AAAAACATCT TTTGTGCGAA AAATAAGCAC ATGTGATTGT 8400

AAAACTTTTT CAGGATCTCC ATGAGGAATC GCCATAAAAT TACCTATGTA TGTAGAAGAT 8460

GATTTCTCAC GCTCTAAAGC TGATTCGATA TATCCTTCTA CAATCGCATG ATGTGCTTGT 8520

AATATTTTTT GAGCTTCTTC AAAAATTTGC ACAGTATGCC GTGATTTTTG TTCAGTATTT 8580

ACGACAAGGA AATTGACAGT GTCCATATGA TGATGTGCTT GAACCGGATT TTGCTTTTGC 8640

TTCACAACGT GTCTGATTTT GTGACGATCA TCTTCAGAAA ATAATGGTGC AACCTTGATA 8700

GTCGTCAGGT GCTTAGGAAG TATGTTTAGC GTTTGTTTAG GAATATCATG GGTCGTTATT 8760

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CCATAATAAC AAGCAATGAC TACATTTAAT TGTGTTTTGG TACGACGCTC GATGGCAGCT 8940

TGAAAATGAA TTGTTAAAAA TGCAATTTCA TCTTCGCTCA TCTCTATATC AGTATCAATT 9000

GCTAATTTAT CAATCGCTTC AAAAAGTGTG TTAAACACAA AGGGATAGAG TTTTTTAATC 9060

TCTATAACTA AAGGATTGTT TAAATAAATG TTTTGAGTGA TACGTAAATA TGCTTTACTA 9120

AAATGATTAT ATAAATTTTG TTGTAAAATC GAATCTTCAT TGAAAGGTAC ATGAATACGT 9180

TGCTGCATCA ATTCGATTAA GCGATCAATA TAACTTTGTA TAAATATACG TTCTATGCCA 9240

ATATCGAGTT TATTAAAATG ATAAGCAATA AAGAATGAAA ACATATTGAT TACTTTTTCG 9300

TTCAAGTCAT AACCTAATCT TTCGTTGATT TGCTTAATGC AAGATTGAGA TATCAATTTT 9360

AGATGAATTA AAAGCTGTTG TATTTGAATA TCAGTTGTTT CAATACTATG TTGTTGAAGT 9480

GTCTCTTGTA TAATATGCGA AATCATCCTT TGGTGTGAAT CAGGTAATTC aTTTAAAATT 9540

AGGTCTTCAA CATGTACATG CCCTGATGAT AATTGATTTA AATGGATGAT GGCATTAGTG 9600

ATATCATTAT CTGTTCCATC GAC 9623

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1021 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ACCGTGGAAA CACGTCTAGT CAATCAGAAA GCGATAAAAA TGTGACTAAA TCATCTCAAG 60

AGGAAAATCA AGCAAAAGAA GAATTACAAA GCGTTTTAAA CAAAATTAAC AAACAATCAA 120

GTAAGAATAA TTAAAAAATT TTGATATTGT CTATGTTTAT AGTTCACAAG CCATTCAACG 180

TATTGTAAAC TAAGGATAGT GTATTTTTTT AATAGTAATT TGTCAGGAGG TGCCTATCTA 240

TGGAAGAACA TTACTACGTA AGTATTGATA TTGGATCATC AAGCGTAAAA ACAATAGTAG 300

GCGAGAAATT TCACAATGGT ATAAATGTGA TAGGTACAGG ACAAACCTAC ACGAGCGGTA 360

TAAAAAATGG TTTAATTGAT GATTTTGATA TTGCGCGACA AGCAATCAAA GACACAATTA 420

AAAAGGCATC AATCGCTTCG GGTGTTGATA TTAAAGAAGT TTTCCTGAAA TTACCTATCA 480

TTGGAACGGA AGTTTATGAT GAATCAAATG AAATCGACTT TTATGAGGAT ACAGAAATCA 540

ACGGTTCACA TATCGAAAAA GTATTAGAAG GTATTAGAGA AAAAAATGAT GTGCAAGAAA 600

CAGAAGTAAT TAATGTGTTC CCGATTCGTT TTATAGTCGA TAAAGAAAAT GAGGTTTCAG 660

ACCCTAAAGA ATTAATTGCC AGACATTCAT TAAAGGTTGA AGCAGGCGTA ATTGCTATTC 720

AAAAATCGAT TTTAATTAAT ATGATTAAAT GCGTAGAAGC ATGTGGTGTT GATGTATTAG 780

ATGTTTACTC TGATGCATAT AACTATGGTT CAATCCTAAC AGCTACTGAA AAAGAGTTAG 840

GTGCATGTGT CATTGATATT GGTGAAGACG TTACGCAAGT TGCTTTTTAT GAACGCGGTG 900

AATTAGTAGA TGCTGATTCT ATCGAAATGG CAGGGCGTGA TATTACaGAC GATaTTGCAC 960

aAGGrTTaAA CACTTCTnAT GAAACTGCTG nAAAAAGTTA AACACCAATn TGGTCATGCA 1020

T 1021

(2) INFORMATION FOR SEQ ID NO: 168:

(A) LENGTH: 7963 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

TAATCTATTA TAAAAACTGT CCATACCCTT TGATTACCTT CTCTTCAGGT ACAGGCCACA 60

CTTGAGGCCA TAAGCCATAT GCTTGCTGTG AATAAAATTG TGCCATTTGT AACAATATAA 120

TATATACAAA TAAACACCCA ATAATTGCTG TCACTAATGG ATATGATAAC CAAACCATTA 180

ATAAAACTGC AATAATTACT AACCTAAAGA TAATATTAAA TGCGTCTCTC CCTCTTATAA 240

AGCTTCTAAT AAATAAGAAT AAATACATCG CATTAGAGTT AAATTTACTA CCCTTTGGAA 300

CTGGTAAAAG TATATCTAGA TAACTTCTTC TGACTGCAGA TTCTTTCAAA TGTTTTACAT 360

CGGTGAACAT ATTAACAAAT TTATAATAAT TCATATGATG TCGATGTTCG ATTGCAATCA 420

TTTTCTCCCA AGGATACAAA AAGCCTGGTT TATATTTTTT AACTAAAAAT TCTATTAACA 480

CAGGCAAAGC AACCATCACA AATGCGATGT ACCATTTTGG AGCTAATAGT AAGTAATATG 540

TTAGAGCAAA GGTGATGAAT GATATTAAAT TAACTTGCCA TGTTTTAAGT CCCGATTGAT 600

ACCATTGCCA TCTTAAGCGT AAACCAACAT ATGGAAAAAT TAATGCACTG ACTCCAAAAC 660

AAATATAAAA TGCCACATTA TGTTGATTAA TATTGTAAAA CAACGGGAAC ATTACAATAA 720

CAATAATGAG TTGGATTAAT ATGCGCGCAA AGTAACTATA TAAAATCGCA TGACGCATAA 780

ATTGAGACAT GTGTTTTTCA AATGGTAATA AAAAGATTTT ATCCgCTTCT TTTAACAGTG 840

GTCsCmTTGG AAAAATAGrT GTCAACGCAA CAATCACTGC TGCTATTaAT GAAAAATTGa 900

TATTCGTTGG AATATGTTTT AACCATTcAC CATATCCArA AATAAATGCA CCCAGCAAAA 960

TAAGTAAAAA GACCATGAAA TGACCATTAA ATATAAACTT ATTATAATAA TTTTtCTCTT 1020

TACGAAGGGC ATGTAATCTT TTATTAAATA ATGTGGTAGC TTGGTTACGC ATGTACATCT 1080

CCACCTTGCG TCACATGAAT ATATATATCG TCTAATGTTT GATTATGTAA GCCAGTTTGT 1140

TGTCTCAATG CTTCTAAATC TCCAAATGCA ACGACTTCAC CTTCGTCTAG TATGaTAAAA 1200

CGATCACAGT AACGTTCAGC TGTTGCTAAA ATATGTGTAC TCATTAGAAC GGTTCTACCT 1260

TCGTTTTTCT TTTCAACCAT TAAATCTAAC ATGGATTGAA TTCCTAATGG ATCTAGGCCA 1320

AGGAATGGTT CGTCTATAAT ATACAATTCG GGATTAACGA TAAACGCACA AATAATCATG 1380

ACTTTTTGTT TCATCCCCTT AGAAAAATGA CTCGGAAAAA CTTTCAACTC ATTTTCTAAA 1440

CGGAATGTCT TTAATAATGG CATTGCTCGA TTCATCGTTT CATCACGATC AATATCATAT 1500

TCCGGAATAT AAGATAACTT TCTTCTATAA GCCTCTATGT CATCATTAAT GTTGATATCT 1620

GAAATTGATA GAGATCCTTC CATAGGTGTA AGCAATCCTA GCATATGTTT AATCGTTGTA 1680

CTCTTACCAG CGCCATTAAG GCCAATAAGT CCAACAATTT CGCCTTTGTT TAATTCAAAA 1740

TTTATATCTT TAATTACAGG GCGTTTTCCA TATCCACCTG TAAGCTGTTC TACTTTAACT 1800

GTCATAAGGC ACCTCCATGA CTTATATTGT ACCAAAAATT ATAAAATGCT CATATTAAAT 1860

ACACATGTCC TAATATCGAA TTTTTAGCGA CAATGTTATA ATGAATGGTA ATACTAGTTG 1920

AAAAGGAGTG TAGTCATCAT GTCAGAAACA ATTTTCGGCA AAATTTTAAC TGGAGAAATT 1980

CCTAGCTTTA AAGTATATGA AGACGATTAT GTCTATGCCT TTTTAGATAT ATCACAAGTT 2040

ACTAAAGGAC ATACGTTATT AATTCCTAAA AAAGCTTCTG CTAATATCTT TGAAACTGAT 2100

GAAGAAACAA TGAAACATAT CGGTGCAGCA TTACCTAAAG TAGCAAATGC TATTAAGCGT 2160

GCATTTAATC CTGATGGTTT AAACATTATT CAAAATAATG GTGAGTTTGC AGATCAATCT 2220

GTATTTCATA TTCATTTCCA CTTAATTCCT CGATACGAAA ATGATATTGA TGGATTTGGT 2280

TATAAGTGGG AAACACATGA AGACATTTTA GATAACGATG CAAAACAACA AATTGCTGAA 2340

CAAATTCAAG CACAATTTTA AATGTATGCT TAATCTAAGC TCGAACGGGT ATAATATGAT 2400

TAATATTATA ACAATTGCGT TTGAAGTGAT AACATCAAGG TTAGCAATTT TAAACAAAAT 2460

GAGTTATCAA GATAACAGAT GTTAAAAGTG AGGAGAATAT AAATGAAAGC ATCACGCATT 2520

cTATTCGGTA TCGGTGTTGG CGTAGCAGCT GGTTTTGTAG TTGCACTTCA AGGACGTGAC 2580

GACAAAAGTG TCAAGAACAA CACGATCGAT CGTACTGCCC CTACTGGTTC AAAATCAGAA 2640

CTACAACGTG AATTTGAAAC GATTAAACAA AGTTTTAATG ACATTTTAAA CTATGGTGTT 2700

CAAATTAAAA ACGAAAGTGC GGAATTTGGT AGTTCAATTG GTGGTGAAAT TAAGTCATTA 2760

CTTGGAAACT TCAAATCTGA CATTAATCCT AATATTGAAC GTTTACAGTC ACACATCGAA 2820

AATTTACAAA ATCGTGGCGA GGATATTGGA AACGAAATTT CTAAGTAGCA GGTTACGTTC 2880

TCGATCACAA CTATTTTTAT TAGTAACAGC ATATTTATTT TTTAAAATTA AATGCCAAAT 2940

AAACGAGATG ACATTAGAAA TTAGATATTT CTTGTCATCT CTTTTTTAAA ACTCAAATGA 3000

ACTTATGTTT ACAAATTATA GGAAGACATT GTTTGTAGTG ATTTTCGCTT AAATCATATT 3060

TATGAATTGA TTGAAAACAT TGCTTAGGAT TCATTGTGTT ATCCtTGCAC TTTGATTACG 3120

CTTTACTTAA ATCATTATCG ACAAACAACA TACTTATATT TTCATTGAGC CGAACCTTAT 3180

ATACACATTA CATATACCTT ACTTGCACAA ATTATTAATC TGGTGTTTAT TATAATTACA 3240

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TTTCATAAGT GATGCTTTAT TAGCAAGAAT ATGTGTTCGC AGAAATTTGT TCTGCATTCT 3420

ACTTCTACGC TAGTCAATCA GACAATTTTA CCAATCCCCA CTTTCGCGTT TCAAATCAAA 3480

CAATACGTCG CTCCTTTCTT CTTATATAAC AATTCTTCTA ACATGATATG TTACTATTGA 3540

ATTACTGAAC CTGAGTTAGT TATAATCTAA CTTATATTGA AAAGAGATGA GGCGTAAGAT 3600

ATGTTTTTAT GTAAAAGACA AATTGATATC AATGCACGAT TTGGTTTGCC TAGAATTGCA 3660

TTTATGAGTG CAGTTGCAAC CATCATTATG TTTTTAGTTA GTTATGAAGT AATGTATTTT 3720

TTATCTAATA CGCCATTATC AGATAGACAT TTTCTCATCT TTTTATTACT TGTATTTATG 3780

ACGTATCCAT TACATAAAAG TATACATTTA TTATTTTTCT TACCATATAG AAAATCGTTT 3840

AAAGTTCATA AGTTAACTAA AAGAAAATGG CTTATATTCT ATAATACCTA CGTCAATCAA 3900

CCTGTACACA AATTTTATTT TTGCATTAAC TTAATATTGC CGTTAATTAT CTTATCTGCA 3960

ATGTTCGTTT ATCTAACAAT TTCATTCCCG CAATATGGAC ATTATTTTAT GTTCTTATTG 4020

GCATTGAATT TCGGTATTTC CATTACAGAT TTATTATATT TAAAAATAAT TATATTTTCT 4080

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AATCCATATC ATTTATAACA AAATAATTAT AGCAAGGTGT TATTATTTGT TTTTAGGCTA 4200

TGTAATAgcT tACAATCAAA TGTATATAGA CCTTGTTTTT TTATTTTCAT CAATTTCTAC 4260

CCCTAAACCT AATGCTCTAG TCTGATGTCA TGGGTTATTG ATTGGTGATA ATATAAAACT 4320

ATGTTATATT CACGATGATT AACTTACAAA GGAGTTTCAA CTATGAAGAT GATAAACAAA 4380

TTAATCGTTC CGGTAACAGC TAGTGCTTTA TTATTAGGCG CTTGTGGCgC TAGTGCCACA 4440

GACTCTAAAG AAAATACATT AATTTCTTCT AAAGCTGGAG ACGTAACAGT TGCAGATACA 4500

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ATTTTAGCTG ATAAATATAA AAATAAAGTT AATGATAAGA AGATTGACGA ACAAATTGAA 4620

AAAATGCAAA AGCAATACGG CGGTAAAGAT AAATTTGAAA AGGCCCTTCA ACAGCAAGGT 4680

TTAACAGCCG ATAAATATAA AGAAAATTTA CGTACTGCTG CTTATCATAA AGAATTACTA 4740

TCAGATAAAA TTAAAATCTC TGATTCTGAA ATTAAAGAAG ACAGCArGAA AGCTTCACAC 4800

ATTTTAATTA AAGTTAAATC TAAGAAAAGC GACmAAGAAG GCTTAGATGA TAAAGAAGCG 4860

AAACAAAAAG CTGAAGAAAT TCAAAAAGAA GTTTCAAAAG ATCCAAGTAA ATTTGGTGAA 4920

ATCGCTAAAA AAGAATCAAT GGATACTGGT TCAGCTAAAA AAGATGGCGA ATTAGGTTAT 4980

GTTCTTAAAG GACAAACTGA TAAAGATTTT GAAAAAGCAC TATTTAAGCT TAAAGATGGT 5040

GAAGTATCAG AGGTTGTTAA ATCAAGCTTT GGATATCATA TTATTAAAGC TGATAAACCA 5100

AAAAATCCAA AATTATTGAC TGATGCATAC AAAGATCTAT TAAAAGAATA CGATGTTGAC 5220

TTTAAAGATC GTGATATTAA ATCAGTTGTC GAAGATAAAA TCTTAAACCC TGAAAAACTT 5280

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GAGCTCATGT TTCAGTATAC TCATCTGTCC GATATCTTTT AATTCTTAAT CGAGTGATTC 5460

AGGATTGTAG AATCTACGAT TTTCAAGACC AAATATTTTA TCTGTAAACT GACCCTTGTC 5520

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ATGAGATAAA ATCATATGTC TTAACAACAT GATTTCTTCT CCTTCAATGT TCAATTCACG 5700

AGCTGCTTCA ACTACTTCAT CACTCGCAAT CGAGATGTGT CCTAATAAGT TACCTTCGAC 5760

TGTATACGAC GTCGCAACAG GACCACTCAA TTCTCTAACT TTACCAATAT CATGCAAAAT 5820

AATACCACTA TATAACAAAC TTTTGTTTAA CAATGGATAA ATGTCaCAAA TTGATTTTGC 5880

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ACTAGCAGCT GGATATGTGT AAAATCGTTC TTGATATTTT TTCAATAAAT GACGTGTGAT 6000

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TGCCGGTGAT AAAGGTGCAC CATCTACAAA TTGTTCTGTT TTTAATTGAT CTTCAGTTGT 6120

CGCTAGTCTA ATTTGGTTGA CTTTCATCTG TTTATTTCCG CGATAGTTTA TGATGTCACC 6180

TTTAACATGT ACAATTTCTT CAGGCTTGAT TGTTGCCATA TCATTTTTTG TAGCCGTCCA 6240

AAATTTCGCT TCAATTTCAC CACTTTTATC TTGCAAATGT AATGTCATAT AATCTTTACC 6300

TTGTGCTGTT ACACCCTGTG TAGCTTTATG CACTAAGAAA AAGTGATCAA CTGAATCTCC 6360

GGGATTTAGA TTCTCTATAT TTCTCATCGT TTCCCGCCTT CCTCTATTTT GTTTAATGTA 6420

ATCACTTCTT TTGATGGAAC AATATTATCT TTTACACATG TAAAGTATAG TACTTGATAG 6480

TGTTCTGATA ATGATCGTAA ATAATTCAAC ATTTTTTCAG TACGTTTTTT ATCAAAATGA 6540

ACAAATGCAT CATCAACAAT TAATGGGAAC GGATAATATG GTCTTAGTAC CTTAATTAAA 6600

CTGATACGTA AAGCTACATA AAGTAATTCT TTTGTAGATT GACTTAGTTC AACAGGATCA 6660

TATAATTGAC CATTAACATG TTTAACCGTA ATTGAATCTT CATTATAGTT AATCATCGTA 6720

TATCTGCCAT CTGTTAAATG CTTCAATATT TCTACCGCTT CATTAATAAC TTGAGGCAAA 6780

CGTTTATCTT TAATTTGTTT AATGTGTTCA TCAACTAAAC TTTGTAAATA ACTTAAACTT 6840

GCCCAATCTT TTGCGATATC ATTAAGTTGA TTTTTAAGAC TGTGATATTC ATGTCTTAAA 6900

GCTTGCATTT CAAGATATTG CTCATTATAT TCGTCAACTT GAGTAGCCAA TAAATGATCT 7020

TCTTCTTCAA GTTGTGCAGT TGTTTTTTCA CTTAAACTAG AACTTAATTC ATAAGAATAG 7080

TTTTGGTTCT CAAGATATTT AGTTAAATCA TTAAAACGAC TCAAATTACT AGTATAAGTT 7140

TGGTAATCTT CATGATGTTG GTAAAAATCT TCTTCAGTAC CAACATTGAT AAAATCGAAT 7200

AGTGCTGTAA TTTCTTTATT ATTTTCTTCT AATTGAGCAT TTAAATGATT TAATTCATTT 7260

GTAACAAGTT TGGTATTTTC AGCATTAATA CGCCATTTTT CATTCGTGTC TTCAGCTGAT 7320

TTCAACCATT GTtGCACATC GTGGAATAAA GATAATTTGT TGAAATAAAC AAATTGTGAT 7380

TTTGTAACAG CTTCAGCATG ATTGTAGAAT GTATCTAATT CTTGAACCAA TTGCTGGCGT 7440

TGTTGATTTA AATCACTGAT ATGTTGATCT AATGCTTTAA TATTCGCCAT TGTAGAAATA 7500

CTATCAACAA TTAAATCATT TGAAATTTTA GATGATAAGT ATAATTCATC CTTAACGTTC 7560

TCAACTGTCG ATTGTAATTC ATCATGACGC CCTTTCGCAT CATTTAAACG ACCTTCAATA 7620

TACTGACGTT TCTCTTCTAA AATATCTTTA TTTTTCAAAG CTTGTTGCCA GTGATCACGA 7680

ATGCGATATT GCTCATCAAG ATCAAAATCT AAGTCATAAT TTTCATCTAA AATGGCTAGT 7740

TGTGCTTTAA TTTCTTCGAT TTCATCTGTG ATGGCCTCGC TATAATCTAC TTCTTTTGAT 7800

TTAGACATGA TGATACCGAT AACAAATACT AAAGTTAATA CTGCGAAAAT AATACCAAAC 7860

AACATGTTGT TTGAAATAAA TGAGAAGGCA GTTAAACCAA TACCTACTAA TGTTAAAAGr 7920

ATAAACGTTG TTCGkAACAA TTTTTGACGT TTTTGttTTT CTT 7963

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3958 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

ATATTGTCTT TACAATAGTT TGCTATGGAG GTAATTAACC AATAGGAGGA ATTTATAATG 60

GCAGTAATTT CAATGAAACA ATTACTAGAA GCGGGTGTTC mCttCGGTCA CCAAACACGT 120

CGTTGGAACC CAAAAATGAA AAAATATATC TTCACTGAGA GAAATGGTAT TTATATCATC 180

GACTTACAAA AAACAGTGAA AAAAGTAGAC GAGGCATACA ACTTCTTGAA ACAAGTTTCA 240

GAAGaTGGTG GACAAGTCTT ATTCGTAGGA nCTAAAAAAC AAGCACAAGA ATCAGTTAAA 300

TCTGAAGCAG AACGTGCTGG TCAATTCTAC ATTAACCAAA GATGGTTAGG TGGATTATTA 360

GAAGATGGTT TATTCGAAGT ATTACCTAAA AAAGAAGTAG TAGAACTTAA AAAAGAATAC 480

GACCGTTTAA TCAAATTCTT AGGCGGAATT CGTGATATGA AATCAATGCC TCAAGCATTA 540

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CCTATCGTAG GTATCGTTGA CACTAACTGT GATCCTGACG AAATTGACTA CGTTATCCCA 660

GCAAACGACG ATGCTATCCG TGCGGTTAAA TTATTAACTG CTAAAATGGC AGATGCAATC 720

TTAGAAGGTC AACAAGGCGT TTCTAATGAA GAAGTAGCTG CAGAACAAAA CATCGATTTA 780

GATGAAAAAG AAAAATCAGA AGAAACAGAA GCAACTGAAG AATAATCAAC TGTTGAATCT 840

GACTTAGATA TAGTTTAAAT GGGTGATAAG ATATTAATGC TTATCACCTT TTTTAAAAAG 900

AAAATCGAGG CAAATTACAA ATATTCAATT AGAGTATTGG CAATCTTGCC TATAATAATG 960

CTAAAATCAT AATATATAAn ATGATAACTT ATTGGAGGAA TAATGAATGG CAACTATTTC 1020

AGCAAAACTT GTTAAAGAAT TACGTGAAAA AACTGGCGCG GGTATGATGG ATTGTAAAAA 1080

AGCGCTAACT GAAACTGATG GTGACATCGA TAAAGCGATT GACTACCTAC GTGAAAAAGG 1140

TATTGCTAAA GCAGCTAAAA AAGCAGACCG TATTGCGGCT GAAGGTTTAG TACATGTAGA 1200

AACTAAAGGT AACGACGCAt TATCGTTGAA ATCAACTCTG AAACAGACTT TGTTGCTCGT 1260

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ACTAAAACTG ATAACGATGC TTTCGGCGCT TACTTACACA TGGGTGGACG CATTGGTGTA 1500

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GCTGCAATCA ACCCTAAATA TGTTTCTTCT GAACAAGTTA GCGAAGAAGA AATCAACCAC 1620

GAAAGAGAAG TTTTAAAACA ACAAGCATTA AATGAAGGTA AACCAGAAAA CATCGTTGAA 1680

AAAATGGTGG AAGGACGTTT ACGTAAATAC TTACAAGAAA TTTGTGCTGT AGATCAAGmT 1740

TCGTTAAAAA CCCTGATGTA ACAGTTGAAG CTTTCTTAAA AACAAAAGGT GGAAAACTTG 1800

TTGACTTCGT ACGCTATGAA GTAGGCGAAG GTATGGAAAA ACGCGAAGAA AACTTTGCGG 1860

ATGAAGTTAA AGGACAAATG AAATAATCTG TCATAAAGTA AAACAAGGAA GAAGACACCT 1920

TTAATGTTGC TTTATTAAAA TGTAAATCAT TCTAATAAAA CGACAACTGT GTCTTCTTTA 1980

CTTGTATATG TTACATATAT TCACGATAGA GAGGATAAGA AAATGGCTCA AATTTCTAAA 2040

TATAAACGTG TAGTTTTGAA ACTAAGTGGT GAAGCGTTAG CTGGAGAAAA AGGATTTGGC 2100

ATAAATCCAG TAATTATTAA AAGTGTTGCT GAGCAAGTGG CTGAAGTTGC TAAAATGGAC 2160

TTAGGTATGG ACCGTGGAAC TGCTGATTAC ATGGGTATGC TTGCAACTGT AATGAATGCC 2280

TTAGCATTAC AAGATAGTTT AGAACAATTG GATTGTGATA CACGAGTATT AACATCTATT 2340

GAAATGAAGC AAGTGGCTGA ACCTTATATT CGTCGTCGTG CAATTAGACA CTTAGAAAAG 2400

AAACGCGTAG TTATTTTTGC TGCAGGTATT GGAAACCCAT ACTTCTCTAC AGATACTACA 2460

GCGGCATTAC GTGCTGCAGA AGTTGAAGCA GATGTTATTT TAATGGGCAA AAATAATGTA 2520

GATGGTGTAT ATTCTGCAGA TCCTAAAGTA AACAAAGATG CGGTAAAATA TGAACATTTA 2580

ACGCATATTC AAATGCTTCA AGAAGGTTTA CAAGTAATGG ATTCAACAGC ATCCTCATTC 2640

TGTATGGATA ATAACATTCC GTTAACTGTT TTCTCTATTA TGGAAGAAGG AAATATTAAA 2700

CGTGCTGTTA TGGGTGAAAA GATAGGTACG TTAATTACAA AATAAATTTA GAGGTGTAAA 2760

ATAATGAGTG ACATTATTAA TGAAACTAAA TCAAGAATGC AAAAATCAAT CGAAAGCTTA 2820

TCACGTGAAT TAGCTAACAT CAGTGCAGGA AGAGCTAATT CAAATTTATT AAACGGCGTA 2880

ACAGTTGATT ACTATGGTGC ACCAACACCT GTACAACAAT TAGCAAGCAT CAATGTTCCA 2940

GAAGCACGTT TACTTGTTAT TTCTCCATAC GACAAAACTT CTGTAGCTGA CATCGAAAAA 3000

GCGATAATAG CAGCTAACTT AGGTGTTAAC CCAACAAGTG ATGGTGAAGT GATACGTATT 3060

GCTGTACCTG CCTTAACAGA AGAACGTAGA AAAGAGCGCG TTAAAGATGT TAAGAAAATT 3120

GGTGAAGAAG CTAAAGTATC TGTTCGAAAT ATTCGTCGTG ATATGAATGA TCAGTTGAAA 3180

AAAGATGAAA AAAATGGCGA CATTACTGAA GATGAGTTGA GAAGTGGCAC TGAAGATGTT 3240

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GATATTATGT CAGTATAAAA CTAATATACA ATGACATATT AAAATGCCAG TATTAAACGA 3360

TAATGTAACA TTTAAAATGG GCATGTTTAA TTAAATCAAA GATGCATGTG ATAATTTAAA 3420

TTCAGAATGA GCATAAAAAT GGTGTTTAAA CAAGTTAATT AAACATATAC TTTATAAATA 3480

ATAGGCATTA GGTATATTGC TATAATAAAG TTATGTAATT TTTAACCTCA GTATGTATGT 3540

CACATTTCTG GTGTAAACTG TACCGAGTCA GACTTTGGTA CAGTTTTTTT ATTTGCTTAT 3600

TCAATGCATT AAATGAGTAT GATAAAATGA TAATGATTGT TTAGTAACTT ATACTATATG 3660

ACAGAGATGA TCAGGCTCGG AGGAAAGACC ATGTTTAAAA AGCTAATAAA TAAAAAGAAC 3720

ACTATAAATA ATTATAATGA AGAATTAGAC TCGTCTAATA TACCTGAACA TATCGCTATT 3780

ATTATGGATG GTAATGGGCG ATGGGCTAAG AAGCGAAAAA TGCCTAGAAT TAAAGGTCAT 3840

TACGAAGTAT GCAAACAATA AAAAAAATTA CTAGGGTAGC TAGTGATATT GGTGTTAAGT 3900

ACTTAACTTT ATACGCCTTT TCCACTGAAA ATTGGTCAAG ACCTGAAAGT GAAGTAAA 3958

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5333 base pairs
(B) TYPE: nucl ic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

ATTAAAACAA CTTAATATAC CTATTTATGG TGGTCCTTTA GCATTAGGTT TAATCCGTAA 60

TAAACTTGAA GAACATCATT TATTACGTAC TGCTAAACTA AATGAAATCA ATGAGGACAG 120

TGTGATTAAA TCTAAGCACT TTACGATTTC TTTCTACTTA ACTACACATA GTATTCCTGA 180

AACTTATGGC GTCATCGTAG ATACACCTGA AGGAAAAGTA GTTCATACCG GTGACTTTAA 240

ATTTGATTTT ACACCTGTAG GCAAACCAGC AAACATTGCT AAAATGGCTC AATTAGGCGA 300

AGAAGGCGTT CTATGTTTAC TTTCAGACTC AACAAATTCA CTTGTGCCTG ATTTTACTTT 360

AAGCGAACGT GAAGTTGGTC AAAACGTAGA TAAGATCTTC CGTAATTGTA AAGGTCGTAT 420

TATATTTGCT ACCTTCGCTT CTAATATTTA CCGAGTTCAA CAAGCAGTTG AAGCTGCTAT 480

CAAAAATAAC CGTAAAATTG TTACGTTCGG TCGTTCGATG GAAAACAATA TTAAAATAGG 540

TATGGAACTT GGTTATATTA AAGCACCACC TGAAACATTT ATTGAACCTA ATAAAATTAA 600

TACCGTACCG AAGCATGAGT TATTGATACT ATGTACTGGT TCACAAGGTG AACCAATGGC 660

AGCATTATCT AGAATTGCTA ATGGTACTCA TAAGCAAATT AAAATTATAC CTGAAGATAC 720

CGTTGTATTT AGTTCATCAC CTATCCCAGG TAATACAAAA AGTATTAACA GAACTATTAA 780

TTCCTTGTAT AAAGCTGGTG CAGATGTTAT CCATAGCAAG ATTTCTAACA TCCATACTTC 840

AGGGCATGGT TCTCAAGGTG ATCAACAATT AATGCTTCGA TTAATCAAGC CGAAATATTT 900

CTTACCTATT CATGGTGAAT ACCGTATGTT AAAAGCACAT GGTGAGACTG GTGTTGAATG 960

CGGCGTTGAA GAAGATAATG TCTTCATCTT TGATATTGGA GATGTCTTAG CTTTAACACA 1020

CGATTCAGCA CGTAAAGCTG GTCGCATTCC ATCTGGTAAT GTACTTGTTG ATGGTAGTGG 1080

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ACCAATGATT TTACCAGTCA TTATGAAGGT AAACGAACAA AAAGAATCAA ACAATAAATA 1440

GCTTTTTCTT TATATATGAT GAGCTTGAGA CATAAATCAA TGTTCAATGC TCTACAAAGT 1560

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TCAGGGGCCC CAACATAGAG AATTTCGAAA AGAAATTCTA CAGGCAATGC GAGTTGGGGT 1680

GTGGGCCCCA ACAAAGAGAA ATTGGATTCC CAATTTCTAC AGACAATGTA AGTTGGGGTG 1740

GGACGACGAA ATAAATTTTG AGAAAATATC ATTTCTGTCC CACTCCCGAT TATCTCGTCG 1800

CAATATTTTT TTCAAAGCGA TTTAAATCAT TATCATGTCC AATCATGATT AAAATATCAC 1860

CTATTTCTAA ATTAATATTT GGATTTGGTG AAATGATGAA CTCTTTGCCT CGTTTAATTG 1920

CAATAATGTT AATTCCATAT TGTGCTCTTA TATCTAAATC AATGATAGAC TGCCCCGCCA 1980

TCTTTTCAGT TGCTTTCAAT TCTACAATAG AATGCTCGTC TGCCAACTCA AGATAATCAA 2040

GTACACTTGC ACTCGCAACA TTATGCGCAA TACGTCTACC CATATCACGC TCAGGGTGCA 2100

CAACCGTATC TGCTCCAATT TTATTTAAAA TCTTTGCATG ATAATCATTT TGTGCTTTAG 2160

CAGTTACTTT TTTTACACCT AACTCTTTTA AAATTAAAGT CGTCAACGTA CTTGATTGAA 2220

TATTTTCACC AATTGCCACA ATGACATGAT CAAAGTTACG GATACCTAAA CTTTTCATAA 2280

CTGCTTCATC TGTAGTGTCT GCAACAACCG CATGAGTAGC GATATCACTA TATTCATTCA 2340

CTCTATTTTC ATCATGGTCG ATGGCCATTA CATCCATGTC TAATGCATTC AACTCACGAA 2400

CGATACTACC TCCAAAACGA CCTAGACCGA TGACTACATA TTCTTTACCC ATACTCGCCC 2460

TCCATTAAAT GATTTTCATC AATTCATTGA AAATATAAAT TTAAAATTAT TATAAATGAG 2520

TACCCCAACT AAATTATCTA AATGCAGTAA TGCAAGTAAA TGAAAGTTGG GGTATCGTCT 2580

CAACTTATGA TTTCTTTCCT TCAACATATT CTTTGTCGAA AACAAATAAT CTTAATAATA 2640

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GCCATTGTCT TGTTAAATTA TATGCTGGTT CGTCATTTGC TTTTTTAGCA TAATATGTCA 3060

AAAATCCTGA TGAAATATAT AAAACTGAAA TAATTGCCAA GAATACTACA GACCAAGCAA 3120

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CTAAATATTT GATTGACTCT GGAAAGAAAC CTACGAATCC TACGAAGAAG AAAACAAAGA 3420

ATACATTCGT AACTTCCCAA ACTGGGTTTA AATAACGTGA AATTAAGTGA TTAATTTTCT 3480

TTTCATCACC AGTTAACTTT GAATGCAATG CGAAGAAACC TGCCCCAAAA TCTATAGAAG 3540

CAATAATGAT ATAGCAAAAT AAAAACAACC ATAACACTGT TATACCTATA AATGCATAAA 3600

TCATTTTTCT ATTTCTCCTC CTTGCTTCTT GGCTAAACGA TTTACATCTT CATACGCCGG 3660

TTTATTTTTA AACATACGAA TTAATACGTA TGCACATGTA TACATTAAAA TGATGTACAA 3720

TATGCCAAAT AAAATTGTAA CGAaGGTTAT TCCGCCTGCT TGTGTTGCTG CTTCTGCCAC 3780

GCGCATATAA CCACGAACAA TCCAAGGCTG TCTACCCATC TCTGTTAAGA ACCATCCAAA 3840

TTCTATAGCT AGCATTGAAG CTGGGCCTGT TAATAATATT CCATAAAGCA TCCATTTATG 3900

AGTAGAAAAC TTTCTAAGCT TTTTAAACAT TAAAGTTAAG ACATAAACAC CTGAAATGAC 3960

AAAACATAAA ATTCCCATCG TTACCATTAA ATCAAAGAAA TAATGGACGA TCATAGGCGG 4020

ATGTAAACTT TTTGGAAAAT CATTTAACCC TTGTACTTTA GTTTTGACAC TATTATCTGC 4080

TAAGAAACTC AATAGTCCAG GTAATTCAAT CGCACCTTTA ACTTGCTGAG TCTTTTCATC 4140

TAACACACCA AATAATAATA ATTTGGCATG GGAAGATGTA TCGAAATGCC ATTCATAAGC 4200

TGCTAATTTT TCAGGTTGGA ATTTATGCAA AAATTTTGCA GATAAATCCC CTGCCAACAT 4260

AGAAAGTAAT GTTGAAAAGA ATCCAACTAT CATAGACATT TTCAAAGCTT TCTTATGGTA 4320

GACAGTATCT TTAGGTTGAC GATTACGCAA TAATTTAAAA GCTGCTATTG ATGCAATAAC 4380

AAATGCCATC GTCATACCGG CTGTAGTAAT TACGTGAAAT GATCGAACTA TAAACGATGG 4440

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AATAATTACT GGTATACTAA TTAAGAAATG TGTCCATTTA TTTTTAAAAC GATCCCAAGT 4620

ATATAAATAT ATACTTAAGA AAATAGCTTC AAAGAAGAAC GCAAATGTTT CCATAAATAA 4680

TGGAAGTGCA ATAACGTGTC CACCCATTTC CATAAATGTA GGCCAAATCA ATGATAATTG 4740

AAGTCCTATA ATTGTACCTG TAACAACTCC CACTGCTACA GTAATTGTAT AAGCTTTAGC 4800

CCATCTTTTG GCCATAGCTA TATATTGAAG ATCATTTTTG CGAATACCTA AAAATTCTGC 4860

AATTGCGAAC ATTAAAGGCA TACCAACACC AATCGTTGCA AAAATGATAT GAACTGCTAA 4920

AGTCATAGCT GTCAAAAACC GACTGATTTC AACTGTATCC ATTTAAAAAC ATCACCTTTT 4980

TCTTTTTTTG ATGACAACAC AATGAACTTA ATTATAATTG CTATAATGTG TATTTTTAAA 5040

GAATTTCAAT GTATAATTGT GTATATTACA TTAGAATAAA GCACGAAGGA GCATGATACA 5160

TGTCAGAAAT AATCGTTTAT ACGCAGAATG ATTGTCCACC TTGTACATTT GTAAAAAATT 5220

ATCTAAATGA GCATCACATT GATTTTGAAG AGAGAAATAT CAACAATCAA CAATATCGAA 5280

ACGAAATGAT AGATTTTGAT GCTTTTTCAA CTCCGTTTAT TTTGTTGAAT GGC 5333

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

ATACGTGACC CTTTATCCGA AAATTTCTTT TCATATTCTG TTAAAATATT ACTGCCATCG 60

TCTTCTTGAT GTAAATTTAG ATTTATTTTT GTAAAATACA TTCCAAATTG AGACATACTT 120

TCTAAACTGT AGGCAAATAG TCCTCTGTTA TCAGTTTTAA AATGTAAATC TCCTTCATCA 180

TTTAAGATTT GTTGATACAA CGCTAAAAAC GTATGATACG TTAAACGTCG TTTTGCATGA 240

CGATTTTTTG GCCATGGATC TGAAAAGTTC AAATAAATAC GCGAAACTTC GCCGTCTTTA 300

AAATATTCAT TTAATTCAAT GGCGTCATTA CAAATAATCT TTAAATTTGT TAAACCCATC 360

TCTTTAACTT TATCCAATAC TTTATAAACG ATACTTTTCT CACGTTCCAT TGAAATATAG 420

TTAATATGAG GATTTTGAGC AGCTAATGTT GTAATAAACT GCCCCATACC CGAACCAATT 480

TCAATGTGTA TCGGTTGCGT TTTaTCAAAC CATTCAGTCA TTTTCCCTGc ATGTTGACCG 540

TCCATGTCAA CCAATTCAGG ATGATCTTTT AAATAATCTT CAGCCCATGG TTTGTATCGA 600

ACTCTCATAT TTTATTCTCC TCTTAAATAA ACATGTTACT ATTCATAACT TCATTTAGGA 660

ATTTAAGCCA AGTGTTCATA TCCTTATATC TTTTTTGCTC TTCATACCAT TGAACAAGAC 720

CTATAGATTG AATTACCGTA TACCATTTCA TACGTTTATT TAAATTCAAG CTCTCTTGAA 780

CACCATATGT TTCAAGCCAT TCAGACCATT GTTGTTGTGG AACATAGTTG TAAAGCAGCA 840

TTCCGATATC AATTGCCGGG TCTGCAATCA TTGCACCTTC CCAATCAACT AAAAATAGTT 900

CATCTCGATC GGATAATAAC CAATTATTAT GATTCACATC ACCATGTACA ACAGTGAAAA 960

AACGCGAATC TAAACTCGGT ATATGCTCTT CTAAATAGGT TAATGATTTT CTCACAATAT 1020

GATGTGTTAA AACTTCTCTT GATAAAGAGG CATTAATTTT ATTAAGCATA ATCTCAGGAG 1080

TAATAGGTTC CATTTCCATA CGCTTTAACA TACTTAATAA AGGTCTAGAA TTGTGTATCT 1140

TTTTCCAATG TTGTGCTGTA ACAACCTCGC CTGTTTCTAT GCGTTTCGTC CATACTAATT 1260

TGGGCACAAT ACCTTCTGCT GATAATGCCG CAATAAATGG ATTTGAATTT CGTTTTAAAA 1320

ACAACTTTTG TCCATCTTGT TCAGCCATAT ATGCTTCACC AGATGCACCA CCTGCTGAAT 1380

CAAGTGTCCA CCCTAATTGA TAAAACTGCT CCAACTCGTC CACCTCACTT TCAATTAGAA 1440

AATGGCTCTA GAAATAGGTT TTTCAAGAGC CATATATTCT AATTTATAAC ACCATACTGG 1500

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TAAATTTAAA TCGTAATGTC TGTCATTGAC ACCATACATT CTATAGTCAC TTACTTGACA 1620

TATAATGTTA CCGTGTCTAA AACTACATGT TTTTGAATCT CTGTAGGCGA TAAACTcTAG 1680

TTTTCAAAAT AATTGCTATC CCATTTTCAT GGTTAGCATA AATTTATGAA CTGTAACATT 1740

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TATAGTCTTC GGCAATTTTT TTAATTACAA TTCGTGTAAT ACCATTAAGA ATATAGTTGT 2220

TAATCGGATG TGTATAAATC ACACCGTCTT TAATTGCATA AGCATTACTT GAAGATCCTT 2280

CAGTTACAGT TtCACCTCGA TGTTGAATTG CTTCAACTGC ATTATATTTC ACAGCATATT 2340

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ATATCTTCAA CGGTAACACC ATTCACACCA TTTTCTAAAT GATCATAAGG ACGATCATAA 2460

CTCTTTGTAT AAGCAACAAT TGCTGGTTCT ACTTCAGGTG TCGGGAAGCT ATGATTCCTT 2520

TCAGCTACAC CACGCGTTGC TyGAATATAA ATTGCCCCAG TTTCAATTTG ATTCATATCA 2580

ACTAATTTAC GAGATAGTTC AATTAATTCT TCTACAGAAT AATTTAAATC TAAACCAATC 2640

TCATTGGCAC TACGTwAAAw TCTTTCATAA TGTTCTGTTA CTGTAAATAA CTTACCATTA 2700

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TGAATCTCAT TTGCAAAACG ATCCATAGCT TTTTCAAATT CAAATCCTTC TGGGTAGCGT 3180

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TTAAATAAGT AGCGATTACT AAATGCTACA AACGCTTGTG CATTATTATC AAGATTTAAT 3360

GATGCTAAGA ATTTTAGTAA GTAAAGACCC GCATTCACAC CGATAGATGG ATCCATACCA 3420

TGAACCGCTT TACCTTCAAC TGTTAAAACT AGAATGCCAC TATCAACAGT ACTATCACCT 3480

TGTAAATGAT TTTGTTCTAA AAAGTACTCA AAGTCTTGAA TAACATCTGT CATATTTTCT 3540

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AAAGTTATTA ATTCATAATC AGGTTCATCT TGATCTTCAG TAAGTTTATT TTGAACTAAA 3660

TCAAATGTTG TAATGCCTTT TTCACCATGA ATACATGGAA ATTCTGCATC TGGTGCAAAA 3720

CCTAATGTTG GCATTTCTTC TGTTTTAAAA TAGCGATCCG TACATTTCCA ATCAGATTCT 3780

TCATCCGTAC CAATAATCAT ATGAATACGT TTCTTCCAAT CCACATTCAT ATCTTCTAAT 3840

ATCTTAATTG CATAATAAGC AGCAATTGTT GGACCTTTGT CATCAAGTGT ACCTCTAGCT 3900

ATGATAGCAT CTTCTGTTAC AACCGGCTCG AACGGATTAC TATCCCATCC ATCACCAGCA 3960

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TATTGTTGAA CTTTTTCTTT CCACATTCGA AATCGACTTC CTTTTTTCTA TAAGTTAAAT 4260

TCTATTTTAC ATGAAAAGAT ATAAAAACTA CAATAAGATG TCAGAAAATA ATAAAAAGGA 4320

ACAAAACGAT GCTATTGATA TGACACAAAT CATAAATAGC TGCTTTGTTC CTTTTTTAAT 4380

TTATATATTT AAAATACACA TATTCAAGAG CTCGAGATAT AAGTCAATGT ACTAGGCACA 4440

CAATTTAATA TTGACAGTAA TTAACCGAAC GAAAATGCGC CCCGGGGCCC CAACATAGAG 4500

AATTTCGAAA AGAAATTCTA CAGACAATGC AAGTTGGCGG GGCCCCAACA TAGAAGCTGG 4560

CCAATAGTTA GCTTTCAATA ATGTGCAAGT TGGGGTAAGG GCCCCAACAC AGAAGCTGGC 4620

CAATAGTCAG CTTTCAATAA TGTGCAAGTT GGGGTAAGGG CCCCAACACA GAGAATTTCG 4680

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CAAGCTTTTT TCAATTCTAG TCAACCTTGC CGGGGTGGGA CGACGAAATA AATTTTGCTA 5040

AAATATGATT TCTGTCCCAC TCCCTTATCA TTTCTGTCCT ACTCACATCT TATTCTTTAT 5100

CAGATAATGC ATTTTTATTC TTTTTTAAAT CTTCTTCAGT GACGATACGT AAATTATTAT 5160

TTGGTGTGCG CCACCTTCAT CATCAAATTT ACCTTTTTCA ATACTTTCGT CAGTCTTATT 5220

GTCATATTCG GTAAATTTTG ATTTTTCTTC TTTGAAAAAT GCTTTTGGAT TATTTTTTAA 5280

TCTATTAGCA TATTCTTTCG GATTTGTTTT TACTTCTTTA ATTGTTTCAT TAGCAATTGT 5340

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ATTAATTCTC CACGAACTGT TATCTTATCG TTTTCTGGTT CTATATGTGT TTTTGGTGAT 6120

TTAATTACTT GTTCGTTGAC ATTTACAAGG CCTTTTTTAA GTAACTGTTT GACCTCATTA 6180

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ACTTGATAAC TACAGAAGCT AAAATAACAT AAACTGTTAA TTTCTGTTTA TCTATACCTT 6660

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ATAATAAGCG ACTACCATCA TGGTTAGGGT CATGACCTAA AACAATTGGA TCGTAACCAT 6780

AGAAAACTGT GAATAATGGT TGTGCCAAGG CCATAATTCC AATACTAGCT GGAACAGTTA 6840

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TCGGAATCAT TACAATTTTA TTAGTTGACA TATTTAGCAT ATTAAAGAAT ATATCTTGTA 7020

ACTGTGAAGG TATACCAACT AAAGATAAAG CACCGTTATG TGTAAATTGA TCTACTAAGT 7080

TAAATAATGG ATAATTCAAA CTTACAATAA CGAACGGTAT ACTATAAGCA ATAATTTCTT 7140

TATACATCTT GCCATATGAC ACATCTATAT CTGTGTAATC AGATTCGACC ATACGATCAA 7200

TATTATGCTT ACGCTTTCTC CAGTAATACC AGAGTGTGaA TATACCAATA ATCGCACCAA 7260

CTGCTGCTGC AAAAGTAGCA ATACCATTGG CTAATAAAAT AGAGCCATCA AAGACATTTA 7320

GTACTAAATA ACTTCCGATT AATATGAAAA TCACGCGTGC AATTTGCTCA GTTACTTCTG 7380

ACACTGCTGT TGGCCCCATA GATTTATAAC CTTGGAATAT CCCTCTCCAT GTCGCTAATA 7440

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AAAGTACGCC CAATACCTTG GTAATTAATA TACTAATGGT AATTAAAAAG GTTCCACGCA 7860

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CATTTTGAGC TTCGGCTTTT ACACCAACAG ATTGACGCGC TGCTGGTTTA ACTTGAACTT 11040

TAGGTAAAAT CACTTTGATG TTGTCGTTGC CATCAGTCnC AGTnCGATCC ACTTCTGCAT 11100

TCGTTTTGTT TTGTGCAATG TCATTT 11126

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3660 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

TTGCCCCGCA CGGCGGTGTG nTTCCTAGAA ATAATGAATA TAAAGaGAAA TATATAACAA 60

CGATTTTGAA TTATGAACCT GGTGATATCG TTACAATCAA ACGTGTGAGA GATAAGACCG 120

ATTTGCTAAT ATATTTGTCT AGTAAAGATA TTTCTATTGG TAATGAAGTG GAAATTGTAT 180

CGAAAGATGA AATGAATAAA GTAATTATCA TTAAACGTAA TGATAATGTA ATTATTGTCA 240

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ATCTTTTGCA CGGCCACCAG CGAGTTTATT AAACAGTACA TGACCAAATT CATGTGTTAA 960

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CGTATTAAAA AAGTTTGATA AATAATTCAT TGTTAACCTC ATATAAGATA TTAATTTAAA 1140

GTTTGCTTAT CACTTATTAT AAATGATATT GGCATCAATA GCGTTAGACT TTAGACTTAC 1200

CTTAGTTAAA CTAATTTTAA TTTTTGAAAA GGTGAATATG TGTTAAAATA AAGCAAAATC 1260

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TAGAAAATTA AACATTGAAT GGATATATAG AGCATTAATA GATTGGAAAC GTATTGGTAG 2040

ATTAAAGAGT ATTCCAATAT TTATGTATAA AATAGCCAAA GCaAAAAGAA AAATAAAAAA 2100

GGCGAAATAA TCATGATGAC AAAAATAAAA CCGAGGAAAT CCTTAAATGG AGATTCTCGG 2160

TTTTTTCGGT TTATTTAATA ACGAAGCGGG ACTCATCGAG TTTGTTTCTA AATTCTTTTT 2220

CATCAAGTTC ACCGTAATCT TTTAACTTTC CGCCTTCAAT CCAAGCAATC TTAGTACAAA 2340

ATTGTCTCAC TTGTCCTAAG TTATGACTAA CGAAAAAGAT GGTTTTGTTT TGCTCTTTAA 2400

ACTCGTAAAT TTTATCTAAA CATTTTTGTG CAAAAGTTTG GTCACCTACA GATAAAGCTT 2460

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TATTGCTCAA CGTTGATTTG CCGGAACCAT TGATGCCAAC AAGCCCTATG ACGTCACCTT 2820

CATATGCTTT TAAACTAATG TCATCTAAAG CGAAAAATGT TTTGTTTTTA TGTTTGGGAA 2880

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TGGCTTGGGA ATTAATTAAC CCTGTTATGC AAATTATGGT TTACTGGATG GTTTTTGGAT 3480

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GTATCAGTAT GTGGTTCTTC ATCAACCAAG GTATTTTAGA AGGTACTAAA GCAATTACAC 3600

AAAAGTTTAA TCAAGTATCG AAAATGAAcT TCCCGTTATC GATAtACCGA CATATATTGT 3660

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13868 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

ATTAATCACT TGTTGTGTAG AGTCTTGTCC GTTTTGGTTA TGATTGTTAG CCATGATATA 120

CCTCCCTTAC AACACTCGTG GACCAGAAGT TTTCTGATCT CTCACATTAA CTTCTAACTT 180

ACGTACTGGC ATTTCTGTGA AATATTCTAC ATTCTTTTTA ATATCCGAAC GAATTGCTTC 240

AGTTAAAGAT TGAACTTGAA CATTATTTGG TACGAAAAAG TCAGTTTTAA TGTCGATATA 300

AGATTTATTT TTTTTGTTAT ATAGTTTCGC AACTACATTT GGTTGTCTTA CTTGATCATA 360

TTTTGCAACC GTATCGAATG CCGTCTTTTC AACAGCTTTA CGAGATACGT AAACATGACC 420

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CGTACGTCCT TTTGACACAC GTGCAATAAA TATACCTACA AATGGTGCCC AAGATATCCA 1440

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ATTTAAAATG TATAGCGTTG GCCCAACAAT AAAAAGACCA ATAAGTACTA CAAAAGCAAG 1620

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ATGAAAGCTA AAATATGCAA ACACTAGCGC GACAATACCA TAGACTGCCC ATGCATGAAT 1980

CCCCCAATGG AAAAATGAAA ACTGCATTGC ATCATTAATT GCAGATTGCG TGCCAGCTTT 2040

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TCCTATTCCC ATACCAGCAC TAAATAACAT AGCAAACCAA GACGGCAATG AGAATTCAGG 2160

ATCTTCGCCT TCTTCACCTA ATGTAATGTT TGCGTATCTC GAAAATAAAA TATACACACA 2220

GACAAATAAA ATAACTAAAA CGAGCAATAA ATAATACCAA GAAAAATGTA GCGCAATAAA 2280

TGTAGTAATG TTTTGCGTGA GTTTTTCTAA CTGTTTCGGA AATATTGCTC CAAAAGCAAC 2340

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CACACTCAAA TTATTTATCA TTGAGCAACA AAGTATTTTA TTGTATTTAA GTAATGCCTT 2580

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TAGACTTATT TCTACCATGT TGCTGAACAA ATTTACTTTA GATAAAAAAT TATTAAATTT 3900

TGGTCAATTA ACAAAGTTAG TTTGTTAAAA CGTgATACTT TATTATTCCG TTACTTTAAT 3960

AACTTGTTTA CCAAAGTTAT CGCCAGTaAA TAAATTTTTA AATGCATGTG GCGCATTTTC 4020

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TACTTGCTTC TTAATAAGCG TACCTTGAAT ACGTGGTCCG ATATCGGCTT CAGGATGATT 4200

ATATGACGAA ATTGCGCCAC ATACTGGTAC ACGTGCAAAA CGATTTAAAT GCTTAAATAC 4260

TTCATCGCCA ACTGTTCCAC CAACATTTTC AAAATAAACA TCAATACCAT CTGGTACTGC 4320

TTGTGCTAAC GCTTCTGCAA AATCCTCTTT CTTATAATCA ATACCAGCGT CAAAGCCCAG 4380

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CGGTTTACCA ATTTCAAAAG GCTGTACATA CGAATCTGCC TTAGTCATAC GTCCTCTCAT 4800

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TTCAGATTGT AACTTAGTCA GTACATTTTT AAACCACGCA GCATTCTTAT CCAAATAGCC 5760

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CCCTCTTTTT TCTGCTTGCT TCACCATAAA CTTTTCAGAA TTGGCACTAC CACCAAATCC 5940

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GAACTGTTTT TTCAGATTCA ATAAATTCAT CTTTATATCC TAAACCATTT TCAGTGATAT 6660

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GAGGATAGAT CATCCAGTCC CAGTCTGTGC GAGGTACGTC GACATCAAAT TCACGTTGTC 6780

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CGCCATTAAC AGATAAGATA TGTTGCACAC CTTCCATCGT TTCACGAGAA TACTTACCTA 7020

AATATGTTGC ATCTAAGATG AATTTATTAT GGATGATATC TTCTAATTCT GCTGCACGAA 7080

CATCTTCAGG ATTTGATGGA TCGAACGGAT ATTTTGTTGG CAATGCGTGT ACAACACCAA 7140

TTTCTCCTTT GTATCCGCCA TCTTTAAATA ATTTTACTGC TCTAGCATGA GCCACCATCA 7200

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CTTCTGGGAA TTCTTTAAAA CAATATTCAG CATAATCTAC AAAGTAGTCA ATCGTTTTAC 7380

GATTTAGAAA ATCGCCATCT TTGTGTAaCA CTTCTGGTGT ATCAAAATGA TGCAATGTTA 7440

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ATAGTTAGAC GCAACTTGTG GCGCTAAAAT GATTAATTGG TACTCTTTCA TAATGTCCAT 7980

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ATTAAGTGCA TTGGCTAATA ATCCACTTGT ACCACCACCG GCACAAAGTA CTAAGACATT 8100

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TGCTAATACA AATGGAATAA AGAACACAGG ATTCAATACT AGTGGTGCAC CAAATAAAAT 8520

TGGTTCGTTT ACACCAAAGA ATGTTGGTAC AACTGATGCA CGTCCAATCG CTTTGTTTCG 8580

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GATGGCTCTT AAATATATGT TACGTGATAA TTTCTCGAAA AATGGCTTCC CTTTTTCAAT 9480

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CTTTCAATGT ATGCTTTCTT TTGAATGTTA ATTTCTTCAG CATCATCAAC ATCATAGTAA 10440

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TACTGCGTTA CTACTAAAGA ACATCTTGCT AAATCTTAGT TTTTCCAACA TGGCGTTCGC 13380

cATTTCACCT ACAAATGCTT CTGTAATATG GCGCATTTCA CCACCAATTA AATAGACACG 13440

AAAATGTGCT GTTTGTTTTT CTAACAAAAT TTTATACACC GGCAAACAAT TCGTAATAAT 13500

TGTGAGCGTA TGATGATTGA CTTCTTCTGC TAATAGTTCC ACTGTTGTTC CTGGTCCGAA 13560

AAACAAAGTA TCCCCATCTT CAATTAATGA TGCAGCTTTT TTAGCTATAA ATCGTTTTTC 13620

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GCCCTTTTTA TTCACTAGTT TAGCAATTTC GTCCAAACGT TCATGTTTAT TCAATGTAAA 13860

ATTGCCTC 13868

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

TTAAGTCAAC TTTGTCTATA CGGTTTGGAT CtTCTaCCCA ATGTCTTATA AAAGACAATC 60

CCGCACCTGA AACATAACTC ATGAAATAAG AAAATGGTAT ACCATTAATT TGATCATTTT 120

AATCTTTACC CATACGAAAC ATCAATTGAT AAAATGCGAT GTCTTTTTCT ATCATTTCTA 240

TTAAAACGGT CATAATTTGA TGTATGTTAT CCGTGGATAA CTTAACTGCT CCATTTAACT 300

TCTCATCATG AATGAAGTCT CTTATTTCCT CCAACTGCTG GTCCTCTAAT TTTTCAAGCA 360

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TAAAGTTGCA TTACGCGGTA GTGACAAATC CAAAGGCGTC TTATCTCCAT GGTCAAAAAG 1080

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GCATAAGTCA TGATTATGAC TACATCGCCT ACTTCAACAA GTCTTGACGC TGCACCGTTT 2640

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GAAAATCATA AGCTGTTACC ATAGAAATTT TAGTTTGCTT TTGTTTCATA TCTATTAATT 4500

GACTTACTGT TTTCAATGTT ATTCAACCTC TTTTTGCAGT ATnATTAGA 4549

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

TTATCTTTTG TTGTTTCCTT AGACAAACGA CTAACCACAT TATAATGGAC TAATTTATTA 60

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ATTTTTTGTA GACGTTCTAA TTCTTTAGAG TTTTCATCAT CTTTCTCTAC AGTTTTTAAA 360

AATGCTAATT TATCATGATA TTCTTTAATC ACGTTACCAT ATTTAAAACT TGTTTCGAAA 420

GTAGATTTTT GATTTAGATA ATCAATAACT TGTTCTAATA TATAAATTCT AGCAACTTTA 480

AACGACATAT TGCCAATTAC TGTTTTAGGT GCAGGTTTCG TTAATAATGG CAATAATACT 540

TGCGCAACTA CCAAACTAAT AATAACCATA CCAGATGCAA TAAATAATAA GTCGTTTCTA 600

ATTGTTCCAT GCACACCACA TAACGTCATA ATTAAAGCGT ATAAACTTCG CTTTGGTGGT 720

TTCTCAGTCG TTGGATTATC ATCATCATTT TTAGTCATCA TTTTTTGGAA TGGACTGATG 780

GCTAAATAAA AATAAGGATA TAAGACATAA ACCCAAACAA ATCTAAATAG ATAGACAGCT 840

AAAGCAACAA CAATAGTGAT GCCTATTAAA AAGATTAAAT TGTGCGGTTC TGTTTTGATA 900

ATTTTAATAA TAACTTCAGG TACTAAAAAT CCTAATATTG AAAAAACAAA GCCATTTAAA 960

ACATAACCTA GTATATTCCA TGTATGATTG TAACTCATTT GCAGTTGTGT ACGTACTTGC 1020

ATAATTCTGT CACGTTCGAA ACCATGTACA AGTCCTGCAA CTACTGCTGC AATGATTCCT 1080

GATGCGTGaA ACAATTCAGC AATTAAATAC GTAACAAATG GTGTTAACAA TTGAATAATT 1140

GTAAACATAT TAATGTTTTC ATATCCTCGA CGCATCAATG TTAATCGGAA CCTTACTAAT 1200

GCCATACCTA TAAGTAAACC AACCACTGCG CCACCAATTG ATGCAATTAA AAACAACTGA 1260

ACAGCATCAA CAAGTGAAAA AGCACCTGTA ACTAATACTC CAACAGCTAT TTTAAATGAA 1320

ATAATACCAG CAGCATCATT CAATAATGAC TCACCTTCAA GAATTGTCAT TGCTCCTTTT 1380

GGCAAGACCT TTCCTTTAGT GATTGCTTGC ACTGCTACTG CATCAGTAGG ACAAAGAATG 1440

GCAGCAATTG CAAATGCTGC TCCAATAGGT AAATCTGGCC AAATCCAATG AATAAATAAA 1500

CCTACACCTA TCACAGTAGT AATGACTAAT CCTAATGCCA TCATCATCAC TGGCTTAATA 1560

TATTTCCTTA AATGGACTCT AGAAACATTA ACACCTTCTA CAAATAACAA AGGCGCAATC 1620

ATTGTTACCA TAAACAATTC AGAATCAAAA TTAAATTGAA CAGGGATTGG GGTAATAAAT 1680

AGTAACATGC CCAAGAAAAT TTGTATAAAT GCTAGGGGTA CTTTAGGTAT GAAAGTATGG 1740

ACAAACGAAC TTAGTATCAC AACAGCTATA AATATAAGAA TTGTTTCAAA TATTTCCAAA 1800

CTTTCACCTC TCTAAAAAGT ATTGTTTAAT TGAAAATTAA GTATCACATC TCGTTGTAAT 1860

TATACTTTAG AGGATAAATT GAGTTAGCGA CCACAAAAGC ACTTTAATAT AGATATATGT 1920

CTACGATTGC AGTACTTAAA TTTGCAATTA TTTAATTTTA TTTTATCACT AATTGTTTGT 1980

ATAAATAAAC AACTTGCTTT CACATAACAA CATTAACTTA TAATACAAAA AATGAGCACC 2040

TTAAAATCGA CTAACCAATT TCaAAGTACT CTTTTAATGA TTAATTTTGA AAACAGATTT 2100

TCaAAAGCAT TGTTATGCTT AACAATTTAG CCAACACTTC AATCGTTTTG ATACCATTTC 2160

TTACGATGCT CTTCTCGTTT TTCAGCACGT AATTGTAATG CTTCTGTAGA GTTTTGTTCA 2220

TTTGAACTTA ATAATATTGA TGCATGTGTG TGAGCATCAT TTTTTCGATA CATATAAGCG 2280

CCGTTGCGAT AAGCAGCGCG AGCGACTAAG TGCATGCCGA CTGGTGAAGT TAAATTAATA 2340

AAAACAAGTG ACAGTAATAA ACGCACACTG AAAAATCCTG TATTCACAAT AAAATAAATT 2400

CTTAAGAAAA CATCTTGGAA TTTCACGATA CCTATTGCAC TAATAAGAGC AATAAAACTA 2520

CCTAACAACA ACATCACAGC AGCAATAAGA CTAAAGATTT CTTTTGTTAT TTCCATTAAA 2580

CACATGCCCC CCACCAATAA AGCGTGATAT TGAAACAGAA CTTACAAAAG ATATAATGGC 2640

AATGAGCATG ATTGAATCTA AGAAAGAAAC GGTGCCCATA AGTACACTTA ACACACCCAC 2700

AATTGACATT ACGACAGCAC TTGTTGTATC AAATGTAACG ACACGATCTG CTGTTGTAGG 2760

TCCCTTGATT AATCTAAATA AACAGATGAT TAATGCAATT CCAAAAATAA TGAGTGAACT 2820

AATAATCATA ATATGTGTTA TTGTTTGTAT CATCGCGACA CCTCCAATAT TAAGTCTTCA 2880

TAATGCTTAA TACTTCTTAA CAAACTATCT TTTTCTTTTT CTGACACGTC GATACTATGA 2940

ATAAAAAACT TTTTAGAGTC TTGAGAAATT CGTATTACTG TAGACCCTGG AGTTATAATA 3000

ATTAAAATTG TTAAAAATGT TATTGACCAA TCACTTGTTA GTCTTGTTTC ATATGAAAGT 3060

AATCCAGGGT TCATATCTTT TGTTTTAAAA AGAATATAAT TAATCGTGCT AATGCTAGAT 3120

GTTATTAATT GATATAAATA AACACCTAAA AATTTAATAG CTACCCATAT TTTTCTAACA 3180

TAAAAATCAT CGCTGAAAAA CCTGTGTAAT ATATAAATGA CAATTAAACC AATTAGATAT 3240

CCAGAAAAGA AAGTCGAGAA TTTAAAATGA TCTTCATCTT GAAATAATAC CCATAAGAAT 3300

GCAATGATAA TATTTAAAAC TATTTGATTC ATTTAGTCCT CTCCTTTCAA ATGCGGATTT 3360

ACAAGTTTTT GATATAATTG ATCACTCGTG TTCAACTCAG TTGCATCACT TGTAACATTT 3420

AACACAACAG GTGCAGCAAT TCCGATTGCG ATAACCACAA CTACTAAAAT ACTTAAAATT 3480

CTTTTTCGAT ATAGCGGGAT TTTCTTAAAA TTAACTTCCT CCCCATCTTT ATCTCCAAAA 3540

TACATATAAA AAAGTATCCT AAATAAACTG TACATTGCAA TTAGACTAGT AATAATCATT 3600

AACGCTAGTC CAATATAATT GCCATTTTGC AATGCACCTT GGAAAATAAG TACTTTCCCC 3660

GGAAAAGCCAC TAAATGGAGG CACGCCGCCA ATAGCAAAAA TCATTATAAT AAACGCAACT 3720

CCAAATAAAG GTTCTTTTTT AGCTAAGCCA TTCAAATATT GATATTGTCG ATAGCCTGTA 3780

ATGTAAACTA AACTACCAAT AATAAAAAAT AGCAATGTTT TTACAACAAT GTCATTTACC 3840

AAATAAAATA TTGCACCATT AATACCTGCA AACGTGTTTG TTCCTAAACC TAAAATGATA 3900

AATCCTATTG AGATTATGAC TTGGTAAGCT GCAATCTTTT TAATATCTTT ATAAGCAATG 3960

ACACCTATAG CGCCGATGAC CATAGTTATA GCAGCCATAG TTGCTAGCAA TGGATGTATG 4020

AGATCATTAT GTTGATCAAA TAGTAAAGTG AAGAATCGAA TTAATGCATA GGCCCCTACT 4080

TTGGTCATTA ACGCTGCAAA TAATGCTGCA AGCTcAGTAT TTAACACAGC GTAGGCTTTG 4140

GGTAGCCACA TAAAAAGGAC CAGCGCTGCT TTCGCACTAA ATGCGACTAA GAAGATTAAT 4200

AAGTTTAATG TACCTACTGT TTTATAAAGT AAACCTATAC CTAATAAGAA TAGCCATGAA 4320

CCAATAATAT TCAAGACAAC ATAAATAATT GCAGCACGTA ATTGTTCTAC AGATTGTCCA 4380

AGTGTAATGA GTACAAATGA CGCTAGTAAC ATAATTTCAA ACATGACGTA TAAATTAAAT 4440

AAATCTGATG TTAGAAAAGA GCCTATCACG CCAACACTTA AAAATAATAT GAACGATGGC 4500

AAGTGATAAC GATTTGCTTT ATGTTCGCCA CGCCCAAATC CGTATGCCAT AATTAAAGTA 4560

ATCACAAACG AAGCGGTTGT AACCATAATT AAACTTAAAG AATCTCCTAA AAACTGTATA 4620

CCAAAGGGCG CTGACCATCC TCCAAAGTCT AGCGTAATTG GACGGTGACG CTGAACATAA 4680

ATTAATAGCA TTAATGAAAT AATTGTGGTG ATAGTCATTG TACCTAAGTA TAAATATTTA 4740

GAAATACGAT CATTATTTTT TAAAAATACA AGGATTAAGG CACAAAGGAA TGGTAATAAC 4800

ATTGGTAAAA TCAATAAGTT ACTTAGCATC ATCTTCCCCC CTTAGGCCTT CAATTTCATC 4860

TTCTTTTGTT ACTTTATAAG TTCTATAAAC AAGTACAAGT AAAAACGCAG TCATCCCAAA 4920

CCCTATAACT ATTGCAGTTA GTACAATAGC TTGTAACAAG GGATCAACAA ACAATTGGTT 4980

TCCACCAGTT ATTAGTGGTT CTGATCTACT AGAACCATAC GTTCCCATAC TCATAATAAT 5040

GAGATTACCA GCATGAGTAT ATATTGAAAT TCCGATTACA ATACGAATTA AATTGATTGA 5100

TAAAATCATA TATGTTCCTA TAAACACTAA AAATCCTATA ACTAGTAATA ATATTAAATT 5160

CATGATCGAC CTCCGCTAAG CGACAACATC ACTGTGACAA TAACACCAAC AACTGAGAAT 5220

AAAATACCTA ATTCAAAAAG TGTTATTGTA CTTACATGAA TTTGTCCTAA AATTGGAAGT 5280

ATCCAAGTTG TTTCATATTG AGACAAAAAT GGTTTTCCAA AAAACATAGG TATTATCGCA 5340

GTAATAGATG ATACCAATGC TCCAATAATC ATTAAAATTC TAAAATCAAT CGGTAAACTT 5400

TCTAAAACCT CTTCAACATT AAAAGCCAGA AACATTAAAA TAAACGCTGA ACTAAATATT 5460

AAACCACCAA TAAACCCACC ACCAGGATTA TTATGACCTG CGAAGAAGAC ATAGAATCCG 5520

AAAGTCAATA AAATAAATAC AACAAGTTTC GTGACCGTTC TTAACACGAC ATCATTCTCT 5580

TTCATCTTGT CCCCTCCGAT CTTGATAATT TAATAATGtg TAAATACCTA GCCCAGTAAT 5640

AATTAACACT AATCCTTCAA ATAATGTATC TAATGCTCTA AAGTCACCAA GTATCGCATT 5700

TACAATATTT TTACCACCTG TTAGTTTGTC AGCTTTTAAA TAAAAGTCTG ATATTGATGA 5760

TAAACCATCT GTTTGTTGTG TAATAAAAAT TAATGATACA ACAATAAGTG CCATCAAGAG 5820

TGATACAGAA ATTTTAATTA TTTCTCTTTT TTTGTTAGCG TTAGATCTTG GCACGTTTGG 5880

TAATCTTGAA AAACTGACAA TAAATAGTAT CGTCGTTATT GTTTCAACTA CTAGCTGAGT 5940

CAATGCTAGA TCAGGGGCTT TCATTGCTAT AAAGAATAAG GTCACAACAA ATCCGATGAC 6000

GACAGTTACG ATTGCTAATA TAATTTCTAA TGCCCCAAAT TCAGAAACAT GTAACTGATG 6120

TACTTTAGGA AGTCCaATTC GAATATAACC ATATCCAATG ATAATCATAA ATATGCCTAA 6180

GGTCATAATA ATGTACTGGT TTAAACGATC TTGCATAACA CGTTTAAATC GCTTCGTAGC 6240

AAACTTTTCA AAATGTCGAT ATACCATCTC ATAGCTTTTT GAAACTGAAA TCTGTCTAAT 6300

TTTACCTGTG AACACTTTTT TCCAATCTAC TTTGATTGCT AGTACACTAC CCAATAAAAT 6360

AATGATGATG GTTAAAAGAA GCGGTATGTT AAATCCATGC CATTGCGAAA CATGTGGTGC 6420

CAATTGATCA ATTTGATGAT TACCACCTGA TACAGCTCTT AATGCnAGAA CGATAATCCC 6480

CTTCCCAAAT ATATnTGGTA CAAAAAAGAT TACAGGTACT AGCACCATTA aTATAAGAGA 6540

TGGTAAACTA aACAACCATG GTTCGTGGAT ATTTTTTTTA GTAAAAACCT TAGAATCATA 6600

TTTTGtCCAA AATACTTCTT TTACCATGTA TAGTGCATAT GTGAATGTAA AAACACTCGC 6660

AATAACACCA ACAAACACGA TAGCTATCAT TGAAATCAAA CTAAATTGGG ATAATTGTCC 6720

AGTTTGTGTT AATGCATCTA AAAACATTTC TTTACTTAAA AATCCATTTA AAAATGGTAC 6780

TCCAGCCATA GATAGAGCCG CTATCGTCAT GACTAGATTC ATTTTAGGAA ATAGTTGACG 6840

CATTCCACTT AAAATTCGTA TATCCCTTGA ACCTGCTTCA TGATCTAAAA TACCTACTCC 6900

CATGAAAAGC GCACATTTAA AGATGGCATG ATTCATTAGa TGAAATAGcG CACCArATAA 6960

TACmAATACA TAAATaGATG CTATTGCGTC TTGTTGGTGT TGAGCATATC CGCCACCTAT 7020

ACCCACCATA GCCATAATCA TCCCAAGTTG ACTGATTGTA GAGTACGCTA GGATACCTTT 7080

TAAATCCCAT TGTTTTAAAG CTGTAATTGA ACCAAATAAC ATTGTTATTA AACCAACAAA 7140

CGTAACGATA TATACGTACA TATTGCTAnG ACCTAATAAT GGTGTAAATC GAAGTAATAG 7200

AAnGATACCA GCTTTTACCA TCGTGGCTGA ATGTAAATAA GCACTTACAG GTGTAGGTGC 7260

AGCCATTGCT CTAGGTAGCC AGTATGAAAT GGAraTTGTG CTGATTTTGT AAATGCACCT 7320

AATAAAAACA TAAAAATCAT AGGGATAAAC AATCCATGAT TCTTAATATG ATCTGCTTGT 7380

CCTAATATCT CTGTGATGTT ATTCGTTCCT GTCATGATAT ACAGCATAAT AAAACCAACT 7440

AATAACGCCA ATCCACCAAA TACTGTAATC ATAAATGATT GAATCGCACC AAATTGACTG 7500

TCACCATTGT TATACCAATA TGAnATCAAT AAAAATGATG ATmCACTCGT TAATTCCCAA 7560

AAaATGTACA TCmATATCGT ATTGTCTGAT AATACaaTAC CAATCATACT GAACATAAAT 7620

AACGTTAAAT AAAAATAAAA CCTTGGTAAA TTGTCTTTTC GAGAGGATAA ATATTGAGTT 7680

GCATAGAAGA ATACTGCAAT TCCAATAAGT GAAATAATAA GAGAAAACAT TAAACTTAAA 7740

CCATCTAAAC GTAAATCTAA ATTAATATCT AATGTCTTAA TCCATGGAAT AGAGGTAGAA 7800

GGTGCAACCA ACGCTATGTA CCCGGCATAT TTAGCCAATG CTCTACGTTT AGACATTAGA 7920

AGTATCATCG CCATAATCAC AAGTATAGCA ATTAATAAAT AAACCAAACT CATTATTAGC 7980

CTCCTTTGTT TCTATAATTG TAATGAAATA TAAATACTAT GTTCACACTC ATTTTCTAAA 8040

CCGATAAAAT TTAGTGTTTC AATAGCAGAT TGATGCCCTA AATACTTTTG AATGACTGGT 8100

ATAAGTATAC CTTTTTGATA AGCATGATAT GCAAATGTCT TACGCAATGT CGTTAGTCCT 8160

ACATTATCTA TACCAGCTTC AATTGATGCT TGGTGAATTA TTCGATATGC TTGCTGTCTA 8220

GATAATACTT GATTTGTTCG TAGTGATTGA AAAAGAACGT CTTCATTCGA AAGACTCCTG 8280

TCCTCTATAT ATTGAAGTAG TTCTTTCGAT AATGTTTCTG GTAACCTAAT TTTAATCAA 8339

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 588 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

CCCGATTTTT TTACGTAATC TAATACATAC GGCAAAATCA ACTTTAATCA AAAAAGACTC 60

ATACACAATG CCTTTAAAGC ACATGTATGA GTCCTTTTTA GTAGTTTATA TCAAAAAATA 120

GTTTAATGTA TAAATTAGTT TTTGTTTACA GATGCGTCGT AGATTGATTC TACAGCATCA 180

CCTAAAGCTT TATCGAATTC TTCTTTAGAT TGATCAGCTC TTAAATCACT AGCTAATGCA 240

CGTGAGAAAC TTGCGATAAG TTCAGCGTTA TCTTTAAGTA ATTCATTTGC TTTTTCTCTG 300

CTGTAACCAC CTGATAATAC AACGACACGA ACAACATTAG GATGTTCAGC TAACTCTTTG 360

TATAAGTTTG GTTCAGTAGG AATTGTTAAT TTCAACATTA CTAATTGATC AGCATTTAAG 420

CTATCTAAAC CTTTTTTAAG TTCAGCTTTT AATACTTTTT CAATTTCAGC TTTGTCTTTT 480

GCATTAATAT TAACTTCTGG TTCGATAATT GGAACTAAAC CTTTAGCAAT AATTTGTTTA 540

GCAACTTCAA ATTGTTGTTC AACAACGTCT TTGATACCTT GCTCATTT 588

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2841 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATAGAGTnCT GGnACTTACT ATGACATATG GCGCTAGAAT GGCTGAGCCA GGTGAATTTA 60

CAAAACGTGC CTTTTTAAAT GGTCGTATTG ATTTATCTCA AGCTGAAGCA GTTATGGACT 120

TTATTCGCTC GAAGACAGAT AGAGCTTCTA AAGTTGCGAT GAATCAAATT GAAGGTCGTC 180

TAAGTGACTT AATCAAAAAA CAACGTCAAT CTATATTAGA GATACTCGCT CAAGTGGAAG 240

TGAATATTGA TTATCCTGAA TACGATGATG TTGAAGATGC GACTACTGAA TTTCTTTTAG 300

AGCAGTCTAA AGAAATCAAA CAGGAAATTA ATCGTTTATT AGATACCGGT GCGCAGGGTA 360

AAATTATGCG TGAAGGTTTA TCTACAGTTA TTGTTGGTAA ACCAAACGTA GGTAAATCAT 420

CGATGTTAAA TAATTTAATA CAAGATAATA AAGCGATTGT AACTGAGGTA GCAGGTACTA 480

CTAGAGATGT CTTAGAAGAG TACGTCAATG TTCGTGGCGT GCCATTAAGA TTAGTTGATA 540

CTGCTGGTAT ACGTGAGACA GAAGATATAG TAGAGAAGAT TGGTGTTGAA CGCTCTAGAA 600

AGGCTCTTAG CCAAGCAGAC TTAATTTTAT TTGTATTAAA CAATAACGAA GCATTGACwC 660

AAGAAGATTA CACATTATAT GAAGTGGTTA AAAATGAAGA TGTAATCGTA ATTGTTAATA 720

AAATGGATTT AGAGCAAAAC ATAGATATTA ATGAAGTTAA AGATATGATA GGTGATACGC 780

CATTAATTCA AACTTCAATG TTAAAACAAG AAGGTATTGA TGaATTAGAA ATACAAATTC 840

gAGATTTGTT CTTTGGTGGa GAAGTACAAA ATCAAGATAT GACTTATGTT TCTAATTCAA 900

GACATATTTC ATTATTAAAA CAAGCAAGAC AAACGATACA AGATGCGATT GATGCAGCAG 960

AATCTGGTGT GCCTATGGaT ATGGTACAAA TTGATTTAAC TAGAACTTGG GAAATATTAG 1020

GAGAAATTAT TGGTGAGACT GCAAgTGATG AACTCATCGA TCAGTTATTC AGTCAATTCT 1080

GCTTAGGTAA ATAGTAATTG AAATAGACGG AATACCGTCT TAAGAAGGCT AGTAAGATAT 1140

CAAATAAGGA GGTTTATATT GTGGTTCAAG AATATGATGT AATCGTTATA GGTGCGGGAC 1200

ATGCAGGTGT AGAAGCAGGT TTAGCATCTG CAAGACGTGG TGCTAAAACA TTAATGCTAA 1260

CAATAAATTT AGATAATATT GCATTTATGC CATGTAACCC ATCTGTAGGT GGACCAGCTA 1320

AAGGTATCGT TGTTCGTGAA ATTGATGCTT TAGGTGGACA AATGGCAAAA ACAATCGATA 1380

AAACACACAT TCAAATGAGA ATGTTAAATA CAGGTAAAGG ACCTGCTGTA AGAGCACTAA 1440

GAGCGCAAgc AGaTAAAGTA CTTTATCAAC AAGAAATGAA ACGCGTGATT GAAGATGAAG 1500

AAAATTTGCA TATAATGCAA GGTATGGTAG ACGAACTTAT TATAGAAGAT AATGAAGTTA 1560

AAGGTGTACG TACAAATATT GGTACAGAGT ATTTATCTAA AGCAGTAATT ATTACAACGG 1620

GAACATTTTT ACGTGGTGAA ATCATTTTAG GTAATATGAA GTATTCAAGT GGACCAAATC 1680

ACCAATTACC ATCAATCACA TTATCAGACA ATTTAAGAGA ACTTGGTTTT GATATTGTTC 1740

AAATACAACC AGGTGACGAT GTAGGTCGTG CATTCAGCTT TGAAACAACA GAATATATAT 1860

TAGATCAATT GCCATGTTGG CTAACGTATA CTAATGCTGA AACACACAAA GTTATCGATG 1920

ATAATTTACA TCTATCTGCA ATGTATTCAG GGATGATTAA AGGAACCGGG CCACGTTATT 1980

GCCCTTCAAT TGAAGATAAA TTTGTTCGAT TTAATGATAA GCCGCGACAT CAACTTTTCT 2040

TAGAGCCTGA AGGTCGTAAT ACAAATGAAG TATATGTGCA AGGATTGTCT ACAAGTCTTC 2100

CTGAACATGT GCAcGTCAAA TGTTAGAGAC GATACCAGGT CTTGAAAAAG CAGATATGAT 2160

GCGTGCCGGC TACGCAATTG AATATGATGC GATTGTGCCA ACGCAGTTAT GGCCTACACT 2220

TGAAACGAAA ATGATTAAAA ACTTATATAC TGCAGGTCAA ATTAATGGTA CATCTGGTTA 2280

TGAAGAAGCA GCAGGACAAG GATTGATGGC AGGTATTAAC GCTGCAGGTA AAGTGTTAAA 2340

CACAGGCGAA AAGATATTAA GTCGTTCAGA TGCATATATT GGTGTCTTAA TCGATGATCT 2400

TGTAACTAAA GGTACTAATG AACCTTATCG TTTACTAACA TCACGTGCAG AATATCGTTT 2460

GTTAcTACGT CATGATAATG CTGATTTGAG ATTGACGGAT ATGGGATATG AACTTGGTAT 2520

GATTTCTGAA GAAAGATATG CACGTTTTAA TGAAAAACGT CAGCAAATTG ATGCGGAAAT 2580

TAAGCGTTTA TCAGATATTC GTATTAAACC AAACGAACAT ACGCAAGCGA TTATTGAACA 2640

ACATGGTGGT TCTCGCTTAA AAGATGGTAT TTTAGCTATC GATTTATTAC GCAGACCTGA 2700

AATGACTTAC GATATAATTT TAGAACTTTT AGAAGAAGAA CATCAATTGA ATGCAGATGT 2760

TGAAGAACAA GTAGAAATAC AAACAAAATA TGAAGGTTAT ATCAATAAAT CACTACAACA 2820

AGTTGAGAAA GTTAAGCGTA T 2841

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3025 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

ATCTAATTTC AAACCCGGTG ATAAATTGCC AAGCGTGACG CAATTAAAAG AACGTTATCA 60

AGTAAGTAAG AGTACTATCA TTAAAGCATT AGGCTTATTG GAACAAGATG GTTTGATCTA 120

TCAAGCACAA GGCAGTGGTA TTTATGTGAG AAATATTGCT GATGCCAATC GTATCAACGT 180

CTTTAAGACT AATGGTTTCT CTAAAAGTTT AGGTGAACAC CGAATGACAA GTAAGGTACT 240

TGTTTTTAAG GAGATTGCAA CGCCACCTAA ATCTGTACAA GATGAGCTCC AATTAAATGC 300

CGAATATTCT TATTATCATA AAGAAATCGT GAAATATTTA AATGATGATA TTGCTAAGGG 420

CTCTATCTTC GACTATTTAG AATCAAACAT GAAACTTCGT ATTGGTTTTT CAGATATTTT 480

CTTTAATGTA GATCAACTCA CTTCAAGTGA AGCTTCATTA CTACAATTGT CTACAGGTGA 540

ACCATGTTTA CGTTACCACC AGACTTTTTA TACAATGACT GGCAAACCCT TTGATTCATC 600

TGACATCGTA TTTCATTATC GTCATGCACA GTTTTATATT CCTAGTAAAA AGTAATAAAT 660

ACATAAAAAC GTCTATATCC CAGTTATAAA CTGGAGTATA GACGTTTTTT TACGATAATA 720

ACAATGGCTC AAATTGCTAT TATCTTGCTT AGGTTTTTCG TTTTAGAAGA ATATTGCTAC 780

AAAGACAGGC ACAACTGCTA CAACAACTAC ACCAACTAAC ACTAAAGCTA TACTTGCCAT 840

TGATTCTTCT ACAGGTCCTA ATTCTTTGGC TGGTGCTACA CCTAATGTGT GACCACTTGT 900

TCCAAGTGCT AATCCTCGGG CAATAGGGTT AGTAATTCGG AAAAGCTTTA AGAATTTATT 960

ACCTAGGGCA TAAATAATGA CACCATTTAA AATAACTGCT AATGATGTTA ATTCTTTTAT 1020

ACCACCGATA CCAGCTGATA CTGGTAACGC AATCGCTGTA GTTGCTGCTT GAGGTAACAT 1080

TGATAAAATA ACATCATTGG CAAATTGTGC TAACTTCGCA AAAGTTAAAA TAATTAATAA 1140

CGCTACAACT GTACCGATAC CAATACCTCC GATGATACGA TGCCAATGTT TAACAAGCAC 1200

TTCACGCTTT TTATATAACG GAATCGCAAA ACAGATTGTT GCCGGTTCTA AGAAGAAGTA 1260

AATAATGTCT CCACCTATTT TGTAAGTCTT ATACGGAATG CCTGTTAAAT AGAGGAAGGC 1320

CACACCAAAT ACCATACTGA CAAATAGCGG TGCGAATAAG AAGAAACGAT TAGTTTTTTC 1380

AAATAATATG GTCGCTAAGA AAAATGGTAT AACGGATAAC AGTATTCCGA AGTAAGGTGT 1440

GTTTaGTGCT AAGTGGTTAA TCaTGAGCTT GTGCCTCCTC TATTTTGATC TTTTTTGTGA 1500

CTTTGTCACC TTTAGATCTC GAAGTAACTT TCATAATAAT TTgTGTGACA TAGCCAGTAC 1560

AAATAAGTAA TAGTATTGTT GAGACGATTA TTAGTCCAAT GATTAAAAAT GGTGCTTGGC 1620

TAATGACACC TAAAGAGTTA ACAACTGAGA TACCGGCTGG TACGAAGAGT AAGCCAATGT 1680

TATTTGTTAG TGTCGTTCCT ACTTTTTCGA CTTCGCCTAA CTTAACAGCA CCAGTACATA 1740

ATAATACAAA TAATAATACT AAACCGATTA CTGATGCAGG CATAGGAATT GGCATAAATG 1800

ATTCAATTAT TTTCGATACA AAGAGTACTA AAGCAATTAC AATGACTTGG TGAAAAAAGT 1860

GTGCTGGTTT TGATGCGTCT TTTTGTTGTT TCACGACCAT TGCCTCCTAC GTTTGATTTA 1920

ACTAAAGTAT AGATGGCTCA CTTCGATTTG CGTGATTTTT AGTCCGAAAT ACAAAATATC 1980

ATAGGTAAAA TGCATAAAAA AAAGGATTAC TGTTAAAGTA ATCCTATCGA CGCTTTAAAA 2040

TCTTTCATAA ATGAACGTCC AACTTGCATC TTGACACCAT TTGTCAATAT TACCATATAA 2100

TGAATACGTA TAAAATAAGT GGGATTCAAT CGTTTTTCAT AACGATTCAA TGGCTCTGTT 2220

GTTTCGTATT TATGATTCGT TGTATGTATG GTTGTAATAC CATTATGTGT GCCAATCCCA 2280

ATAATATTTT GTTGCTTTAA CATGTGAATT TTATCGTCAA TTTCAACAGG TAAGCTTTGA 2340

TCAAAATTCG CCGACATATC ATTCGCAATT GCACTTGCGT TATTATCATC TTTGGCTTTA 2400

GTCGCACGCA CTTTATTGAC TGCTTGTTCA ATACGTTTTT GACCAAACGG TTTCAAAATA 2460

TAGTCTGTCG CATTTAATTC AAATGCCTGT ACTGCGTATT GGTCATGTGC AGTTGCAAAA 2520

ATAATCGCAG GTGGCTCTTT CATCTTTTGA ATCTTAGCTC CTAATTCGAT CCCATTTTCA 2580

TCCATTAAAT TGACATCTAA AAATATAATG TCATATTGAT TGATCAGTAG TGCTTCCAAT 2640

GTTTCTTTTA CATTTTCTGC CTCATTAATT TCTTCAAAAC CACCAATTTC ATTTAATAAA 2700

TATGTTAATT CATTACGTGC TAATGGCTCA TCATCTATGA TTAATGCTTT CATATTTATT 2760

CCTCCTCTTG TCTTTCATAA GGAAGTACAC ACCAAAAAGT GGTACCGCTC GATGTCGATT 2820

CAAATTGTAA TGCTGCGGAT TTTCCAAATA ATCCTTTTAG GCGTAAGTTT AAATTTTCTA 2880

AAGCACTACC AGTTCCAGAC TCTGATTCTA CAGATGTnTC TCCCaACAAA TGCATTTTAT 2940

CTTTAGAAAT ACCCTGACCA TTATCTTGTA CAATAATACG TACATGTGTT GCAGTTTCTT 3000

TAATCACTGA CACGTCAATA TCGTT 3025

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1689 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

ACAGAATTTC ACAGCATTTT TAGATGAAAA AATAAGCCAG TCATAGCGTT GATTTAACAA 60

ATGAATATCA AAATTTAGTG GCTTTATATC AATAAAGGGT TTGTGAATAA TTGATACTAA 120

ATCACTTTGC ATGTCATTTG TTTGTGTCAT AACTACAACT GGCTTCATAT TTAAACGTCA 180

CTCCATTATT TAATGTTGTT CATTTAAGCG TTTTATAATT TCATAAGCAC CTTGCTCTTT 240

TAATTTGTTA CTCACTGTTT TGCCTAACTC AACCGGATCT GTTCCGTTCA TTGTATATTC 300

AAATCGTTCT TTACCATCTG GGGTCATAAT TAAACCTGTA AATTCGATTT CGTTTTGATC 360

TGAGATTGTA GCATATCCTG CAATTGGCAC CTGACAACTA CCATCCATTT CTGCTAAAAA 420

CGTTCGTTCA GCAGTCACAC ATTTTGCAAC CTCATCATTA TGTACTTTGC TTAATAATGT 480

TAACAATGTA TCTCTATCAA GATAAGATGT TnCAATATCA TCTGACCAGC CCATTCTTCT 600

TAAACCAGCT GCAGCTAAAA TAATCGCATC ATAATCTTCA GTTTGTAACT TTTCTAATCG 660

TGTATCTATA TTACCTCTAA TCCATTTAAT CTCTAAATTA GGATACTTAG ATAATATTTG 720

TGCACCACGA CGTAATGAAC TAGTACCAAT AATACTGCCT TCTGGCAATT GGGATAGTGG 780

TGTATGTGTT TTAGAAATAT ACGCATCAAA AGGTAATTCT CTATCAGGGA TACAACCTAA 840

TGTTAAACCT TCCGGAATTA CACTTGGTAC GTCTTTAAGC GAGTGTATTG CCATATCGAT 900

ATTTTTTTCA AAAAGTTCAT GTTGTATTTC TTTAACAAAT AAGCCTTTGC CTCCGACTTT 960

AGACAATTGT TTATCTACTA TACGATCGCC TTTCGTGaCA ATTTCTTTAA TTTCAATTTC 1020

TAGATTTGGC TCGACAGCTT TTAATTTATC AATAAATTGC TGGCTTTGTG TTAAAGCTAA 1080

TTTACyTCTT CTGGAGCCAA CGACTrATTT ACGCATGTTC AATTCCTCCT AGGAACGGAT 1140

TGCTCTAGAT TATTTTCTCA ATTCACAAAA TGTGTTGCAA AAAATAAATT AATCATATTT 1200

AAGCAAAATA AAATAATGTT ATAGTATATT AAATATCTTG AATTCAACCA TTTGTTGATT 1260

CTAAGTAAAA TATAACTTCC ATATAATACT GTAATAATTG AAGAGAGTAT TACCTTCGGG 1320

TCAATGAATA TACGTTCACC AACTGAAATT ACACCCCACT GTGTACCTAA AATAATACTA 1380

AATATGAGAA TTATCCACCC ACTTAACGTT GAGTAAAACA CAATTGATTC AAGTGTAGCA 1440

ACGCTACCAA TTCTAAAGTA TTTTTGATCA AAACGTTTTT CCTTCAAATT ACGGTATTGC 1500

ATGATATACA GTAATGCATT GACAAAAGCT AAGGCAAAGA AGACATAACT TAACACAGCT 1560

AGACCGATAT GGACTAACAG TAACTCGTCT ACAACAGCAA TTTTCTGAAC CTTATTAGTA 1620

TAATGTGTCG GTTGAAATGT ATTCATCCCT AAnAGTGTTA ACCCTATTAA ATTCCAAGGA 1680

AAAACACAG 1689

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

nTGGnTGGCT TTTCCTATTG GACCAAATGG ACCnTTTACC TGGCCnTTCC CAGGACACCC 60

CGCTTGTGCC CACATTCCAA TCGGAAAAGG TGTATGTGGT ACAGCCGTTT CAGAACGTCG 120

TACACAAATT GTAGCTGATG TTCATCAATT CGAAGGACAT ATCGCTTGTG ATGCTAATAG 180

CGATGCCCCT ATAACGGATC GATTTGATGA CAATGACAAa GAaCATCTTG AaGCAATTGT 300

TAAAATTATT GAAAaGCAAC TCGCATAAAA GGACATCAGC ATTTTCAATA AAGTGTTGAC 360

AGTTAGCAGG AAAATGTTAC AATAATCTTT GTGTGAATTA ACGAAAGTAG CAGTTGTATA 420

TTATTGAGCG CTATGTTGTT CCCAATGCGG ACGTGTCACG TAACTGTCGC TATAAGGTGA 480

AGACACATAA AACAATATAT CTTAGTAAGC ATGCAACACT CTTTTTTGTT TATTCATAAC 540

AACAAAAAAG AATTAAAGGA GGAGTCTTAT TATGGCTCGA TTCAGAGGTT CAAACTGGAA 600

AAAATCTCGT CGTTTAGGTA TCTCTTTAAG CGGTACTGGT AAAGAATTAG AAAAACGTCC 660

TTACGCACCA GGACAACATG GTCCAAACCA ACGTAAAAAA TTATCAGAAT ATGGTTTACA 720

ATTACGTGAA AAACAAAAAT TACGTTACTT ATATGGAATG ACTGAAAGAC AATTCCGTAA 780

CACATTTGAC ATCGCTGGTA AAAAATTCGG TGTACACGGT GAAAACTTCA TGATCTTATT 840

AGCAAGTCGT TTAGACGCTG TTGTTTATTC ATTAGGTTTA GCTCGTACTC GTCGTCAAGC 900

ACGTCAATTA GTTAACCACG GTCATATCTT AGTAGATGGT AAACGTGTTG ATATTCCATC 960

TTATTCTGTT AAACCTGGTC AAACAATTTC AGTTCGTGAA AAATCTCAAA AATTAAACAT 1020

CATCGTTGAA TCAGTTGAAA TCAACAATTT CGTACCTGAG TACTTAAACT TTGATGCTGA 1080

CAGCTTAACT GGTACTTTCG TACGTTTACC AGAACGTAGC GAATTACCTG CTGAAATTAA 1140

CGAACAATTA ATCCGTTGAG TACTACTCAA GATAATACGG TCAATACCAA CACCCACAAT 1200

TGTGGGTGT 1209

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 698 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

AAATCCCTTt GTtaAAgTsC AAAtTTTTCc AACrgCTTTA AtArGACCCA TATTACCtTC 60

TTGGATTAAA tCmAGGaATG AcATACCACG ACCaCGTATC TTTTAGCAAT ACTTACAACT 120

AAACGTAAGT TCGCTTCTGC AAGTCTTGAT TTTGCTACTT CATCACCTTG TTCAATACGT 180

TTGGCTAATT CGATTTCTTC TTGTGCACTT AATAAGTTAA CACGCCCAAT TTCTTTAAGG 240

TACATACGAA CTGGGTCATT TATTTTAACA CCTGGAGGGG CACTAAGATC ACTTGGATTC 300

AGTTTCTCGT CAGTATCTGA ACTATCTTTT TCATTAACTA GTGAAATATC ATTATCATTT 360

GCAATTTCTT CATGACTTAA ATGACCCTCT TTTTTACCTT TTTCAATTAA TTGCTTCTTA 480

ACATCTTCTA ATGTTAATGT CGGATCAATT GTTTGTTTTT TAATTTTAAC TGTGTTATCA 540

GACATGAAAC GGCCTCCCGA TTTTAAATAT GAACATTCGA AATTTATTCA ATATTGCTAT 600

TTTAAACGAA ATTCTTAATT AATTCCATCC ATATTTTnAA TTTTATTTTA CAAATTGGGA 660

ACTAAATCCC CAATATTTAT TTTTCAATAG TGGTGGTT 698

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

ACTTGATGAT GTATACAATG TATTTCAAGA ATATTATCAA AAAACATCTA ACATTAAGTT 60

TTGTAGAATT CACAATTCTA GCTATTATCA CTTCTCAAAA TAAAAACATC GTTCTTCTTA 120

AAGATTTAAT TGAAACAATC CACCATAAAT ACCCTCAAAC TGTTAGAGCT CTCAATAATT 180

TAAAAAAGCA AGGCTATCTA ATAAAAGAAC GCTCAACTGA AGATGAAAGA AAAATTTTAA 240

TTCATATGGA TGACGCGCAG CAAGACCATG CTGAACAATT ATTAGCTCAA GTGAATCAAT 300

TATTAGCAGA TAAAGATCAT TTACATCTTG TTTTTGAATA ATATCTCTAT TACGCAAGTG 360

TGCTGTATTC TAAAGTGCAC TTGTGTTTTC TATTTTTTAA TAAAACCTCA GCACATAATG 420

AACAACTTTC TATTTTCTAT ATCACTTAAA ACCATTTCCG AAATTAAACC TCAGCACATT 480

CAAAGCCCCA CTTTATTCTT AAAAATATTT TTTAACTCAT ATGTATTAAA CCGCTTTCAT 540

TATAAAAAAT ATCTCTATAT TtTATCTGtT TtTATTAATC GAAATAGCGT GATTTTGCGG 600

TTTTAAGCCT TTTACTTCCT GAATAAATCT TTCAGCAAAA TATTTATTTT ATAAGTTGTA 660

AAACTTACCT TTAAATTTAA TTATAAATAT AGATTTTAGT ATTGCAATAC ATAATTCGTT 720

ATATTATGAT GACTTTACAA ATACATACAG GGGGTATTAA TkTGAAAAAG AAAAACATtT 780

ATTCAATTCG TAAACTAGGT GTAGGTATtG CATCTGTAAC TTTAGGTACA TTACTTATAT 840

CTGGTGGCGT AACACCTGCT GCAAAtgctG CGCAACACGA TGAAGCTCAA CAAAATGCTT 900

TTTATCAAGT CTTAAATATG CCTAACTTAA ATGCTGATCA ACGCAATGGT TTTATCCAAA 960

GCCTTAAAGA TGATCCAAGC CAAAGTGCTA ACGTTTTAGG TGAAGCTCAA AAACTTAATG 1020

ACTCTCAAGC TCCAAAAGCT GATGCGCAAC AAAATAACTT CAACAAAGAT CAACAAAGCG 1080

AAAGTCTTAA AGACGACCCA AGCCAAAGCA CTAACGTTTT AGGTGAAGCT AAAAAATTAA 1200

ACGAATCTCA AGCACCGAAA GCTGATAACA ATTTCAACAA AGAACAACAA AATGCTTTCT 1260

ATGAAATCTT GAATATGCCT AACTTAAACG AAGAACAACG CAATGGTTTC ATCCAAAGCT 1320

TAAAAGATGA CCCAAGCCAA AGTGCTAACC TATTGTCAGA AGCTAAAAAG TTAAATGAAT 1380

CTCAAGCACC GAAAGCGGAT AACAAATTCA ACAAAGAACA ACAAAATGCT TTCTATGAAA 1440

TCTTACATTT ACCTAACTTA AACGAAGAAC AACGCAATGG TTTCATCCAA AGCCTAAAAG 1500

ATGACCCAAG CCAAAGCGCT AACCTTTTAG CAGAAGCTAA AAAGCTAAAT GATGCTCAAG 1560

CACCAAAAGC TGACAACAAA TTCAACAAAG AACAACAAAA TGCTTTCTAT GAAATTTTAC 1620

ATTTACCTAA CTTAACTGAA GAACAACGTA ACGGCTTCAT CCAAAGCCTT AAAGACGATC 1680

CTTCAGTGAG CAAAGAAATT TTAGCAGAAG CTAAAAAGCT AAACGATGCT CAAGCACCAA 1740

AAGAGGAAGA CAATAACAAG CCTGGCAAAG AAGACAATAA CAAGCCTGGC AAAGAAGACA 1800

ACAACAAGCC TGGTAAAGAA GACAACAACA AGCCTGGTAA AGAAGACAAC AACAAGCCTG 1860

GCAAAGAAGA CGGCAACAAG CCTGGTAAAG AAGACAACAA AAAACCTGGT AAAGAAGATG 1920

GCAACAAGCC TGGTAAAGAA GACAACAAAA AACCTGGTAA AGAAGACGGC AACAAGCCTG 1980

GCAAAGAAGA TGGCAACAAA CCTGGTAAAG AAGATGGTAA CGGAGTACAT GTCGTTAAAC 2040

CTGGTGATAC AGTAAATGAC ATTGCAAAAG CAAACGGCAC TACTGCTGAC AAAATTGCTG 2100

CAGATAACAA ATTAGCTGAT AAAAACATGA TCAAACCTGG TCAAGAACTT GTTGTTGATA 2160

AGAAGCAACC AGCAAACCAT GCAGATGCTA ACAAAGCTCA AGCATTACCA GAAACTGGTG 2220

AAGAAAATCC ATTCATCGGT ACAACTGTAT TTGGTGGATT ATCATTAGCC TTAGGTGCAG 2280

CGTTATTAGC TGGACGTCGT CGCGAACTAT AAAAACAAAC AATACACAAC GATAGATATC 2340

ATTTTATCCA AACCAATTTT AACTTATATA CGTTGATTAA CACATTCTTA TTTGAAATGA 2400

TAAGAATCAT CTAAATGCAC GAGCAACATC TTTTGTTGCT CAGTGCATTT TTTATTTTAC 2460

TTACTTTTCT AAACAACTTC TGAAACGCCT CAACACTTTC TACTCTGATT ACATATATGA 2520

CATTTTTAGG CATTAAAAAA TCGAACTAGA CAAGATGCTC ATTGCATTTC GTACTAGTTC 2580

GATTCATGAA TAATTAGATT TAAAATGTCA TTTGAATCCA AGTGACAACA TTATTTATAT 2640

TTAGAATATT AACGTTAGTA TAAACGTCCA AACACAAATA AAAGCAACAA ATATAATACT 2700

GTATTTTAAC GTCATTTTTA ATAATGCAGA TTCTTCACCA ACTTTTTTAA CAGCTGCAGT 2760

CGCAATGGCA ATTGATTGTG GTGAAATAAG TTTCGCTGCT ACACCACCTG CAGTGTTAGC 2820

TGCCACAAGT AATGAACCGC TTGTTGAAAT TTGTTGTGCC ACTGTCGCTT GAATAGGTGC 2880

TGGAGAGAAT AATGGGAAAA TTGCTCCCGC TTTAGCAATA CCTTGTCCAA TTGCTACAGT 3000

CAAACCACCG TATGTCATAA CTTTAGCAAT AGCTAGGATA GCTGAAATTG TAAGGATCGG 3060

TAACCATAAT TCTTTAATTG CTTCGACCAA TAAAGCACCT GCACTTTTCC ATTTTAACTT 3120

CGTAATTAAA ATTGTAATAA TTACTGTTAA TAAAATCGCT GTCCCAGTTG CACCAATTAA 3180

ATCGAGACGC AACGCAATTC CTTTAGGCGA TAAATCACTC ACAGTATTTG GAATTGGCAA 3240

TTTTATTACT AAACTTTCAA GTGCACCTCC AGGTTGGAAT AATTTTTTGA AGAATGGTGC 3300

ACTCCATACT AATACAAAGG CAGTTAAAAT TACGAACGGA CTCCAAGCAA AGACAATTTC 3360

TTTAGGCGTT CGTTTTTGAA TTTTATGTTC AGACGCTTCC AATCTGAAAA TGTTTTTCGG 3420

TTTAAATTTA CGACAAACAA ATGCTAACAC CACCATTGTT GCTAGTGATG GAATAATGTC 3480

TGCTAGTTCT GGACCATGGA ATATTGTTAA TAATAATTGT AATCCAGTAT ATGTACCACT 3540

CACTGTTAAA ATGACAGGTA AAATTTCTTT AATACCTTTC ATACCATCTA CAATGAATAC 3600

TAAAACAAAT GGAATAATAA AGTTTAAAAT TGGAAGTGTT AATGCTGAGT ATCTCGCAAC 3660

ATCTAATGTT GTAACGCCTC CACTTAAGTT AAACGTATCA ATAATACTAA CTGGTAAACC 3720

AATTGCACCA AAGGCACCCG CCGCACCATT AGCAATTAAA CATAACATCG CTGCTTTTAA 3780

TGGTTCAAAT CCAAGTTGAA TTAATAATAC TGCACAAATC GCAATTGGCA CACCAAATCC 3840

TGCTGCACCT TCTAAAAATG CGTTGAAACA AAATCCAATT AATAATAGTT GGATTCTTTG 3900

GTCCACTGAA ATACTTGCAA TACTATCTTG AATAATAGAA AATTGTCCTG TTTTAATAGA 3960

AACTTTATAT AACCAAACTG CCATTAAAAC GATATATCCT ATTGGGAAAA TACCGGCAAC 4020

AACGCCTTCT GTAATCGCAC CTGCTGATAC ACGCGCTGGT AATTCAAATA CAAATAAAGC 4080

CACAATCAAT GTAACAACCA AAGTTGTCAA TGCTGCATAA ATGCCTTTCA TTTTAAAAAC 4140

GGTTAAAGCAT AATAAAAATA AAATAATAGG TACTGCTGCA ACTAAGGCTG ATAATCCGAC 4200

ATTATCGAAT GGATTTACAG TAAGTAGTGT CATAATGACT CCCTCTCTTT ATATAAAATA 4260

TTTATCATTC TGATTAATCT ACAACCTATT TCAACTTATA TTTTGCGATG ATCACATATT 4320

TAAAATGTAA CACTCCTATA TGTGACAGGC AATCGAATTT TTACAAAAAG TTCACAAAAT 4380

ATACACAATA TTTAACTATA ATAmATAATA TATCaTntTA ATTATAAATA CTAGATATTA 4440

TTTATAATAA TCTCAGGAAT TCGCTTCAAA ACTGCATCAT GAGAGTTTAT ATTTTTATTG 4500

AGAATCTCTC ATTTTATGAA TTGTAGGAAG TAAACAAAAT ATGACAAGCG TCAAACCAAT 4560

GATAATGATA AATATCATAT TAAACCATAG TAAATTGAAT TGATGATGGT GTTGTATTTG 4620

CCAAATTTCT AATACTGTGA AGATAGACAT ATAGCTCATA ATCTCTAAAT TTAACGTACT 4680

AAATCGTTCA TAGTATCTAC CTGCAATGAA AAATATAAGC CAAATCACTA TAAATGCGCT 4800

ATTAATCAAA AGCAGCACCC ATTTATCAGC AAAATTATCA GCATCCCCTG CTAAATTATA 4860

ATGAATAGGC ACTTTGGTTG GTAATTTTGG ATAGGTCACT ACTGTATAGC ACATCATAGC 4920

TAAGTAAATA AGTAGACTTA ATATTGTAAA AGACCTGATT TTAGACATTC TATCGCCTCT 4980

TCTTTACATT TTATGTATAA CACTCTGCCT ATTTTACCTT TTAATACATT ACCCCAACGA 5040

TTAAACAATA TGTAATGATA CTATAATTGC GTCAGGAGTA TCCGCTTGTT AAATGTGCAT 5100

AGCTTATATT TAGCTGTTTA ACATGCCACA TAATGATTCG AATTATT 5147

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

CACTTACTTC CACCATTATC ATAACTTTAA AATGGATATA nTTCATCAAA CATTATCTAA 60

AGGCGTCGCA CCTACACCAA CACCATCCAA CAATTAACTT ACAACTCTGC GATTACTTCT 120

TCAGCAGCAA CTTTCACnTG CGTAATACAA TCAGGTAGTC CAACCGCTTC AAAAGATGCA 180

CCAGTTACTC TAAGTCGTGG ATATGTTTGT TTAATATGTG CTTGAATCTG TCTAATTTGT 240

TGAATATGAC CGACATGGTA CTGTGGCATA CTTTTCGGCA AACGATTGAC AATTGTAAAT 300

TCAGGATCAC CTTTAAATGT CATCATTTGA CTTAAATCTC TACGTACAAT CGATACTAAT 360

TCATTATCTG TATGATCATC AACCACAGTA TCACCTGGTT TACCTACATA CGCACGAATC 420

AAAACCTTAC CTTCCGGTGT AGTAAATGGC CATTTTTTCG ATGTCCAAGT ACATGCGGTA 480

ATGTCTGTAT CACTCGTTCT CGCAATTACG AAGCCAGTAC CATCATGGGT ATTTTCAATG 540

TCTTTTTCAT CAAATGCCAA TACAACAGTT GCAACAGTCG TACTATCCAT CGTTTTAAAG 600

TAATCAAATG CTGGATCTTG TCCGAACCAA TTTAAAAACA CTTGATGTGG TGTCGTTACT 660

AATACGCCAT CATACACTTC TTCTAGTTGA TCATTGTAAA CAATTTTATA TTGTTTTTGA 720

GATGTAATTA TATCATCCAC TGACGTATTG TAGCGTATTG TCACACCTTT ATTTTTAACA 780

TCTTGTTCTA ATGCTTCAAT AAATGAGCTT AAACCATGCT TAAATTGTTT GAATTGTCCT 840

TTCGGTGCGC CAGGATATAA TTGTCTTTGT TTCAGACGCT TATTTTTCTC ATCCTTCATA 900

CCTTTTATCA GACTTCCGAA TGCCTCTTCT TTTTCTTTAA AATTAGGAAA CGTACTCATC 960

TCAAGTACCT CATTACCTAA TCTTGCTCTG AAAAATGCAC CAACAGAAAT GTCACCATCC 1080

TGCATTTGAG TAGGTTTTTT TAATAAATCA AACCCTGCTC TTAATTTACC AAGTGGCGAT 1140

ATTAATTTTG TAGTAACAAA TGGTTTAATA TCTGTTGGAA TACCCATAAT TGAACCACCT 1200

GGAATCGGAT ATAATTTATT TTTCGCAAAA ATATATGATT GTCCAGTCGT ATTTGTAACA 1260

ATATCTTGTT CTAATCCAAT ATCTTTCGCT AATTCTGTCA TAATCGTTTT TC 1312

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TTTTACAATA AAAATATGAT ATACTACTTG TCGTATATAA GGAACGGAGG ACAATTTATG 60

CATACATTTT TAATCGTATT ATTAATCATT GATTGTATTG CATTAATAAC TGTTGTACTA 120

CTCCAAGAAG GTAAAAGCAG TGGACTTTCA GGTGCCATCA GTGGTGGTGC TGAGCAGTTA 180

TTCGGTAAAC AAAAACAACG TGGCGTCGAT TTATTCTTAA ATAGATTAAC AATTATTTTA 240

TCAATATTAT TTTTTGTACT TATGATTTGC ATAAGTTATC TTGGTATGTA AGGTCCGGCG 300

ATGTAAATGT CGGGCTTTTT TATTTATAAT TAAGAATGTA ATAGTTTAAC AATAAGCTAT 360

GTAAAATATA TAGCCTAGTT AAGTATGCAA AGGGAGCGTT AGATTTATGC AGATAAAATT 420

ACCAAAACCT TTCTTTTTTG AGGAAGGTAA ACGTGCCGTG TTATTACTAC ATGGTTTTAC 480

AGGCAATTCG TCTGATGTTC GTCAATTAGG TCGATTTTTA CAAAAGAAAG GTTATACATC 540

ATATGCACCG CAATATGAAG GCCACGCGGC ACCACCAGAT GAAATACTGA AATCTAGTCC 600

TTTCGTTTGG TTTAAAGATG CGTTAGATGG TTATGATTAT CTTGTTGAAC AAGGTTATGA 660

TGAAATTGTT GTTGCTGGTC TATCATTAGG TGGGGATTTT GCTTTAAAAT TAAGCTTAAA 720

TAGAGATGTA AAGGGTATTG TAACGATGTG TGCTCCTATG GGTGGCAAAA CTGAAGGTGC 780

CATTTATGAA GGCTTTTTAG AATATGCACG CAATTTTAAA AAGTATGAAG GTAAAGATCA 840

AGAGACTATT GATAATGAAA TGGATCATTT TAAACCAACT GAAACTTTAA AAGAACTAAG 900

TGAAGCATTA GATACGATTA AAGAGCAAGT TGATGAAGTG TTGGATCCTA TTTTAGTGAT 960

TCAAGCAGAA AACGACAATA TGATTGATCC ACAATCCGCA AATTATATAT ATGACCATGT 1020

AGATTCTGAT GACAAAAATA TCAAGTGGTA CAGTGAATCT GGACATGTTA TTACGATTGA 1080

AGAATAAAAA GAGATTTTAA CATTAGAAAG GAGGGGCATA ATGAATTTAA AGCAATCTAT 1200

AGAAGAGATT ATTAATCAAC CTGAATATGA ACCTATGTCA GTGTCAGATT TTCAAGATGC 1260

ATTAGGTTTA AGCAGTGCCG ACTCGTTTAG AGATTTAATT AAGGTGCTTG TGGAGTTAGA 1320

ACAATCAGGA TTAATCGAAC GTACAAAAAC AGACAGATAC CAAAAAAAGC ATAGTTATAG 1380

AGGTCAATCA AAATTGATAA AAGGAACGTT AAGTCAAAAT AAAAAAGGCT TTGCATTCTT 1440

AAGACCTGAA GATGAGGATA TGGAAGATAT ATTTATTCCC CCGACGAAAA TTAATCGTGC 1500

CTTGGATGGA GATACTGTTA TTGTAGAAAT CCATCAATCA AAAGGTGAAC ATAAAGGTAA 1560

AATCGAAGGG GAAGTTAAGT CGATTGAGAA GCATTCTGTA ACTCAAGTTG TTGGTACGTA 1620

TAGTGAAGCT AGACATTTTG GCTTTGTTAT TCCGGATGAT AAACGTATTA TGCAAGATAT 1680

TTTCATTCCT AAAGGTCAAA GTTTAGGCGC AGTCGATGGT CATAAGGTAC TTGTACAAAT 1740

TACTAAGTAT GCTGATGGTT CAGATAATCC AGAAGGACAT ATTTCTGCTA TTTTAGGACA 1800

TAAAAATGAT CCTGGCGTAG ATATTTTATC TATTATCTAT CAACATGGCA TAGAAATTGA 1860

ATTTCCTGAT GAAGTGTTAC AAGAAGCTGA AGCAGTACCT GATCATATTG AAAATACTGA 1920

AATTAAAGGC CGTCATGATT TACGTGATGA ATTGACAATC ACAATTGATG GTGCTGATGC 1980

TAAAGACTTA GATGACGCAA TTAGTGTTAA AAAGTTAGCG AACGGTAATA CGCAATTAAC 2040

TGTAAGTATT GCTGATGTCA GCTATTATGT AACAGAAGGT TCTGCATTGG ATAAAGAGGC 2100

ATATGATAGA GCGACAAGTG TATATCTTGT TGACCGTGTA ATTCCAATGA TTCCACATCG 2160

ATTAAGTAAT GGTATTTGTT CATTGAATCC TAATGTTGAT CGTTTAACTC TAAGCTGTCG 2220

CATGGAAATC GATGCTAGTG GTCGCGTTGT TAAACATGAA ATTTTTGATA GTGTTATACA 2280

TTCTGATTAT CGAATGACGT ATGATGCGGT AAATCAGATT ATTACTGAAA AGGATCCTAA 2340

CATTCGCGAA CAATATAATG AAATTACGCC TATGCTAGAT TTAGCACAAG ATTTATCTAA 2400

TCGTTTGATT CAAATGAGAA AACGACGTGG TGAAATCGAT TTTGATATTA GTGAAGCAAA 2460

AGTATTAGTT AACGAAGACG GTATACCAAC AGATGTTCAA TTAAGACAAC GTGGCGAGGG 2520

TGAACGTCTA ATTGAATCAT TTATGTTAAT TGCAAATGAA ACAGTTGCTG AACATTTTAG 2580

TAAGTTAGAT GTACCTTTTA TTTACCGAGT GCATGAGCAA CCTAAATCAG ATCGCTTAAG 2640

ACAATTCTTT GATTTTATTA CAAACTTTGG CATCATGATT AAGGGTACTG GCGAAGATAT 2700

TCATCCAACA ACACTTCAAA AGGTTCAAGA AGAAGTAGAA GGTCGACCTG AACAAATGGT 2760

CATTTCAACA ATGATGTTGC GTTCAATGCA ACAAGCGCAT TATGATGATG TGAACTTGGG 2820

ACATTTTGGC TTATCAGCTG AATATTATAC GCATTTTACA TCACCAATTA GACGTTATCC 2880

AGAAGTGAAG CGTTGGGAAG ACAAATTGCC TGAGTTAGCT GAACATACTT CTAAACGTGA 3000

ACGTCGTGCT ATTGAGGCAG AACGTGATAC TGATGaATTG AAAAAAGCAG AATATATGAT 3060

TCAACATATT GGTGATGAAT TTGAAGGTAT TGTCAGCTCA GTAGCTAACT TCGGTATGTT 3120

CATTGAATTG CCAAATACGA TAGAAGGTAT GGTTCATATT GCGAATATGA CTGATGATTA 3180

TTACCGTTTT GAAGAGCGTC AAATGGCATT AATTGGTGAG CGTCAAGCTA AAGTATTTAG 3240

AATTGGTGAC ACAGTTAAGG TTAAAGTGAC GCATGTTGAT GTAGATGAAC GATTAATTGA 3300

TTTTCAAATT GTAGGTATGC CTTTACCGAA AAATGATCGA TCACAGCGCC CAGCGCGAGG 3360

TAAGACAATT CAAGCCAAAA CGCGTGGTAA ATCATTAGAT AAATCAAAAT CTGATGATAA 3420

GGGTCGTAAG AAAAAAGGTA AGCAACGTAA AGGTAAAAAC CAACGTAATA ATGATAAATC 3480

AGGTAATAGT AAGCATAAGC CATTTTATAA AGATAAAAGT GTGAAAAAGA AAGCACGTCG 3540

TAAGAAAAAA TAAGCAGCAA TGAGGTGAGT ATGAATGGCT AAGAAGAAAT CACCAGGTAC 3600

ATTAGCGGAA AATCGTAAGG CAAGACATGA TTATAATATT GAAGATACGA TTGAAGCGGG 3660

AATTGTATTG CAAGGCACAG AAATAAAATC AATTCGCCGA GGTAGTGCTA ACCTTAAAGA 3720

TAGTTATGCG CAAGTTAAAA ACGGTGAAAT GTATTTGAAT AATATGCATA TAGCACCATA 3780

CGAAGAAGGG AATCGTTTTA ATCACGATCC TCTTCGTTCT CGAAAATTAT TATTGCACAA 3840

GCGTGAAATC ATTAAATTGG GTGATCAAAC ACGTGAGATT GGTTATTCGA TTGTGCCGTT 3900

AAAGCTTTAT TTGAAGCATG GACATTGTAA AGTATTACTT GGTGTtGCAC GAGGTAAGAA 3960

AAAATATGAT AAACGTCAAG CTTTGAAAGA AAAAGCAGTC AAACGAGATG TTGCGCGCGA 4020

TATGAAAGCC CGTTATTAAG CGATTTAGTT GCTTAATCGG GCTATATTTG ATATAGTTAT 4080

ATGTGCTTTT GTAAATTACA AAAGTATGAT TTGTTTGATT TATTATTTCG GGGACGTTCA 4140

TGGATTCGAC AGGGGTCCCC CGAGCTCATT AAGCGTGTCG GAGGGTTGTC TTCGTCATCA 4200

ACACACACAG TTTATAATAA CTGGCAAATC AAACAATAAT TTCGCAGTAG CTGCCTAATC 4260

GCACTCTGCA TCGCCTAACA GCATTTCCTA TGTGCTGTTA ACGCGATTCA ACCTTAATAG 4320

GATATGCTAA ACACTGCCGT TTGAAGTCTG TTTAGAAGAA ACTTAATCAA ACTAGCATCA 4380

TGTTGGTTGT TTATCACTTT TCATGATGCG AAACCTATCG ATAAACTACA CACGTAGAAA 4440

GATGTGTATC AGGACCTTTG GACGCGGGTT CAAATCCCGC CGTCTCCATA TTTGTAGCCT 4500

ACAGCCTTTG TGGTTGTGGG CTTTTTTATT TTGTGTTTTT CAGGGGATAA TGCATTGCAG 4560

AATTTGTTGT GAGTATTGAT ATAGCAGTGT TTGTATAGGT GTTTATTTGA TGGAGGAAAG 4620

AGTAATAAGT GATTATGAAT TAGTTTTTGA GATATAAGGG GACAGTGATG TGTGTCAAAT 4680

TTATACGCAA AAAATTCTCC ATGTTATATA TGTCAATATA AAAATGTGAA TCGTCTACAC 4800

TTAATTGGAT AAATGGCTAC TGAAAAAGAA CTTTTCATTT TTGTTACGTC ACTAAGTGGG 4860

TGTAGTTATA AAGAGATGAG CCGAGTTTTG ATATTTTCAT TAGAATCAAT ATGCCTATTA 4920

ACACAATCAG CAATAGTTGA CGAGACGGAA ATAAAAGAAG TCGTAGTTAA GAAATGCATT 4980

TCACAACATA CCATTGTAGC CATTTTTATT GTTTTGGATG ATAAACTCTT TTTGGAATTT 5040

TTAGTTTTTA TAATTTGCAA CTACACTACT TCTTTTACTA ATATTAATGT CTAAGTAATC 5100

GATAAAAAAT TTTCCATTGA ATAAATGAGA AGTTAAAAAC TTTACTTAAC CTTTCycATT 5160

GCATTTTCCT ATTCACGATT TTAAGAACCC AACATACTAC AAACGAATTT TAAAAGGCGA 5220

GAGTAAAGCT TACTTGTTTA TTATACATAT TTAAAATCCA AGAGTCAGAA CAGACTACTC 5280

CTCTTTATAA CTATAAAAAA TAGCTATGAA AAAATCTATC GTCATAGATT CCTTCATAGC 5340

TAATCTTAGT ATGTTTATTT TTATTTTAGG ATGCTATTTA TCAACTCAAC ATATAACTCA 5400

CTATTTTTAT AACCTTCTAA TATATCATTA ACTTGTCTAA TAGGTATTTC TGGTACTTCT 5460

CTAATGTTTT CCAATTTTGT TTTAAATTGT TTTTTTGTTA TTTGCTCTTT ATTTGTAGCC 5520

AATTGGAACA AGTAAGAATC TAGCATATTA ATTTCTTTAT ATGAATACAT ATATCTTAAT 5580

AACACTAAAT CTCTAGTTTT TAAGTTAGGC GCTAGTTCTT CTTGTAATTG TTCTATTGAT 5640

TGTyTCATTA ATAACAATCT CATTTCTAAT TCTTCATTAT TCATTTTATC ACACTCTTtT 5700

TATATTAATG CTTGACCAAC TTGGGAAACC CAAAACCCTA TGCTTCTTGC AGTAGAATCT 5760

TTAATACCAG TTCCCATCAA TGCTTGTGAA ACTTGACCTT GTACATTTCC CCATGTAGCC 5820

TCTTCTTGTT TTAATGCATT ATTCAATGCG GGATTTACAA ATTTATCCCA TCTTTTTTTT 5880

ATGATTTTCC GGCACGGGGA CTGATTTCTT TAACACCATT AAACACAGAT TTTTTATTTT 5940

TAATCATAGC TTTATAGTAT CATGTTGGCT AAGCTATAAA TAAGTCAGTT TCTCTAAAAA 6000

TTAAATAACT GAATGTAAGA CAATCAACAA wCCAAATTTA TACTTCATCT AAACCACTGT 6060

GGTCGTCATC TTTTTGCTTT TCTTTTTCTT TCTCTCGTTC TTGTTCTTTT TTGTACTCTT 6120

CTTCAAATTC TTTTTCTTTC TTTTCTACTT CTTCTCT 6157

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 884 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CATTTGTTAT TCTGAGTAGC CAATTTGGCA AAGATGAACA AACGTCTGAA CAAACGTATC 60

AAGTTGCAGT CGCATTAGAG TTAATTCATA TGGCAACACT TGTTCATGAT GACGTTATTG 120

ATAAAAGCGA CAAGCGTCGA GGCAAGTTAA CCATATCAAA GAAATGGGAT CAGACAACTG 180

CTATTTTAAC TGGGAATTTT TTATTGGCAT TAGGACTTGA ACACTTAATG GCCGTTAAAG 240

ATAATCGTGT ACATCAATTG ATATCTGAAT CTATCGTTGA TGTTTGTAGA GGGGAACTTT 300

TCCAATTTCA AGACCAATTT AACAGTCAAC AGACAATTAT TAATTATTTA CGACGTATCA 360

ATCGCAAAAC AGCACTGTTA ATTCAAATAT CAACTGAAGT TGGTGCAATT ACTTCTCAAT 420

CTGATAAAGA GACTGTACGA AAATTGAAAA TGATTGGTCA TTATATAGGT ATGAGCTTCC 480

AAATCATTGA TGATGTATTA GACTTCACAA GTACCGAAAA GAAATTAGGT AAGCCGGTCG 540

GAAGTGATTT GCTTAATGGT CATATTACGT TACCGATtTT ATTAGAAATG CGTAAAAATC 600

CAGACTTCAA ATTGAAAATC GAACAGTTAC GTCGTGATAG TGAACGCAAA GAATTTGAAG 660

AATGTATCCA AATCATTAGA AAATCTGACA GCATCGATGA GGCTAAGGCA GTAAGTTCGA 720

AGTATTTAAG TAAAGCyTTG AATTTGATTT CyGaGTTACC aGATGGACaT CCGaGAtCAC 780

TACyTTTAAG TTTGACGAAA AAAATGGGTT CAAnAAACAC GTAGTATTTA TGnAAAAGTA 840

TTGAAAGCGC TTTACCAACC TGTTAATATA TAATAGTAAT ATAC 884

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6876 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

AATTTCATCT GCTCGTGCAA AATCTTTGTT TTTCCTTGCT TCATTACGCT CTTCGATTAA 60

TTTTTCAACA TCTTCATCCA ATAATTCATC TGCATTTTTA GATTTTAACG GTACACCTAA 120

AACATCGCTG AAAATTTGAT AAACTGCTTT AAATTTATCA ATTACTTCTG TTGATGTTGT 180

GTTCTCTAGT ACATATTTAT TCGCAAGTkT TGCTAAATCA TACCAAGCTG TAATTGCATT 240

AGCTGTATTA AAATCATCAT TCATAACTGT TTCAAAACGA TTTAAAATCG CATCAATTTG 300

ATCAATATAT GTCTGTTGAT TTTCAATATT AGTAGCAATT TGTGCGCGCT CTTCAATTAA 360

TTGATAACTA TTGCGAATAC GCTCTAGTcC aCTACGTGCT GATTCTACCA ATTCTAGATT 420

ATAGTTAATT GGGCTTCTAT AATGTACGCT AATCATAAAG AATCTTAGTA CATCTGGATC 480

ATTATCAATA TTAATGAAAC CATTATGCAT CCAATAATTA GCAAATGGCG CATGATTATG 600

TGCTTCTGAT TGTGCTATTT CATTTTCATG ATGTGGAAAT TGTAAATCTG AACCACCCGC 660

ATGTATATCA ATTGTAGGTC CTAGCTCATG AAATGCCATT ACAGAACATT CTATATGCCA 720

TCCTGGTCTA CCTTCACCAA ATGGGCTATC CCAACTAATC TCGCCAGGTt CGCTTTTTTC 780

CACAATGTAA AATCAAGTGC ATCTTCTTTA TGCTCTCCTG CATCTATACG AGCACCCACT 840

TTTAAGTCAT CTATGGATTG ATGACTTAAT TTACCATAAC CTTCAAATTT ACGTGTTCTA 900

AAGTAAACAT CGCCACCACT TTCATATGCA TAACCTTGAT CCACCAAATC TTTAATAAAT 960

TGAATAATGT CATCCATATG GTCCATTACC CTTGGATTTG AAGTCGCTTT TCTAACATTT 1020

AACGCACCAA CATCTTCATG AAAAGCAGCG ATATATTTTT CTGCAATTTC GGGAACAGAC 1080

TGATTTAATT CTTGAGAACG TTTAATTAAT TTATCATCTA CGTCTGTAAA ATTTGATACA 1140

TATTCTACAT TATATCCTTG GTATTCAAAG TAACGTCTCA CTACGTCATA ATTAATTGCw 1200

GGTCTTGCGT TACCAATATG AATGTAGTTA TATACAGTAG GACCACATAC ATACATTTTT 1260

ACTTTCCCTG GTTCTATAGG CTTGAACACT TCTTTTTGAC GTGTAAGCGT ATTATATAAT 1320

GTAATCATCT TGAATCTCTC CATTCCTAGT CTTTTCAAGT TGTCGTTCTA AATGCTTAAT 1380

TTGTTCATAA ATTGGATCAG GTAGATGGCG ATGATCAAAT GTTTTTCCAA CTCGAACACC 1440

ATCTTGCTTA ACAATATGTC CTGGTATACC AACAACCGTT GAATAACTTG GAACTGATTG 1500

TAAAACAACT GAATTTGCAC CAATATTTAC ATTTGAATTT ATTTTAATAT TTCCTAAAAC 1560

TTTCGCACCG GCTGCTATTA AAACATTGTC TCCTATATCT GGGTGTCTTT TCCCTCTTTC 1620

TTTCCCTGTC CCACCAAGTG TCACGCCTTG ATAGATTGTC ACATTATCAC CAATTGTACA 1680

TGTTTCTCCT ATTACAACGC CCATACCATG ATCTATAAAT AGACGCTTTC CAATTTTAGC 1740

ACCTGGATGG ATTTCTATAC CTGTGAAAAA TCTTGAAATT TGAGATATCG CGCGTGCTGC 1800

AACATATTTT TTTTGGTTGT ATAACTTATG TGCAATCAAA TGACTCCAAA CTGCATGTAA 1860

ACCTGCATAC GTTGTAATGA CTTCTAATGT TGAACGTGCC GCTGGATCCT GCTCAAATAC 1920

CATTTTTATA TCGTCTCTCA TTCTTTTTAA CAAGATCATT TCCTCCTCAA TGATTGAACT 1980

ACGTAAATAC ATAATTGAAG TACCTGCGAA ATTAAATATC AAAAAAGCAC CACTAACATA 2040

CAAATTGTAT TGTTAGAGGC GCTTCCGCAC GGTTCCACTC TGAATTTAGC GAATAACATT 2100

AATAATATTG CGGGCGCTTC CAAATTATCA AGGAAACTAA GTCAACTTAA TGCTCATCAC 2160

TCTCATTATA TATTTAATTC ATTTTACGAA GGTGCATTCA TTAATTTCTA CGTTGTACTC 2220

ACAGCAACCG TACACTCTCT GCATCGTATA AATTTAATTA CTAATCCTTC GTTTTATATA 2280

ATAAAATTCA AGTATATACT ACCTTGATCT TGTCTATTTC ATTACTTATA TTGTTTTAAA 2400

CGGTTTAGCA CTTTTTCTTT ACCAAGTACT TCAATTGTAT TTGGTAATTC AGGACCATGC 2460

ATTTGGCCTG TTACAGCAAC ACGAATAGGC ATAAATAATT GCTTGCCTTT TATTCCTGTT 2520

TCTTTTTGAA CTTCTTTAAT TGTCTTTTTA ATTTCAGCCG CTTCAAATGG TTCAAGTGCT 2580

TCTAATTTAC TGAATAAGTG CGTCATTAAC TCTGGTACTT GCTCTCCATT AATCACTTGT 2640

TGTTCTTCTT CACCAAGAGC TGGCATTTCT TTAAAGAACA TTTCTGATAA AGGTACAATT 2700

TCACCGGCAT AACTCATTTC TTTTTGATAA AGCGCAATTA ATTTGCGTCC CCAAGATAAA 2760

TCCTCTTCTG ACGGCACCTC AGGAATCAAA TTTGCTTTAA TTAAATGAGG TAATGCTAAT 2820

TGGAATACTG TTTCAGTATC TTTTTGTTTC ATATATTGGT TATTAACCCA TGCTAATTTT 2880

TGCTTATCGA AAAATGCTGG TGATTTTGAC AAACGCTTTT CATCAAAGAT TTTGATAAAT 2940

TCTTCTTTAG AAAAGATTTC TTCTTCACCT TCAGGAGACC AACCTAATAA CGCAATAAAA 3000

TTAAATAACG CTTCAGGTAA ATAACCTAAG TCACGATATT GCTCAATAAA TTGTAAAATT 3060

TGCCCATCAC GTTTACTTAA CTTTTTACGT TCTTCATTAA CAATTAATGA CATATGACCA 3120

AAACGAGGTG GCTCCCAGCC AAATGCTTCA TAAATCATAA TTTGTTTAGG CGTGTTTGAA 3180

ATATGATCAT CACCACGAAT TACATCTGAA ATTTGCATGT AATGATCATC TATAGCTACT 3240

GCAAAATTGT ACGTTGGAAT GCCATCTTTT TTTACGATAA CCCAGTCACC AATACCATTT 3300

GAATCAAATG AAATATTTCC TTTTACCATA TCATCAAATG AATACGTTTG GTTTTGAGGT 3360

ACTCGGAAAC GAATTGATGG TTGGCGTCCT TCTGCTTCAA ATTGTTGACG TTGTTCTTCA 3420

GTCAAATGCG CATGTTGACC ACCATAGCGA GGCATTTCAC CACGAGCGAT TTGCGCTTCA 3480

CGTTCAGCTT CTAATTCTTC TTCTGTCATA TAGCATTTAT ATGCTTTATC TTCTGCTAGT 3540

AACTGATCTA TTAATGGTTG GTAGATATGT TGACGTTCAG ATTGACGATA TGGTCCGTAG 3600

CCATTGTCTT TATCTACAGA CTCATCCCAA TCTAATCCTA ACCATTTAAG ATTATCAAAT 3660

TGTGATGTTT CTCCATCTTC TAAATTACGT TTTTTATCAG TATCTTCAAT TCGAATCACA 3720

AAATCTCCGT TGTAATGTTT AGCATACAAG TAATTGAATA ATGCTGTTCT TGCATTACCA 3780

ATATGAAGAT ACCCAGTTGG ACTTGGTGCA TATCTTACTC TTATACGATC GCTCATTTTT 3840

TTCACTCCTA AATTAAATAT CAGATTTTCA AGTTAGTTCA TATAAATTGT TCATTTGCTA 3900

TCTTCGACCG TCATAACAAA TGTCTAACTC GTCTTATTGT TAAAACGAAA CAATGCTTTT 3960

TAACATGACC TTAAAATAAT TTCATTGTTT AATCATAACA TAATTCCCTG GGTAATATGC 4020

TTAAATTTTA AATAGAAAGC TGTTGTTTTT TCAACACTTT AAAAAAGCTA TCCCTAAGAA 4080

TTAAACTTCA AATTAACTAT TCAAATACGT TAAAATTGAT TCTAATTTTG TATGTCTTGA 4200

TTGCTATAAG AATAACTTTA TTAATATCTA AAATTTAACA CTTAATGAAC TTGTTTCAAT 4260

GATATATTAG CACTATTTGT ATTTTTTGAT AACTAATATG TTTTGCATTT ATTTATAGTT 4320

ATACTTCAAA TTACAAACTt CGCCATTTCA TATACCTTTT AATATCTATT TTGTTTTCGT 4380

CAACTACAGT TTTTATAATG ATACTGTATC TTCGATTTTT TTAGCAAAAA CAATTCTTCC 4440

TGAAGATGTT TGCAATAAGC TGACTACTTC TAAATTGACA TGACTGCCAA TAAGATTTTT 4500

AGCATTATCA ACAACTACCA TCGTACCATC ATCTAGATAT CCTACTGCCT GACCAGGCtC 4560

CTTACCCATT TTTGTCAGTA AAATATGCAG TTGATCACCT TGATGTACAT TAGGTTTGAT 4620

TGCTTCTGAT AAATCATTAA CATTTAATGC TTTGATACCA TGTACATGAC AAACTTTATT 4680

TAGGTTGAAA TCTGTCGTTA TAATACTTGC ATGATATTGT TTTGCTAATT TTAATAACAT 4740

CGTATCAATA TCACTATGTG TTTTAGTTGG ATGTATAACC TTTGTAGGAT AGTCTAAATC 4800

ATACAATTCA TTTAAAATAT CTAAGCCTCT TTTACCCTTT TCaCGTTTAA CACTGTCATT 4860

TGAATCTGCA ACAATTTGTA ATTCATTAAT AACACCTTGT GGAATTAAAA TATTGCCATC 4920

GATAAAACCG CAACGAATGA CTTCTAAAAT ACGACCATCA ATAATTGCGC TTGTGTCGAT 4980

AATTTTTGGC GTAgcaCTTT TaGTATGTTG TGACATGGAA CGCGCTATAT TCTCAGGTAA 5040

AAACATTAAC ATTTCATCTC GTTTTTTAAG GCCAAATTGG AAACCGAAAT AACATAGTAA 5100

TATCGTAATT ATGACAGGAA TGAAATGATT AAAAATAGAG TTGCCAATTG ATTCTAATAT 5160

AAACGACACC ATAACAGAAA TAAGTAATCC GATTATTAAA CCTATTGTTG CGAATAGTAT 5220

TTCAACAGCA CTTCTACGCA TAATAAAATG TTCTAAACCT TTTATAGCGT TAGTAACTCG 5280

TCTAATAAAT ACACCAAAAA TTAAGAACAT AAAAATACTA CCGATAATGC CATCTACATA 5340

GTGATTTTTT AAAAAGCTGG AGTTTTGTAA TCCAAGATCA TTTGCAATTT CAGGAATAAT 5400

AATTATTCCT AATGCGCTCC CAATAATTAA GTAAATAATA ATAACCATTA GTTTAACGAT 5460

ATTCACACAA TGTCCTCCTT TCTTGATGTT TTATGAATGA AGAGCAAATG ACAATACTTC 5520

ATGTACAGTA GTTACACCTA TTACTTGTAT ACCTTCAGGA TATGTCCATC CGCCTATATT 5580

ATTTTTAGGA ATAATTACAC GTTTGAAACC TAGTTTTGCA GCCTCTTGCA CGCGTTGTTC 5640

TATCCGAGAT ACACGACGTA CCTCACCCGT TAAACCAACT TCTCCAATAT AGCAATCTAA 5700

TCCGTCGACA GCTTTATCTT TAAAGCTAGA TGCAGTTGCT ACAATTACAC TTAAATCAAC 5760

TGCTGGCTCC GTTAACTTTA CACCGCCAGC TACTTTGATA TAAGCATCTT GTTGTTGTAA 5820

TAGATAATTT TCTTTCTTTT CCAAAACAGC CATCAACAAA CTTAATCGAT TATGATCAAT 5880

TATTAAAAGT GGTCTGGTTC CCTCCATGGT TGCAACAATT GTTGAACCTG GAACATTTGT 6000

TGAACGTTCT TCTAAAAACA TTTCAGATGG ATTATTTACA CCTTTTAATC CACTTTGCTT 6060

CATTTCGAAG ATTCcCATTT CATTCGTTGA ACCAAAACGG TTTTTAACAG CTCGCAAAAT 6120

TCGATATGCG TGGTGTTCAT CGCCTTCAAA ATAAAGCACA GTATCaACCA TGTGTTCTAG 6180

CAATCTTGGG cCCAGCAATT TGACCTTCTT TCGTTACATG ACCCACTATA AAAGTTGCaA 6240

TGTTCATTTG TTTAGCAATA TTCATTAAAC TTTGTGTACT TTCACGAACT TGTGAAACAG 6300

AACCTGGCGC AGAGCTGATT TCAGGATGAT ATATTGTTTG AATCGAATCC ACTACTAATA 6360

AATCAGGTTG TTCTTCTTTT ACTGTTTGAT AAATAACTTC AAGATCTGTT TCAGCTAATA 6420

CTTGCAATTC ACTTGAATCT TCATCTAATC GCTCTGCACG TAATTTAGTC TGACTAAGCG 6480

ATTCTTCTCC AGTAATATAT AGTACTTTTT TCTTTTGAGA TAACGATGCA CAAATTTGTA 6540

AAAGTAACGT TGACTTACCA ATACCTGGAT CCCCACCAAT AAGTACTAAC GATCCGCTCA 6600

CAATACCTCC ACCTAATACA CGGTTGAATT CTGCTGAATC TGTTAACACT CTCGGCGTTG 6660

TTTCATGTTT AATACTATTT AATTTTTGTA CTTTACCTGC TAATTCCTTG GTTTTAACTC 6720

CATGTTTAGG ATTGGCTGCT TTTTCAACAA TTTCCTCCAT TTGATTCCAA GCGCCACAAT 6780

TAGGACATTT CCCCATCCAT TTAGGAGATT GATAACCACA AGCCATACAT TCAAAAATCA 6840

CTTTTTTCTT GGCCArAATT GCAcCTCCAC TTTCTT 6876

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

CAACTCAAAC AGCAGAACAA CGTCGTGAGT TGATTAATGG TGTATTTACT GACATTAATC 60

CCATACATTA AAAATATGAT GTACGTGTTA GCAGATAATA GACATATCTC ATTAATAGCT 120

GACGTATTCA AGGCGTTCCA AAGCTTATAT AACGGACACT ACAATCAAGA TTTTGCAACA 180

ATTGAGTCAA CATATGAATT GAGTCAAGAA GAGTTAGATA AGATTGTCAA ACTAGTAACT 240

CAACAAACGA AGTTATCTAA AGTTATTGTA GATACAAAAA TTAATCCAGA TTTAATTGGT 300

GGATTTAGAG TTAAAGTCGG CACAACTGTA TTAGATGGTA GTGTTAGAAA TGATCTTGTC 360

CAATTACAAA GAAAATTTAG AAGAGTTAAT TAATTATAAA GAGGAGTGAC ATAGATGGCC 420

ATGTCCGTAA CTGATGTAGG TACTGTATTA CAAATTGGTG ATGGTATTGC ATTAATTCAC 540

GGATTAAATG ACGTTATGGC TGGTGAGCTA GTAGAATTCC ATAACGGCGT ACTTGGTTTA 600

GCCCAAAACC TTGAAGAGTC AAACGTGGGT GTGGTTATTT TAGGACCATA CACAGGTATT 660

ACTGAAGGTG ACGAAGTTAA ACGTACTGGT CGTATCATGG AAGTACCAGT AGGTGAAGAA 720

CTAATCGGAA GAGTTGTTAA TCCATTAGGA CAACCTATTG ATGGACAAGG ACCGATTAAC 780

ACAACTAAAA CACGTCCAGT AGAGAAAAAA GCTACTGGTG TAATGGATCG TAAATCAGTA 840

GATGAGCCAT TACAAACAGG TATCAAAGCA ATTGATGCTT TAGTACCAAT TGGTAGAGGT 900

CAACGTGAGT TAATCATCGG TGACCGTCAA ACAGGTAAAA CAACAATTGC AATTGACACA 960

ATTTTGAACC AAAAAGATCA AGGTACGATT TGTATCTATG TTGCTATTGG TCAAAAAGAT 1020

TCAACAGTAA GAGCAAATGT TGAAAAGTTA AGACAAGCAG GCGCTTTAGA CTACACTATT 1080

GTTGTAGCAG CATCAGCTTC TGAACCTTCT CCATTATTAT ATATTGCACC ATATTCAGGT 1140

GTAACAATGG GTGAAGAATT CATGTTTAAC GGTAAACATG TTTTAATCGT TTA 1193

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

TGCTAAGAAG TCAAAATAAA CTAACTATnA AACATCTAGT ACGATTATTA AAGTGACAGA 60

TnATAAAATT GAATTATTnA GAGAAGGAGA TATAAAGTTT GAAGAAATAA AAGAAAGACT 120

AGGTACAGGT ATTATTTATG AATAAGTTAA TACTTGGGAT TTATTTATAC CGAATTTTTT 180

CACGAGCATA CTTTTATTTA CCGTTTTTAT TAATTTACTT TTTGATTCAA GGTTATTCCA 240

TAATACAATT AGAAATATTA ATGGCGTCTT ATGGCATTGC AGCATTTTTA TTCTCTCTAT 300

ACAAAGAGAA GTGTTTTAAA ATTTGTAACT TAAAAGATTC TAATAAATTA GTTGTTAGTG 360

AAATATTCAA AATCATCGGT TTATTGTTGT TATTATATCA AAATCAATAT TTAATTTTAG 420

TAGTGGCACA AATATTATTA GGGTTAAGTT ACTCAATGAT GGCGGGTGTT GATACCGCAA 480

TAATTAAAAG AAATATAACA AATGAGAAAT ACGTACAAAA TAAGTCAAAT AGCTATATGT 540

TCCTATCATT ATTAATTTCA GGGATTATAG GTAGTTATCT TTATGGAATA AATATTAAAT 600

GGCCTATAAT AATGACTGGT ATATTTTCAA TTCTAACAAT TATAATTATT CGATGCACAT 660

TACCAGAAGA GAAGTTTTGG ATATTGCATT ATTCTTTTTT AAGAGCGTTA ATATTAGGAT 780

TTTTTATAGG ATTTATTCCA ATTAATATAT ATAATGATTT AAAACTGAAT AATTTACAAT 840

TTATTTCAGT ATTAACTTGT TACACAGTTA TGGGTTTTGT ATCTTCACGT TATTTAACTA 900

AATACTTGAA TTATAAGTTT GTGTCAGAAA TTTGTTTAGT AATATTTTTA ATAATATATA 960

CATATCAAAG TTTCATAGCA GTTACTATTT CTATGATATT TTTAGGTATT TCTTCAGGGT 1020

TAACTCGTCC ACAAACTATA AATAAACTTT CTAGCAGTAG TAACTTAAGA GTGATGCTTA 1080

ATTATGCAGA AACGTTATAT TTTATTTTTA ATATCGCATT TTTACTTATG GGTGGTTACT 1140

TATATACAAT AGGAACTATT CAATACTTAA TATTATTTAT TTCGTTATTA ATTTTTATAT 1200

ATTTAATAAT AATATTTyAT TTTACAAGGA GAGAGCAACA TGAAAATAAA AACTGAATTT 1260

AAAGGGAACA ATATACCATA TGAATACGCA GCAGGTGCAG ATGTGAGTGA TTCTATTAAC 1320

GGGAATCCAA TTAAGTCATT TCCATTTGAA GTAATTGAAT TACCGGAAGG gACTAAATAT 1380

CTTGCTTGGT CTTTAATTGA CTATGATGCA ATTCCTGTAT GTGGCTTTGC TTGGATTCAT 1440

TGGAGTGTAG CTAATGTAAG TGTTAGTGGC AATTCAATTT CTATAAAAGC AGATTTATCA 1500

AGAACAAAGG GCGACTATGT ACAAGGTAAA AATAGCTTTA CTAGTGGGTT GTTGGCTGAA 1560

GATTTTTCAG AAATAGAAAA TCACTATGTA GGACCTACAC CACCTGATCA AGATCATCAA 1620

TATGAATTAA CAGTTTATGC GTTAGATCAT TCTTTAAATT TGAAGAATGG GTTCTACTTG 1680

AATGAATTTT TAAAAGAAGT AAATCAACAT AAAATTGATC AAACAAGTAT TAACCTTATA 1740

GGAAGAAAAA TTTAATACTA AATATCTCAT CAATATAAAA TTGTTCAATT AAAAGTACAA 1800

AGAAACAAAG GTTTTAATTT ATATATTAGG TACGGCGTTC GCTATAATGC AAAGAAGTAA 1860

TTAAATTTAA GAAATGTAAA CTTAGTTATT GTAATGTGAA TTTATTTGAA AAAATAGAAA 1920

GTATTAACAA TTATAGCTTT TACATTAATT AAAATTTATT TTTAAAAACA AGTAAACAAT 1980

TTACATACTT ATAATTTTTG AAAATTTTCA ATTTGTGTTA TATTGATTTT GTAAGATACT 2040

TTAACTCACA AAGGAGAGAG AGTATATGAA ATTAAAATCA TTTATAACTG TAACTTTGGC 2100

ACTGGGCATG ATCGCAACGA CTGGCGCTAC TGTGGCAGGT AATGAGGTAT CTGCAGCAGA 2160

AAAGGACAAA CTACCGGCAA CTCAAAAAGC TAAAGAAATG CAAAATGTTC CATATACAAT 2220

TGCAGTAGAT GGCATTATGG CTTTCAATCA ATCTTACTTA AATTTACCAA AAGATAGCCA 2280

ATTATCATAT TTAGATTTAG GAAATAAAGT TAAAGCTTTG TTATATGATG AACGCGGTGT 2340

AACACCTGAG AAGATTCGAA ATGCAAAATC TGCCGTTTAC ACGATTACTT GGAAAGATGG 2400

TAGTAAAAAA GAAGTGGATC TTAAGAAAGA TAGCTACACA GCAAACTTGT TTGATTCAAA 2460

CAACATGAAG CATTTAATTT TACAGTGATG ATTATAAAAT AATTGCCTTG ATACAAAGAT 2580

TACTCGTAAA TGACATCTTT GTATTAAGGC TTTTTCTAAA TTTAAAAGTG ATGGGTTAGA 2640

GGTCATTGAG CTTTAAAATA TTCAAAATAC AAAACATTAA TGGCCAAAAA TAAAAGCCGC 2700

CTTTATCTGG GCAGCTTCAA TAATAAGAAA GACATATTTC ATTTTATACT AAATAGTTAT 2760

TGTGATGAAT CTTTCGGCGG TTTAATTACT GCAGCAAAAA TTGCTGTGAA AATCGTGAAC 2820

AATACTGCCA TGATAATTGG ATTCACTACA TTTAAGCTGT CTCCACCTAC TAGGCTATTA 2880

AGTACAAAGT TAACCATTTG CATTAATAAT AATGCCCAAA AGAATGTTAC GAGGTGTTTC 2940

ATGTCATTCT ACCTCCACTT TAATTATATA TATTTTATTT TAAGTGAAAG TTAGAAATTT 3000

GTATAGTAAC ATCTCATATA TTTTGACCAT ATTATACAGT TTAAATAAAT GATTTTATCT 3060

GAATGGCTAT TCTAAATTAA GCGCATTAAA ACCAATTTCA TACTGAAATT TGACGATAAT 3120

AAAGCATTAA AATTTTATTA ACTAGTCAAT ATTCCTACCT CTGACTTGAG TTTAAAAAGT 3180

AATCTATGTT AAATTAATAC CTGGTATTAA AAATTTTATT AAGAAGGTGT TCAACTATGA 3240

ACGTGGGTAT TAAAGGTTTT GGTGCATATG CGCCAGAAAA GATTATTGAC AATGCCTATT 3300

TTGAGCAATT TTTAGATACA TCTGATGAAT GGATTTCTAA GATGACTGGA ATTAAAGAAA 3360

GACATTGGGC AGATGATGAT CAAGATACTT CAGATTTAGC ATATGAAGCA AGTTTAAAAG 3420

CAATCGCTGA CGCTGGTATT CAGCCCGAAG ATATAGATAT GATAATTGTT GCCACAGCAa 3480

CTGGaGATAT GCCATTTCCA ACTGTCGCAA ATATGTTGCA AGAACGTTTA GGGACGGGCA 3540

AAGTTGCCTC TATGGATCAA CTTGCAGCAT GTTCTGGATT TATGTATTCA ATGATTACAG 3600

CTAAACAATA TGTTCAATCT GGAGATTATC ATAACATTTT AGTTGTCGGT GCAGATAAAT 3660

TATCTAAAAT AACAGATTTA ACTGACCGTT CTACTGCAGT TCTATTTGGA GATGGTGCAG 3720

GTGCGGTTAT CATCGGTGAA GTTTCAGATG GCAGAGGTAT TATAAGTTAT GAAATGGGTT 3780

CTGATGGCAC AGGTGGTAAA CATTTATATT TAGATAAAGA TACTGGTAAA CTGAAAATGA 3840

ATGGTCGAGA AGTATTTAAA TTTGCTGTTA GAATTATGGG TGATGCATCA ACACGTGTAG 3900

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TTAGAATTAT GGAATCAGCT AGAGAACGCT TAGGTATTTC AAAAGACAAA ATGAGTGTTT 4020

CTGTAAATAA ATATGGAAAT ACTTCAGCTG CGTCAATACC TTTAAGTATC GATCAAGAAT 4080

TAAAAAATGG TAAAATCAAA GATGATGATA CAATTGTTCT TGTCGGATTC GGTGGCGGCC 4140

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CGACAAAAAA GAAGCGCGTC GTATGGATAG ATTTACTCAA TATGCAATTG TAGCAGCTAG 4440

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ATGGATTGGT TCTGGTATCG GTGGTATGGA AACATTTGAA ATTGCACATA AACAATTAAT 4560

GGATAAAGGC CCAAGACGTG TGAGTCCATT TTTCGTACCA ATGTTAATTC CTGATATGGC 4620

AACTGGGCAA GTATCAATTG ACTTAGGTGC AAAAGGACCA AATGGTGCAA CAGTTACAGC 4680

ATGTGCAACA GGTACAAATT CAATCGGAGA AGCATTTAAA ATTGTGCAAC GCGGTGATGC 4740

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CAGTGCAAGT CGAGCGCTTT CTACAAATGA TGACATTGAA ACAGCATGTC GTCCATTCCA 4860

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AGAATCAGCA CAAGCTCGAG GTGCCAATAT TTATGCTGAG ATAGTTGGCT ATGGTACTAC 4980

AGGTGATGCT TATCATATTA CAGCGCCAGC TCCAGAAGGT GAAGGTGGTT CTAGAGCAAT 5040

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AGCGCAAGAC CTTGATATTA CTTATGCAAT GAGTAATAGC TTAGGATTCG GTGGACATAA 5400

CGCAGTATTA GTATTCAAGA AATTTGAAGC ATAACTATAA nAATCTTCAG TAACGTTGTT 5460

TTAGTTACTG AAGATTTTTT CaGTTTCTTT ATACTAAGAT GAGCGACAcA CAATCGTCAT 5520

AATAAAAATAT GAATATTTAT TAATAATAA 5549

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4832 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

AGATTATAGT AAGATTGATA GTTTGGCGAC TGaAGCgCGa GaAAAATTAT CAGaAGTAAA 60

mCCTTTAAAT ATTGCACAAG CTTCTAGAAT ATCAGGGGTA AATCCAGCAG ACATATCTAT 120

TGGTTAGCAG AACAATTAAA AGAACATAAT ATTCAATTAA CTGAGACTCA AAAACAACAG 240

TTTCAAACAT ATTATCGTTT ACTTGTTGAA TGGAATGAAA AGATGAATTT GACAAGTATT 300

ACAGATGAAC ACGATGTATA TTTGAAACAT TTTTATGATT CCATTGCACC TAGTTTTTAT 360

TTTGATTTTA ATCAGCCTAT AAGTATATGT GATGTAGGCG CTGGAGCTGG TTTTCCAAGT 420

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GCAAGAGCAg TAGCTAGATT ATCCGTGTTA AGTGAATTGT GTTTACCGCT AGTTAAAAAA 660

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TACAACTAAC ATAAAAGGAG CGAATGGATA ATGAAAAAAC CTTTTTCAAA ATTATTTGGT 960

TTGAAAAACA AAGATGACAT CATTGGACAT ATTGAAGAAG ATCGCAATAG TAATGTTGAA 1020

TCCATTCAAA TTGAACGTAT CGTTCCCAAC CGTTATCAAC CAAGACAGGT GTTTGAACCA 1080

AATAAAATTA AAGAACTTGC TGAATCAATA CATGAACATG GTTTACTACA ACCTATTGTT 1140

GTAAGACCGA TTGAAGAAGA TATGTTTGAA ATTATTGCTG GAGAGCGCCG ATTTAGAGCA 1200

ATACAATCAC TAAATTTACC TCAAGCAGAC GTTATTATTC GTGATATGGA TGATGAAGAG 1260

ACGGCTGTTG TTGCATTAAT TGAGAATATT CAAAGAGAAA ATTTGTCTGT TGTTGAAGAA 1320

GCGGAAGCCT ATAAGAAATT ATTGGAAATT GGTGATACAA CGCAAAGTGA ATTGGCAAAA 1380

AGTTTAGGTA AAAGTCAAAG CTTTATTGCA AATAAGTTGC GTTTATTGAA GTTGGCGCCG 1440

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ACCTTCGCTT TGCACAAGAT GTCACTCAAG CACGAGATGA GGTAGGCAAA AGTATCCAAG 1680

CGATTCAACA AACAGGATTA CATGTTGAGC ATAAAGACAA AGATCATGAA GATTATTATG 1740

AAATAAAAAT TCGAATATAT AAACGTTaGT AGTAGGATGT CGTATACATG ATGACTAACA 1800

CATAAAAGAC AAAGCTAAGA TCATAACAGC TTTGTCTTTT TTTTTTGTTT TACGTGAAAC 1860

ATAAAAATTT ATATTTATAT GTTGATCAGG CTGGTACATA AATCAATGTT CTATGCTCTA 1920

TTCTAGTCAA CCTTGCTGGG GTGGGACGAC GAAATAAATT TTGCGAAAAT ATCATTTCTG 2040

TCCCACTCCC TAATTTGAGC TGGATATACT TTCATTTGAA CCCTTTATTG CTAGTTTATG 2100

AAAGTATCAT GAAAGCTTTA TGAACATCGC TTGAGTTGCC TTTACAGTAG AAAATTTAAG 2160

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CAGTTGTTTG TTGGTTTGTC ATTTCCCTCG CAATATTCAG TATTAGACAT TTATAGTTTG 2580

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ATTGTATCTG TAACACTACC TTGGAAAGAA TTTGGCGGTA TATTTGCaAC GTTTCCGGCA 2760

GTATTTTTAG TGTCTATGTT TATTACAGGT ATGCAATATG GTGATAAAGT CGCTGTGCAT 2820

GTAAGTCGTG GCGCAGTGTT TGGTATGACA GGGGTATTAG TTTGTATTTT AGTTACATGG 2880

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AAGCATAGTT GGAAAGCTGG AAAATCGAAT AGTAAATAGT GTGAACGTAA TCTCTTAACT 3060

AGGACTAACT TTGCAAGCAT TGAATAGCAT GGAAAAGTTG CATCATTAAT AAGTGAAATT 3120

CAAGTTGGCA TTGAGAAAAT TACAAGCGCG TAATCATACa GGTCTGTCTT AAGGGAGTCT 3180

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aTTCATTTAT AATGAGTCGT TTTATGTTGT AAGATTAAAC AGTTTGTACG TTAACTGCTT 4020

GGTCTCCACG TTGACCTTCA GTGATTTCGA AAGTAACTTT TTGACCTTCT TCTAAAGTTT 4080

TGTAGCCATC GCTAGCGATA CCTGAGAAAT GTACGAATAC GTCTCCGCCA TTTTCTTGTT 4140

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ATCCTCATAT GATTGTTTTA CTAATTCTCT AAATTTCATG ATTCAATCTC TCCTTTTTTA 4800

TAAATCTTTA GATTGTCAAA TTAAGCTGGA CA 4832

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5727 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

CAAAGCTGTT CAAAAGGCTT ATAATTTAAA TTTAGATAAC ATACGTACAA TGGAACCTAA 60

GTTGAGATAT CAAGCGATCA ATAAAGGTAA TATTAATTTA ATAGATGCAT ATTCAACTGA 120

CGCTGAATTA AAACAATATG ATATGGTTGT GTTAAAAGAT GATAAGCACG TATTTCCACC 180

ATATCAAGGA GCACCATTAT TTAAAGAAAG CTTTTTAAAG AAACATCCAG AAATTAAGAA 240

ACCGTTAAAC AAACTAGAAA ACAAAATATC TGATGAAGAT ATGCAAATGA TGAACTATAA 300

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TATTATCACA ATGCGATTGT TGAATCAGCT AATGTGATAC AAGTACCTTT AAAAGATGGT 1020

GGCTTCGATT TAGAAGGTAT TTTAAAAGAA GTTAATGAAG ATACGTCATT GGTATGGTTA 1080

TGTAATCCAA ATAATCCTAC AGGTACATAT TTTAATCATG AGAGCTTAGA TTCGTTTTTA 1140

TCTCAAGTAC CTCCACATGT ACCAGTAATT ATAGATGAAG CTTATTTTGA ATTTGTGACA 1200

GCAGAGGACT ACCCGGATAC ACTTGCTTTG CAACAAAAAT ATGACAATGC TTTCTTATTA 1260

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AATGTAGGGT GTATTACGCG ACCATTTCCA ACTGGTGTTA GAATTACAAT TGGTTTTAAA 1620

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CGATTATGTT TACAGCAGTG CATAATATTA ATGATGATCG ATTTGAACGC GTAAATAGCT 2520

GGAAAGATGT AGAACAGTAT TTTTTAGATA ATATTGAGAA ATAAAATATA TCACTTGAAA 2580

AATTTCATGT AGAAAAGATG ATGGATAGGC TATAAAGTAA TTGTGACTGA GATGAACTTT 2640

TATGTCTTAG ACACTACAAC ACTATATTGG CAGTAGTTGA CTGCGGGGCC CCAACATAGA 2700

GAAATTGGAT TCCCAATTTC TACAGACAAT GCAAGTTGGG GTGGsCCCCA ACATAAAGAA 2760

ATACTTTTTC TTTAGAAATT AGTATTTCTT ATGCATGAGT GTAACTCATG CATTCATATT 2820

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GTTCTTTATC ATTTCCGTCC CGCTCTCAAT AAATGTTAGT CTATCTTATT ATTATAAATC 2940

GGATGAATGT GTTAATCTAT GGCAGATTAC ACGTCATCCG ATTTTTTATA GAATTTGAAA 3000

AAGACGCATA AACCACTATG ATTTAAAATA CAACATCAAT CATTTTAGTG gCATGCGCCA 3060

AAATTATATG TCTGTTTTTG AAACAGGGTA ATAGCTTAAA GCTAATAAAA ACGAATATAA 3120

GGTGCGTTGA ATCTTATGAT TACACTCCAA ACCTAATATA ATATCGGGTT AAGATCATTC 3180

CGGATGCTTA CAAATCATTG ACAGTAAGTA ACTGAATGGC ATTTGGTATA ACCTCAATAT 3240

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TGAGACCTAA GCCAACAAAG TTGAGTGCAT ATTGATTATT TATTTTAATT ACATCGTATG 3720

TACCAACTTG TGCAGAAATC ATTTGTTCAC TAGCTTGTTT ATGATTAGGT GCTATATTTA 3780

GCGTTTTTGT AAAATCATTA AAAGTACCGC CTGGTAAAAT GCCAATAGGG AGTTGAAGGT 3840

CATGTGTCAT AACACCGTTT ATAAGTTCGT TAACCGTGCC ATCACCGCCA AGAATAAATA 3900

CACCTTCGTT TTCACTCAAT TGAATAGAAA GATGCTTACA AATTGAACTT AATGCTGTTG 4020

TAACTTCCCC AATACCTTGA TTAATATTTT TTAATCCACT GTGTTCATGG TAAAAGAGGA 4080

CACCATGTGT ATATTTATTT TCCATAGTTT AGCCTACTTT CTAAAAATTG GTTCATTAAA 4140

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TTGGGCATTA AATGCTTTAG GTGCTAACTT AACAGCAGCA CTATTACCCG TTGGTGATAA 4620

GCATAGCTCA CCGATAACAC AAATAATGTA CGATAAAATA ACCCAGTTAA CTGAAAAGTT 4680

TGATGAACCT GATGCATAAC CTACAATACC AATTAGTATG TATGACGCAC CTGCTAAGAA 4740

CGTACCAATT GCAAATTTTA CTGGCAGGCT AGGTTGTTTA GTTCCAAGCT TTTGCCATAA 4800

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CATATAGATT AATGAACCAT ArACTGACAT AATTGACATA GCTGTTGTTT TATCAATTCC 5700

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14078 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

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ATCACAGATG ACCCAGCATT AGCTGATCAG ATTAAAGAAG AAAAGAAAGA CGAAACATAC 120

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AGATGATACC TTCAGAGGTC TTTTTAATGT TGCCATCTAT GGGATAGGCA ATCGTTTCAT 240

TCGTTTATAT TCATATGACA AGTATTTGTA TGGCAATTTG GCGTCACAAA CACTTACATG 300

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TACTTTCTAA TCTTTGTTTC GCTTTAGTCA TTTGATCCAA ATTTTTAGTG CGTATAGCGG 420

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GATAATAAAC CTAATTTTGA TAAATTAGTT GAAGAAACGA AAAAAGCAGT TAAAGAAGCA 1740

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GTAGTAAAAG AAGAGAAGAA AGTTGAAGAA CCTCAAGCAC CTAAAGTTGA TAACCAACAA 1860

GAGGTTAAAA CTACGGCTGG TAAAGCTGAA GAAACAACAC AACCAGTTGC ACAACCATTA 1920

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TATAGAGATG CTGGTACAGG TATCCGTGAA TACAACGATG GAACATTTGG ATATGAAGCG 2340

AGACCAAGAT TCAATAAGCC ATCAGAAACA AATGCATATA ACGTAACAAC ACATGCAAAT 2400

GGTCAAGTAT CATACGGAGC TCGTCCGACA TACAAGAAGC CAAGCGAAAC GAATGCATAC 2460

AATGTAACAA CACATGCAAA CGGCCAAGTA TCATACGGAG CTCGTCCGAC ACAAAACAAG 2520

CCAAGCAAAA CAAACGCATA TAACGTAACA ACACATGGAA ACGGCCAAGT ATCATATGGC 2580

GCTCGCCCAA CACAAAACAA GCCAAGCAAA ACAAATGCAT ACAACGTAAC AACACATGCA 2640

AACGGTCAAG TGTCATACGG AGCTCGCCCG ACATACAAGA AGCCAAGTAA AACAAATGCA 2700

TACAATGTAA CAACACATGC AGATGGTACT GCGACATATG GGCCTAGAGT AACAAAATAA 2760

GTTTGTAACT CTATCCAAAG ACATACAGTC AATACAAAAC ATTACGTATC TTTACAACAG 2820

TAATCATGCA TTCTATGATG CTTCTAACTG AATTAAAGCA TCGAACAATC GGAAGCATAT 2880

TTCTAAATTA TTTATTCATT ATAGTCTTAA ACATAACATG ACCTAATATA TTACTAACCT 2940

ATTAAAATAA ACCACGCACA TCTAAGTGAT ATACGACAAT CACAGCAATA ATAATTGCTT 3000

TAGAAAGTCG TGCCGAACTG GAACTTACAA GTCTAGTTCG AACACACACT GATGTGAGTG 3060

GTTTTCTTTA TTTTAAACAT GAACAATCAG ATAAGTTACT AGCATTAGCA AATATTATTA 3120

AATCAAAGGG CTTCGATTCA TAAAATTTAA AACAATGATT AAAATTAGAC GTGTAAATGT 3180

TATTTCACAC AGCTTCATTA ATAAAACGAA ATTGCTTCAA CCCGCTTCAA CTTCAACTGG 3300

CTTCAACTTC AGCCTACTTC ATTCAATAAC AAAACGAATC CGCTTCATCC AAAATCAACC 3360

ATTCTAACGC ACATATTCAA ATATAGCAGC TGCACCCATG CCGACACCAA TACACATCGT 3420

AACCATGCCG TAACGGCTAT CGGGACGTCT ACCCATTTCA TTAAGTAAAC GCGCGGTTAA 3480

CATTGCGCCT GTAGCACCTA ATGGATGACC TAAAGCAATA GCGCCACCAT TCACATTCGT 3540

ACGTGATATA TCTAGACCTA CTTCTTTAAT AGATGCAATC GTTTGAGAAG CAAATGCTTC 3600

GTTCAATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA ATACTTCAGG 3660

AATCGCATAT GCAGGCCCAA TACCCATAAT TTTCGGGTCA ACGCCTACTG CCTTAAAACC 3720

AACGAATCGT GCAATAGGTG TCACGCCGAG TTCTTTCACT TTATCTCCAG ACATTAAAAC 3780

TACAAATCCT GCACCATCAG AAAGTGGGGC AGATGTTCCT GCAGTCATAG TGCCGTCAGC 3840

TTTAAATACT GTACGTAATT TGGCTAATGC CTCCATCGTG GTGTCAGGGC GTATAAATTC 3900

ATCTTGGTCA AAGATATTTG TGTGTACTTT TGGTCCTGCG TTTGTATATT CAACTGAGTT 3960

TACTTGTATT GGAATAATTT CATCTTTGAA CCGACCATCA CGTTGTGCGT CATAGGCACG 4020

TTGATGACTT CTGACAGCAT AAGCATCTTG ATCTTCGCGT GATACGTCAA ATTGGGATGC 4080

TACATTTTCA GCAGTTAAAC CCATAGGATA TGACGCACCT ATATCATCAT ATTGTAAGGT 4140

TGGATTGTTT GTGGGCTCGT TGCCACCCAT TGGTACGGCA CTCATCAATT CAACGCCACC 4200

AGCTACAAGT ATATCTCCTT GACCAGCCAT AATTTGATTG GCTGCAATCG CGATGGTTTG 4260

TAATCCTGAT GAGCAGTAGC GATTCACTGT TTGACCCGGT ACCGTGTCAG ATAATCCCGC 4320

ACGCAATGCA ATCGTTCGTG CAATGTTTTG GCCTTGTAAT CCTTCTGGAA AAGCCGTACC 4380

AACAATGACA TCTTCAATCA TATTCTTATT GAATTTTCCG TCAATACGTT TCAATACGCC 4440

TTGTAATACT TTGGCTGCGA CATCATCAGG TCTTTCGTGG AATAATGCGC CTTGCTTTGC 4500

TTTCGCTGCG GCTGAACGCC CATAAGCTAC AATGTATGCT TCTTGCATGG TTATCATCCT 4560

CTCTTAATGA CTATCTTTTA ATTACGTAAT GGCTTACCAG TTTTTAACAT ATGTGCAATT 4620

CTTTCATATG ATTTTTTAGA TTTTAGTAAG TCAATAAAGC CAATTTTCTC CAACGATTGA 4680

ATGTAACGTT GATTGATAAA TGTATTTCTT GGTAAATCAC CACCCGCTAA AATTGTGGCG 4740

ATATTTAAGG CAATATGATA ATCATGGTCG CTAATAAAAT GACCCCGTCT TTGCGCATCT 4800

AATTGTCCTT GGATCAATGC TTTGAAGTCT TCACCTAAAG CGATATATTG ATGTCTAGGA 4860

TTCGGAATAT AGTTTGTTTC TGCTTCATAT TTCGCACGTT TGAGCGCAAC TTCGACACGT 4920

TGTGCTGTAT TGAAAATAAT CGTATCTGTA TCACGTAAAT AACCATAACG ACGTGCCTCA 4980

TGTTTGTCAT CAAACTTATG CGATGTGCGT AATATGCGAT CAGCCATTTC TGCAAGGCCA 5100

CCGCCACTCG GTAATAAGCC AACACCTGCT TCAACAAGAC CGATATATGT TTCACTTGCA 5160

GCGACAACAA TAGGTGAGTA AAGTACAAGC TCACAGCCAC CGCCTAAGGC ACGACCTTGA 5220

ACAGCTGTGA CTACTGGTTT CAAACTATAC TTCAAACGAT TAAAGCTATA ATGTAATTTA 5280

TCAATTGATT GTGCAACGAC ATCATCTACA AGACCGTCTT CATGCGCCTT TTTCATTAAG 5340

AAAAGGTTAG CACCCACACT GAAATTGTTA CCATCTGCAT AAATAACCAT ACTTGTGTAA 5400

TGGTCATTTT CCAGTAAATC AATCGCATCA ACTAACGCAT CGTTGAATTC ATCGGTAATG 5460

ACATTATTTT TACTTTGTAA TTTCAGTAAC AGTTGATCAT CATGAGTTAC GGAAAGTTTG 5520

GCATCACCTT TATCCCAAAG TTCATCTTTT ACGAAGTGAG AAATAGGTGT TGCATATTCA 5580

ATGGTCTCAT CTTGTTTATA AAAGCCACCA TCTAAATCAC TAATCCATTG TGGTAAGTCT 5640

CCAAGTTCGT CTTCCATACG TGTTTTAACA CGTTCGTATC CCATTGCATC CCATAATTGG 5700

AATGGACCAA GTTTCCAGTT GAACCCCCAG ACAAGCGCAC GGTCTATGTC TCGGAAATCA 5760

TCGGTAGCTT TAGGTACATT GATAGCAGAG TAATAGAAAT TATTACGTAA TGTCTCCCAT 5820

AAAAATAGTC CCGCTTCGTC TTGCGCATTG AATATGGTAT CAAGGTTATG CACTAAGTCT 5880

TTATTAAATT CATTTAAAAT TGGTAATTGT GGTTGCGATA CAGGTACATA ATCTTGTTTT 5940

TCAACATCGT AAACAAGTCG AGCTTTAGTT TCTTTATCCT TTTTGTAAAA TCCTTGTTTC 6000

GTTTTACGTC CGAGTGCGCC ATTGTCAAAC AACGTATTTA CAATTTTGAC ATCATGAAAA 6060

TAAGGTGTTT CTTCAGGTAC TTGTTGCATG CCTTTAATTA CAGACACTGC AATATCTAAA 6120

CCGACTAGGT CAGATAGCGC ATATGTACCT GTTTTAGGAC GACCAATCGC TTGCCCAGTT 6180

AAAGCATCCA CATCTACAAT GCTTATCTTG TGTTGCTCGG CGCGATACAT AATATCATTC 6240

ATTGTTTGCG TGCCGACTCT ATTTGCGACA AAGCCAGGCA CATCATTGAC GACAATGACA 6300

CCTTTACCTA ACACATTTTG CGCGAAATTT TTTACATCTA ATATAATAGA TTCCTTCGTG 6360

TGTGACGTAG GTATTAACTC CACTAATTTC ATAATACGTG GTGGGTTAAA GAAATGTAGA 6420

CCAAAGAATC GTTCTTGATC CTTCTCGTTA AATGCTTGAG CAATCGCATT AATTGGAATA 6480

CCTGATGTAT TTGTAGCGAA TAAAGCATCT TCTTTAGCAT GTTGTAGAAC TTGTTGCCAA 6540

ACAGCATGCT TAATTTCAAT ATCTTCTTTG ACTGCTTCGA TATATAAATC AGCATCATCA 6600

TTTACCAAGT CATCATCAAA ATTACCATAT GTTAAATGAC TCGCTAGATT TAAGTCGAAT 6660

AGTAGCGGCC GTTTCTTATC TGTAATTTTA TCGTAAGATT TTTTCGCAAT GAGATTTGGA 6720

TCGTTTTTGT CCACTACAAT ATCTAATAGT TTTACTTTAA GTCCAGCATT CACAAAAAGT 6780

GTGATTCCTC CAATTTAGTT GAGGATAAGA TAACCATTAA GATAATTGGA ATAACGTTGC 6900

TATTTTATAA AATTAATTAA GTATCTTTGA CAGTCATCTT AGCCTCTTAT TTAAGGAAAA 6960

AGCTTTATGC TTAAAATAAG TCTTTTTTAG TGAAATTAAT GCATCTCATA TAATTATTTG 7020

CTATTTATAC GAAAGCAGAA TCTCCAGTCA AAGCGCGTCC AATTACTAAG GCATTAATTT 7080

CATGTGTACC TTCGTACGTG TAAATCGCTT CTGCATCAGA GAAGAAACGT GCAATATCAT 7140

AATCGTCAGC TAGTATGCCA TTACCACCTG TAATACCGCG GCCCATAGCT ACTGTCTCAC 7200

GCAAACGTAA GGCATTCATC ATCTTCGCCG TTGAAGTTGC AACCTCGTCA TATTCACCAT 7260

GTGCTTGCAT ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGAGCTAAA TTACCTTGCA 7320

TCATTGCTAG CTTTTCTTGT ATTAACTGAT ATTTACTAAT TGGTTTGCCG AATTGcTTAC 7380

GCTCAGTGAC ATAATCTAAT GTGGCACGTA AAGCGCCAGC CATACCACCT GTAGCCATAT 7440

AAGCAACGCC TGCTCTCGTT GAATAAAGAA TTTTGGCAAT ATCTTTAAAG CTTGTTATGT 7500

TTTGTAAGCG ATCCGCTTCA TCTACTTTGA CATTAGTTAA TTTAATTAGG GCGTTAGGAA 7560

CAATGCGAAG TGCGATTTTA TTATCAATGA CTTCAATATC GACGCCATCT TGTTCTGGTC 7620

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GGCGTTCAGC GACTGTTTCA AGACCTCCCG CAACGTCCGA ACCGTGTTCT GGTTCAGTTA 7800

AAGCAAAGCA TGTACGCAGT TCATGTGACT GTAATTTAGG TACATATTTC GCAATTTGTT 7860

CTTTGCTACC TCCGAAATAG AAAGTGTTAT GCCCTAAACC TTGGTGAACA CCGAGTAGGG 7920

TAGCTAAGGA AATATCAAAT CGCGCGAGTA GGTAAGACAT GAAAAACTGA AATAGTTGAC 7980

TAGGCATTTT GGCGTTTGGA CGATCCTTGT AAAGTAATGG ATTGTTAAAA TAATTTAATT 8040

CTCCCAGATC TTTAAAATAG TCCTCGGGTA CAGTAGCGTC TATCCAATGT TGATTAATAT 8100

TTTCACGGTA CTTACTTTCT AGCAATGAAT CTACTTGTTG TAAAAATTCG ACTTCACCGT 8160

CTGTTAAACC TTTAGCAATA CTAAGTACAT CTTCAGGAAA TAATGTTTTT AAGACCGTTT 8220

CTTTTTCAAA TGTCATATAA ATTCCTCCTA AAAATAATAT GAATACTAAT GTGAAATGCA 8280

TTTAATTCAA AAACAACACG CTTTATTTGT AAACGCTTAC ACTAAATGTC AAAAATTTTT 8340

ATCACCTTTA AAGTGTTTGC GAGACTTTGT CATTCATCAT TTGTCGAATC GCAAGTTTAT 8400

CTGGTTTCTG CGTACTGTTT AACGGCATAT GTGTCACTGG TACATACATT CTTGGGACTT 8460

TATAACCTGC TAAACGACTt CGCATATGTT GATTTAAAAT TTCAGCGTAA TGAGGTTCAT 8520

CTTCGCGAAG TATAATGGCT GCAGCAATTG ATTCACCATA TTTTGGATGA TCATAGCCAA 8580

AGACATTTTC GCCACCAGTT ATGATTAATT CTTTTTTGCG GTCAATAATA AATATATCGC 8700

CATCGTTGTC CATCTTCGCT AAGTCACCAG TTAATAAATA TCGACCATGA AATGCTTTGG 8760

CAGTCTCTGC TGGTTTATTC CAATATCCTG GCGTGACATT TTTAGCCTTA ATTGCAAGTT 8820

CGCCAATCTC ACCAGTAGGT ACTTCCTCAC CGTTATCATC AAGGATACGT GCATCAACGA 8880

ACATGACTGC TTTACCAATA CTCATTGGCT TACGTTTTGA ATTTTCCGGT GTATTAACAA 8940

GTACAAGAGG TGCTTCAGTT AAACCATAGC CGTTAATAAT GTTTATGCCA TATTGTTTAA 9000

AAGCTGCTTG GATACTTGGT AATGGTTGTG AACCACCTTG GATGATATAA TCCATAGCTC 9060

TAAAATTTTC AGGATTAAAA TTACTAGCAC GTAGCGTACT ATAATACATT GTCGGAATCA 9120

TGATAATAAA TGTAGGGTGA TATTGTGCAA TCATGTCATT CAATTCTTCG CCGTTAAAGT 9180

AACGTTGAAG AATAAGTGTG CCACCTGACA TTAATACTGG TAATACAGTA TCGTTAAACC 9240

CTAAAACATG GAACATTGGT GTTGATACAA TCGTAATATA GTTTGAATTG AACTTATACG 9300

TCAGCTCTAA GTTTGCACCG TTATGAACAA ATGATTCATA TGAGAACATC ACACCTTTAG 9360

GTGATCCGGT TGTACCACTT GTATAAATTA ATGCTGCAAG ATCTTGTGGT TCAACAGGTG 9420

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AGAAGAGCAG TTTTAATTGT GCATCTTCCA CAATGGCTGC AATTTCTTTT GGGTTAAGCC 9600

GCCAATTCAA TGGTAAAAAA ACCGCACCTG TTTTAAAACA AGCAAACAAT AAATCTAATA 9660

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TTAAGTTGTC CCCATTTTTC TTTGTAAATG CTGGTATCAA TTAATTTTAA ATGATCAGCA 9960

ATAATTGGTT TAAAAGCCAT TTGATTCAAA ATATCTTTAT GCAAATCAAG ACCTGGTGCA 10020

ATTTCAATTA GTTTCAAGCC TTGATTGGTG AGTTCGAATA CTGCACGATC AGTAACAAAA 10080

TAGATTTCTT GCTCGAGTGA TTGTGAATAT TGTGCATTAA AGTCGATATG GCTCACATCT 10140

GATACAAATT TCTGGTTTTG TCCTTCAGTT TCAATGTTTA ATCGTTGATT ATGGCATGAG 10200

ACATGACTGC CAGCTACAAA AGTACCTGAA AAGATAATTT TATTTACAGA TTGCGTAATG 10260

TCTATAAAGC CACCACATCC ATTTAGTCGG TCATTGAAGT AAGACACGTT GACATTGCCG 10320

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TTTTGATGGT CGATAACAAT TGTAATATCA AGGGTTTGTA ATGAATTGAA TATCATTAAA 11640

ATACTTATAT AAAAATATTG TTCGGAATAT AAAAAGTTAA ATAGGTTTTG ATTTTTAAAT 11700

ATGAAATACA AAGTGCCCAA TCGAACAAAG TATTTATATT AAAATATGGA AAATCCATCA 11760

ATATTAAATT AAAATAGTTT TATTATGAAA AGTGAAAGTA GGTAAGTCTA TGGAAGGTCT 11820

TAATCATCGA AGAAATACAG AAAAAGAAGA GACAACACAA ACGCAATCaG TTGCACCTAA 11880

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GGGCAATGAT GAAAGCTTAA ATCTTAATTT AAAAGATATG CTTTCTGAAG TATTTAAGCC 12120

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TTTCACAGTA ACATTTATTG GATTATGGGT CATGGCAGCA ATTTTTAATA ACACTAACGC 12300

GATTCCGGGT CTCATTTTTA TAGGGGCTTT AACAGTACCA TTATCGGGTT TGTTCTTCTT 12360

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TGGCGGCGTA TTTTCATTAC TAAGTACGAT GGTATTATAT AGATTTGTCG TTTTTAGTGA 12480

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TGGCAGTGAT ACGTTGAAAA TATTTATTTT AATCGTTATT GTGTGGATAC TTGTATTCaT 12960

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GAAAAAAGTA GACGAATAAT AATTAAAGCT TATGTTGCTC ATATGTTTGT GACATAAGCT 13080

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GGCTGAGACA TAAATCAATG TCCCACACTC CCTTATCGTT CAATCGTTGT TCGATAATCG 13380

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TCATTAGAAA TATTGTGACG TTCCTTAACA TCTACAGTAT GATTCAATTG ATTAATTAAA 13560

TCATCGACGT TGCTATTATT GTAGTCTCCT TTATTAATAG CACCATCTTT TTTATATGCT 13620

TGATTAAAGA AATAACCTGT ATCTCCACGA GGAATTGTTC CGAAACTATA CATCGTTGCA 13680

TCCCATGCAG AACGGTCTTT TAAGTAACCT TCTATGTCAT CAACACTTTT AATGTCGATT 13740

TCAATATTTG CTTTTTTAGC ATCTGATTGT AATACTTGCG CAATTTTCGA TAGCTCTGGA 13800

CGACCGTCAT ACGTAATTAA CTTAATTTTT AAAGGGTGTT CTTTTGTATA ACCATCTTTA 13860

GCTAATAACA TTTTTGCTTG TTCGATATTT TGTTTGGTTA ACTTAGGTTC TTTAATATAT 13920

GGAATTTTAT CATTAAATGG ACTCGTTGCA GGTTTCGCAT AACCTTGATA AATATGATCT 13980

TTATtAGTAT GATTATACAT AAGTaAGAAG TTCTAAAn 14078

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

TGAAAACTAA AGTGTTTCTA ATGCGTGACT AAAATTAGTA ATAATTAAGT TCTCATGATA 60

ATAGGTATTT TTGAAAAATG GAGGAGTCTA TAAATGGGTA AAAAAATGGG TCTAGGTTTA 120

TCTATTGCAT TGGTTGTTAT TGGTATTGCC GTTGTATGTT TAATGATTTT TTCTAGTCAA 180

AAAACGACTT ATTTTGGTTA TATGAATAGT AATACAAATG CAGAAAAAGT TGTCAGTGAA 240

AAAGATGGAT TAGTCAAACA TAATATCAAA GTAGAACCAT CTAATGATTT CAAGCCGAAA 300

AAAGGAGACT TTGTAAAATT AGTTTCTAAA GATGATGGGA AGACATTTTA TAAACAAGAG 360

ATTGTTAAAC ATGATGACGT CCCACACGGT TTAATGATGA AAATTCACGA CATGCATATG 420

AATTAATAAA AAAGCATCTA TAACGTAATT TTGAAGAAGT AGAGTTATCT TCTTATGCGT 480

TTTAGA 486

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1626 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

GAGGTCTATA TACAATTATG GTTGTTCCAG TTAAACGAAC TGATGGCTTT ATTACTAAGT 60

TTAATAGATT AATTGAAAGA CGATTATTAC GTCATTTCAG TAAAAAAGGT TATATCACAT 120

GGGAGGAAAA TTGATTGTCT GACATTTTAA AATGTATCGG TTGTGGTGCG CCACTTCAAT 180

CTGAAGATAA AAATAAACCT GGTTTTGTAC CAGAGCATAA TATGTTTCGT GATGACGTGA 240

TTTGCAGACG TTGTTTCCGC TTGAAAAATT ATAACGAATT CAAGATGTAG GATTAGAAAG 300

TGAAGACTTT TTAAAATTAT TATCAGGACT TGCGGATAAA AAGGGTATTG TCGTCAATGT 360

CGTGGATGTA TTTGACTTTG AAGGATCATT TATTAATGCA GTTAAACGTA TTGTCGGAAA 420

TCGAGTTAAA GAATGGTTAA AACGAACAGC AAGAAAATAT GGTTTGGAAG CTGACGATGT 540

CGTATTAATT TCAGCTGAAA AAGGCTGGGG CATAGACGAC TTATTATCAT CAATTGCGAA 600

TATTCGAGAA AATGAAGATG TGTATATTGT AGGGACAACG AATGTTGGGA AATCTACATT 660

GATTAATAAA CTGATTGAAG CTAGTGTTGG TGAAAAAGAT GTAGTAACAA CTTCAAGATT 720

CCCTGGAACA ACTTTAGATA TGATAGATAT TCCTTTAGAT GAAACATCAT TTATGTATGA 780

TACACCAGGT ATTATTCAAG ATCACCAAAT GACGCATTTA GTTAGTGAAA AAGAATTGAA 840

AATTATTATG CCTAAGAAAG AAATAAAACA ACGCGTATAT CAATTAAATG AGGCGCAGAC 900

ATTATTCTTC GGCGGTCTAG CGCGCATAGA TTATGTATCA GGTGGTAAAC GTCCGTTAGT 960

TTGTTTCTTT TCTAATGACT TGAATATACA TCGTACTAAm ACGGAGAAGG CTAATGATTT 1020

ATGGCGTAAT CAACTTGGCG ATTTATTAAC GCCACCTGGA AATCCACAAA ATTTTGATCT 1080

TAATGAGGTA AAGGCTGTTA GACTTGAAAC AGGCAAAGAG AAACGCGATG TTATGATCTC 1140

TGGTCTAGGC TTTATAACTA TAGGACCAGG GGCTAAAGTA ATCGTTCGTG TTCCTAAAAA 1200

TGTTGAkGTT GTATTAAGAA ATTCTATTTT ATAAGGTGaT TAAAAAAATG AAATTTGcAG 1260

TTATAGGAAA TCCTATTTCA CATTCCTTGT CGCCCGTTAT GCATAGAGCA AATTTTAATT 1320

CTTTAGGATT AGATGATACT TATGAAGCTT TAAATATTnC CAATTGAAGA TTTTCATTTA 1380

ATTAAAGAAA TTATTTCGAA AAAAGAATTa GAAGGCTTTA ATATCACAAT TCCTCATAAA 1440

GAACGTATCA TACCGTATTT AGATTATGTT GATGAACAAG CGATTAATGC AGGTGCAGTT 1500

AACACTGTTT tGATAAAAGA TGGCAAGTGG ATAGGGTATA ATACAGATGG TATTGGTTAT 1560

GTTAAAGGAT TGCACAGCGT TTAnCCAGAT TTAGAAAATG CATACATTTT AATTTTGGGC 1620

GCAGGT 1626

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 635 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

AGGGTTAATT GTCGGTTTAA TTGCAATGAA TAAGTTCCAT GTATTAGCTG GCTATAGAGC 60

GAAATTCATC TTAATGGTGA TTTTAACTAT GATGGTCTTC GTACTTATTA ATACGTATTT 120

ACTAAGACAG GTAAAATCTA TCGGTATGTT CTTAATGATT GCTGCATTGG GTCTATACTT 180

GTCTTATATC GATAACATGT TCTTCAATTA TTTAAATGCA GAGCATCCTA TAGGCTTGGT 300

GCTAGTAATA TTAACAGTAC TTGTGATTAT TGGCTTTGTA CTGAACATGT TTATAAAACA 360

CTTTAAGAAA GAGAGATTAA TCTAATGTTG ATGAATAGCG TGATTGCTTT AACTTTTTTA 420

ACAGCATCTA GCAATAATGG CGGACTTAAT ATTGATGTGC AACAAGAAGA GGAAAAGCGA 480

ATCAATAATG ATTTAAATCA ATATGATACA ACGCTATTTA ATAAAGACAG CAAAGCGGTT 540

AATGATGCGA TTGCTAAGCA GAAAAAAGAA CGACAACAAC AAATAAAAAA TGATATGTTT 600

CAAAATCAAG CGAGTCACTC GACTCGCTTG AATGA 635

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13715 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

CTGAAATGGG TATTATTTGT CTTCTTCATC ATAAAGTAAT AAAGATTGTT CATCATTGCG 60

ACGTTGCCAA TTTTCATTTG GCGATCTTGG AACGTATAAT AATTGCCTAG TAGCATACGC 120

TTTGATTGAA ACATACAAGT CATTCCTTGA ACTTGCACCT CAATTTCCAC ATTTGAATTT 180

TCTTTTATAT TAATAATTTC ATCCAAATTC AGCTCACGTG CTAAGACAGC TCTTGATGCG 240

CCTCTTTTAC CCCAGTAATT ACATTGAAAA TGATTAGTTA CTAACGTCTC TGCATTCCAA 300

TGAAGTGGTA TTGGATTTTC TTGCGCCTTC ACATACATTA CTACTGCTGG ATCCCCGAAA 360

ATAATTCTGT CAACTCGTAT TTCATGTAAA AAATTAATAT AATCTTCTAC AGCATCTAAA 420

TGATAATTAT GAAATAATCC ATTCACTGCC GCATATACTT TTTTATCGTT TTTGTGAGCT 480

AATGCGACAG CCTCTGTCAT TTGTTGTCTA TTGAATTCCC CTGGAAGTCT TAAACCAAAC 540

TTTTGCTCGC CAATTACAAA AGCATCTGCA CCTAAATCAA TAAGTGTTTC CATATGGCTT 600

AATGACTTGG GTGTGACAAG TAATTCTGTC ATAGTCATTC TCCTTTAATT GAAATCGCTA 660

ATCCATCGTC TATATTTAAA AAATTCGTTG TATATCCTGG TTGCTTTATT AACCACTCAT 720

TATAATCTTG AACCTTTTTA ACCATTTGTC TTACATTTCT CGATCTAACA ATCCCAATAT 780

CCGATACAAA ACCGTGATAT AAAACATTAT CTGTAATTAC GAGACCTTGG TGCTTTAAAA 840

GTGGTGTATA TATTTCAAAA AATTTCTTTG ATTGCGCTTT TGCTGCATCA ATAAATATCA 900

TATCATAAAC TTTGTCATTT ACATTTTCAA ATTGCTCTAA AGCATTACCT TCAATAATTC 960

CATTACGCTC TATCGTTGTG ACATGAATGT CATCAGATAT AGAAGCGAAT TGCATAGAAC 1080

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GCTTAATTAA ATCTAATGTT AAACGATCTA CAATTGGCAC TTCATTTACC TCGGCAAATT 1200

CACGCAAAAC TTCGATTGAA CTATTTTGAT GTTGATGTAA ATCTATTAAA TATTTTTTAT 1260

TTAGGTCATC CATGTTTTAA ACTTCCTTTA TGTAAAATAA GTCAATATGA TTATGACAAT 1320

AAAATAAATC AGCCTTCACA ATTGATTATA ATTTTGCCAA CCAATTAAAT GACTGATTTC 1380

GTGTTAGACG CAAAGCTATT TTATTTATAG AAGCGAATCA TTCATATAAA ATTTAACTTT 1440

AGATATTTTA CCATATTTTC AATAAAATTA TAAGCGTTAA TTATTTATAC ATTGCTTGAC 1500

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GAATAAAGTT AATAATTCTT CTTCGTTATT AATTTCTAGT TGTGAATCAT GATTATGTTC 1860

AGTCATAGTA AAATCTCCTT TTAATGTAGT GAATCTAAAT AGCCTTGTAA AATAAATACC 1920

GCTGCCATTT TATCAATCAC TTGTTTTCTT TTTTGTCTTG AAACATCTGC TTCTAATAAT 1980

GATCGTTCAG CAGCCATTGT GCTTAATCTT TCATCCCACA TCACAATCTC AATAGAAGGA 2040

TAAGCTTCTA ATAATTTTTC TTTATATGTT AACGAAGCTT CGCCTCGAAA TCCTATTGAA 2100

TTATTCATGT TTTTAGGTAG TCCTATTACG ACTGTACCCA CATTATGTTT TTTAATAATG 2160

TCTACTAATT GGTCAATACC TAATTCATTA TTTTCTTCAT TGATTCGGAG TGTGTCTAAT 2220

CCTTGTGCCG TCCAACCCAT TATATCACTA ATTGCAATTC CTACCGTTCT ACTACCGACA 2280

TCGAGTCCTA AAATTTTATG TTGTAACATA AATTATTTAT TTTGCTCTTT TAAATAGTAA 2340

GAAACAAGCT CTTCCATAAT AACATCTCTA TCAATATGAC GAATTTGATT TCTTGCTTCA 2400

TTTTGGCGTG GAATATACGC AGGGTCACCT GATAATAAAT AACCTACAAT TTGGTTTACG 2460

GCATTATATC CTCGTTCATC TAATGTTCGA TAAACATTAT TTAAAACATC TCTTACATCT 2520

TGCGTTGGAA GTTCTTCATA GTCGAATTTC ATTGTTTTAT CAAAGTTTTC CATTTGCGAC 2580

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TACGACGCAC ACCAGCTCCT GTACCTGACT CACTTACTAT TTTGAATAAG CCAATTTCAG 3240

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CACGCACAAC ATCACCATAT TTTTCACCGA ATAATGCCAT TGCGCCCATT TCTTTAGcTG 3360

AAGCAATATC CATTTCTTGA ATGTTAACGT CAATACCTTT CCAAATTTCT TCATTTACTA 3420

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TGTATATCAA GTGTGTTAGT GTTGTTTGAG ctGTCGCAGT ATCATAACCA ACAAAAGTAC 3900

TTGCAGATGT AATATTTTTC AATACTTCAC TTTGAACTTG CATTGATTGA GAATTTTGAC 3960

GTGCTTGACG TGCACGATCA CGTTGTTGTT GCATTTCTGA CTCGAATGTT GTCATATCAA 4020

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TAATGTCTGC AACAATATCA ACAAGTTTGT ACATAAATGG CTCATTGATT CCTAACGTTT 4320

GACTAAAACG AACGGCACGA CGTAACAATC GACGTAATAC ATACCCTCTA CCTTCATTGG 4380

CAGGTAATGC ACCATCAGAA ATTGCAAATG CAATCGTACG AATGTGGTCA GCAATTACTT 4440

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TTTAATTCGA CTATACAGTT GTGCATAAAG TAGCGTTCAC TAATGTTTGT tGTACTTTTC 5520

ACCAACCAGT ACATCTCTGA TAAACAAATC aTTAACTACT CATCTTTATA CGAATTTAAT 5580

TCTATTTTAG TTACATTTAC GCTTGTTGTC AACGTTCTAT AAAGTCATAC GGCGTGATTT 5640

CTCCCATATT AATCATTGGG TCAATTTTAA ACATTGTAGC TTCCGTTAAT ACATTTGTAT 5700

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TCGTTTTCGC TCTAGTTAAA CCAGTATATA ATATCGGTCT TTGTAACATT CTAAAATACT 6000

GTTTAACAAT AGGCATGATA ACAATAGGAA ATTCTGAACC TTGTGATTTA TGGATTGATG 6060

TACAATAAGC ATGTGTTAAT TCCATCATAT CTTGTTTCGT AAATGTAATT TCATTACCTT 6120

CAAAATCCAC AACAAGTACA TCTTTATTAA GGGCATTTTC TTTCGCCCAA AAAATACCAA 6180

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TCAATTGATA TGGATTTCGA TCTAAAATAG TCAGTGTATC GCCGAGATAA AACTGATAAA 7560

TTGCCATTGA AAGTTTAGGA CCAAACCCTA AATCATGTAA ACGAATCATT ATTTTTTCAG 7620

ATTCTTGATT TGCTGAAATT TGTTCTGCAA TTTGTTTCTG TTTCTTTTTA GATAATCCCG 7680

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ATAATATACA TTTGCTAGAT TAAAAAATAC GACGCCATTC TTCGGATCTA TTGTnAAAGC 8580

TTTTTGGAAA AAACGCTCTG CCTTTyCAAy CyCATTCgCA TCAGCAAGTA CGATmCCaGC 8640

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CAtGGtCGTT TTCACGTTTC ACAAAAACTT TCGTATCTTT TTGGCGATAT CTAAATTTAG 9420

CTGtACATTC AAAACCTTGA TCTAAGTCAT TATCTTCTGG ATTTACAAAT GAATAGTCTG 9480

AAGCAATTAA GTAATCACTG TATAATGCAT CGTGATGGAA TCCTTGTTCT ACATATAAAA 9540

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ATCCATGTCT TTGTCCTATT GTGTAATACA TCAAACCACT ATGTTTACCC ATTTTCTTAC 9660

CATCAAGTGT TATCATATCA CCCGGTTGTG CAGGTAAATA TTGTGATAAA AATGTTTTAA 9720

AGTTTTTTTC GCCGATAAAA CAAATGCCTG TAGAATCTTT TTTCTTAGCA GTAACAAGTC 9780

CTTGTTCTTC AGCAATTCGA CGCACTTCAC TCTTTTCGAT GTCGCCAATT GGGaACATCA 9840

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CTACAATTGC ATTAATTTCA TTTTCAGTAG TCAATTCGTT AAAACTAAAT CGAATCGAAT 10440

GATTTGATCG CTCCTCATCT TCGAACATTG CATCTAAAAC ATGCGACGGT TGTGTAGAGC 10500

CTGCTGTACA TGCAGATCCA GACGACACAT AGATTTGTGC CATATCCAAC AATGTTAACA 10560

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TTGAACCATT TAATTCAAAT GGAATCGCTC TTTCTTGTAA TTTAACTAAA AATTGTTCTT 10680

TTAAATTCAT TAAATGAATA TTGTTATCGT CTCGATTCTT TTCTGCTAAT TGTAATGCTT 10740

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CCTGGAACAG ATATGATGAC CGcAAGTGCA TTAAGACGAG ATCAACATGA TGGTGTTTAT 12180

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CCACTAAGGA GGTTCGCTmm mCAyymyAAT ATGAAGTTTT TATGTTATAG TATAGTATTT 13500

ATACGATTAA ATATAAAACA TGTATCCGTC TAAATCTTCA CTTGTATCTA CATATTCCGC 13560

TAGTTGTTTT TGCGCAGGTG GTTCTGATTC AATACTTTCA ACAAATGTAA TTGGACCTTC 13680

TAACAGTCTT ATAATATCCC CTGCTGAGAT TTCTT 13715

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 873 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

AAATCCATAA TGTCATGATA ATCTGCATAT GCTTCATATA ATTCAATCAT TGTGAATTCA 60

GGGTTATGTC TAGTTGATAC ACCTTCATTA CGGAATACTC TACCAATTTC ATATACTTTT 120

TCAAGTCCAC CGACAATTAm ACGTTTTAAA TGCAACyCAA TAGCAATACG CATGTATAaC 180

GTTGCATCTA ATGCATTATG ATGTGTTACA AATGGTCTAG CAGCTGCTCC ACCAGCAATT 240

TGGTGCATCA TAGGTGTTTC TACTTCCAAG AAACCTTTAT TATTTAAATA ATTACGCATT 300

TCTTGAATGA TTTTACTACG ATTAATAAAT GTACGAGTGC TATCTTCGTT CGTAATTAAA 360

TCTAAATATC TTTGACGATA tCTCTGTTCA ATATCCTGTA AACCGTGGAA TTTATCCGGT 420

AATGGTCGCA ATGATTTAGT TAGTAGCGTG AATTTCTTCG CTTTAACCGA TAATTCGCCA 480

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CATAAATCAA ATTCGTCATC GCCAACTTGA TCTTTACGAA CGTAAATTTG AATTTGTCCA 600

GCTAAGTCCT GAACGTGTGC AAATCCTGCT TTACCTTTAC CACGCTTAGT CATTAATCGT 660

CCAGCTATAG CGACATGACT ATCCGCTTCT TTTTCTACCA ATTCTTCTTT AGAATACTGG 720

TCCCACTCTT CTTTCAAATC ACTAGATAAA CCTGAACGGT CAAATTTAGA ACCAAACGGG 780

TCTATACCAA GATCATATAA TTCTTGTAAT TtTTGACGTC GAACCAACAT TTGGTCATTC 840

ATTTCTTCTG ACATAACTtT CTCTCCTTTA ACT 873

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 452 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

ACCATAATAT GAATGGCTTC AGGATCAAAA TAAAGACCAA CTTCACTGCC TACTTCAGCT 120

TTTTTAGTCG TTTGTATTAC CCATTCATAA CCTTTATTGT CTATACAACA TATTTCATAG 180

TGGACCCCTC TAAATAACAT AGAATCAACA GTTGCTTTAA ATAATCCTTC TTCAGCTTTG 240

ATTAATGATA TATCTTCTGG TCGAATAACG ACTTCTACTT TTTTATTTTC AGGAATACCC 300

ATATCGACAC ATTCGAAATC TTGCCCATAA ATATTCACGA CATAATCTCT AACCATGCGC 360

CCTTCAACAA TATTAGATTC TCCAATAAAA TCAGCTACAA ATCGATTCAC TGGTTCGTCA 420

TaTATATCTG TTGGTGTGCC AAATTGTTGA AT 452

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

TAGGTTGGGT TCTAACATAC GATAAAGCTC AACAAATCAA CACAGCTTTC TTTGTAAAAT 60

TGTTTAATAC TGCATTAGCA GAACGTGATT ATTATTTTAA TATAGATGGA ACAAATGCTT 120

TTAGATTATT TAATGCTGAA GGTGATGGTG TTGGGGGATT AACAATCGAC AATTACGATG 180

GTCATTTGTT GATTCAATGG TACTCAAAAG GTATTTATAA ATTTAAATAT GCCATTCTTG 240

AAGCGGTTAG AAAAGTATTT GATTATAAAT CTATTTACGA AAAAGTAAGA TTTAAAGACA 300

GCGAATATAG TGGTGGTTTT GTTGAAGGAG ATGCACCTGa GTTTCCAATT GTTATCGAAG 360

AAAACTTCAC ATTTTATAAT GTAGACCTTG AAGATGGTTT GATGACAGGT ATCTTTTTAG 420

ATCAAAAAGA AGTGCGCAAG AaATTAAGGG ATCAATATGC CAAAGAACGC CATGTTTTAA 480

ACTTATTTAG TTATACAGGT GCTTTTTCTG CAATAGCAGC AAGTGAGGCA TCTTCAACAA 540

CAAGTGTAGA TTTGGCTAAT CGTTCTCGTA GTTTAACTGA AGAAAATTTT GGATTAAATG 600

CTATTGATCC TAAATCCCAA TATATTTATG TCATGGACAC TTTTGATTTC TATAAATATG 660

CTGCACGACA TGGACATAGT TATGACACGA TCGTGATTGA TCCACCTAGC TTTGCGCGTA 720

ACAAAAAACG TACATTTTCA GTGCAAAAAG ATTATGACAA ATTAATTAAT GGCGCCTTAA 780

ATATCTTATC ATCTGAAGGA ACATTATTGT TATGTACAAA CGCAAGTGTA TATCCATTAA 840

AGCAATTTAA AAATACTATT AAAAAGACGC TTGAAGAGAG TGGCGTTGAT TATGAATTAA 900

CTGAAGTTAT GGGATTACCA AAAGATTTTA AAACGCATCC ACATTATAAG CCATCTAAAT 960

TATTGAGAAA AAGAAGGGTG ATAATATTAT GGGATTCAAA AACAATTTAA CATCAAATTT 1080

AACAAATAAA ATCGGTAATT CAGTCTTTAA AATAGAAAAT GTTGACGGAA AAGGTGCAAT 1140

GCCAACGACG ATTCAAGAAT TGAGAGAAAG ACGACAACGT GCTGAAGCAA TTGTAAAGAG 1200

AAAGTCTTTA ATGTCATCAA CAATGAGCGT TGTTCCAATT CCGGGTTTAG ATTTTGGTGT 1260

TGATTTAAAA TTAATGAAAG ATATTATCGA AGATGTTAAT AAAATTTATG GTTTAGATCA 1320

TAAGCAAGTT AATAGCCTTG GGGATGATGT GAAAGAAAGA ATTATGTCTG CAGCAGCAAT 1380

TCAAGGTAGT CAATTTATTG GTAAAAGAAT TTCAAATGCA TTTTTAAAAA TTGTAATTAG 1440

AGATGTAGCT AAACGTACTG CTGCAAAACa AACAAAATGG TTTCCTGTTG TAGGACAAGC 1500

TGTGTCTGCA TCTATTAGTT ACTATTTTAT GAATAAAATT GGAAAAGATC ACATTCAAAA 1560

ATGCGAAAAT GTTATTAAAA ATGTCATGTA GGTGCTATAA TAGTTTTGCA ATTTGCAAAT 1620

TTTACTGAAA CCGGTTTTAA ACGAATTGAA TTTAAAGcAT GGTTTTGGTA AAGTTAATGT 1680

ATAAAACTAA GTTAGyATTG TAATAATATk GAAGATTCTA ACTATACGAA GGAGAAATGT 1740

AATTATGGAA CAAAATTCAT ATGTAATCAT CGACGAGAmT GGTATTCACG CTAGACCAGC 1800

AACAATGTTA GTACAAACAG CTTCAAAATT CGATTCTGAT ATTCAATTAG AATATAACGG 1860

TAAGAAAGTA AACTTAAAAT CAATCATGGG TGTTATGAGC CTTGGTGTTG GTAAAGATGC 1920

TGAAATTACA ATTTATGCTG ACGGTAGTGA TGAATCTGAC GCCATTCAAG CAATCAGTGA 1980

CGTCTTATCA AAAGAAGGAT TGACTAAATA ATCATGTCTA AATTAATTAA AGGTATTGCC 2040

GCATCTGATG GTGTCGCAAT TGCTAAAGCT TATTTATTAG TTGAGCCAGA CTTAACATTC 2100

GACAAAAATG AAAAAGTCAC TGATGTTGAA GGAGAAGTTG CAAAGTTCAA TAGCGCTATC 2160

GAAGCTTCTA AAGTTGAGTT AACTAAAATT AGAAATAATG CAGAGGTTCA ACTAGGTGCT 2220

GATAAAAGCTG CTATCTTTGA TGCAcaTTGG GGGGTGGTAG ATGACCCTGA ATTAATTCAA 2280

CCAATCCAAG ATAAGATTAA AAATGAAA 2308

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5559 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

AAGTAATAAA TCGTCTCATT TGGCAACTGA CGCATAATTT CTTTAGCTAC TGTCAAACCT 60

TTTAATTTTT AGTTTATCAT AACTAAGCAT TGGATTTTAG TATTATGCAC TGTGTTTACC 180

ATTTTTGTCA TTATAATATT TATTTTAAAT CAGCCCACTA TCATATTGTC ATGTAATCTG 240

CTTATTAAAA AAATCCCTTC CAAGTTATTG TGTATCTCCA TTCAATTTAA TTTTGAAAGG 300

AACATAACwT TTTAACTCAA AAGGGATTAA TTTnTAnTCT ACTTCATGGT CTGAACCAAA 360

GAATGATTTA AACATGTGGA ATGTTGTTTC TCTGTTCATT GCTGCAATGG ATGTTGTTAA 420

TGGAATACCT TTAGGGCAAG CATTAACACA GTTTTGTGAA TTACCACACT GCTGTAAGCC 480

ACCAGTACCC ATTAATGCAT TTAAACGTTC ATCTTTAGTC ATAGATCCTG TTGGGTGCAA 540

ATTAAACAAA CGAACTTGCG AGATTGCTTG TGCACCAACG AaTTTATTAT TTTCAGTAAC 600

ATTAGGACAA ACCTCTAAAC ATACACCACA TGTCATACAT TTAGATAATT CATAAGCTGT 660

TTGACGTTTT TTCTCTGGCA TACGTGGTCC CGGACCTAAA TCATACGTTC CATCAATTGG 720

GATCCATGCT TTCATACGTT TTAAGTTATC GAACATTCTA GAACGATCAA CTTGTAAGTC 780

ACGGATAACT GGGAAAGTAT TCATTGGCTC TAAACGAATA GGTTGTTCTA ATTGATCAAC 840

AATCGCAGAA CAAGATTGTC TTGCACGACC ATTGATAACC ATAGAACATG CTCCACATAC 900

TTCTTCTAAG CAGTTCATAT CCCAGACAAC AGGTGTTGTT TTTTCACCTT TAATATTAAC 960

TGGGTTACGT CTAATTTCCA TTAAACAAGC AATGACGTTT AAATTTTCAC GATATGGAAT 1020

TTCAAATGTT TCTTCATAAG GCTTAGAATC ACTTGTATCT TGTCGTTTAA TAATTAATTT 1080

TACTGTTTTT TGTTTCGGTT TAGATTGTGT TTCATGTTGT GGAGTGTTTT TCACTGATTG 1140

TTCAGTCATT ATTTTTTACC CCCTTTAGAC TTACTTGTGT AATCACGTTT ACGAGGTGGT 1200

ATTAAACTCA CATCGACGTC ATCATAAGTA AACTGCGGTT TTTCAAATGC GCCTTGGAAT 1260

GAGGCCATTG TCGTTTTTAA CCACTCTTCA TCATTACGCT CTGGGAATTC TGGTTTATAA 1320

TGGGCACCGC GTGATTCGTT ACGGTTATAT GCACCAATCG TAATAACACG TGCAAGTACT 1380

AACATGTTCC ATAGTTGACG GGTAAAGAAT ACCGCTTGGT TACTCCAAGT TTGAGTATCT 1440

TCCATATCAA TATCTTCATA ACGTTTCATC AATTCAACAA TCTTTTTATC TGTTTCTAAC 1500

AGTTTTTCAT TTTCACGAAC AACAGTTACA TTTGCTGTCA TAATTTCACC AAGTTCACGG 1560

TGTAATTTAT ATGCATTTTC TGTACCGCGC ATAGCTAATA ATTTATCAAA ACGTTCTTGC 1620

TCTTCAGCTT TACGCTTTTC AAAAATACTT TCGTCCATAT CAGTATATGA TCGATCAATA 1680

TTTGAAATAT AATCAATCGC GTTTGGACCT GCTACTGTAC CACCATAAAT CGCTGATAAC 1740

AATGAATTGG CACCTAAGCG GTTACCACCA TGTTGAGAGA AGTCACATTC TCCAGCTGCA 1800

AATAACCCTT TAATATTTGT CATTTGATCA TAATCTACAT ATAGACCACC CATTGAATAG 1860

TAAATCTCAA TGATACCACC TAGTTTTACA TCTAACTCAT GTGGATCTTT ATGTGACAAA 1980

TCAAGATATA CCATGTTTTC GCCATTTATA CCTAATTTTT GGTTAATACA TACATCGAAA 2040

ATTTCACGCG TTGCGATATC ACGAGGTACT AAGTTACCAT AATCAGGATA TTTCTCTTCT 2100

AAGAAGTACC AAGGCTTACC ATCTTTATAT GTCCAAATTC GTCCACCTTC ACCACGTGCT 2160

GATTCACTCA TTAGTCGCAG TTTATCATCA CCAGGGATTG CAGTAGGATG AATTTGAATG 2220

AACTCACCAT TAGCATAAAT AGCGCCTTGT TGGTAAACAA TGGAAGCCGC TGATCCTGTA 2280

TTAATCATTG AGTTTGTTGT TTTACCGAAA ATAATACCAG GGCCACCCGT TGCCATAATA 2340

ACTGCATCTG AACCAAATGT TTCAATCTCA GCAGTTGTCA TATTTTGTGC AnCGATACCT 2400

CTTGCACTAT CATCGTCACC TTTAACTATG CCAAGGAATT CCCATCCTTC ATACTTCGTA 2460

ACTAATCCAT CTACTTCATA TGCACGAACT TGTTCATCCA ATGCATATAA TAATTGTTGT 2520

CCAGTTGTTG CCCCTGCATA TGCTGTTCTG TGATGTAATG TACCACCGAA ACGTCTAAAA 2580

TCTAATAGAC CTTCATTTGT TCTATTGAAC ATTACGCCCA TACGGTCTAA TAAATGAATA 2640

ATTTTAGGTG CTGCCTCTGT CATCGCTTTA ACAGGTGGTT GGTTTGCAAG GAAATCGCCA 2700

CCATACACTG TATCATCAAA GTGAATCCAA GGAGAATCGC CTTCCCCTTT AGTATTGACC 2760

GCACCATTAA TGCCACCTTG GGCACAAACA GAGTGCGAAC GCTTTACTGG TACAACTGAG 2820

AACAAATCTA CATGTGCACC TTTTTCTGCC GCTTTAATTG TTGACATTAA GCCCGCTAGG 2880

CCACCTCCGA CAACAATAAG ATGTTTCTCT GCCATAAAAA TTTCACTCCC CTAAATTTTC 2940

AATCTATATT TGTTAAATGC GATGTATTAC ATAAAGGCAA TAATTGCAGT AACACCAATA 3000

TACGAAATAA CTAAAAATAC GATTAATGAA ACCCATGTAA ATACTCGTTG TGATTTTGGA 3060

GATTGAAGTC CACCCCAAGT AACTAAGAAT GACCATAAGC CATTTGCAAA GTGGAACACA 3120

ACAGCAATAA TACAAATAAT ATAAAATATT GCCCATCCAG GATGTTGCAA TGTTTCGTGC 3180

ATTAAATCGT AATTCACTTC TTTGCCGTAA AATGCTTTTT GTAAACGTGT TTGCCATAAA 3240

TGGATACCAA TAAAGATAAA TGTTAAGATA CCACTCACTC TTTGGAAGAA GAACATCCAG 3300

TTTCTAAAAA TCGAGTAATG TCCAACATTT TCTTTTGCTG TAAATGCAAT GTGTATACCA 3360

AACAAACCGT GATATAACAA CGGAATGTAT ATAAATAAAA ATTCTACAAT AATTAGAAAT 3420

GGTAATGATT CCATAAAGTT AGATGCCTTA TTAAACGCTT CAGCACCTTG TGTTGCTTGG 3480

TGATTCACTA ATAAATGAAC GACCAAAAAT GCACCTATTG GGATAATACC TAATAACGAG 3540

TGAATACGTC TTAGATAAAA TTCATTTTTT GATTGAGCCA AAAGGAGTCC CCCCTGTGAA 3600

CGAATATTTA ATTTATTGAG CTATTTATAT TAAACGTACG CTTAACCCCC TAAAGTGATA 3660

CGATCACCAA ACTGCATGTC GAACAATGTA ACATTTGGAT TCGATATTTA AAATTGCTTG 3780

TGATGATAAA CTTTCTCATT TAGAAAACGC TTCCACGTAC ATTCAAAAAA ATAACTTTGT 3840

TAACCATATT GTAACATTAT TTCATATATT TTGGGGCATG AGAATGATTC TCACGCCCAG 3900

TAATTTATTT ATGCAATTGT TCATGTAGGT TCTTTGCGAC GTTTTCAGGA ATACCTATAT 3960

TTTTAAAATC TTCAAGTGTA GCTTCCTTCA TTTTCTTGAT TGAACCGAAT GAACGCAATA 4020

ATAATGTTTT ACGTTTGTTA CCGATACCAT CTATATCATC AAGTATTGAT TTCAAGCCTG 4080

TCTTTTGACG TGTTTGTCTA TGAAATGTGA TTGCGAATCT GTGAACCTCA TCTTGGATAC 4140

GGTGCAACAA ATAAAATGCC TGGCTATTTT TCTTCAGTGG TACAATTTCT GCACTAGCGC 4200

CATATAATAA TTCAGATGTT TGGTGTTTAT CATTTTTCTG CAAACCTGCA ACAGGGATAT 4260

CAAGACCTAA TTCGTTTTGT AGCACATCAA TAACCCCGTT CATATGTCCT TTACCACCAT 4320

CTACTATTAT TAAATCAGGT AATGGTAATC CTTCGTTTAA AACGCGAGAA TATCGTCGTC 4380

TTACTACTTC TCTCATTGAT TTGTAATCAT CTGGACCTTT AACCGTTTTG ATTTTATACT 4440

TTCTATAATT TTTCTTATCT GGTTTACCGT CGACAAATGT AACCATTGCT GACACTGGAT 4500

CCACACCTTG AATATTAGAA TTATCGAATG CTTCAATTCT AATTGGTGTT TGAATTCCCA 4560

TTTGTGTTCC AAGTTCTTCA ATAGCTTTAA TCGTTCTGGA CTCATCACGT GATATTAATT 4620

CAAATTTATT ATTTAAGGAT ACTTTAGCGT TATGTGCAGC TAGGTCAACC ATATCTTTTT 4680

TGGGACCTCG CGCGGGTTGA ACGATTTTAG TGTCCACAAC AGATTGAATC ATTTCTTTAT 4740

CCAAATTACG TGGTACATGA ACTTCCTTAG GTAAAATATG TTGGTTTAAG CTATAAAATT 4800

GTCCAATAAA TGTATAAAAT TCTTCTTcTT CTGTTTGCTG TAATGGAATC ATCGTTGTAT 4860

CTCGCTTTAT CATATTACCT TGTCGTATAA AGAAAACTTG GATACACATC CATCCTTTAT 4920

CAACACTATA ACCAAAGACA TCACGAATCG TTTTATCTGA TGACATAATT TTTTGTTTGT 4980

TTGTCAGATT TTGAATATGT TGAATTAAAT CTCTATATTC TTTAGCCCGT TCAAAATCAA 5040

GTGATTCACT TGCAGTTAAC ATTCGCTCTT CTAAACTTTT TAAAATTGTT TTGTCTTCCC 5100

CATTCAGAAA ATCAGTAATT TCCTTCGTCA TTTGTGCGTA TTTACTCAAA TCAACGTCAT 5160

ATACACATGG TCCTAAACAT TGTCCAATAT GGTAATAAAG ACATAATTTA TCTGGCATCT 5220

TATCACATTT GCGATATGGA TATATTCTGT CTAATAACTT TTTAGTTTCT TGAGCAGAAT 5280

ATGCATTCGG ATACGGTCCG AAATATTTGC CAGTACCTTG TTTTACAGTT CTCGTCACTA 5340

GTAGTCTAGG ATATTTCTCC TTCGTAATTT TAATAAATGG ATAACTTTTA TCATCCTTTA 5400

ATAATATATT ATATCTTGGT TGATATTGTT TAATCAGATT CAATTCCAGT AAAAGTGATT 5460

TTTTAGCATC ATGAGCACCC GTAAAATATG ATCGCAATC 5559

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4594 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

AAATCAATCG AGTGGCATGT CAAGGTCATA TCAATATTTT AGAATCTGCG ACTATGAGAG 60

AGGAAATAAA TGAAATTGCG CGACGTATCA TCGTTGATAT TCGTGATAAG CAATTACGAT 120

ATCAAGATAT TGCTATTTTA TATCGTGATG AATCTTATGC TTATTTATTT GATTCCATAT 180

TACCGCTTTA TAATATTCCT TATAATATTG ATACAAAGCG TTCGATGACA CATCATCCGG 240

TCATGGAAAT GATTCGTTCA TTGATTGAAG TTATTCAATC TAATTGGCAA GTGAATCCAA 300

TGCTACGCTT ATTGAAGACT GATGTGTTAA CGGCATCATA TCTAAAAAGT GCATACTTAG 360

TTGATTTACT TGAAAATTTT GTACTTGAAC GTGGTATATA CGGTAAACGT TGGTTAGATG 420

ATGAGCTATT TAATGTCGAA CATTTTAGCA AAATGGGGCG TAAAGCGCAT AAACTGACCG 480

AAGATGAACG TAACACATTT GAACAAGTCG TTAAGTTAAA GAAAGATGTC ATTGATAAAA 540

TTTTACATTT TGAAAAGCAA ATGTCACAAG CGGAAACTGT AAAAGATTTT GCAACTGCTT 600

TTTATGAAAG TATGGAATAT TTCGAACTGC CAAATCAATT GATGACAGAG CGAGATGAAC 660

TTGATTTAAA TGGTAATCAT GAAAAGGCGG AGGAAATTGA TCAAATATGG AATGGCTTAA 720

TTCAAATCCT TGATGACTTA GTTCTAGTAT TTGGAGATGA ACCAATGTCG ATGGAACGTT 780

TCTTAGAAGT ATTTGATATT GGTTTAGAAC AATTAGAATT TGTTATGATT CCGCAAACAT 840

TGGACCAAGT AAGTATTGGT ACGATGGATT TGGCTAAAGT CGATAATAAG CAACATGTTT 900

ACTTAGTAGG TATGAATGAT GGAACGATGC CACAACCAGT AmTGCGTCAA GCTTGATTAC 960

AGATGAAGAA AAGAAATACT TTGAACAGCA GGCTAATGTC GAGTTAAGTC CAACATCAGA 1020

TATTTTACAG ATGGATGAAG CATTTGTTTG TTATGTTGCT ATGACTAGAG CTAAGGGAGA 1080

TGTTACATTT TCTTACAGTC TAATGGGATC AAGTGGTGAT GATAAGGAGA TCAGCCCATT 1140

TTTAAATCAA ATTCAATCAT TGTTCAACCA ATTGGAAATT ACTAACATTC CTCAATACCA 1200

TGAAGTTAAC CCATTGTCAC TAATGCAACA TGCTAAGCAA ACCAAAATTA CATTATTTGA 1260

AGCATTGCGT GCTTGGTTAT ATGATGAAAT TGTGGCTGAT AGTTGGTTAG ATGCTTATCA 1320

GTTTGACAAT GAAACTGTAA AATTAGGTGA AACGTTGTCT AAAGATTTAT ATGGTAAGGA 1440

AATCAATGCC AGTGTATCCC GTTTTGAAGG TTATCAACAA TGCCCATTTA AACACTATGC 1500

GTCACATGGT CTGAAACTAA ATGAGCGAAC GAAGTATGAA CTTCAAAACT TTGATTTAGG 1560

TGATATTTTC CATTCTGTTT TAAAATATAT ATCTGAACGT ATTAATGGCG ATTTTAAACA 1620

ATTAGACCTG AAAAAAATAA GACAATTAAC GAATGAAGCA TTGGAAGAAA TTTTACCTAA 1680

AGTTCAGTTT AATTTATTAA ATTCTTCAGC TTACTATCGT TATTTATCAA GACGCATTGG 1740

CGCTATTGTA GAAACAACAC TAAGCGCATT AAAATATCAA GGCACGTATT CAAAGTTTAT 1800

GCCAAAACAT TTTGAGACAA GTTTTAGAAG GAAACCAAGA ACAAATGACG AATTAATTGC 1860

ACAAACATTA ACGACAACTC AAGGTATTCC AATTAATATT AGAGGGCAAA TTGACCGTAT 1920

CGATACGTAT ACAAAGAATG ATACAAGTTT TGTTAATATC ATTGACTATA AATCCTCTGA 1980

AGGTAGTGCG ACACTTGATT TAACGAAAGT ATATTATGGT ATGCAAATGC AAATGATGAC 2040

ATACATGGAT ATCGTTTTAC AAAATAAACA ACGCCTTGGA TTAACAGATA TTGTGAAcCA 2100

GGTGGaTTAT TATACTTCCA TGTACATGAA CCTAGAATTA AATTTAAATC ATGGTCTGAT 2160

ATTGATGAAG ATAAACTAGA ACAAGATTTA ATTAAAAAGT TTAAGTTGAG TGGTTTAGTT 2220

AATGCAGACC AAACTGTTAT TGATGCATTG GATATTCGTT TAGAACCTAA ATTCACTTCA 2280

GATATTGTAC CAGTTGGTTT GAATAAAGAT GGCTCTTTGA GTAAACGAGG CAGCCAAGTG 2340

GCAGATGAAG CAACGATTTA TAAATTCATC CAACATAACA AAGAGAATTT TATAGAAACA 2400

GCTTCAAATA TTATGGATGG ACATACTGAA GTTGCACCAT TAAAGTACAA ACAAAAATTG 2460

CCATGTGCTT TTTGTAGTTA TCAATCGGTA TGTCATGTAG ATGGCATGAT TGATAGTAAG 2520

CGATATCGAA CTGTAGATGA AACAATAAAT CCAATTGAAG CAATTCAAAA TATTAACATT 2580

AATGATGAAT TTGGGGGTGA GCAATAGATG ACAATTCCAG AGAAACCACA AGGCGTGATT 2640

TGGACTGACG CGCAATGGCA AAGTATTTAC GCAACTGGAC AAGATGTACT TGTTGCAGCC 2700

GCGGCAGGTT CAGGTAAAAC AGCTGTACTA GTTGAGCGTA TTATCCAAAA GATTTTACGT 2760

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ATGAAGCATC GTGTAGACCA ACGTATTCAA GAGGCATCGA TTGCTGATCC TGCAAATGCA 2880

CACTTGAAAA ACCAACGCAT CAAAATTCAT CAAGCACAAA TATCTACACT CCATAGTTTT 2940

TGCTTGAAAT TAATTCAACA GCATTATGAT GTATTAAATA TTGACCCGAA CTTTAGAACA 3000

AGCAGTGAAG CTGAAAATAT TTTATTATTA GAACAAACGA TAGATGAGGT CATAGAACAA 3060

CATTACGATA TCCTTGATCC TGCTTTTATT GAATTAACAG AGCAATTGTC TTCAGATAGA 3120

AATCCTACAA ATTGGTTGGA TCAATTGGTG ACACCATACG AAGAAGAAGC ACAACAAGCG 3240

CAACTTATTC AACTACTAAC AGACTTATCT AAAGTATTTA TCACAGCTGC TTATGATGCT 3300

TTAAATAAGG CGTATGATTT GTTTAGTATG ATGGATAGCG TCGATAAACA TTTAGCTGTT 3360

ATAGAAGATG AACGACGTTT AATGGGGCGT GTTTTAGAAG GTGGCTTTAT TGATATACCT 3420

TATTTAACTG GTCACGAATT TGGCGCGCGT TTGCCTAATG TAACAGCGAA AATTAAAGAA 3480

GCAAATGAAA TGATGGTCGA TGCCTTAGAA GATGCTAAAC TTCAGTATAA AAAATATAAA 3540

TCATTAATTG ATAAAGTGAA GAGTGATTAC TTTTCAAGAG AAGCTGATGA TTTGAAAGCT 3600

GATATGCAAC AATTGGCGCC ACGAGTAAAG TACCTTGCGC GTATTGTGAA AGATGTTATG 3660

TCAGAATTCA ATCGAAAAAA GCGTAGCAAA AATATTTTGG ATTTTTCTGA TTATGAACAT 3720

TTTGCATTAC AAATTTTAAC TAATGAGGAT GGTTCGCCTT CAGAAATTGC CGAATCATAC 3780

CGTCAACACT TCCAAGAAAT ATTGGTCGAT GAGTATCAAG ATACGAACCG AGTTCAAGAG 3840

AAAATACTAT CTTGCATCAA AACGGGTGAT GAACATAATG GTAATTTATT TATGGTTGGA 3900

GATGTTAAGC AATCCATTTA TAAATTTAGA CAAGCTGATC CAAGTTTATT TATTGAAAAG 3960

TATCAACGCT TTACTATAGA TGGAGATGGC ACTGGACGTC GAATTGATTT GTCGCAAAAC 4020

TTCCGTTCTC GAAAAGAAGT ACTGTCAACG ACTAACTATA TATTCAAACA TATGATGGAT 4080

GAACAAGTCG GTGAAGTAAA ATATGATGAA GCGGCACAGT TGTATTATGG TGCACCATAT 4140

GATGAATCGG ACCATCCaGT AAACTTAAAA GTCCTTGTTG AAGCGGATCA AGAACATAGT 4200

GATTTAACTG GTAGTGAACA AGAAGCGCAT TTTATAGTAG AACAAGTTAA AGATATCTTA 4260

GAACATCAAA AAGTTTATGA TATGAAAACA GGAAGCTATA GAAGTGCGAC ATACAAGGAT 4320

ATCGTTATTC TAGAACGCAG CTTTGGACAA GCTCGCAATT TACAACAAGC CTTTAAAAAT 4380

GAAGATATTC CATTCCATGT GAATAGTCGT GAAGGTTACT TTGAACAAAC AGAAGTCCGC 4440

TTAGTATTAT CATTTTTAAG AGCGATAGAT AATCCATTAC AAGATATTTA TTTAGTTGGG 4500

TTAATGCGCT CCGTTATATA TCAGTTCAAA GAAGACGAAT TAGCTCAAAT TAGAATATTG 4560

AGTCCAAATG ATGACTACTT CTATCAATCG ATTG 4594

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGTTTTCnTG GAAAGATAGT GAAAATCTCG TGTTTTTTGG TTTTgAGGTG TTGTTTGTAT 60

TTTaTAAAAT GGCTTACATA TATGAAGCGT TGATTAAGTA TGGAATTGTT AATTAATTGA 120

ACCTATTTAG CTTTAAGAAG GCATAACAAG ATGACCTTAT TTTATGCTAT AATATTTCTA 180

TTATGCGAAG ATTAAGGTGA GTAGTAAATT GGATAAAAAA GTAAGTATTC AAACAAAGCA 240

AGTGTTGAAA CAGCACAACG AAAAAGAAAA ATTTGAATTT ACTACTGAAG GAACTTGGCA 300

ACAAAGGCAA TCTAACTTTA TTCGGTATGT AGAACAAATT GAGGATGCAA CAGTTAATGT 360

TACAATAAAA GTGGATGATG ATAGCGTTAA GTTGATTCGT AAAGGCGACA TTAATATGAA 420

TTTGCATTTT GTTGAAGGAC AAACGACAAC AACTTTTTAC GATATATCGG CTGGACGAAT 480

TCCACTAGAA GTTAAAACAT TACGCATTTT ACATTTCGTA AGTGGAGACG GTGGCAAGCT 540

AAAGATTCAT TATGAATTAT ATCAAGATAA TGAAAAAATG GGTTCTTATC AATATGAAAT 600

TAACTATAAG GAGATAGGCG AATGAATATT ATTGATCAAG TGAAACAAAC ATTAGTAGAA 660

GAAATTGCAG CAAGTATTAA CAAAGCAGGA TTAGCAGATG AGATTCCTGA TATTAAAATT 720

GAAGTTCCTA AAGATACAAA AAATGGAGAT TATGCTACTA ATATTGCGAT GGTACTGACT 780

AAGATTGCAA AGCGTAATCC TCGTGAAATT GCTCAAGCGA TTGTTGATAA CTTAGATACT 840

GAAAAAGCAC ATGTAAAACA AATTGACATT GCTGGTCCAG GATTCATTAA TTTTTACTTA 900

GATAATCAGT ATTTAACAGC AATTATTCCT GAAGCAATTG AAAAAGGTGA TCAATTTGGA 960

CATGTAAATG AATCAAAAGG TCAAAATGTA TTGCTTGAGT ATGTTTCAGC TAACCCTACA 1020

GGAGATTTAC ATATTGGTCA TGCTAGAAAT GCAGCAGTTG GTGATGCTTT AgcTAAtATT 1080

TTAACTGCAG CTGGCTATAA TGTAACACGT GAATATTATA TTAATGATGC TGGTAATCAA 1140

ATTACTAACT TAGCGCGTTC GATTGAAACA CGTTTCTTTG AAGCTTTAGG TGACAATAGT 1200

TATTCAATGC CAGAAGATGG CTATAATGGA AAAGATATTA TTGAAATAGG TAAAGATTTA 1260

GCAGAGAAAC ACCCTGAAAT TAAAGATTAT TCTGAAGAAG CACGTTTGAA AGAATTTAGA 1320

AAATTAGGCG TAGAATACGA AATGGCTAAA TTGAAAAATG ATTTAGCAGA GTTCAATACG 1380

CATTTTGATA ATTGGTTTAG TGAAaCATCT TTATATGAAA AAGGAGAAAT TCTTGAAGTT 1440

TTAGCAAAAA TGAAAGAATT AGGTTATACG TATGAAGCTG ATGGCGCTAC ATGGTTACGT 1500

ACAACTGATT TTAAAGACGA CAAAGACAGA GTATTAATTA AAAATGACGG TACATATACG 1560

TATTTCTTAC CAGATATTGC GTACCACTTC GATAAAGTAA AACGTGGTAA TGACATTTTA 1620

ATCGATTTAT TTGGTGCTGA TCATCATGGT TATATTAATC GTTTGAAAGC ATCTCTTGAA 1680

ACGTTTGGTG TAGATAGTAA TCGTTTAGAA ATTCAAATCA TGCAAATGGT TCGTTTAATG 1740

ATTATGGACG AaGTTGGCGT TGACGCTGCA CGTTATTTCT TAACTATGCG TAgTCCTGAT 1860

AGTCACTTTG ATTTTGATAT GGAATTAGCG AAAGAGCAAT CTCAAGACAA TCCAGTTTAC 1920

TATGCTCAAT ATGCACATGC GCGTATTTGT TCAATTTTAA AACAAGCGAA AGAGCAAGGT 1980

ATTGAAGTGA CTGCTGCGAA TGATTTTACA ACGATTACTA ATGAAAAAGC GATTGAATTG 2040

TTGAAAAAAG TAGCTGATTT CGAACCTACA ATTGAAAGTG CTGCTGAGCA TAGATCGGCA 2100

CATAGAATTA CTAATTATAT TCAAGATTTA GCTTCTCATT TCCATAAATT CTATAATGCT 2160

GAAAAAGTGT TAACAGATGA TATTGAAAAA ACAAAAGCAC ATGTTGCTAT GATTGAAGCG 2220

GTCAGAATTA CATTGAAAAA TGCATTGGCA ATGGTCGGTG TAAGCGCACC TGAATCAATG 2280

TAAGAACATT TATATACACT CCAACGTAGA GTTTCTCGAA AGATACTTTG TGTTGGAGTG 2340

TTTTTTTTAG GTATGTGACA TATTGGGGAA TGCTTAGTAT GTGAATAAGG TTAAGAGGAA 2400

CACAGTTGGA TGCTCTGCAC AACTGCATAA GAGAGCCTGA GACATAAATC AATGTTCTAT 2460

GCTCTACAAA GTTATAATGG CAGTAGTTGA CTGAACGAAA ATTCGCTTGT AACAAGCTTT 2520

TTTCAATTCT AGTCAACCTT GCCGGCGGGG CCCCAACAAA GAGAAATTGG ATTCCCAATT 2580

TCTACAGACA ATGCAAGTTG GGGTGGGACG ACGAAATAAA TTTTACGATA ATATCATTTC 2640

TGTCCCACTC CCTCTAAAAT GGAGGGTGTA AATGTTAGGA ACTGATGAAT TATATAAAGT 2700

TTTATATGAA CATCTCGGAC CACAATTTTG GTGGCCTGCT GATAATGACA TTGAAATGAT 2760

GTTAGGTGCA ATTTTAGTTC AAAATACTAG ATGGCGAAAT GCAGAAATTG CATTGAATCA 2820

GATTAAAGAA CATACGCATT TTAATCCAAA TCATATATTA GAACTACCTA TTGAAACGTT 2880

ACAATCATTG ATACATTCAA GTGGCTTTTA TAAAAGTAAA TCACTGACGA TTAAAACATT 2940

ATTAACATGG TTAGCACGAC ATCATTTCAA TTATCAAGAG ATTAATGAGC GATATAAAGG 3000

TGGATTAAGA AAAGAATTAT TATCTTTGAA AGGTATTGGA AGTGAAACAG CAGATGTCTT 3060

ACTTGTTTAT ATATTCGGAC GTATTGAATT TATTCCAGAT AGCTATACAA GAAAAATATA 3120

TGATAAATTA GGATATGAAA ACACTAAAAA TTATGATCAA TTAAAAAAAG TAGTCaCATT 3180

ACCAAATCAT TTTACAAATC AAGATGCTAA TGAATTTCAT GCTCTGTTAG ATGTATTTGG 3240

TAAACATTAC TTTAGAGACA AAGATATAAA GAATTATGAT TTTTTAGAAC CTTACTTTAA 3300

AAAGTAAACG CTGTGAAGTT AGATAGATGA GTTTATATGA AATATAAAAA ATAATTTACT 3360

ATTTTCTTTT AGTATGTGGA CTTATATAAT AAATAGAAGC ATATAAAGAA AAAAACAGTT 3420

GTTTGTTTGT GCAGCAACTG CATAAGAGCC CCTAATCGCT AAAGCTCAAG GGGAGTAAAG 3480

GAATACAGTT GTTTGTGCAG CAACTGCATA AAAGCCTCTA ATCACTAAAG GTGAAGAGGA 3540

AACGCAGTTG GATgCTACCG CACAACTGCA TAAATCCCTC TaATCgcTAA AGCGAAAAGT 3660

GGGATTAAAA AGGAGATGTG ATAGTGTGAA GAAATCGTTA ATTGCTTTTA TTTTGATTTT 3720

TATGCTTGTC CTGAGTGGCT GTGGTATGAA AGATAATGAT AAACAAGGTA GCAATGATAA 3780

TGGCTCGTCT AAATCGCCGT ACCATAGAAT TGTTTCGTTA ATGCCTAGTA ATACTGAAAT 3840

TTTATATGAA TTAGGATTAG GTAAATACAT AGTTGGTGTT TCAACGGTTG ATGATTATCC 3900

AAAAGATGTG AAAAAGGGTA AGAAACAATT TGATGCTTTG AATCTAAATA AAGAGGAACT 3960

TTTAAAGGCA AAGCCAGATC TAATTCTTGC GCATGAGTCG CAAAAGGCAA CTGCTAATAA 4020

AGTATTGTCA TCATTAGAGA AACAAGGCAT CAAAGTAGTG TATGTTAAAG ATGCACAATC 4080

AATTGATGAA ACTTACAACA CATTTAAGCA AATTGGGAAA TTAACGCATC ATGATAAGCA 4140

GGCTGAACAA CTTGTTGAGG AAACTAAAGA TAATATCGAT AAAGTCATAG ATTCAATTCC 4200

TGCTCATCAT AAAAAATCAA AAGTATTTAT TGAGGTTTCA TCAAAGCCTG AAATATATAC 4260

AGCAGGGAAG CATACATTTT TTAATGATAT GTTAGAAAAA TTAGAAGCCC AAAATGTGTA 4320

TAGTGACATT AATGGTTGGA ACCCTGTAAC GAAGGAAAGT ATTATTAAAA AGAACCCAGA 4380

TATATTAATT TCGACGGAAG CTAAGACAAG ATCAGATTAT ATGGATATCA TCAAAAAAAG 4440

AGGTGGATTC AATAAAATTA ATGCTGTCAA GAATACACGT ATTGAAGTTG TAAATGGTGA 4500

TGAAGTATCA AGACCAGGTC CACGTATTGA TGAAGGATTA AAAGAATTAA GAGATGCAAT 4560

TTATAGAAAA TAAACCATTC TAATTATGCC CCTTATTGCT ACATGTAAAA AATACATGTT 4620

TGAGATAAGG GGTTTTTaAA ATATATTTAG TGAATGATAG CAACGCGAGT ATGTGATTGC 4680

TATAATGAAT GTAATTATCG ATGAAcaaAA GAGAATGCTA TGACATTTAA TAAAGTATTA 4740

TTGAGCTGGa TAGTCmTATT GATTATAACA ACTAGCATAT ATCTATTTTG GCAGTTGGGC 4800

GATATCAATG ATGTATTTAA CCAGTCTATT TTAATCAATG TTAGATTACC GAGATTATTA 4860

GAAGCATTGT TGACAGGTAT GATATTAACT GTTGCAGGCC TTATATTTCA AACAGTTTTA 4920

AATAATGCAT TGGCAGATAG CTTTACATTA GGATTGGCAA GCGGCGCTAC ATTTGGTTCA 4980

GGATTAGCAT TATTTTTAGG TTTAACAACG TTATGGATTC CTGTATTTTC AATAACATTT 5040

AGTTTGATAA CATTAATAAC TGTATTAGTC ATTACGTCGG TATTGAGCCA AGGCTATCCA 5100

GTTAGAATCT TAATATTAAG TGGTTTAATG ATTGGTGCGT TATTCAATTC ACTTCTATAT 5160

TTTTTGATTT TATTAAAACC TCGCAAATTA AATACAATTG CCAATTATCT GTTTGGTGGT 5220

TTTGGTGATG CAGAATACTC AAATGTATCT ATAATAGCAA TCACATTTAT CATTGCATTG 5280

TTTGGTATAT TTATCATTCT TAATCAACTA AAGTTATTGC AATTAGGAGA ACTAAAAAGT 5340

ATAACGGCGA TAAATGTCGC ATATGTTGGC ATCATTGGAT TCATTGGTAT GGTGATACCG 5460

cAACTCATTA GAAAATGGCA GTGGAAACAA TCATTAGGAA GACAATTGGC TTTAAATATT 5520

GTAACTGGAG GACAAATAAT GGTTATGGCA GATTTTATTG GTAGCCATAT ATTGTCACCA 5580

GTACAAATAC CGGCAAGTAT TATCATTGCA TTAATTGGTA TACCAGTGTT AtTTTACaTG 5640

CkAAwAtCtC aGTCgAAAcG GTTACaCTAG CACACGACaT TTGCTAAAAT AAAAATAACT 5700

ATAAACATAA AGAGGGCATA AGCGATGGAT TTGAATCAAA TTAAAGCAGT TGTATTTGAT 5760

TTAGAAGGTA CGTTGTTGGA CAGAGTTAAA TCTCGAGAGA AATTTATCGA AGAGCAATAT 5820

GAACGATTTC ATGACTACTT AATTCATGTT CAACTGGCAG ATTTTAAAAA AgCATTTATT 5880

GAGCTAGATG ACGATGAAGA TAATGATAAA CCTGATTTAT ATAAAGAAAT CATTAAACGT 5940

TTCCATGTAG ATAGGTTAAC TTGGAAAGAC TTATTTAATG ATTTTGAAAT GCATTTTTAT 6000

CGTTATGTAT TTCCTTATTA CGATACTTTG TATACACTAG AAAAgCTATC GCAAAAAGGC 6060

TTTCAAATTG GTGTTATCGC AAATGGTAAA TCTAAGATTA AACAATTTCG ATTACATTCA 6120

CTTGGTTTGA TGCATGTTAT TAATTATTTA TCAACATCAG AAACAGTTGG TTTTCGTAAA 6180

CCACATCCTA AAATTTTTGA AGATATGATT GATCAACTAG GGGTATTACC TGAGCAAATT 6240

ATGTATGTTG GCGATGATGC GTTAAATGAT GTAGCTCCAG CACGAGCTAT GGGCATGGTT 6300

AGTGTATGGT ATA 6313

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

CCGTAAACAC ATCAACAAAA GAAGGCTATA TTACAAAAGA AGACTTGGAC TTATGCTGCA 60

CGTCGCTCTA ATTCAGCTGG AATGCAAGTC ACCGGACGAC TGGCTTACAT TGAACCTTAT 120

GGGGCAACAA GTCGCACAAA ATAAACGCGC GAGAAGCaAG AATAGGAAGT GATATCTATG 180

AAATGGTTAT CACGAATATT AACAGTAATA GTGACCATGT CtATGGcGTG TGGTGCATTG 240

ATATTTAATC GTAGACATCA GCTAAAGGCG AAAACGCTGA ACTTCAATCA TAAAGCATTA 300

ACAATTATTA TTCCGGCTAG AAACGAAGAA AAAAGAATAG GTCATTTACT ACATTCGATA 360

ATACAACAGC AAGTTCCAGT AGATGTCATT GTTATGAATG ACGGATCGAC AGATGAAACA 420

AAATGGTATG GGAAATCACA TGCTTGTTAT CAAGGTGTGA CGCATGCATG TACGAATCGC 540

ATTGCCTTTG TAGATGCTGA TGTAACTTTC TTAAGGAAAG ATGCTGTTGA AACGTTGATT 600

AATCAGTATC AATTACAAGG TGAAAAAGGA TTGTTAAGCG TACAGCCTTA TCATATAACA 660

AAGCGTTTCT ACGAAGGGTT TTCAGCGATA TTTAATTTAA TGACAGTCGT TGGTATGAAT 720

GTATTTTCTA CCTTAGACGA CGGTCGGACT AACCAGCATG CATTTGGACC GGTGACATTA 780

ACAAATAAAG AAGATTATTA TGCAACTGGA GGTCATAAAA GTGCAAACCG TCATATTATT 840

GAAGGATTTG CTTTAGGAAG TGCATATACT TCACAATCAT TGCCCGTAAC AGTTTATGAA 900

GGGTTTCCAT TTGTTGCATT TCGCATGTAT CAAGAAGGAT TTCAGTCATT ACAAGAAGGA 960

TGGACAAAGC ATTTGTCAAC TGGGGCAGGT GGCACAAAGC CTAAGATCAT GACAGCAATT 1020

GTGTTGTGGT TGTTTGGTTC TATAGCGAGT ATTTTAGGGC TATGTCTTAG TTTAAAATAT 1080

CGCCAAATGT CTGTAAGAAA AATGGTAGCA CTTTACTTGA GCTATACTAC ACAATTTATT 1140

TATCTGCATC GAAGGGTCGG CCAATTTTCT AATTTATTAA TGGTATGTCA TCCATTGTTA 1200

TTTATGTTTT TTACTAAAAT TTTCATCCAA TCTTGGAAAC AAACGCATCG TTATGGTGTA 1260

GTTGAATGGA AAGGTCGTCA ATATTCTATA TCTAAAGAAC AATAAATCAA GGTAATGGCA 1320

TTTCAATATA GGAGGACTAG TATGACAATG ATGGATATGA ATTTTAAATA TTGTCATAAA 1380

ATCATGAAGA AACATTCAAA AAGCTTTTCT TACGCTTTTG ACTTGTTACC AGAAGATCAA 1440

AGAAAAGCGG TTTGGGCAAT TTATGCTGTG TGTCGTAAAA TTGATGACAG TATAGATGTT 1500

TATGGCGATA TTCAATTTTT AAATCAAATA AAAGAAGATA TACAATCTAT TGAAAAATAC 1560

CCATATGAAC ATCATCACTT TCAAAGTGAT CGTAGAATCA TGATGGCGCT TCAgCATGTT 1620

GCACAACATA AAAATATCGC CTTTCAATCT TTTTATAATC TCATTGATAC TGTATATAAA 1680

GATCAACATT TTACAATGTT TGAAACGGAC GCTGAATTAT TCGGATATTG TTATGGTGTT 1740

GCTGGTACAg TAGGTGAAGT ATTGACGCCG ATTTTAAGTG ATCATGAAAC ACATCAGACA 1800

TACGATGTCG CAAGAAGACT TGGTGAATCG TTGCAATTGA TTAATATATT AAGAGATGTC 1860

GGTGAAGATT TTGACAATGA ACGGATATAT TTTAGTAAGC AACGATTAAA GCAATATGAA 1920

GTTGATATTG CTGAAGTGTA CCAAAATGGT GTTAATAATC ATTATATTGA CTTATGGGAA 1980

TATTATGCAG CTATCGCAGA AAAAGATTTT CAAGATGTTA TGGATCAAAT CAAAGTATTT 2040

AGTATTGAAG CACAACCAAT CATAGAATTA GCAGCACGTA TATATATTGA AATACTGGAC 2100

GAaGTGAGaC AGGCTAACTA TACATTACAT GAACGTGTTT TTGTGGaTAA GAGGAAAAAG 2160

GCAAAGTTGT TTCA 2174

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4715 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

GAAnCAGnTA GACAAATTAT GGaAAmCGGT GTGAATCaAG GATTCtTTGG TGTAGCTGGT 60

TTTGACCTAC TCGTCGATGA GGATGATAAC GTTTATGCGA TTGATTTAAA CTTTAGACAA 120

AATGGTTCaA CGAGCATGTT ATTACTTGCT AACGAGTTGA ATTCAGGATA TCAAAAGTTT 180

TATAGTTATC ATTCAAAAGG TGATAACACA CATTTCTTCA ATACGATTTT GAAATATGTC 240

AAAGAAGGTA GTTTATACCC GTTATCTTAT TATGATGGTG ATTGGTACGG TGAAGATAAA 300

GTTAAATCAA GGTTTGGCTG TATTTGGCAT GGTGATTCAA AAGAAACAGT ACTGGAGAAT 360

GAACGCGCAT TTTTAGCTGA ACTTGAACAC TATTAGAGTT CGGAACATAA GGCGCTACAA 420

TGTTGTGTTG CCAGTAGTTG ACTGAATATG CGTTTGTAAC AAGCTTTTTT CGATTCTAGT 480

CAACAGTAAT TAAATTTATG ATATGGCAAT ACTTTGTAAT ACTAATATTA AATGGCGACT 540

TTTATTTCAC TATGTTATAA GAGTTGCCAT TTTGTTGATA AAGGTATACT AAAGGTTATC 600

GTTTTGAAAT TTTTAGTAAC TAGATATGTT TCGTGTTATA GACCGAATTT GTGTATACGT 660

AAAATTTAAT GCTATTGAAT TTTTAAAATG AAAAACATGA CATTAAATTG AATTCATAAT 720

ATGTCTAATT GACTAACTTG TTGGAGTCAT TTACTATTTT ATGTATGACA TATTTTAAAA 780

AGTGAGGGTC AAGCATGTCT TATAAAGCAT ATCCATTCTT TAGAGATATA TTAATAAATG 840

AATGTATTTA TTTCGCCTCT AAAAATAAAA AACTAGTACG CCTAAATTAT AAAAGTGAAG 900

CGnATGTAGG CGTTTGGACA GAAGAAAGTG TGGCCGTATC ATTTTTAACA AGTCGTGATA 960

TTCCATTTGA TAAAGTTGTA AAAATGGACG TTGATCGTTT TGCTACTTAT GAATTAGATG 1020

AATTGTTTGA TGAACAAGAC CATATTATTA TGAATCAAAC AATGGAAGAw GAAGGGCATC 1080

TACTAAACGT TGTAGCTGTT ACACAAGAAG TGATGACGGA ATTAGATAAA ATTAGAATCA 1140

AAGAATTTGT CCAAGATGTA GCGAAATATG ATGAAGTATA CGGCTTAACT AAAAAAGGTA 1200

GTAAGCAGTT TATTCTCATT AGTGAAAATG ATAGCGACGA AAAAAAGCCG CATATTATGC 1260

CTGTATGGAG TATTAAAAAC AGAGCGTTAA AAGTTCGAGA TGAAGATTTT GAAGAGTGTG 1320

ATTTAATTAC GATTGAAGGT TCTGTTTTCG GAGAATGGCT AGATGAACTT AGAGATGATC 1380

ATAAAGCCGT TGCGATAGAT TTAAAAACTG GCGTGGTTGG TACAATTGTT TCAGCGCAAA 1440

ATGGAACAAT ACGTATTCAA AACACTTAGA CCATAAAATA AAAGGCCATT TATATAGCGT 1560

TTATTTAAAA CAACGCGCAT ATAAATGGTC TTTTTCTATT TTTCTAAATA TAATGCACCA 1620

ATAGCACCTG nAAAATGCGC CGTTTTCAAC ATAGTACGGT TTGCAACCGC GTAACACAGT 1680

ATAATCTTCC ACAACTTTGC GTAATAAAGC GTTATTATGA AATGAAGAAC CGATATAAAC 1740

GATATTTTCA GTTTTAAATT CACGTGCAAC AGTAATGGCC ATTGTCGTAA CAACTTCGCC 1800

AACGACACCA ATAACGGCTG CTAATTTATT GCTAGGTGTA AAATCAGCAT CTAAATGATG 1860

TAGTACATGA CCAAAATTAG CTGCTGTTAA ATCACCGGGA ATGGGTGGTT CGGTATCTTT 1920

ATAAATATGT CTAACCTTTA AATCGATAGT GTTACGATCA CCGTGTTGTG CCATGTCAGT 1980

TAACTGTTTA TAATCAGTGA TTTGACTTAG TAAATAACCG AGTCCTTGAA TCATGCCTCC 2040

ACCTGTACCG ATACCGCCTA CACGACGTTG TGATTGGCCG TCGAAATAAT GTAGTGACGT 2100

ACCGGTACCA ACATTTGCAA AAATATAATC TGCTAAGTCA TGGCCTTGCT CTTTTAACAA 2160

AATACCTAGT CCTTGAGATG CAGCATCAAA CTCTACAAAA ATTTGTGCAG GAATGTTGAT 2220

GTTTTCAGCA ATGACACCTG CATTACCTCC AGTTAAGCAT AATTTTTCAA TTTGCTGTTG 2280

GTTTAACCAT TCCACAACTT GATCAATATT TTTAGTTAAT TCAGTTTTAA AAGTACGTTG 2340

GTTATCTTGC TCTTGAACGA TTTTAATTAG TGTACCGCCA GCGTCAATGC CAACTTTCAT 2400

AAGATTCCCA CCTCATTATT AATGTCTATC CTTAAATAAT AGTATAGTAA AATGACTAAA 2460

AAACAAGTAA TAATAGTAAT TATTAACAAA TTTGATGCCa TTGCATTTCA ACATTGTAAG 2520

cGTATCGCAA TTAAtGTTTT ACAAACGTGG ACGTTAAGTt ATATATATTA TTTTCTAGGA 2580

ATTTTGAAGT TGTATAGGAT TGTTAGTTAG TGACGCAATA TTAAAAGTAG TTCGTACGCA 2640

GTGTATTTGT AAGTCTCTGA TTAAAATGAT AAGTAATGAG GAATAGTACA TTAATTTTGA 2700

AATTTAAAAA ATATAAATAA GTAATTTATT TAACTTAGAG CAAATAATGG TATCGTAGTG 2760

AAATAATAGG TAAAATAATA TGGGGATTCA TGCTTCATAT ATAAAAAGAT AGGGGTTAAA 2820

TATATGGCTA AAGAACTTTG TTTTGAAGGT ATCACTTTAA AAGCATTTGA TGAACAATAT 2880

CGTTCAGCAA TTAATGATTT TGACTTGAAT GAAAGACAAC AAATATATTC ATCTTTACCT 2940

AAAGAAGTTA TTGATGATGC AATTAATGAT GCTGATAGGA TTGCTAACGT AGCAwTAAmC 3000

GATAAAAATG AAGTGGTGGG CTTTTTTGTA TTACATCGTT ACTATCAGCA TGAAGGTTAT 3060

GATACACCTG AAAATGTCGT TTATATTCGT TCATTATCGA TTAATGAAAA ATATCAAGGT 3120

TTTGGATATG GCACGAAAAT AATGATGTCA TTGCCGCAAT ATGTTCAAGG TGTATTTCCT 3180

GATTTTAATC ATCTATATCT AGTAGTAGAT GCGGAAAATG ACAATGCTTG GAACCTATAC 3240

CTATATTACT TGGACTTAGA TTCAAAACAT GTTTCATCAT TAAAGCTTGA AGAAGAAAGT 3360

CGTTCAGAAG TGACCAATGT ACATATCATT AATTTAATGA TTGATGGCCA AAAGGTTGGC 3420

TTTATCGCAT TGGAGCAGAT TGGTGAACGC ATGAACATTG CTGCTATTGA AGTGGATAAA 3480

TCATATCGCT TTAATGGTAT TGGTTCAAGT GCTCTGCGAC AATTGCCAAC TTACTTAAGA 3540

AAAAACTATG ACAACCTTAA TGTGATTACG ATGATTCTGT TTGGAGAGAA TAATGATTTT 3600

AAACCATTAT GTTTAAATAG TAATTTCGTT GAAATCGAAC AAACTGATGA TTATGTCGTT 3660

TTCGAAAAAT ATTTAAATTA CTAACAGTGA TTGCGAAATA TGATATTGTC ATTTATAATT 3720

TAGTTTTGTT ACTATATATA AATGAATTCA GACGTATAAA TTTAGATTAT ATCCTTCGAA 3780

AGGAAGTATT GGGCAATGAA AATTCAAGAT TATACAAAAC AAATGGTTGA TGAAAAATCA 3840

TTTATTGATA TGGCTTATAC ATTATTGAAT GATAAAGGCG AAACAATGAm mTTATATGAT 3900

ATyATCGATG AATTTAGAGC GTTAGGTGAT TATGAGTACG AAGAAATTGA AAATCGTGTT 3960

GTACAATTTT ACACGGATTT AAACACAGAT GGTCGTTTTT TAAATGTTGG AGAAAATTTA 4020

TGGGGATTAC GTGATTGGTA TTCGGTAGAT GATATTGAAG AGAAAATCGC ACCAACTATT 4080

CAAAAATTCG ATATTCTGGA TGCAGATGAT GAAGAAGATC AAAACTTAAA ATTATTGGGC 4140

GAAGATGAAA TGGATGACGA CGATGATATT CCAGCTCAAA CAGATGATCA AGAAGAACTA 4200

AATGATCCAG AAGATGAGCA GGTTGAAGAA GAAATCAATC ATTCGGATAT AGTCATTGAA 4260

GAAGATGAAG ATGAACTAGA CGAAGACGAA GAAGTGTTTG AAGACGAAGA AGACTTCAAC 4320

GATTAATTTT TTGTTTGACT TTTAGTTGAA AGATGATAAA ATTTTATTCG GGCTCCTTTA 4380

AATAGGACAC GTGTATAAAA TTTATACGCT CCCCTTACAG AATTTGTGAG AGGGAGCGTT 4440

TTTTtATTTA ATTGAGTAAA TCAAGAAATG ATAACGCAAA AATCAAAGTT GTAAATGATA 4500

TACATAGTGA CATAGCAGTA TGGAAACGGT AAGTAAACAG AATTTAATTT TGTCGAtTCG 4560

ACAAtAAaCA aCTtGAaTGA GCTTGCTTTA ATGTTATGTn nTACGTAATT TTTACAATTG 4620

ATGAGGAAGC ATTCCCTTTA ATAATTAGGA GGTCAAGACA TGACAAAATT TATTTTTGTA 4680

ACAGGTGGCG TAGTTTCATC CATTAGGGGA AGGGT 4715

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATAATAACTG AAATTAAAAT TGCTAAATmG TGTTaAgCTA TCGCmACAAT GAAAATwCCG 60

ATTTTGCGTT GTTGAAAATA TCTTTCCAAA CCAAGAATCG ATAATGGCAA TAAATATAAT 120

AAATTTCCAT AAAATGACCA AGTAAAATTA AAGTATATAA CGACAGTTGA CATGCCGTAT 180

AAAATCGTAG CGATCATATT TGCTGAGCGT TTAAAGTGTA ATATTTTAAA TAAGTAGAAG 240

GTCACGACAA ATGTTATGAT AGCTCGTATC ATAGCCATAA TAAGTTGGTT TGTCGGCCAA 300

AAATGTATTG TCGTCGGATT AAATATACCA ACCGTTTCTC CTATTTTAAT GAAkAGAAAA 360

TTTAGCCACA TTAAAGGTGA CAGCGAATAA TAATnTGATA GTCCTTTCAT ATAATCGCCA 420

CCTAmTCCAA ACGATGCATC ATrTAAACTA GAAnAACTAC GTAGATGTTC ATACAnATAC 480

ATTTGAAATG GCATCATTTG ACGGAATCCA TCTCCAGCCC CGCTAAAAAC AGTACCATTC 540

ACAATATAAT CATAGATATG AGTAGAAAAT AAAATAAGCG TTAATATTAC ACTAATGAAA 600

GTTATAACAA AGAATTGTTT GACGTTTGAA TTTAGCCACT TTTTTAACAC AACATTATCC 660

TCAACTTTCA AATTTAAAAT TAAGTTTAAC TGAAACTAAA GTTAATGAGG TTCTTGATAG 720

GTAAAGACGA AGATGACTGT GGAACAGATA CCTTATCATA GTTACTTAAA CTTTGGATCA 780

TTTTCAGTTT ATCATTAAAC AAATATATTG AATAATAAAa aTGTCATACT GATAAAGATG 840

AATGTCACTT AATAAGTAAC TTAGaTTTAA CAAATGATGA TTTTTAATTG TAGAAAACTT 900

GAAATAATCA CkTATACC 918

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

TCGCCCnATA ATCAATTTAT TTTTCATGTG CCACTCCTAT ACAAGCTnAC AATGCTTCTT 60

CAGTTAAGGC AATATCTTTT AATTTTGTTT GATATTTTTG TTCAAAGTCA TATTGTAACT 120

GAACAATTTC TGGCAAACCA ATATGCCAAT CCGCCAATTT TTTTTTAyCT TtGAAGAGCT 180

CTTTTGGTGA TGkTTGcGAC ACTATACTAC CTTCTTTCAT AACGATGACT TCATCTGCAT 240

AACGCGCGAC TTCATTCATA TCATGTGAAA TTAGGATAAT TGCCTTATTT TCATCTGTTT 300

GTAGTGACTT TAGTAATCTC ATTACTTGTC GTTTACTTTG TGGATCAAGT CCTGCTGTAG 360

GTTCATCAAC CACGATAATA TCAGGATTCA TTGCCAATAT CGATACAATC GCTATTTTAC 420

AATCCATCAA CAGACGATGG GCATAGTTTT TGGCTTCATC TAAATTCATT TTAAAGTTTT 540

TAGGTCCAAA TATCATTTCA CGCTCTACTG TGTCCTCAAA TAATTGAGAT TCGGGAAATT 600

GAAATACCAT TCCAATTCTT TTTCTTACAG GTCTAATATA TTTATCTTTG GTCTTATGTG 660

TAATAGTAAT GTCATCAACT GTAACTGTCC CAGTAGTCGG CTTTAACAGC GCATTAATAT 720

TTTGTATCAA CGTTGATTTA CCACTACCCG TTTGTCCAAC GATGGCGTAA TATTTACCTT 780

GTTCAAATTC TGTATTAACA TCATGAATAG CTTGATGCTG ATATGGTGTC CCTTTTTGAT 840

AGGTATAACT TACATTGTCA AACCGTATAG TCATAGTTGA TCCACCAGCC CTTCATAAGT 900

TAAGAATGAT GTTTGGTGTC CCAGCATTTG ATTTATTTTG ATTGGGAATG GCAAATCTAG 960

ACCTATTCTT GTTAACTCTT CTGCATTGTC GAAAATTTCA GTCGCTGTGC CTTCTTTATA 1020

GACAGTCCCT TTATTCATAA CGATAACATG ATCTGCTTCC ATCGCCTCAG ATAAATCATG 1080

CGTAATAGAA ATGATTGTAA TATTATGTTC TGATTTAACT TTTCTCACTA AATCCAATAA 1140

ATTTTGACGT GCATCAGGAT CTAACATAGA AGTCGCCTCA TCTAATATAA TGACAGAGGG 1200

GTTAAGTGCT AATACACTTG CTATAGCCAC ACGCTGCTTC TGTCCCCCCG ATAATGCATT 1260

AGGTTCATAA TCTGCACGTT CTAACATATC AACTTGTTTA AGTGCTTCGC TGACTCTTCT 1320

ATGCATTTCG TCATATGGAA CCGCATGATT TTCGAGTCCA AATGCCACAT CGTATTTTAC 1380

AATTGAACCA ACAAATTGAT TATCCGGATT CTGAAATACA ATTCCTATGT CTTTTCTTAA 1440

CTTTTCAAAA TTATCATCAG TTATAGCTTG ATTATTATAA AAAATTTCTC CAGATTTAAC 1500

TTTCTCTATG CCAATCATTA ACTTGGcAAT TGTAGATTTT CCAGAACCGT TATGACCAAC 1560

AATAGATGTC CACTGACCTT TAGGTATATT AAAAGAAACA TCTTTCAATG TGAAGGATGC 1620

ATCACTTTGA TATTGAAATG AAACATTTTT AAATACAATA ACTGAATTCT TATCCTCCAC 1680

TTGTCTCTCT CCTTTACGAT TCGTGTATCT ATCATATTTT ACAATATTTA TAAATCGCTG 1740

TATATGACAT TGACTGGGTT CTCTATATAT TACTAGTATT TTCTGACTCA TTTCTAGTCT 1800

TTAAAGTGTT GTTTAACAAC TAATGATAAG GACTTTTATT CCTCTCTAAC AATTATGTAT 1860

AAACGTTAAT AAAATAAATG ATTTACTAAT ATAGGGGTGG TCGCGTTTGA TTCAACGATA 1920

ATACTTTCAC TTCATTCAGT TCTAGTGAAA TTGATCAAAC TAGCTTCATC ATATTTTTAG 1980

ATTCGCACTC AAAAAAGTAA ATATAAAGAA ATCGGACTTA AAAACATTTC TGTTCATAAG 2040

TCCGATATTT TATTCAATAA AAAAGCGCGC ACCCCATCAT AAGTTTGTTG AGTTCACGCT 2100

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CTTCAGATTT GTCAGCTAAC TCTTGAACAG AATTGATTCC TGCGCGTTTT AAGCAGTTAT 2760

ATGAACGTAC AGATAAGTCT AATTCTTCAA TAGACATTTC TAATACTTTT TCTTTTTGAT 2820

CTTCTTCTTT TTCAATCATG ATTTCAGCGT TTTGCGCTTC ATCAGTAAGA CCAACGAAGA 2880

TATTCAAGTG TTCAGTCATT ATTTTTGCTG CTAATGAAAC TGATTCTTGT GGTGTGATTG 2940

AACCATTAGT CCAAACATCC AATGTTAATT TATCAAAATC ACTGCTTTGA CCTACACGTG 3000

TATTTTCAAC AGTATAGTTC ACACGTTCAA CAGGTGAATA CAATGAATCA ACAGGGATTA 3060

CACCAATTGG TAAATCACTA GTATTATTTT GTTCTGCTAA TGCGTAACCT CTACCCTTGT 3120

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AATTATCTAC CACCAAAGCC TTTATATTCT TTTTGAGATA CTTGAGCTTC TAAAGATTTC 5700

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CTGTCTAACA CATACTTTTA TATTTnACTT TATATACTTA GTCAGTTCAA CTATTTTCGA 16380

GATATTTTnA ATTTCCn 16397

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29555 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

TnAGTTGTTT CTGCCACGAA AGATTCAATG GCTTTTCTTG CTTTACGCTT TTCTTTCAAT 60

GGCAAATCAC CAATCATTTT TTTAAGGTGA TGTGGGTTTA CAACACCACT ATACTGGTAG 120

TCATTTGAAn TTGTTTTTAG GGCTTGTTCA TCGATAGATC TCTCTCCAGC AAATCCTTTG 180

AACTCCGCTT CTTTTTTAAT ACTTTCGAAA TTAACATATT CTTGATCGAT ATCATCATCC 240

TTATTTAAAG AAGGTACAAC ATTGTCGATG AATTCTCTAA TTAGATCTCG TTTTAACCTC 300

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ACATTTATAT TTTAGGTAAG GCATTGGGTG GCGGCTTATA CCCTGTATCT GCTGTACTTG 15480

CAAATAATGA TGTCATGCGT GTTCTAACAC CAGGTACACA TGGTTCAACA TTTGGTGGTA 15540

ACCCTTTAGC CATTGCAATA TCGACGGCAG CGCTTGATGT ACTTAAAGAT GAACAACTGG 15600

TTGAACGATC AGAACGCTTA GGTTCATTTT TATTAAAAGC GTTGCTACAA CTTAAACATC 15660

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TGACTTAACA TATCTGTTAA ATATAGTGCT ATAAACGGTA TAAATGCTGT CGTAATAATT 29520

AGCTGTAAAA nATTGCTAAT CAATCGTACT TTCAA 29555

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1539 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

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AAACGCTTAA TGACACTTAT TTTTTGAAAA TAATAGTAAT ATCATTTTGT TAAATGAAAG 120

AATAAAGCTA TAATmATTAT AGAATAACTA TTTAAAGGAG ATTATAAACA TGCCAATTAT 180

TACAGATGTT TACGCTCGCG AAGTCTTAGA CTCTCGTGGT AACCCAACTG TTGAAGTAGA 240

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ACCAGTACCA ATGATGAACA TCGTTAATGG TGGTTCTCAC TCAGATGCTC CAATTGCATT 660

CCAAGAATTC ATGATTTTAC CTGTAGGTGC TACAACGTTC AAAGAATCAT TACGTTGGGG 720

TACTGAAATT TTCCACAACT TAAAATCAAT TTTAAGCAAA CGTGGTTTAG AAACTGCAGT 780

AGGTGACGAA GGTGGTTTCG CTCCTAAATT TGAAGGTACT GAAGATGCTG TTGAAACAAT 840

TATCCAAGCA ATCGAAGCAG CTGGTTACAA ACCAGGTGAA GAAGTATTCT TAGGATTTGA 900

CTGTGCATCA TCAGAATTCT ATGAAAATGG TGTATATGAC TACAGTAAGT TCGAAGGCGA 960

ACACGGTGCA AAACGTACAG CTGCAGAACA AGTTGACTAC TTAGAACAAT TAGTAGACAA 1020

ATATCCTATC ATTACAATTG AAGACGGTAT GGACGAAAAC GACTGGGATG GTTGGAAACA 1080

ACTTACAGAA CGTATCGGTG ACCGTGTACA ATTAGTAGGT GACGATTTAT TCGTAACAAA 1140

CACTGAAATT TTAGCAAAAG GTATTGAAAA CGGAATTGGT AACTCAATCT TAATTAAAGT 1200

TAACCAAATC GGTACATTAA CTGAAACATT TGATGCAATC GAAATGGCTC AAAAAGCTGG 1260

TTACACAGCA GTAGTTTCTC ACCGTTCAGg aAACAGAAGA TACAACAATT GCTGATATTG 1320

CTGTTGCTAC AAACGCTGGT cAAATTAAAA CTGGTTCATT ATCACGTACT GACCgTATTG 1380

CTAAATACAA TCAATTATTA CGTATCGAgA TGAATTATTT GAAACTGCTA AATATGACGG 1440

TATCAAATCA TTCTATAACT TAGATAAATA ATTTTCTnTA TAATCAAATG CTGACATAAT 1500

TTTAGTTGAG GATTATTATG ACGGTATAAA TAAATAAAG 1539

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CAATTTCTAT CTATCAATGA TGTGCATACT TCCAnTTAAA TTAAtCGAAA TGaATCAAGG 60

TATATCATTC CTGCCTCTTT ATATAACaAC AAATAGTGAT TACAATATTT CGGTTATTAA 120

CACGAAAATT TTACAAGCAC CTATTTCATT TACATATATA TACAGCAAAA AAGAAAGCCC 180

AGAAATATTG GTGTTTATTA AATCATTTAA AAAGTATATT GCCAATGAAC AATTATAATA 240

AATTTCAAAT CTAAAAAACC AAGAATGCGA TTAATCATCA CATTCTTGGT TCAATTTTAT 300

TCATGAATTT TTTCAACATT AAACGTTAAG TTATTGTCTG AATTTAAATT AACTTTAATC 360

CGTTGTACAA AACGTTTTAA TGGTCTTGCA CCGTATTGAG GTTCATAAGC TTCTTGACCT 480

AGCCAAGCTT TAGCATCATC AGAAACTTCA ATTGAGATTC GTTGTTCTAA TAATCTTATA 540

TTTAATTGCG TTAAGATTTT ATCTACAATC ATACTCATGT CATCAATAGA TAATGGTTTA 600

AATAATACGA TATCATCCAT ACGATTCAAA ATTTCTGGTT TGAAATATGC ATTTAAACTT 660

GTCATAACAG CTTTTTCTGT TGATTCTGTA ATTTCACCAG TCTCTTTTAC GTTTTCTAAT 720

AAAACTTGAG ATCCAATATT ACTTGTCATA ATAATAATAG TATTTTTAAA ATCAACGCTA 780

CGTCCTTTAG AATCAGTTAA ACGGCtTCAT CTAAAATTTG CAATAATACA TTAAAGACGT 840

CAGTAT 846

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1674 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

nTGGGAACAG TAAGCCAGTA TTTTTAGAAA GTTGCCATAC ATGAGCGTCG ATTTTTCCAA 60

TATGGCTATG ACACTAGAAC AATGGGAATT TGGAGGAAAA GTAAATGATT AAACCTAAAA 120

TAGCATTAAC CATTGCAGGT ACTGATcCaA CAGGTGGTGC CGGCGTAATG GCTGATTTAA 180

AATCATTTCA TTCATGTGGT GTATATGGTA TGGGCGTCGT TACAAGTmTT GTTGCTCAAA 240

ATACATTGGG CGTACAACAT ATTCATAATT TAAATCATCA ATGGGTAGAT GAACAACTTG 300

ATAGTGTCTT CAATGATACC TTACCTCATG CTATTAAAAC GGGGATGATT GCTACAGCAG 360

ATACTATGGA AACGATTCGT CATTATTTAA TGCAACATGA ATCTATTCCA TATGTAATtG 420

ATCCTGTTAT GTTGGCGAAA rCggTGATTC ATaATGGwTA ATGACaCAAg CaAAACTTGC 480

AGCATaCGTT ATTGCCATTA GCTGACGTAG TAACACCGAA TTTACCAGAA GCTGAAGAAA 540

TAACGGGACT AACCATTGAT AGTGAAGAAA AAATTATGCA GGCTGGCCGC ATCTTTATTA 600

ATGAGATTGG TAGTAAAGGT GTCATCATTA AAGGCGGTCA TTCAAATGAT ACTGATATAG 660

CAAAAGATTA TTTATTTACT AACGAAGGTG TTCAAACATT TGAAAATGAA CGATTTAAAA 720

CAAnACATAC GCATGGAACA GGGTGTACAT TTTCAGCAGT TATAACGGCA GAACTTGCAA 780

AAGGTAGACC ATTATTTGAG GCTGTACACA AGGCTAAAAA GTTTATTTCA ATGAGTATAC 840

AATATACGCC TGAAATCGGC CGTGGTAGAG GTCCAGTGAA TCATTTTGCA TATTTAAAGA 900

TGTTATACAA ACGATGTAGT TAAAAATTTT ACAGCGAATG GTTTATTAAG TATTGGTGCT 1020

AGCCCTGCAA TGAGTGAAGC TCCCGAAGAA GCTGAAGAAT TTTACAAAGT TGCACAAGCG 1080

CTATTAATCA ATATCGGTAC TTTAACAGCA GAAAATGAAC AAGATATTAT TGCGATTGCT 1140

CAAACGGCAA ATGAGGCAGG CTTACCTATT GTATTTGACC CTGTAGCTGT TGGTGCTTCT 1200

ACATATCGAA AGCAATTTTG TAAATTATTA TTGAAATCAG CGAAAGTATC AGTAATTAAA 1260

GGCAATGCAT CTGAAATATT AGCGTTGATT GATGATACAG CAACTATGAA AGGTACAGAT 1320

AGTGATGCTA ATCTTGATGC GGTTGCAATA GCGAAAAAGG tTACGCAACA TATAAAACTG 1380

CAATAGTAAT CACAGGTAAA GAGGACGTTA TTGtTCmAGA TAATAAAGCC TTCGTATTAG 1440

CTAATGGATC TCCATTATTA GCACGAGTAA CTGGAGCTGG TTGTTTATTA GGAGGCGTTA 1500

TTGCTGGATT TTTATTTAGA GAAACAGAAC CAGACATAGA AGCGTTAATT GAAGCGGTAA 1560

GCgkATTTAA TATTGCTGCT GAGGTAGCTG CTGAAAATGA AAATTGTGGT GGTCCTGGTA 1620

CGTTTTCACC ATTGTTGCTT GATACGTTAT ATCATTTAAA TGAAACAACC TATC 1674

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

ATGAGTTGCC GATGAATTTA GCACCACCAA CGATTGCnTT TGATACTGTG TCCCAACCAG 60

CTTGTTTAGC ATATTTAATA CCTTCACGTA AAGGATCGTT ATCATATGCA GCAATACCAA 120

ATACGTTATG GTATTTCGTG TTTGAGTTAG TTACAACTTT GTnTTGCACT ACATCTGCAC 180

CTTTCGCTAA TTGAGAAGTA CCGTTACCTG TTTCTAATAG GGCATGTGAG ATAAGATAAA 240

CTTCATTAAT GCCATACATT TGAGCAGCTT TGTTAAATGC AGCACCTTGG TTTTCTAATA 300

CACCTTTACC TTTTAAGAAT TGATTAATTT TATCAATAGA AATATTTTGT GGTTGGTCTA 360

AGCGTAAGAA TTGATATTTT AATGCTGGAT CTTGAGCTAA ACGCTTCGTA TCCATTGCAT 420

GCTTAACATC ATTAAATTTA GCATCTGTCC ACTTACCTGG TACACGTTGT ACTTGTGGTT 480

TATATTGTAA ACCAGCTTGT ATTTGAGCAA CTTGGTTTAA TGTCATACCT GTTTGATTAT 540

ACTTAATTAA TTCTTTAGCT AAATCAGTTG ATTTAATCCA TGCtAATTTA CCGTTAGATA 600

ATTTACCATA GTACCAAGTT TGTCCATTAA TGACTTGTTC TTTAACAACT GCGAATGGTT 660

AACCATTACC ATTTTTAATT ACATAAGTGT AGTTATAATC TTTGGcAGCT GATGTAGTTG 780

GTTTCACAGC AGTTGGTGCA GTTAAATCTT TTGCATTTAC CCAACCAGTG CGGTTATTAA 840

TAGTACCGTA TAAATAAACA TCTTTGCCTA CAGATACTTG TTTCGTTGCA TTAAATGTAC 900

CTTGAGCAAT GTTATTGCCT GTTAAAATGA CTTGGTTTTT AGTACCCCAA GGAACCATTG 960

ATAAGCCGTT ATTTGATTTA TTAACAGTAT ATTTTTGAGT CGTTTTAACT TCTTTGCCTA 1020

AGTTTTGAAC ATTTAAGTCT TTTACATTGA ACCAACCTAA TGGGATGTTA TGGCTTGTAT 1080

TGTTTAATAA TACATACGTT TCATTACCAT GAGCACGCTC TTTTGTTACA TAGAACGTAC 1140

GGTCTGCATA TTTCGCACCG TTTTTCGCTG TTTTTTCATA AACAGAAGCA CGAATACCAG 1200

TGTTGTTTGG TTTAACTTGA GCAATCTTGC TAACTGTTTG AGTCGTTTGT GGTTTAGTAA 1260

CAGTATAAGC TTTTACAGCT GTTTTTGGTT GTGCTACTGC TTTTTTAGGT GCAGCAGGTA 1320

CAGCTAAATA TGCTTTACTT ACCCAACCAG ATTTACCATT TACAGTTCCA AATAAATAGA 1380

TAGATTTATC AATTTGTTGT TGCTTAGTCG CTTTAAAAGT TTGGTTACCT GTACCAGAAA 1440

CTGCACCAGC TTCTTGTTTA TAAGTGCCCC AAGGTACTGA ATATAATTTA GTGCCTGGgT 1500

TTACTGTATA TGTTTGCATT ACATTTACAG GTGATTTTGC ATtGtTATAA ATACGTCACC 1560

TTGTTTAACC CAACCAATTA AAGTTGGACT ATTGTAATCT TTAACTAAGT AGAATTTGTT 1620

TCCACCTAAA CTTGCTTCTT TTGTTACAGC AAATGTTTTT TGAACTTCTT TCGTTGGCTT 1680

ACCAGTTTTG TCATAAACTG TAGTGAATAA GCCATTGTTT TTAGCATTAA TTTGAGCAAC 1740

ACCGTTTAAT GATGAAACTG TTAATTTATT ATTTGTTGTA GGTGTTGATG GCTTAGGTGT 1800

TGGTGTAGGC GTAGGTTTAG CAGTATCAAC TAAATATGCT TTACTTACCC AACCAGATTT 1860

ACCATTCACA GAGCCATATA AATAAATTGA TTTATCAATT TGTTGTTGCT TTGAAGCCTT 1920

AAATGTTTGG TTTCCAGAGC CAGACACACT ACCAGCAACT TGTTTAGATG TACCCCAAGG 1980

TACTGTATAA AGTTTCGTAC CAGGTTTGAT TGAATATGAT TGATTTACAT TTACAGGTGA 2040

TTTAGCTGTG TTGTAAACCA CATCGCCTTC TTTAACCCAA CCAAATTTAT TACCAGAATT 2100

GTAATCTTGA ACAAGATAGA ATTTTTGATT ACCTAATGTA GCTGTTTTAG ATACAGCAAA 2160

TGTTTTTTGA ACTTCATTAG TTGCTTTACC AGTTTTGTCG TATACAGTAG TATATAAACC 2220

ACTATTTGTT GG 2232

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2082 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

GATTTAAATA AAATTAATGG ATATCGTGAT CGTACGATGT TAGAACTTCT GTACGCAACG 60

GGAATGCGTG TATCTGAATT GATACATTTA GAGTTAGAAA ACGTGAACTT AATAATGGGA 120

TTTGTACGCG TATTTGGTAA AGGCGATAAA GAAAGAATTG TACCATTAGG CGACGCAGTC 180

ATTGAGTACT TAACTACTTA TATTGAAACG ATTAGACCGC AACTTTTAAA AAAGACTGTT 240

ACTGAAGTCT TATTTTTAAA TATGCATGGT AAACCTTTAT CACGACAAGC AATATGGAAA 300

ATGATTAAAC AAAATGGTGT AAAGGCAAAC ATTAAAAAGA CGTTAACGCC ACATACGTTA 360

CGCCACTCTT TTGCGACACA TTTATTGGAA AATGGCGCAG ATTTAAGAGC AGTGCAAGAG 420

ATGTtAGGtC ACTCTGaCmT ATCTACTACC CmaCTCTATA CmCATGTTTC GrAATCTCAA 480

ATTAGAAAAA TGTATAACCA ATTTCATCCT AGAGCATAAA GTGAACAATA ACTCAAAAGT 540

CACAATACAC ATGACTAAAA ATGTCTGTGC TATTGTGGCT TTTTTAAATT GGTTGATTAA 600

TTACGTCTAT GTTTTCTTAA TTGAATCGCT TCTTCTTTTG CTGCAATCAC TTCTGAACGA 660

TCACGGCGCA TGTGATGGTC TACAATAAAA GGATCTGTTG CTGTTTCCTG ATTATAATCA 720

TAGTCTGGAT AGTTGGCCTT GATGATGCGT TCAAAGACTG GAGTTATTGG TAATATAACA 780

GATGAAAAAG GCTTTGCTGC ATTCAATTTT GCAATCTGTT GCTCAATTAA CAACTGATAA 840

TCATTTAAAT TAAGGTATAA CGCATCTCTA TCTTTAGCAT TTTGTATTAT TTCTTTAGAT 900

TTATTAAAAG ACTTATAGGC GCCTTTTAAA TTATTGCGGC GATAATGGTA ACAAGCAGTT 960

GCAAACAAGA TTAAACTAAC AACTGCATCT TGCTTACTGT AGTTATTTTC AGCTTTCCAT 1020

GCATCTTCTA AAATGTCATG ACATAGGAAA TAATGTTGCT TAGTATGAAA TTGATAATAG 1080

AAATTTATCA GTGCCTGTTG CATTTTGTTA TCACCCCAAT TTAAAAGTAA GTTATTTTCA 1140

TGCTATAATA TTTTAGAGAA TTATGCACAT ATGACGCAAT ACGAGGTAGA TATTATGTAT 1200

GAAGTTAAAT TAGATGCTTT CAATGGACCA TTAGATTTAT TGCTGCATCT TATCCAAAAA 1260

TTTGAAATAG ATATTTATGA TATTCCTATG CAAGCATTAA CAGAGCAGTA TATGCAGTAC 1320

GTTCATGCAA TGAAACAGCT TGAAATTAAT ATTGCAAGTG AATACCTAGT ATTAGCGTCA 1380

GAACTCTTAA TGATTAAAAG TAAGATGCTA TTACCACAAT CAACATCAGA TATGGATGTT 1440

GATGATGACC CACGGGAAGA TTTAGTtGGG CGTTTAATAG rATATCaAAA TTATArAGAA 1500

TATACTGCtA TTTTAAATGA CATGAAAGAA GAAAGAGATT TTTATTTTAC CAAAAAGACC 1560

GACAGATTTA TCtCATTTGG AAAcAGATGA ATCyTGGGAT CCaAATCATA CGATTGATTT 1620

ATCTGTTGAA ATCCGAAAAG AGACATTTAC CATTCAACAA GCTACAGAAC AAGTGACATC 1740

GAGATTGAAA GATAAAGATC ATTTTAACTT CTTTAGTCTG TTTACGTTTT CTGAGCCAAT 1800

TGAACAAGTA GTCACTCACT TTTTAGCTAT TTTAGAGATG TCAAAAGCAG GAATAATTAA 1860

TATTGAGCAA CAACGTAATT TTGAAGATAT TAACATTATT AGAGGAGTGA ACTACCATTT 1920

TGGATAATCA TGGTATATTA GAGTCGCTTT TATTTACAGC TGGCGATGAA GGTTTAGATG 1980

AAAAACAACT ATTAGAAATA TTAGATATGT CGAAAGACCA ACTCGTTGAA TTAATTGAAA 2040

ATTATTCATC ACATGGATTA ATGATACAAC GATTTGGAAT GA 2082

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

TCTATTCTCG TTCTTCCAAG ACCCTGaATT AGAAGTTAAG AAAATCGAAG AAGATGAGAA 60

AGAATCTATT AAAAAAGCTC AAAAAGGTAT TTATAAAGAC CCTAGAGACA TCAATGATGA 120

CGAACAAGAT GATGATACAA AAGATACTGT TGATAAAAAG GAATGATTGT AATTGCCTAA 180

CAAAAACACT CAAGAATATT GGGAAGAACG CGGACGCAAA GCAATCGAGA ATGAGTTGAA 240

GCGTGATAAA ACTAAAGCTG AAGAAATAGA ACGTATATTG AATATGATGA TTAAGCGCAT 300

TGAAAAAGAG ATCaATGCGT TTATTGTCAA GTACGGAGAT TTTGCAGGCG TTACATTACA 360

AGAAGCACAA AAGATTATTG ATGAGTTCGA TGTAAAAGCG TTTCAAGAAG AAGCAAAAAG 420

ATTGGTCGAA AACAAGGAGT TTAGCGATAG AGCAAATGAA GAATTAAAGA AGTATAACAC 480

GAAAATGTAT GTATCTAGAG AACAGATGTT AAAGATTCAA ATAGAATTCT TAATTGCTTA 540

TGCAACAGCT CAAACAGAAT TATCGATGAG GGAATATTTC GAATCAACAG CTTATCGTGT 600

GTTCAGTGAT CAAGCGGGTA TTTTAGGTGA AGGTGTACAA GTAGCTAAAG AAGTTATAGA 660

TACAATCGTT GATACACAAT TTCATGGTGT CGTTTGGTCA GAGCGATTAT GGACTAATAC 720

CGAAGCAATG AAACAAGAAG TAGAAGAAAT AATTGCTAAT GTAGTTATTA GAGGTCGACA 780

TCCTAATGAA TATGTTAAAG ATATGCGCAA cACTTAAATA AATTCGAAGG CACAGCACGA 840

CAAAAGACCG CAGCAATTAA ATCATTGCTT TATACGGAAT CGGCACGTGT TCACGCACAA 900

TCAAGCATTG ACAGCATGAA AGAAATTTCA CCGGAAGgAT ATTATATGTA TATTGCAAAA 960

GACGCTAAAA TTGGTGTTAA TTTCTATCCT ATGCATATCA ATTGTCGTTC AGATTGCGCT 1080

TTACTACCTA AATCTATGTG GCCGAAAAAA CCAAGCAAGA AACGAAAAAC AAAATACTTC 1140

GGAGGGAAAG TGAAAAGCGG TGATTGATTT AAAAGTGAAG TTTTTTAAAG GCAAGTTAGT 1200

TTTGTATGAC AGTAAATTAA ATGTTTGGAG GATACTAATA TGAGTAATAC TGACAAATAC 1260

CTTAGAGACA TAGCAAGAGA ATTAAAAGGT ATACGTAAAG AGTTACAAAA GCGAAACGAA 1320

ACAGTTATTA TTGATGCAAA CTTAGACAGT TTAAGGTCGG CAGTATTAGC CGATAAAGAA 1380

AAATCGAAAT ATAATGAACC TCTCTTTTAA TAGCTAGCAC TTAATTGTGT TGGCTATTTT 1440

TTATGTCCAA AACGTGCTGA TGACATAAAA AGCACGCATG GAAAAACAGT CGACAGACTA 1500

TAAATGGAGG TATATCTCAT GGAAGAAAAT AAACTTAAGT TTAATTTGCA aTTTTTTGCA 1560

GACCAATCAG ATGATCCGGA CGAACCAGGC GGAGATGGTA AAAAAGGAAA TCCTGATAAG 1620

AAAGAAAATG ACGAAGGTAC TGAAATAACT TTCACGCCAG AGCAACAAAA GAAAGTTGAT 1680

GAAATACTTG AACGTCGTGT AGCCCACGAA AAGAAAAAAG CTGATGAGTA TGCAAAAGAA 1740

AAAGCAGCAG AAGCTGCTAA AGAAGCTGCT AAATTAGCGA AAATGAACAA GGATCAAAAA 1800

GATGAATATG AACGCGAACA AATGGAAAAA GAACTGGAAC AATTACGTTC AGAAAAACAA 1860

TTAAACGAAA TGCGTTCAGA AGCACGAAAA ATGTTGAGTG AAGCGGaAGT TGATTCATCA 1920

GATGrGGTTG TCAATTTAGT TGTAACAGAT ACTGCTGAAC AAACTAAATT GAATGTTGAA 1980

GCTTTTTCTA ATGCAGTAAA AAAAGCGGTT AATGAAGCGG TTAAGGTTAA CGCTAGACAA 2040

TCGCCATTGA CTGGTGGAGA TTCATTTAAT CACTCGACTA AAAATAAACC GCAAAACTTA 2100

GCTGAAATAG CTAGACAAAA AaGAATTATT AAAAATTAAC GGAGGCATTT AAATGGAACA 2160

AACACAAAAA TTAAAATTAA ATTTGCAACA TTTTGCAAGT AACAATGTTA AACCACAAGT 2220

ATTTAACCCT GACAATGTAA TGATGCATGA AAAGAAAGAT GGCACGTTGT TAAACGACTT 2280

TACAACACCT ATCTTACAAG AGGTTATGGA AAACTCTAAA ATCATGCAAT TAGGTAAGTA 2340

CGAACCAATG GAAGGTACTG AGAAGAAGTT TACTTTTTGG GCTGATAAAC CAGGTGCTTA 2400

CTGGGTAGGT GAAGGTCAAA AAATCGAAAC GTCTAAGGCT ACTTGGGTTA ATGCTACAAT 2460

GAGAGCGTTT AAATTAGGGG TTATCTTACC AGTAACAAAA GAATTCTTGA ATTACACTTA 2520

TTCACAATTC TTTGAAGAAA TGAAACCTAT GATTGCTGAA GCTTTCTATA AAAAGTTTGA 2580

CGAGGCAGGT ATTTTGAATC AAGGTAACAA TCCGTTCGGT AAATCAATTG CACAATCAAT 2640

TGAAAAAACT AATAAGGTTA TTAAAGGTGA CTTCACACAA GATAACATTA TTGATTTAGA 2700

GGCATTGCTT GAAGATGACG AATTAGAAGC AAATGCATTT ATCTCAAAAA CACAAAACAG 2760

TGATTCGTTA GACGGTCTAC CTGTGGTTAA CCTTAAATCA AGCAACTTAA AACGTGGTGA 2880

ATTAATCACT GGTGACTTCG ACAAATTGAT TTATGGTATC CCTCAATTAA TCGAATACAA 2940

AATCGATGAA ACTGCACAAT TATCTACAGT TAAAAACGAA GATGGCACAC CTGTAAACTT 3000

GTTTGAACAA GACATGGTGG CATTACGTGC AACTATGCAT GTAGCATTGC ATATTGCTGA 3060

TGATAAAGCG TTTGCTAAGT TAGTTCCTGC TGACAAAAGA ACAGATTCAG TTCCAGGAGA 3120

AGTTTAATAA ATAATTAGGA GTGGTAACAT GCCCGAAATC ATTGGAATTG TTAAAGTAGA 3180

TTTTACAGAT TTAGAAGATA ACAGACATGT CTATATGAAA GGGCATGTCT ACCCTCGTAA 3240

AGGTTATAAT CCTACAGATG AACGTATCAA AGCTTTAGCT AGTGTTGAAA ATAAACGCAA 3300

CAAACAAATG ATTTACATTG TAAATGACAA ATTAACCAAA AAAGAACTTG TCGAAATAGC 3360

AAGTGTTGCT GGCTTACAAG TTGATGAAAA ACAAACAAAA GCTGAAATTA TCAATGCTTT 3420

TGAGTCACTA GAGTAGGTGG TTATATGACT ACGCTAGCTG ATGTAAAAAA ACGTATTGGT 3480

CTTAAAGATG AAAAGCAAGA TGAACAATTA GAAGAAATCA TAAAAAGTTG TGAAAGCCAG 3540

TTGTTATCAA TGTTACCTAT TGAAGTTGAA CAAATACCGG AAAGgTTTAG TTACATGATT 3600

AAAGAAGTTG CAGTTAAACG CTACAACAGG ATTGGTGCTG AAGtATGACA TCAGAAGCGG 3660

TTGACGGACG TAGCAATGCG TATGAATTGA ACGATTtCAA GGAGTATGAA GCTATTATTG 3720

ATAATTACTT TAATGCTAGA ACGAGAACTA AAAAAGGAAG GGCTGTGTTC TTTTGAGATA 3780

TGAAGATAGA GTTATTTTTC AATTAGAACA AGTAGCAACT TACAATCCTA AAACTAGCAA 3840

AAAAGAAAAC ACACTAATCA CTTATGATGC GATACCATGC AATATTAACC CCATTTCTAG 3900

AGCAAGAAAG CAACTTGAAT TTGGTGATGT AAAAAACGAT GTAAGTGTTC TGAGGATAAA 3960

AGAATCAATA TCTTACCCTG TTAGCCACGT GTTGGTTAAT GGCATTCGCT ACAAGATAGT 4020

TGATACAAGG ATATACAGAC ACGAAACGTC ATATTATATC GAAGAGGTCA ATTGATGAAT 4080

ATAGATGGAT TAGACGCACT GTTAAACCAA TTTCACGATA TGAAAACCAA CATTGATGAT 4140

GATGTAGATG ATATTTTACA GGAAAACGCC AAAGAATATG TAGTACGAGC TAAATTGAAA 4200

GCTAGAGAAG TAATGAATA 4219

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GCTTACAAGT ATATTCATAA TTACATATTC AAGGTCCTTG CATGTGGTAT TTTGCTATGG 60

yCtTTaACTA CAACGGGGTC TAAGACTGCG TTTATCATAT TAATCGTCTT AGCCATTtAT 120

TyCTTTATkA AAAAGTTATT TAGTAGAAAT GCGGTAAGTG TTGTGAGTAT GTCAGTGATT 180

ATGCTGATAT TACTTTGTTT TACCTTTTAT AATATCAACT ACTATTTATT CCAATTAAGC 240

GACCTTGATG CCTTACCGTC ATTAGATCGA ATGGCGTCTA TTTTTGAAGA GGGCTTTGCA 300

TCATTAAATG ATAGTGGGTC TGAGCGAAGT GTTGTATGGA TAAATGCCAT TTCAGTAATT 360

AAATATACAC TAGGTTTTGG TGTCGGATTA GTGGATTATG TACATATTGG CTCGCAAATT 420

AATGGTATTT TACTTGTTGC CCATAATACA TATTTGCAGA TCTTTGCGGA ATGGGGCATT 480

TTATTCGGTG CATTATTTAT CATATTTATG CTTTATTTAC TGTTTGAATT ATTTAGATTT 540

AACATTTCTG GGAAAAATGT AACAGCAATT GTTGTAATGT TGACGATGCT GATTTACTTT 600

TTAACAGTAT CATTTAATAA CTCAAGATAT GTCGCTTTTA TTTTAGGAAT TATCGTCTTT 660

ATTGTTCAAT ATGAAAAGAT GGAAAGGGAT CGTAATGAAG AGTGATTCAC TAAAAGAAAA 720

TATTATTTAT CAAGGGCTAT ACCAATTGAT TAGAACGATG ACACCACTGA TTACAATACC 780

CATTATTTCA CGTGCATTTG GTCCCAGTGG TGTGGGTATT GTTTCATTTT CTTTCAATAT 840

CGTGCAATAC TTTTTGATGA TTGCAAGTGT TGGCGTTCAG TTATATTTTA ATAGAGTTAT 900

CGCGAAGTCC GTTAACGACA AACGGCAATT GTCACAGCAG TTTTGGGATA TCTTTGTCAG 960

TAAATTATTT TTAGCGTTAA CAGTTTTTGC GATGTATATG GTCGTAATTA CTATATTTAT 1020

TGATGATTAC TATCTTATTT TCCTACTACA AGGAATCTAT ATTATAGGTG CAGCACTCGA 1080

TATTTCATGG TTTTATGCTG GAACTGAAAA GTTTAAAATT CCTAGCCTCA GTAATATTGT 1140

TGCGTCTGGT ATTGTATTAA GTGTAGTTGT TATTTTTGTC AAAGATCAAT CAGATTTATC 1200

ATTGTATGTA TTTACTATTG CTATTGTGAC GGTATTAAAC CAATTACCTT TGTTTATCTA 1260

TTTAAAACGA TACATTAGCT TTGTTTCGGT TAATTGGATA CACGTCTGGC AATTGTTTCG 1320

TTCGTCATTt AGCATACTTA TTACCAAATG GACAGCTCAA CTTATATACT AGTATTTCTT 1380

GCGTTGTTCT TGGTTTAGTA GGTACATACC AACAAGTTGG TATCTTTTCT AACGCATTTA 1440

ATATTTTAAC GGTCGCAATC ATAATGATTA ATACATTTGA TCTTGTAATG ATTCCGCGTA 1500

TTACCAAAAT GTCTATCCAG CAATCACATA GTTTAACTAA AACGTTAGCT AATAATATGA 1560

ATATTCAATT GATATTAaCA ATACCTATGG TCTTTgGTTT AATTGCaATT ATGCCATCAT 1620

TTTATTTATG GTTCtTTGGT GAGGAATTCG CATCAACTGT CCCATTGATG ACCATTTTAG 1680

CGATACTTGT ATTAATCATT CCTTTAAATA tGTTGaTAAg CaGGCAATAT TTAtTAAtAG 1740

TATGTAyTAT TTTGATATAT TTTTATGGAA TTTACGGTGC TGCTATTGCG CGTTTAATTA 1860

CAGAGTTTTT CTTGCTCATT TGGCGATTTA TTGATATTAC TAAAATCAAT GTGAAGTTGA 1920

ATATTGTAAG TACGATTCAA TGTGTCATTG CTGCTGTTAT GATGTTTATT GTGCTTGGTG 1980

TGGTCAATCA TTATTTGCC 1999

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7769 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TCATTATTAA GACTATTATA TATAATGAAT TTTAACTGGT TTATTAAACG AGAACGTCGG 60

GAATTAAGTA ACTACAATAA AAATAAGATA TGACAATAAG GAGACTACAC GCGTGATCAT 120

TGCCATAATT ATATTGATAT TTATTTCGTT TTTCTTTTCA GGAAGCGAGA CGGCATTAAC 180

GGCTGCCAAT AAAACAAAAT TTAAAACTGA AGCTGACAAA GGTGATAAAA AAGCAAAAGG 240

CATTGTAAAG TTACTTGAAA AACCAAGTGA GTTTATTACA ACGATTCTAA TTGGGAATAA 300

TGTCGCGAAT ATTTTATTAC CAACACTTGT TACAATTATG GCTTTACGTT GGGGGATTAG 360

CGTTGGTATT GCATCAGCTG TTTTAACAGT TGTTATCATT TTGATCTCCG AAGTGATTCC 420

CAAGTCTGTC GCTGCAACAT TTCCAGATAA AATAACAAGG CTTGTATATC CAATTATTAA 480

TATTTGTGTC ATTGTGTTCC GTCCTATCAC ATTACTTTTA AATAAGTTGA CGGACAGTAT 540

TAATCGAAGT TTATCTAAGG GCCAACCTCA AGAACATCAA TTTTCAAAAG AAGAATTTAA 600

AACAATGTTA GCAATTGCTG GACATGAAGG TGCTTTAAAT GAAATTGAGA CGAGTAGGTT 660

GGAAGGTGTC ATTAATTTTG AAAATTTAAA AGTAAAAGAT GTAGATACAA CACCTAGAAT 720

TAATGTGACG GCATTTGCTT CAAATGCGaC ATACGAAGAA GTTTATGAAA CGGTTATGAA 780

TAAGCCATAC ACTAGATATC CAGTGTACGA GGGAGATATT GATAACATTA TTGGGGTGTT 840

TCATTCTAAA TATCTGTTGG CTTGGAGTAA TAAAAAAGAA AATCAAATTA CAAACTATTC 900

AGCTAAGCCA TTATTTGTGA ATGAACACAA TAAAGCTGAA TGGGTATTAC GTAAGATGAC 960

TATTTCTAGA AAACATTTAG CAATTGTGTT GGACGAATTT GGTGGTACTG AAGCGATAGT 1020

GTCACATGAA GACTTAATTG AAGAATTATT AGGTATGGAA ATTGAAGATG AGATGGATAA 1080

AAAGGAAAAA GAAAAACTTT CTCAACAGCA AATTCAATTT CAACAACGGA AAAATCGCAA 1140

GTATTGAATA TCCAATTATA CAAGCAGGTA TGGCAGGAAG TACGACACCG AAATTAGTTG 1260

CATCAGTAAG TAACAGTGGT GGGTTAGGCA CAATAGGCGC AGGTTACTTT AATACGCAGC 1320

AATTGGAAGA TGAAATAGAT TATGTACGCC AATTAACGTC AAATTCTTTT GGCGTAAATG 1380

TCTTTGTACC AAGTCAACAA TCATATACCA GTAGTCAAAT TGAAAATATG AATGCATGGT 1440

TAAAACCTTA TCGACGCGCA TTACATTTAG AAGAGCCGGT TGTAAAAATT ACCGAAGAAC 1500

AACAATTTAA GTGTCATATT GATACGATAA TTAAAAAGCA AGTGCCTGTA TGTTGTTTTA 1560

CTTTTGGAAT TCCAAGCGAA CAGATTATAA GCAGGTTGAA AGCAGCGAAT GTCAAACTTA 1620

TAGGTACAGC AACAAGTGTT GATGAAGCTA TTGCGAATGA AAAAGCGGGT ATGGATGCTA 1680

TCGTTGCTCA AGGTAGTGAA GCAGGTGGAC ATCGTGGTTC ATTTTTAAAA CCTAAAAATC 1740

AATTACCTAT GGTTGGAACA ATATCTTTAG TGCCACAAAT TGTAGATGTC GTTTCAATTC 1800

CGGTCATTGC CGCTGGTGGA ATTATGGATG GTAGAGGAGT TTTGGCAAGT ATTGTCTTAG 1860

GTGCAGAAGG GGTACAAATG GGCACCGCAT TTTTAACATC ACAAGACAGT AATGCATCAG 1920

AACTACTGCG AGATGCAATT ATAAATAGTA AAGAAACAGA TACAGTCATT ACAAAAGCGT 1980

TTAGTGGAAA GCTTGCACGC GGTATCAACA ATAGGTTTAT CGAAGAAATG TCCCAATACG 2040

AAGGCGATAT CCCAGATTAT CCAATACAAA ATGAGCTAAC AAGTAGCATA AGAAAAGCCG 2100

CAGCAAACAT CGGCGACAAA GAGTTAATAC ATATGTGGAG TGGACAAAGC CCGCGACTAG 2160

CAACAACGCA TCCCGCCAAC ACCATCATGT CCAATATAAT CAATCAAATT AATCAAATCA 2220

TGCAATATAA ATAATCGACC GCAATCCACA AAAGCACAAG CACCCCCAAA CATTATTTTA 2280

GTGCTTGCCA TTTTTGTGGA TTGCGTTTCT ATTTTACCAA TTTAATCAAA CGAAAACATC 2340

AAGCTGAAGA TCGCCGAAAG ATTTTAATCA AGCAAAAACA TCAAACTAAA GTTCGCTGAA 2400

ATGATTATGA TAAAAGTTAT ATGGTATGAT GACATTGGTG ATATATATGA TAAACATCGG 2460

ATTAACAGGT TGGGGTGATC ACTATTCATT ATATGAAGAT TTAGAACGCC AAACCGATAA 2520

ACTTAAAACA TATGCTGGAC ATTTTCCGGT TGTCGAATTA GATGCGACAT ACTATGCGAT 2580

ACAACCGGAA AGAAATATAT TGAAATGGAT AAAAGAAACG CCTGATACAT TTGAATTTGT 2640

GGTCAAAATT CATCAAGCAC TcACATTGCA TGCAGACTAC AAAACATTTG CAGATACAAG 2700

GCAAGAACTA TTTGATCAAT TTAAGAATAT GTTAGAGCCC TTACATACAC AGAAAAAATT 2760

AGCAATGGTA TTGGTTCAAT TTCCGCCATG GTTTGACTGC AATGCACAAA ATATCAAATA 2820

TATTTTGTAT GTAAGACAGC AATTACAAGC ATTTCCAATG TGTGTAGAAT TTAGGCATCA 2880

ATCATGGTTT AGTGATGCAT TTAAAGAACA AACATTGGCA TTTTTAACAG AACATCAAAT 2940

AATCACAAAT GAAATTGCGT TTGTACGTTA TCATGGACGT AATCATTACG GTTGGACTAA 3060

GAAAGATATG TCAGATCAAG AATGGCGCGA TGTACGCTAT TTATATGATT ATAATGAGCA 3120

AGAATTAATA GACTTGGCAC AAAAGGCACA AATATTAGCA CAAAAAGCTA AGAAAGTTTA 3180

CGTCATATTT AACAATAATT CTGGTGGTCA TGCAGCAAAT AATGCCAAAA CATATCAGCG 3240

ATTATTGAAT ATAGAATATG AAGGGTTAGC ACCACAACAA TTAAAATTAT TTTAAGAGGC 3300

GACGACTATG TTATTAACAA TTACATTATT AGTTTTAATC GGAGGTTTGT CAGCGATTAT 3360

AGGGTCTATC GTAGGCATTG GAGGCGGTAT TATTATCGTT CCAACAATGG TTTACCTCGG 3420

TGTTGAACAT GGATTACTAC ATAATATTAC AACACAAGTA GCGATAGGGA CGTCTTCAGT 3480

CATTCTAATT GTGACAGGAC TTTCTTCATC ACTTGGATAT TTAAAAACAA AACAAGTTGA 3540

TATTAAAAAT GGTTCCATCT TTTTATTTGG ACTATTACCA GGTTCATTGC TTGGGTCCTT 3600

CATTAGTAGA TATTTAACAT TTGAGTCATT TAATTTATAT TTTGGTATCT TTTTAATTTT 3660

CGTAGCCATT TTATTAATGG TAAGAAATAA GATTAAACCG TTTAAAATTT TCGATAAACC 3720

CAAGTATGAA AAGACTTATG TAGACGCTAA AGGTAAAACA TATCATTATA gTGTTCCACC 3780

ATTGTTTGCT TTTATTACAA CGTTTTTAAT TGGTATATTG ACAGGTTTAT TTGGTATTGG 3840

AGGTGGCGCA CTAATGACGC CACTAATGCT TATTGTATTT AGATTTCCAC CTCATGTAGC 3900

TGTTGGAACA AGTATGATGA TGATTTTCTT TTCAAGTGTC ATGAGTTCTA TAGGGCACAT 3960

TGCTCAAGGT CACGTAGCTT GGGGTTATGC AATCATnTTA ATTATTTCTA GTTATTTTGG 4020

TGCGAAAATC GGTGTCAAAG TGAATCAATC AATTAAGTCA GATACGGTAG TAACATTATT 4080

GAGAACAGTA ATGTTGTTAA TGGGTATATA TTTAATTATT CGTGCGTTGA TTTAATACAA 4140

CTTTAAAAGG AGGACGTCAA TTTGAGGCTT ACAATTTATC ATACGAACGA TATTCATAGT 4200

CATTTACATG AATACGAACG CATTAAAGCA TATATGGCAG AACATCGGCC ACGACTTAAT 4260

CATCCTTCTT TATATGTTGA TCTAGGTGAT CATGTAGATT TATCCGCACC TATAACTGAA 4320

GCAACTTTAG GTAAAAAGAA TGTGGCATTA CTAAATGAAG CAAAATGTGA TGTTGCAACA 4380

ATCGGTAATA ATGAAGGGAT GACCATTTCA TACGAAGCTT TAAATCACCT TTACGACGAA 4440

GCAAAATTTA TAGTGACATG TAGCAATGTT ATAGATGAAT CAGGTCATTT ACCAAATAAT 4500

ATCGTTTCTT CTTATATTAA GGACATAGAC GGTGTGAAAA TACTATTCGT TGCAGCGACA 4560

GCACCTTTTA CCCCATTTTA TCGTGCACTA AATTGGATTG TTACCGATCC ACTTGAATCT 4620

ATAAAAGAAG AAATTGAACT TCAACGAGGT AAATTTGATG TATTAATCGT GCTAAGTCAT 4680

TGTGGCATTT TCTTCGATGA AACATTATGC CAAGAATTGC CTGAAATTGA TGTCATTTTT 4740

GCAgCTGGAA AGTATGGTAA TTATCTTGGA GAGGTTAATT TAACTTTTGA GGCACATAAA 4860

GTAGTACATA AAACTGCAAA GATTATTCCT TTAGAAACAT TACCTGAAGT TGAAACTTCA 4920

TTTGAAGAAG AAGGAAAAAC GTTAATGTCC AATTCAGTAA TTCAACATCC AGTAGTGCTT 4980

AAGCGTAGTA TGAATCACAT AACTGAAGCT GCATACTTAT TAGCTCAAAG TGTTTGTGAG 5040

TATACACATG CACAATGTGC CATCATCAAT GCTGGCTTAC TCGTTAAAGA TATTGTAAAA 5100

GATGAAGTGA CAGAATATGA CATTCATCAA ATGTTACCGC ATCCGATTAA TATGGTAAGG 5160

GTTAGACTTT TTGGTGTGAA ATTAAAAGAG ATTATAGCTA AAAGTAATAA ACAAGAATAT 5220

ATGTATGAAC ATGCACAAGG TTTGGGTTTC AGAGGGAATA TATTTGGAGG ATATATTCTT 5280

TATAATTTAG GGTACATTCA TTCTACAGGG CGTTACTATC TGAATGGAGA AGAAATCGAA 5340

GACGACAAAG AATATGTACT AGGTACGATA GATATGTATA CGTTCGGTCG TTATTTCCCA 5400

ACATTGAAAG AATTACCAAA AGAGTATTTA ATGCCAGAGT TTTTAAGAGA TATATTTAAA 5460

GAAAAATTAT TGGAATATTA AAAAGTAAGA TTATTGGATT TTCATTTGTC ATGAATTTCG 5520

ATATAATGTT TAAAGATACA CTTAACAGGA GGGTATGTGT TGTTATGGCG ACAAAAAACG 5580

AGGAAATATT ACGTAAACCG GATTGGTTGA AAATAAAATT AAATACCAAC GAAAACTATA 5640

CAGGACTTAA GAAGATGATG AGGGAAAAAA ATCTTAATAC TGTATGTGAA GAAGCTAAAT 5700

GTCCTAATAT ACATGAATGT TGGGGTGCAC GTCGTACAGC GACATTTATG ATTTTAGGTG 5760

CCGTATGTAC AAGAGCTTGT CGTTTTTGTG CGGTTAAGAC AGGTTTACCT AATGAACTTG 5820

ATTTAAATGA GCCTGAACGT GTAGCTGAAT CAGTTGAATT AATGAATTTG AAACACGTTG 5880

TTATCACTGC TGTTGCGCGT GATGATTTAA GAGATGCTGG TTCAAATGTT TATGCTGAGA 5940

CAGTACGTAA AGTTAGAGAA AGAAATCCAT TTACAACGAT TGAAATTTTA CCATCAGATA 6000

TGGGCGGGGA CTATGATGCG TTAGAAACAT TAATGGCGTC AAGACCTGAC ATTTTAAACC 6060

ATAATATTGA AACTGTTCGT CGCTTAACAC CGAGAGTTCG TGCGCGTGCG ACTTACGACA 6120

GAACATTAGA GTTTTTACGT CGTTCAAAAG AATTACAACC GGATATCCCA ACTAAATCAA 6180

GTATTATGGT TGGATTAGGT GAAACTATAG AAGAAATTTA TGAAACGATG GATGATTTAC 6240

GTGCGAATGA TGTAGATATT TTAACGATTG GTCAATATTT ACAACCTTCA CGTAAACATT 6300

TAAAGGTTCA AAAATATTAC ACGCCTTTAG AGTTTGGTAA ATTAAGAAAA GTGGCAATGG 6360

ATAAAGGGTT TAAACATTGC CAAGCTGGAC CTTTAGTACG TAGTTCTTAT CATGCGGATG 6420

AGCAAGTAAA TGAAGCTGCT AAAGAAAAGC AACGCCAAGG TGAGGCACAG TTAAATAGTT 6480

AATATTTAAC CATTAATAAG GCATAAAGGC TTAGTTTGTA CAAAACGAAC GTGTCATAGA 6540

AGGTGAAGAA TTTGATAAAA GTAGATCAAC ATTACTTTGA ATTAATAGAA AATTATCGCG 6660

AATGTTTTAA TGAAGAACAA TTTATTGCTA GGTATTCAGA TATTTTAGAT AAATATGATT 6720

ACATAGTTGG TGACTATGGT TACGATCAAT TACGATTAAA AGGTTTTTAC AAAGATTCTA 6780

ATAAAAAAGC AGAGATGAGT AAACGTTTTT CAAATATTCA AGATTACATA TTTGAATATT 6840

GTAACTTTGG TTGTCCTTAC TTTGTATTAA GACATTTGTC TAAACAAGAG GTTAAAAAGT 6900

TAATCGAAGA AGTTCATCCG TCTGATGTGA TAGATGACGA CAATAAACTT CAAGATGTGA 6960

AGATTAAGCC AACCATTCAA GATACTGAAC ATTAATAAAA CCCTTAGCTA GATTGAAAAT 7020

GGGAATCATG CAATTCAAGC ATGGACCTGT AATCTAGTTA GGGGTTTTTA TCTTTAATGA 7080

ATGACTTCAT TTAAATACTC AGTAATTTCA TCGCCTTCTT CAGCATTTAC ACCTAAAATA 7140

TGAGCGATAT AGCCTTCTTC TTTTAAATCA TCAGTACCGA TAATACCGAA TTTATTTGTT 7200

TGCATATTAA GTACGAGTGT CTTACCATAA TGTCTATTTG TATGGACTAA CATCAAATCA 7260

TATCGACTAT GCTCGCCAAC AAAACCAACA AACTGAACTT GACTCTCTTC GTTGTCATCA 7320

TATAAATACA TATCAATCAT TTTGTAGCGA CTCCTTTTAA AAGTAGTAAA GTTAGTATAA 7380

CGACAAATGA AGTATACTGC AAAATTATGA TAATATATAA GTGAGAGGTG ACAAGGAATG 7440

TATTTTGTAG ACAAAGATAA ACTAACTCAG AAATTAGCCT ATTTACAAGC ATTAACTGAT 7500

GATTATCATG AGAGCAAGCA CAATCATTAT GCATTTGAAC GCATTGCTCA AATGTTGATA 7560

GAATCATCGG TAGATATAGG GAATATGATT ATCGATGCAT TTATTTTAAG GGATCCTGGT 7620

AATTATAAAG ATGTGATTGA TATATTAGAA CTAGAAAATG TTATTACTAA AGAAACACAG 7680

CAGGCGATTA ATAAAACTGT CGGTATTCGT AAACAATTTA CATATGATTA CACAGCCTTA 7740

GATGTTGAGA TTATCATGCC AATGTTTGA 7769

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 644 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

ACCGCCACCC ATTAATGATT GCTTAAAATC AATAGTCGTA CCATTTAATA CGGGTGCATC 60

TTTTTTGTCT ACTAATACTT TTAATCCAAA GTATTCTAAG ACTTCATCAT TTTCACCAGG 120

CGCTTCTTCT GCACCCATAC CGTATGTTAA ACCAGTGCAC CCGCCACCAT TCACTTTAAT 180

TGCTTCTGTT AATATAACTG TTGGCATGAT AACTCCTCCT TAAAAAATCC AAGTTTCTTT 300

TATATGTGCA TATATATTTT GTAATAATTC TTCCGGCGAA TCACCTTCAA CAATATCACC 360

ATTTACTAAA GCATACAACC CGGCTGAACA TATACCACAA TGTGTCAGGC AACCATACTC 420

TAACACATCG ACATCTGGGT CATTTTCCAG TTGATTAAAA ACATAATCTC CACCTTTTGC 480

CATGTTAGAG AGACAAAATT CTACGATCGG ATTCATACTT CACCTTCTTA TTTCATTTGT 540

TACAATATTA TAGCATTTTA AAACTGGTAT TTTAACATGA TGTGCTCAAT TAGCAACAAC 600

TGATGTTTCT TATCCCAGTT ATGTAATAGT GCCTTAGTTA GTAC 644

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1578 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

GAATGATGAA AGGAATAGAA AAGAAAAGAT AAATAATGTA ATAGATTTAT CCGAGAAAAT 60

TGAAAGAACA AAAGATATGC CAATCAAGAA TACTATAACT ACTCAATTAG GAAATAAACT 120

TATTGGCACA AAAAAAGCTC GTTTTGATGA TAAGAAAGTA GTGTCGTTTG GAGCATTTGA 180

AGATGAATAA AATAAATGAT AGAGATTTAA CAGAATTGAG TAGCTATAGG GTTTATCAAG 240

ACATCAATAA AGATAATGAC TTTACAGTTA ACGAAAAACG ATTTAAGCAG GCAGATGTAT 300

TTGAAGATTT ATATAGAGAG AAACTAAAAG ACACAAATAA ATTAAGAGAG TATAATTATT 360

TACAAAATGA AACTTTTAAA AGCGCATAAA TAGGTGATGA GATATGCTTA AAAAAGCAAA 420

ATTTATCTTA ATGGCAACGA TACTACTATC AGGATGTTCA ACTACCAATA ACGAATCCAA 480

CAAAGAAACA AAATCTGTAC CAGAAGAAAT GGATGCTTCA AAATATGTAG GACAAGGATT 540

CCAACCACCT GCAGAAAAAG ATGCGATTGA ATTTGCAAAG AAGCATAAAG ATAAAATTGC 600

TAAGCGAGGC GAACAATTTT TTATGGATAA CTTCGGTCTA AAAGTTAAAG CTACAAATGT 660

TATAGGTAGT GGCGATGGTG TAGAAGTATT CGTGCATTGT GATGACCACG AyATCGTATT 720

TAATGCGAGT ATTCCATTTG ATAAATCAAT wATTGAsAGT GATAGCTCAT TAAGAAGTrA 780

GGAyAAAGGy GATGATATGA GTACTTTAGT TGGTGCAGTA CTCAGTGGGT TTGAATATCG 840

AGCACAAAAA GAAAAATATG ATAAATTATA TAAATTTTTC AAAGATAATG AAGAGAAATA 900

TCAATATACA GGATTTACAA AAGAAGCAAT TAATAAGACG CAAAATAGTG GTTATGAAAA 960

ACCATTGTTA AACAAAAGTG ACAGTGAATT TTCAAAAGAA TTGTCAAATG TTAAGAAGCA 1080

ATTAAAAGAT AAGTCTAAAG TTTCGGTAAC TACTACTCTA TTTAGTAAAA AAAAGAACTA 1140

TACTAAAAAA AGTAACAGTG AAAATGTAAT AAAAATGGCA GAAGAAATAA AAAAAGATAA 1200

AGAGATACCA AACGGTATAG AGCTTAGTAT AAAATTTTCG GACAATAAAA TAAATACGGT 1260

TAAACCAAAT TTTAACGGTG aAAGCACTTC AGAATATGGT GTGTTTGATC AAGAATAAAA 1320

TTAATGATGa AAATTTAACG GAGAATAGTG TATATTGAGT AGATCmAGAA TAAAAAGATA 1380

ATTCTACTAT TGTTGTGAAG GCAAATAAGT AGAAGATTTT AAGTGTAATT TCTGGTGATT 1440

TAAATAATAA TATAnATGGn AGTACTGATA TAAnACTTTT TAACCTACTA GATTCTTATA 1500

ATTTGCTTTC CATTTTATGA CGATTTTTAC TCCAATTGAG TGATAGAATC CAAAAAAGCC 1560

ATCTCCAAAA ATTAATCC 1578

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

TGTTTTCCTT GGGTTAAAAC ATGCTTGCTA TGCGTTTGTA AATATGACTT GCTGTTTTnA 60

CCTGnATACC CGTCACACCA TGGAAGTAAA AATGTTTCTT GCTCTTGGCT TACAATTTTA 120

GCTTTAATCG CTTCATATGC TTTATATTGG TCTTCTGTTA ATTGCTGTTT TGATTCTTGT 180

TCGAAAACAC GATCTTTAAA TGGGTCTCTT TCAACAACCG CGTCATATTT TTCAACATAA 240

CCTTTTTTGA TAAGTCCATC TAAACTGGAT TTTGAAAAGC CCATATCCTC AATATCAGTT 300

AAAAATATTG TTTTATGTTG TTCTTCAGAC AAGTAAGCAT ACAAATCGTA TTGTTTAATA 360

ACTTTCTCCA ACTTAGCTAA TACTTCATCA GGATGATACC CTTCAATGAC ACGAACAGCA 420

CGCTTGGTTT TTTTAGTTAT ATTTTGTGTG AGAATCGTTT TTTCTTCAAC GATATCATCT 480

TTTAACAACT TCATAAGCAA TTGAATATCA TTATTTTTTT GCGCATCTTT ATAATAATAG 540

TAACCATGCT TATCAAATTT TTGTAATAAA GCTGAAGGTA GCTCTATGTC ATCTTTCATC 600

TTAAATGCTT TTTTATACTT CGCTTTAATA GCACTCGGAA GCATCACTTC TAGCATAGAA 660

ATACGTTTAA TGACATGAGT TGAACCCATC CACTCACTTA AAGCTATTAA TTCTGATGTT 720

AATTCTGGTT GTATATCTTT CACTTCTATG ATTTTTTTTA ACTTCGAAAC GTCAAGTTGT 780

ACAATTACAC GCACACCAGG TTGGATGACA GATTCGAGTT GTTCGGGAAT TATATAATCA 900

AATTTATAGT CAACGCTCTT CGACGCGACA TCGACTATGA CTTTCGCTAT CATTATTGCC 960

ACCTAGTTTC TAGTTCATCT AAAATTTGTG CAGCTAATAC TACTTTTTTT CCTTTCTTGA 1020

TATTTACTTT TTCATTATTT TTAAAATGCA TTGTCAATTC ATTATCATCA GAACTAAATC 1080

CGATAGACAT ATCCCCAACA TTATTTGAAA TAATCACATC TGCATTTTTC TTGCGTAATT 1140

TTTGTTGTGC ATAATTTTCA ATATCTTCAG TCTCTGCTGC AAAGCCTATT AAATACTGTG 1200

ATGTTTTATG TTCACCTAAA TATTTAAGAA TGTCTTTAGT ACGTTTAAAA GATACTGACA 1260

AATCACCATC CTGCTTTTTC ATCTTATGTT CTAATACATC AACCGGTGTA TAGTCAGATA 1320

CGGCTGCTGC TTTTACAACA ATATCTTGTT CGTCAAATCG GCTTGTCACT TGTTCAAACA 1380

TTTCTTCAGC ACTTTGAACA TGAATAACTT CAATATCTTT TGGATCCTCT AGTGTTGTAG 1440

GACCAGCAAC TAACGTCACG ATAGCTCCTC GATTTCGCAA TGCTTCAGCT ATTGCATAGC 1500

CCATTTTTCC AGAAGAACGA TTGGATACAA ATCTGACTGG ATCGATAACT TCAATAGTTG 1560

GTCCTGCTGT AACCAATGCG CGTTTATCTT GAAATGAACT ATTAGCTAAA CGATTACTAT 1620

TTTGAAAATG AGCATCAATT ACAGAAACGA TTTGAAGCGG TTCTTCCATA CGTCCTTTAG 1680

CAACATAACC ACATGCTAGA AATCCGCTTC CTGGTTCGAT AAAATGATAC CCATCTTCTT 1740

TTAAAATATT AATATTTTGC TGCGTACGTT TATTTTCATA CATATGCACA TTCATAGCAG 1800

GCGCAATAAA TTTCGGTGTC TCTGTTGCTA GCAACGTTGA TGTCACCAAA TCATCAGCAA 1860

TACCTACACT CAATTTTGCA ATTGTATTTG CCGTTGCAGG TGCAACAATG ATTGCATCTG 1920

CCCAATCACC TAATGCAATA TGCTGTATTT CTGAAGGATT TTCTTCTATA AAAGTATCTG 1980

TATAAACAGC ATTTCGACTT ATTGCTTGAA ATGCTAATGG TGTCACAAAT TTTTGTGCGT 2040

GATTCGTTAA CATAACGCGA ACTTCATACC CAGATTGTGT TAACTTACTT GTCAAATCAA 2100

TTGCTTTATA TGCCGCAATG CCACCTGTAA CGGCTAATAA TATTTTCTTC ATATTCAATC 2160

TCCCTTAAAT ATCACTATGA CATTTACGCT TTACATCATC ATATGCGCAC AAATGCTCAT 2220

TACTTTTTTA TAGATACAAA TTTAGTATTA TTATAACATC AATCATTGGA TAAACTAAAA 2280

AAACACACCT ACATAGGTGC GTTTGATTTG GATATGCCTT GACGTATTTG ATGTACGTCT 2340

AGCTTCACAT ATTTTTAATG GTCGAAACTA TTCTTTACCA TAATAATCAC TTGAAATAAC 2400

AGGGCGAATT TTACCGTCAG CAATTTCTTC TAACGCTCTA CCAACTGGTT TAAATGAATG 2460

ATATTCACTT AATAATTCAG TTTCAGGTTG TTCATCAATT TCACGCGCTC TTTTCGCTGC 2520

AGTTGTTGCA ATTAAATACT TTGATTTAAT TTGTGaCGTT aATTGGTTtA AAgGTGGATT 2580

TTTArGTGcT CAGCTTCTAC AATACATTGA ATTCtATTCy TCGcAAGtTC TACTTCAtCA 2700

TTAACTACAA cGTAAyCGTA TAAATTCATC ATTTCrACTT CTkTACGCGC yTCGTTAATA 2760

CGACTTTGTA TTTTCTCATC AGATTCTGTT CCTCTACCTA CTAATCGCTC TCTCAAGTGT 2820

TCTAAACTTG GAGGTGCTAA GAAAATAAAT AGCGCATCTG GAAATTTCTT TCTAACTTGC 2880

TTTGCACCTT CTACTTCAAT TTCTAAAAAT ACATCATGAC CTtCGTCCAT TGTATCTTTA 2940

ACATATTGAA CTGGTGTACC ATAATAGTTG CCTACATATT CAGCATATTC TATAAATTGG 3000

TCATCTTTGA TTAAAGCTTC AAACGCATCC CTAGTTTTAA AAAAGTAATC TACGCCATCA 3060

ACTTCACCTT CACGCATTTG ACGTGTTGTC ATTGAAATAG AATACTTATA TGATGTACTT 3120

GGATCTTCAA ATATnCGTnT TCTAACAGTA CCTTTACCTA CTCCAGATGG TCCTGATAAA 3180

ACGATTAACA ATCCTTTTTC ATTATCCATG CCTTACGACC TCTCTAAGCT AATCTTCTAT 3240

TATTTAAATA TGATATCACA TTGTTCTTTA TATTGTATAG CATATTTGAA ATTGCATGCC 3300

ATAATTTCTA TTAAGTCTAA CAATATCGTT ATATTGCACG ATTAATTTTA ATTAAATAAA 3360

TTGAATTGCA AACTTTTAGA TAATGTAAAA TGTATGGCAT AATGTATGGT TCAATAACTA 3420

TACTGAAAAG TTACAATCAT GTTAAAATGA AACGAATGAT ATGAAGAAGG TGGAAGATAA 3480

ATTATGGCTT ATGATGGCTT ATTTACAAAG AAAATGGTTG AGTCTCTACA ATTTTTAACA 3540

ACAGGACGTG TTCACAAAAT CAATCAACCT GATAATGACA CGATACTAAT GGTTGTACGT 3600

CAAAATAGAC AAAACCATCA ATTGTTATTG TCAATCCATC CAAACTTTTC AAGATTACAA 3660

TTGACTACTA AAAAATATGA TAATCCATTT AATCCACCCA TGTTTGCGCG TGTTTTTAGA 3720

AAACACTTAG AAGGTGGTAT TATCGAATCG ATTAAGCAAA TTGGTAATGA TCGTCGCATT 3780

GAAATCGATA TAAAGAGTAA AGATGAAATT GGCGATACTA TTTACCGCAC TGTCATCCTT 3840

GAGATTATGG GTAAACATAG TAACTTAATT TTAGTAGATG AAAATCGCAA AATAATTGAA 3900

GGATTTAAAC ACTTAACACC AAATACGAAT CACTATCGTA CAGTAATGCC AGGATTTAAT 3960

TATGAAGCAC CACCTACTCA GCACAAAATA AATCCGTATG ATATTACAGG TGCAGAGGTG 4020

TTGAAATATA TCGATTTTAA CGCAGGTAAT ATTGCTAAAC AATTATTGAA TCAGTTTGAA 4080

GGATTTAGCC CTTTAATTAC GAATGAAATC GTTAGTCGTC GTCAATTTAT GACTTCATCA 4140

ACATTACCAG AAGCATTTGA CGAAGTAATG GCAGAAACCA AGTTACCACC TACTCCTATT 4200

TTTCATAAAA ATCATGAAAC AGGTAAAGAG GATTTCTATT TTATAAAGTT AAATCAATTT 4260

AATGATGATA CAGTTACATA CGATTCATTA AATGATTTGC TTGATCGTTT TTATGATGCG 4320

CGTGGCGAAC GTGAACGCGT TAAACAACGT GCGAATGATT TAGTTCGATT TGTTCAACAG 4380

ATAAAGATAC TGAACAGTTA TATGGTGAAT TGATCACTGC TAATATATAT CGAATTAAGC 4500

AAGGCGATAA AGAAGTGACG GCATTGAATT ATTATACGAA TGAAGAAGTT GTCATTCCTT 4560

TAAATCCTAC AAAATCCCCA TCAGCAAATG CTCAATATTA TTATAAACAA TATAAyCGTA 4620

TGAAAACGAG AGAmCGTGAA TTACAACATC AAATTCAATT GACGAAAGAC AATATAGATT 4680

ATTTTTCAAC AATCGAACAA CAATTACATC ATATTTCTGT CCATGACATT GATGAAATTA 4740

GAGATGAATT AGCAGAACAA GGCTTTATGA AACAGCGTAA AAATCAAACT AAGAAAAAGA 4800

AAGCGCAGAT TCAATTACAA CATTATGTAT CAACTGATGG CGACGATATA TATGTTGGTA 4860

AGAATAACAA GCAAAATGAT TATTTAACAA ATAAAAAAGC TAAAAAAACT CACACATGGT 4920

tACACACAAA AGATATTCCT GGTTCACATG TCGTTATATT TAATGATGCA CCAAGTGATA 4980

CGACAATCAA GGAAGCGGCT ATGTTAGCAG GATACTTTTC AAAAGCTGGT AATTCTGGAC 5040

AAATACCTGT TGATTATACA TTAATTAAAA ATGTGCATAA ACCATCaGGT GCAAAGCCTG 5100

GGTTTGTAAC ATATGACAAT CAAAAAACTT TGTATGC 5137

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

GTTTTATCGC AGCAGTAAAG CTATCAATCG GCGGTTCAAT TGATGATGCA TTAGCAGAAA 60

TCAnACAATC ATTTTAGTTA AAATTTACTA ATAATGAaAA ATGTAAACCT TTTTCAAATG 120

AAACTTTATa AaAAATATGA TAGTATATAT GTAAATGTTT AATAAAATCT GGAGAAATAG 180

GAGGACATTG CCATGCAACA CCTTATAAAA AAACATGTAT TGAATGGCGA GTTTGATTTA 240

GTACGACAAT TGATGTCCGA AACAGATTTT ATGGAATTTG AAGAAGCATA TATTTCAAGT 300

GCGCATGAAG TAGAAAGTAT GATGTTTTAT ACATGTATTT TAGATATGAT TAAGTACGAA 360

GAATCATCTG AAATGCATGA CTTAGCATTT TTATTGCTTG TGTATCCACT AAGTGAATAT 420

GAAGGTGCTT TGGATTCTGC TTATTATCAT GCAGACGCTT CCATAAAACT TACTGACGGC 480

AAAGAAGTTA AAAGTTTGTT ACAAATGTTA TTATTGCATG CGATACCAAC ACCTGTTATT 540

TCAGATAAGA AGGCTTTTGA TATCGCCAAG CAAATTTTAA AATTAGATCC TAATAATAAT 600

GTTGCTCGTA ACGTCTTAAA AGACACTGCC AAACGTATGc gACAaCGTTG TTGTTGATAT 660

AGTTTTAACA TTTGGTTGGG TTGGGCATAT GTTCCAGCCT TTTTTAATAC TTAAAAACTA 780

ACGAAgTATA CTTGTGTGCA CAAATGGTTT TTATACAACA TTTTATAAAT TTATACATTT 840

TAATAAAGAA CATACGATAG ATGGTTTAAA CCTTGTTAAC TGAGAAATTT TGATATGTAT 900

TCTTCGAAAT TTAACTAAAT ATACGAAATT CAAGAAGCAC AATAATTAAT CATTTTTCCT 960

ATACAAAAGT TCGTATGACT GCATTATAAA AGCATAAATT TATAATTTTT TTAAATGTCA 1020

TTGAACGTGA TAATGTGAAT GGATTGAGCA ATTTTGAAAA AGTGAAAAAT AACCTATGCG 1080

ACTTGCAATT AATTTTCAGT ACGTTATAAT GCACACTGTG CAAAATTAAG GAGGTCTATT 1140

ATTCACATGA TGATGAaTAA AGAAGCAACA AAAATTGGAT TTGCCTACGT CGGCATTGTA 1200

GTGGGCGCAG gATTTTCAAC TGGACAAGAA GTTATGCAAT TTTTCACTAA ATATGGCTTG 1260

TGGGCTTATT TAGGTGTTAT TATATCTGGT TTTATTTTAG CTTTTATTGG GCGCCAAGTA 1320

GCAAAAATTG GTACTGCCTT TGAAGCGACA AATCATGAAT CAACATTACA ATACGTATTC 1380

GGTGAAAAGT TTAGTAAAGT CTTTGaTTAT ATTTTAATCT TCTTCTTATT TGGTATAGCT 1440

GTAACCATGC tAGCTGGTGC AGGCGCAACA TTTGAAGAAA GTTATAACAT ACCTACATGG 1500

CTAGGTGCTT TaATTATGaC ATTAGCGATT TATATTACGT TGCkATTAGA CTTTAATAAA 1560

ATAGTACGTG CACTAGGTAT CGTTACACCA TTTTTAATTG TTTTAGTTGT ATTAATCGCT 1620

GGCGTTTATT tATTTAAAGG TCATGtTTCA TTAGCAGAAG TTAACCAAGT AGTGCCtGAA 1680

GCAAGTATTT GGAAGGGAAT CTGGTTTGGT ACAATATATG GTGGATTAGC TTTTTCTGTA 1740

GGTTTTAGTA CCATCGTAGC AATCnGTGGG GATACTGAAA AGCGTACAGT GTCAGGTGCA 1800

GGCGCGATGT ATGGTGGTAT TATCTATACT GTATTACTAG CATTGATCAA CTTTGcATTG 1860

CAAGTGaATA TCCAACTATT AAAAATGCCT CAATTCCTAC ATTGACGTTA GCAAATAATA 1920

TCCATCCTTT AATAGCAACA GTGkTATCTG TTATTATGCT GGCGGkTATG TATAATACTA 1980

TTCTAGGACT AATGTATTCA TTTGCAGCAC GTTTTACAGA ACCATACAGT AAAAATTATC 2040

ATATCTTTAT TATTATAATG ATGGTAGCAG GTTATTTATT AAGTTnCGTA GGATTTGCTG 2100

AATTAATTAA TAAGTTATAT ACnATTTATG GGATATGTAG GCTTATTnTA TTGTAGTAGC 2160

TGTAATTATn AAATATTTCC AAACGTAAAA ATGGCGGATA AAAAACATAT TGCTTTAATA 2220

TCATATGGAG GGGATATCCG AAACTTTACA ATTTGAATCA CTTTGGT 2267

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

GTCAATGTAA CCTAATAGTT TATGTCTATC TTGTGTACCA ACTACTACAT CGACACCAGG 60

AATTTCCATA ATTTCAGCTG ATGAAGTTTG CGCATAACAA CCTGTTACAC AGATTACAGC 120

ATCAGGATTT TGTCTTATTG CACGTCTAAT TATTTGACGA CTTTTTTTAT CACCCGTATT 180

CGTTACTGTA CAAGTATTAA TAACAAATAC ATCAGCATTC GCTTCAAAGT CAACGCGCTC 240

ATAGTTTGCT TCTTTAAATA ATTGCCAGAT TGCTTCAGTT TCATAATGGT TTACTTTACA 300

ACCTAATGTG TGaACGCAAC TGTTGACATA AATATTCACC CCATTAATTC TTTTTCATAA 360

CTTATTGCAC TTAACGCATA CAATGGCGCA GTTTCTGCCC GTAAAATTCT CGGCCCAAGA 420

CCAACAACTG TACTAGTATT ACTAAATAAT GAAATTTCAT TTTCTGACAA ACCACCCTCA 480

GGaCCAAAAA TCATCAACAC TTTATCCTGA GCATTGAATT GTTGTAAAGT TTGCTTGAAA 540

TTGCTTAACT CACCATCTTT TGCTTCCTCT TCATATGCAA TAAGAATATA GTCATAATTA 600

TCAATAGTAT CACAAATTAA TTTTAAATTC GACTCGAATT GAATAGATGG AATCACTAAA 660

CGATAGCTTT GTTCAGCAGC TTCTTTAATT ATTTTTTGCC AACGCTCTAT CTTTTTGGCA 720

ACTTTTGCCT CGTTTAATTT AACAATTGAA CGTTCCATGC TCACAGCTAT AAATGATGAA 780

GCACCCAATT CAGTAGCTTT TTGTAGCAAC CACTCATATT TGTCAGCTTT GATTAGTCCA 840

CTGCAAATCG TAACATCAAC TGGCAATTCT GTATTAATAT TTTGTTTTTC TTTTAAATCA 900

ACTTCAATTT TATCACTTGT TATGTCAGCA ATTTCACATA AATAAACTGT TTGATCATTA 960

AAAGTTAAAA TAATTTTACT ACCAACATCA TATCTCATTA CATTTGTTAT ATGATGAATA 1020

TCTTCTTTTT TTGTAATAAA AAAACGCTGA CTTACATCAG CGTTTTGGnT CTATGAAATA 1080

ACGTTGCACA TTATTCACTC ACTTTCTGGC CAACAAGACA AACCCAACCG TTGTCATGTT 1140

GTTCTGAAAT AATTTTAAAA CCTACACGCT CCATATGTGA CTGTATACCT TCATACTTCT 1200

CTTTTATAAT ACCAGAAGTA ATAAAATAAC CGCCTTCATT TAGAGTATTA TAAGCATCTT 1260

CAATCATTTC ATCAATAATA TGCGCTAAAA TATTTGCTAT TACAATATCA AATTTTTCTG 1320

TTTCGTCTTT CAATAAGTTA CCTGGAACAG CTTCAATTAA CGTTTCACAA TGATTTCTTC 1380

TGAAGTTTTC TTTAGCTACA CTCACTGCCA TTTCATCAAT ATCCAACGCT TTAATACGTT 1440

TTACACCGAT TAGATGACTT GCAATACTTA ATATACCTGA GCCAGTACCA ACATCAATTA 1500

CTGAATGCTG TGGCAATACA TATGTTTCTA TTGCCTTCAA ACACATACTT GTAGTCGGAT 1560

GATCACCTGT TCCAAAAGCC ATACCTGGGT CGAGCTCAAT GCAAAGCTCT TCATCCGCTT 1620

GGAAATAGTT TTTCCATTCA TTTTCCCAAT CCGTCTCTGC AATAATTTGC TCACTGAATT 1740

GAACGTTATG TTGATCAAGT TCATCTAAAT TTAATAACTC ATCTTTAATT TGCTGTCGCA 1800

ACTTATCATC ATAAGTCATT TCATTAAAAT AGGCTTTCAA TCTTACTCCC TTATCTGGAT 1860

AATCCTCTTT TTTCAAAGCG TAAATTTCAC CGTATTTATC TTCTGGTTGG TTAATTAAAT 1920

CATCTGAATC TTCTATCACG ACACCATTTG ATCCATGATT TTCAAGTATA TTGGTAGCCA 1980

ATTCTACTGC TTCATGATTA ATAATAATTG AAAGCTCTGT CCAGTTCATA CTTTATTCTC 2040

CCTTAAAGAA TCTTTTTGCT CTATCTTTAA AATTCGAAGG TTGTTCATTA ATTTCTTCAC 2100

CATTTAATTG GGCAAATTCT TTCATTAGTT CTTTTTGTCT ATCTGTTAAT TTAGTAGGCG 2160

TTACTACTTT AATATCAACA TATAAATCTC CGTATCCATA GCCATGAACA TTTTTTATAC 2220

CCTTTTCTTT TAAGCGGAAT TGCTTACCTG TTTGTGTACC AGCAGGGATT GTTAACATAA 2280

CTTCATTATT TAATGTTGGT ATTTTTATTT CATCGCCTAA AGCTGCTTGT GGGAAGCTAA 2340

CATTTAATTT GTAATAAATA TCATCACCAT CACGTTTAAA TGTTTCAGAT GGTTTAACTC 2400

TAAATACTAC GTATAAATCA CCAGCAGGTC CTCCATTCAC GCCTGGAGAG CCTTCACCAG 2460

CTAATCTAAT TTGTTGTTCA TTGTCGACAC CTTCAGGTAC TTTCACTTCT AATTTAACTG 2520

TTTTATTTTC AGTACCTTTT CCGTGACATG TTGGACAAGC TTCTTCAAAT TCTTGACCAC 2580

TTCCATTACA TTTAGGACAA ACTTGTTCAG TACGAACTCT ACCTAAAATT GTGTTTTGTT 2640

CTACAGCTAC ATGACCAGCG CCATTACAGT AACTACAAGT CTTTTTACTT GTTCCAGGCT 2700

TTGCACCATC ACCATGACAT GTTTCGCATG TTACATCTTT ACGGATTGAA ATTTCTTTTG 2760

TTGTACCAAA TACCGCTTCT TCAAATGTTA ATGTCATTGT ATACTGAAGA TCATCACCTT 2820

TTTGCGGTGC ATTTGGATCT CTTTGTCTGC CGCCACCGAA GAAAGAGCTA AAGATATCTT 2880

CAAAGCCGCC GCCACCGAAG CCACTAAAAC CGCCAAAGTC AGAGCCATTG AATCCTTGTC 2940

CACCAAAACC TTGTGGACCA TCATGTCCAA ATTGATCATA GcTTGCGCGT TTATTATCAT 3000

CACTTAAAAC TTCATAGGCT TCAGAAATTT CTTTAAACTT TTCATCTGCA CCTTCTTCTT 3060

TGTTAATATC TGGATGATAT TTTTTCGAAA GCTTTCGATA CGCTTTTTTG ATTTCATCTT 3120

TTGAAGCATC CTTACTAATG CCTAAAACTT CATAATAATC TCTTTTGGCC ACAGCTATCT 3180

CTCCTTTTCT TAATTAACTC ATATAGTTTA ACGTAATATG TCATACTATC CAAATAAAAA 3240

GCCAAAGCCA ATGTTCTATT GACTTTGACT TTTCAGATCA TGACAACATT CTAATTGTAT 3300

TGTTTAATTA TTTTTTGTCG TCGTCTTTTA CTTCTTTAAA TTCAGCATCT TCTACAGTAC 3360

TATCATTGTT TTGACCAGCA TTAGCACCTT GTGCTTGTTG TTGCTGTTGA GCCGCTTGCT 3420

TATCTTCTAT ATCTTGACCT TCTAAAGCAG TTTTAAGAGC GTCTTTTTTC TCTTCAGCAG 3540

ATTTTTTATC TTCTTCACCG ATATTTTCGC CTAAATCAGT TAAAGTTTTT TCAACTTGGA 3600

ATACTAGACT GTCAGCTTCG TTTCTTAAGT CTACTTCTTC ACGACGTTTT TTATCTGCTT 3660

CAGCGTTAAC TTCAGCATCT TTTACCATAC GGTCGATTTC TTCGTCTGAT AATGAAGAAC 3720

TTGATTGAAT TGTAATTCTT TGTTCTTTAT TTGTACCTAA GTCTTTTGCA GTTACATTTA 3780

CAATACCGTT TTTATCGATA TCAAACGTTA CTTCAATTTG AGGTTTACCA CGTTCAGCTG 3840

GTGGAATATC AGTCAATTGG AATCTACCAA GTGTTTTATT ATCCGCAGCC ATTGGACGTT 3900

CACCTTGTAA TACGTGTACA TCTACTGATG GTTGATTATC TACTGCTGTT GAATAGATTT 3960

GAGATTTAGA TGTAGGAATC GTAGTGTTAC GTTCAATTAA CGTATTCATA CGTCCACCTA 4020

AAATTTCAAT ACCTAAAGAT AGTGGTGTTA CGTCTAATAA TACTACGTCT TTAACGTCAC 4080

CTGTGATAAC GCCACCTTGG ATTGCAGCTC CCATTGCCAC TACTTCGTCC GGGTTTACTC 4140

CTTTGTTAGG CTCTTTACCG ATTTCTTTTT TGACAGCTTC TTGTACTGCT GGAATACGAG 4200

TTGATCCACC AACTAAGATA ACTTCATCGA TATCTGAGTT TGTTAAGCCA GCGTCTTTCA 4260

TTGCTTGGCG TGTAGGTTCC ATTGTTCTTC TAATTAATGA ATCTGATAAT TCTTCAAATT 4320

TAGAACGAGT TAAGTTTACT TCTAAGTGTA ATGGACCGTT TTCACCAGCT GAGATAAATG 4380

GTAATGAGAT TTGAGTTTGT GATACACCTG ATAAGTCTTT TTTAGCTTTT TCAGCAGCAT 4440

CTTTCAAACG TTGTAATGCC ATTTTATCTT GAGATAAGTC TACGCCATTT TCTTTTTTGA 4500

ATTCTGCAAC TAGGTAGTCA ATAATTACTT GGTCAAAATC ATCACCGCCA AGTTTGTTGT 4560

CACCGGCTGT TGATAGTACT TCGAATACAC CGTCACCTAA TTCTAGGATA GATACGTCAA 4620

ATGTACCGCC ACCTAAGTCA AAAACAAGAA CTTTTTCATC TTTATCAGTT TTGTCTAAAC 4680

CATATGCTAA TGCTGCAGCT GTTGGTTCAT TAATGATACG CTCAACTTCT AAACCAGCAA 4740

TTTTACCAGC ATCTTTAGTT GCTTGACGTT CAGCATCGTT AAAGTATGCA GGTACTGTAA 4800

TTACAGCTTT GTCAACTTTC TCACCTAAaA TAgTTTCAGC TGTATTTTTT AAGTTTTGTA 4860

AAATCATAGC TGAGATTTCT TGTGGTGTGT ATGATTTACC TTCAATATCT ACTTTATAAT 4920

CAGTACCCAT ATGACGTTTA ATAGATTGAA CAGTGTTTGG GTTTGTAATA GCTTGACGTT 4980

TTGCTACTTC aCCAACTTGA GTTTCTCCAT TTTTGAAAGC TACAACAGAT GGTGTTGTAC 5040

GTGAACcTTC AGGGTTTTGA ATTACTTTTG GCTCATCGCC TTCTAATAcT GTnACACATG 5100

AATTTGTTGT ACCTAAGTCT ATACCAATAA TTTTACTCAT AATAAAATTC CTCCATTTAA 5160

TCATTAAATT AATTTAATTT TAAACAATGT CTTTTCGCCA AATTTAAGTT ATTGGTTTAC 5220

AGTGATTTCG CCAGATTCAA AATCAGGGTT ATCATCTTGA ACTACAGCTT GGTGAATATT 5340

TGGATCAAAT GCTTCACCTT CAGTTTTAAT AACTTCAAGA CCATTATCTT TTAGTGCGTT 5400

AATCAAACTT TCATGCACCA TTTGTACACC TTTTTGAAGA GATTTAAAAG TCTCATCATC 5460

ACCTTCAATT TGAAGTGCAC GTTCTATATT GTCTATTGCT GGTAAAATAT CTGTTAACAC 5520

ACGTTGTGCT TGATATGTTT TGTTTATTTC ATTTTCTTTT TGAATTCTAC GCTTATAATT 5580

TTCAAACTCA GCGTAGAGCC TTAAATATTT CTCTTCGTTT TCATCTGCTA ATTGTTGAAG 5640

TTCATTAATT TTTTGATCTT TTGGATCTAT TTCTTCAATA ACATTCTCGT CAGACGTTTC 5700

TTCTATTGCT TCATCTTGTA AATGACCTTT ACTTTCTTCA GCTTGTTCAA CTGAATCATC 5760

AATATTTTGT TTGACGTTTG TTTCTTCAAC TGTTGATTCA GTGTTTTTTT CAACTGATTC 5820

GTCTTTATTT GTCATTTTCT GTCCTCCAAT ACTTTCTAAT CCATCATTAC CAAATTCTAT 5880

TTAATAATTG AATGACATTT TGATAATGCA TAGCTGTAGG TCCAATCACA GCGATTTGAC 5940

CTTTTAACGT TTCATCAAAA TGATATTGAC TTGTTACAAT TGAAATATCA CTTAAGCTGT 6000

CATCAATTTC ATTACCAATT TTTACATTAA TATTTGGTGA AGATATATCT TGTAATAATT 6060

CTGCAATTCT ATTTGATTCT ATATATTGTA GAATGGGCTG AATTGAAGAT ACATTACTTT 6120

CATTCAATGC ATCAATAAGT TTAACCTTTC CACCCATATA AATGCTATTA CTTTGATTAG 6180

AAATATGATT ATTCATCGTA TTTAACAATT TATTGATAAA AATTTCTTCC TGCTCTGATT 6240

GAaCAAAAGA GACAATATCA TCTTGTAAAT TCTGATTAAA CTCAGTTAGT TTGTTTGTAA 6300

CAAAATTTGA TATTGTATTT AGTTTGTCAT TATTAA 6336

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13059 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

TTCATGATTA TTATCTGTTG TAGACACTGC TGGATCTTCC GATGTATCTT TCGATGCATC 60

TTTCGATTTG TGTATTTGCT GATTCAAATG GTCTAGGTCT TCTAACGCCT TATTTACCAT 120

TGCTTCATCA TTTTTATCAT CTTTTTCTCC ATGTTTTGTT GTAGCCGTTT GTGACATATC 180

ATTTTTCATT GCATTAAGAT CGTCCTCGCC ACTTTGTTGA CCCCTATCAA CATTTGAAGA 240

AACCTCATTT AAATCTTTAA GCAATTGATC TAATTTACTG TCTATATCAC TTTGACCGTT 300

TTCATCTATT TGCGATGCTG TTTTCGCTTC ATTTAGTTGT GCTTTATAAT GTTCTTTAGA 420

TGAAGCCGAT AACTGTTTTA ATTGCTCAAT TTGACGAATT GCCTTGTCAA CTTTGTCTAA 480

TAAATCTTGC TTAGATAATA TCTCTTTTGT AATTTCAGTA TCCTTTTCAG ATGCAGCTTG 540

GGCATCGTAC GGCAAGATAT TCGTTAAAAT GATACTTGTC GCCATCATTG TCGAACACGA 600

TAACTTTACA TATAATTGAA ACGGTTTCCC TCGATATTTA GCCATCAACA TACTCCTTCC 660

TCACTTACTT CCTTCAAAGA ATTACATACT ATTATATACC TGTTTACAAG AAATTTACAC 720

TTATCTATCT AGTTATTGTT GTTAGTAATT ATCTACTTAT TACTTAGCTT ATATTTAAGT 780

AAACAAAACA AGCATGACGT AATATCATAT TGTCCATGTC GCTAACATCA TATTACGTCA 840

AATCTTTTAT ATTAAATGAT GTTTTATTTT AGACTGCTTT TTCCTTTTAG CTTTCGAGCG 900

CCTGTTTAAA AACTTGCTCG AATTGTTCAC GCGAGATTTC GTGTGCATGT GCTTTTTGTG 960

CTAATAAAGC ATCTCGAAAC TGTTGTTGAT CTTTCAAACT TTCTAACATT TGTATTAATT 1020

GGTCTTTACT TTCCATTGTT ATCTCATCAT TATGCTCAAA TAAGTGCTCT GATAATGTTA 1080

CTTTAGCATG GTGTGCGGTT TGACGATAAC CTAAAATCAA CAACTCATAG TCAAACGCTT 1140

GTTCCACCGC ATTTAAAATT TCATTACCCT CATTGATATC AAGATAAATA TCACATAACT 1200

GGTATAGTTC ATTTACCCTG TCAATATTAA TAGATGGGTA TAAATGCACA TTAGCATATT 1260

GATCAAGTTG CATTAGCTTA TCAGACATCT CTGTAATAGC AGCGATGTGn AACTTAAAAT 1320

CTGGTAAAGt TyCAACCAAT ACCTTGATGT TACGAatTGa TCCgAGTTAG TTAATATTAC 1380

AATTTCTTTA GTATATCTAT TACGACTACG ATAGTTATAT AGATATCCGC CTTGTAAAAT 1440

ACGAGATTGA ACCTTTGCGT CTGCTATATT GAGCATCGTT TCATATTCGT TTTTATCTGG 1500

AATAATAATA TTACAATGTC GTTTCATATC ACCTTTACAC ATCAATTGCA TATTTCCCGG 1560

GACATTACCA TTACAGTGTT CTTGCCATAC CAAAACATCA CTACCTTTTG ATGGCAAATT 1620

ATATAACACT GAAAATGGTA GGGCTAGTGA GTTAATAACG AAATGATGTT CCGTAATTTC 1680

AAGTTGCTTG ATAAAAAATA ATGCGAATGC GAGCTTTGAA GGGAAAAAGT AAGACTTCCC 1740

TTGCCAATCC AATATGACAT CAGATGTTAC AAAATTTTCA TAAATCACTT CTTTACCTTC 1800

TGCTGTCATA TATTTCTTCA AGATCGCTTT ACGATTTAAA TCGTAAACAG TTTGTGCAAA 1860

TTTAATACCA TTCTTAGAAT AATAATCGAC AAATCGGACA CGTTGTTGGT CATCAAACCA 1920

TTCGACACGA CTAACAATTC TAGGGCGCTC TCCACTTTGA yAAAATATTT TACCTCGyAG 1980

ACGTCCCATA TCATTaATTG TAGCCGAATT GTTGTTACCT TTAATTTCCC AAAAAGCTGG 2040

TACAGTAACC TGATTAAAAA ATCGTGGTTT CATATTTTCT GTATTATGAT TATCTGCAAA 2100

TAAATCTTCT TCCAACTTAC TGGCTTTAAA AGACTCATAT AACTTTCGTG AATGATCGTT 2220

AAAGTAATCA AATAATTTAA TCATGTAGCA CCTCTTGaAC TAATGTTTCC CATTTTAAAA 2280

TAATATCTTG AGTCATAAAT TGCTGTGCCA CTTCATAAGA GATGTCATGT GGTGTCTGGG 2340

GACCATTGTT AAAATACATT ACAATGGcAT GAGCTAGTTT TGCGATAACA TCATCCACAC 2400

TATCTTCGTC GGTATCAAAA GGTACCAAGT AGCCATTTTC CCCATCTCGA ATAAAGGTTG 2460

GGTTACCATA ATTCACATTT AATCCAATCA TACCTAGTCC TGAGCCTACC GCTTCCATTA 2520

GTGTTAACCC AAAACCTTCG CTAGTTGATG CAGAAAGAAA TAACTCATAA TCATTATAAA 2580

TTTCATCAAG TTTAACATGC CCTAGTAAAC GAATATAATC TTGTGCGCGG TGTGTATCAA 2640

TAATTTTACG CAGTCGCGTC TTCTCGCTAC CTTCTCCATA AATATCAAAT GTTAATTCTG 2700

GCACTTGTCG TTTAGCCACG ATAACCGCTT TGACAAGCCA ATCAATATGT TTCTCATTCG 2760

CTAAACGAGA TGCACTAATC ATCGCATATG GCTTTCTTGA TAATGTTGGA TATGATAATG 2820

CATCAATGCT TCCCACAGGA ATAGTATAAA CACGTGGGCG ATAACCTTGA TATTGCTCAA 2880

ATTGTCGACA AACCATATGA TTTTGAATAT CTGTTGCTGT AATAAAGAAA TCAATGTATT 2940

TAGCTTTTGA AAATTGATAT TCATAATAAT TGTTCCATAG TATATGCTGC TCACTCATCA 3000

TATTATTACT ATAATGATCA GCATGAATCA CAACACCAAC TTTACTATCA CCTTTATGCT 3060

GCAAAACAGC CTGACCAATA TCAGAAGCGC GGTCTAATAT GACAATATCG TCTCGGGTTA 3120

AATTCAATCG TTGTAAAAAG TATGCAATAA ATTCCGTTTT GTTATACAAC ACCGCATCTT 3180

CAAACACATA TATAGAGCTG TCTCCATCAA TATATTCGTT ATAAGCGATG GAACCATCTT 3240

GATTATAAAA TTGTCGCATA TATAATTTCG CTTTATTATC AGCTGGTGCA TAATACTCAG 3300

AAAATATGCG CGTATAACTA TAAAAATCTT TACGTACTAA CATACTATTA ATTACAAATT 3360

CTGCACGATC CACAATATCT TTTTGTTCAT TTTGCAGATA ACATGTTACA AATGATGATT 3420

TCCCATTAAA ATATAGGCGG ACTATCTTAC CATTTCTTTC TCTAAAACTA ATGTCATGAC 3480

CAAGCTCACG TTCAATGTCA TCTAACGTGT ACGTTGTTGG TGCTAAAGAA ATATCACTAA 3540

AATACTGATA CAACCAAATA ACTTCTTGAT CTTTAAACCC AATGTTTTGC GTTAATGTCT 3600

GTATGTTCTC TGACTGTATA AAATCTAAAA ACACAAATTT AGTGTCTTGA TTTGTACGTC 3660

TCAATAATTT AGCACGGTAA GCTTGTGCAT ATTCAACACC GCTACTCGCC CAGCCTATAC 3720

CAAAGTTTAT ATTATATATT GTCATGCGCT ACCCCTTTTC ATTTATGGAA AATGTATAAC 3780

TGGCATACCC TCTTTATCAA ATGTAATCAT GCTTTGACAA ATATTTTTCA CCATTCTTTT 3840

TTTGATATTT CGTGTCATAA CTTCAAATGA ATCTAAGGCA ACTCTATGGT ATTCAAAAAT 3900

GACTTGTTCT AACCAACATG AATCAATTGC TTTCAAAAAG ACTTTTTGAA CGAAAATATT 4020

ATAATAATAT GCACTTTGCA TGTTTTTACG ATTCAAAGCT AATTGCTTTT CAAATTGCTC 4080

TAATAAAAAT GTCACTACTG CTTGCTTATC TTTAAAATTA ACACAAGCCA CATCTTTATT 4140

AAATTGGAAA CTTAAATTTT GATAAATATA CTCGACAACA CGCGATTTTG TTAGCACCTT 4200

TTCCTCATTT ACAAACATTT CAAATACATC TTTAGCTAAC GCTTTAAAAT CTTGATTCTC 4260

AGCATCATCT ATTTCTAAAA CTCGATTGCG TTCCTCGTAT ACAAGATCTC GCTGTATACT 4320

AATGCTTTTT TCAAATTCAT TAGCCATTTC ACGAGCTTTA ACCCCTTGTT CTTCCGAGAt 4380

aCGcTGCGCT TTAACTACAA TTTGCTTAAC TTTGCGATTA AACAAATTAC TTTGCGATAA 4440

TCGTTGTGCA TCTAATGAAT ATAATTGATT ATTTTCCGCT AAATTACTAT CGCTCCATCG 4500

CTTAACTAAA TAATCATCTA GTGAAATATA TATACAAGAT GATCCCGGAT CCCCTTGTCT 4560

ACCAGAACGA CCACGTAATT GCCTGTCTAC ACGGCTATTT TCCATATGTT CATGAATAAT 4620

AACAGCTAAT CCACCTAATG CTTCGACACC TTCACCAAGT TTAATATCTG TGCCTCGACC 4680

TGCCATACTA GTCGCAACAG TCATGGAACC AATTTGCCCT GCTTCAGCTA TCATCTGCGC 4740

TTCTTTTGCA ACATTTTGCG CAATGAGTAA ATTATTAGGA ATATCCATTT GGAATAATAC 4800

TTTCGAAAAG TATTCAGCCG CTTCAGCAGT TCTCGTTATG AGTAAAACCG GTCGCCCCGT 4860

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CACTTTATCT GGTTCATCGA TACGTTGAAT CGCTTTATCA GTTGGTACTT GTACGACTAT 4980

TTTTGAATAC AAATCAAAGA ACTCTGATTC GCCTAATTTT CCTGTAGCTG TCATACCTGA 5040

AAATGATTCA AAAAGTTTAA ATAAATTCTG GAAGGTAATT GTTGCCATAA CACTTTTATC 5100

TGTTGAAACC TCCATACCTT CTTTCGCTTC AATAGCTTGG TGAAGTCCAG CTTGCAACTT 5160

AGTTCCCGGT AACATACGAC CTGTAATACG GTCAATTAAA ACAATATCAC CATTATATAC 5220

AAAGTAATCG ACATTAGATT CAAACAAATA TTGTGCGCGC AGTGCTAAAT TAATATTACG 5280

CACTAGGACC ATCGCTTGTT CGCTATATAA ATCTTCAACA TTAAAGTATG ATTGTGCCGC 5340

TTCAATACCT TGATTTAACA GCCATATTTC TTTTTTGGTC TTCTTCATTT TAAAATGCAC 5400

GTCTTCAATC AATGTATCTA CAAACTCTTT CACAATATGA AATAGATTTG ATTGTAATCT 5460

TGGTGCACCC GAAATAACTA ATGGTGTTTG AGCAGCATCT AAAATGATTG AATCCACTTC 5520

ATCAATAATA CCGTAATTTA ATTGTGGTAA AAATTTCCCT TCCGCACTAT CAGCCAAATT 5580

ATCAATTAAA TAATCAAAAC CGAGACGTCC ATTAGTTGTA TATATAATAT CATGTTCATA 5640

TATATTACGT TTTTCCCCTT TTTGATACTC ATAATCCACA ATATCAACAA AACCTAATGA 5700

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TTTGAATCAC TTAATGAATC AGATTCACTC ACGCTTTCTG AACTTCTTAG TGACGTCGAT 13020

ACACTTAATG ATGACGAATC GCTTGTGCTT ACTGAATCG 13059

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10758 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

AGGGATGGCC TTACCTAAAA AACCGGGnAA ACCCTCCAAA ACCCATTAAA AGGnTGGnTA 60

CCCTTTAAAA TGGTAGCATT TAACCGCCAC CCGCCAAGGT GGGTGGTTTA TTCTTCCGTT 120

ATTTAAATTA GTACACCATG CAGATTCTGT AGTTGAGGGA TATTTTAACG AAAGCTTATT 180

AGCAACTGAT AAAAAAATAC GTCCTAAGGC ATATATTGCT TCATGGAAGG ACATCGAGCC 240

GGCTAAGAAA ATAGAATTTA AAATTAAAAA AGGTATTAAA TGGCATGATG GTAATGAATT 300

GAAAATTGAT GATTGGATTT ATTCAATTGA AGTCTTAGCT AACAAGGACT ACGAAGGTGC 360

TTATTATCCA AGTGTAGAAA ATATCCAAGG TGCGAAAGAT TATCATGAAG GAAAAACTGA 420

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TGCTCAATGA TGATACCACC TCTAAAATAT TCGCCGTTTG TAATAAATGT ATCACCCGTC 7560

AATGTATTCC AATTGAGTAA AATGAGTGGA CGCTTTAGGC GATGACGATG CATTAAGTCG 7620

ATAAGGTAAT TCGTTTTATT AATAATCATT TGACTCGCGG TTTTAAATTC ATCATCATTC 7680

ATTTTATTAA AATCAACAGC GTCATTTGAA TTGGCATCAA ATACAAAATG GTCGATGTGT 7740

GGCTCAAGTC GTTTCAATAA TGGTAGATGT CTTTCCGTAG CTTGATCTAA GTGAATGTAC 7800

AAGCCACCAT TAGGGAATAA TGCTTTAAAA TAATCAATCA TTTCAATCAA AGACGTGTGC 7860

AATGTCGTCA CATACAAGTT GAACTTCAAA TCTTTTCTAT GACTGACATG CAGGGCAACG 7920

TGATGGATAA AAATTTTAAA TGCATCGATA TAATCACGTG AGTCATACTG ATCCAAATGC 7980

ATGGTCAAAC TAAAGTTATG ATCTAATAAA AAGTCTAAAC ACAAATCAAT ATCATAAAAT 8040

ATATTCGAAA TTTCTGCATC ATACGTGAAT GGCGCATTGA GCTTTTTCAT GATATATGGA 8100

ATCACATCAT ATGCTAATAC TTCATTGACT TGAAAATCAT GATGACATGT AAGCAACTGT 8160

GATTGATACT GTGTATTGAG CAAATTCCTC AAATAGCCCA CTTGAATAAT ATGATTAAAT 8220

TGATTTAGTT GGTGATTGGT TGGTTGAAAG GCAATCTCTT TATAGTTCAT CTTTTCAATA 8280

TCTTCAATAA AATGATTCAT TTCTTCAATG TAGTCATTTA AAAGTAATAT CAATTCACGG 8340

TCGTGATAAT CATGTTGTGC CGATTGCTGG TTTTCAGTGA TTGCTGGACG ATCACCTCGA 8400

TATTGTTTAG GTGTTTGATG CGTAAAGTGT TTAAATGTTC TCGCAAAGCT CGCTGCACTT 8460

TTCGCATGCT CAATTCGCGT CGTATTTAAG AAATGATGGA ATCCTACACC TAGCGATTCT 8580

GTAAACTTTT TAGACAGATG GCTCTCTGAC CACCCAACGT ATTCGCTTAA TTCTGAAAGG 8640

CTTAAATCTT CATGAAAATG TAACTCGATA TAGTCGCATA CTTGATTCAC TTTATCATCA 8700

TTTAAGATAC TTTGGTTCGA ATGATATGTA cGCGGGACAT AATGAATCAT ATGCATAAGC 8760

AACTGAATCA CAAGTTGTTG CTCAGTCAAT TTAGACAACT CATTATGTCG GATATGTGTT 8820

GAAACCAGTC TTGCCATTAT ATTTCTCAGT TGATGTATAT TCTTTGTTGT GGTCGCATCT 8880

GTTAAGTGAA AATATAGACA ATGCACATCA TCAAACTTGT CTGCTAAATA TTTCATTTGG 8940

AATTGGATAT AACATATGAT GCCATCTTGT TGAAGTTGAA ATCGATACAA GTCGCGGTGG 9000

TTAATGATGA AAATGTCGCC ACTGTTGCAT TGCGTCATAT TATTTTCATC ATAAATGTGT 9060

GCCTCnCCTT TAATAACAAA ACCAATCATT AAACTATTGA GCCTTTTGAA ATCTGACATA 9120

CTCTCAGTTT CTACTCGAAT TAAATAATCA CGTTGCATAC TATCCCTCAA TTCAGTAATA 9180

TGAATACGTT TATTTTACAT TATTTTACAG CAACATATTT GAATTTCATA TTGAATCGTG 9240

TGTGTGGATG ATTATTTATC CTCACTCGGT TCAAGATGTA GACTATCAGT AAAAAAAGTA 9300

TTTTCACCTT TTTTCTCCAC AAAAGTAAAT TCAATGTCTT TATATCCAAC TGrTGaACCT 9360

TTTAAGTCTC CCgAACCTTT CaACaATAAC TTTGGTGCTT TATTCGTTGG TATTTTATAT 9420

CTTTTTCGTA ATTGTTTTAC ATTATAGTCA TCATTAGTTA ATTGATATTT TGCTGAATAA 9480

CTCGGTACCT CTGGATTATA TGATATATCG CCGTCTTTGT ACTTCGACAA ATCTTTAAAG 9540

CTGCCATATT GCGCGAAGAA CTTAAAATTC TCGATTTCTT TTTTTATATT TTCGTCTTTG 9600

ATACCTTTAG TTGGAATGAT TTTATTGTCT ACCATTTTAA CGGGATATTC TTTATCTTTA 9660

CTCTTAGGTC TACCATCTTC ATCATGAAGT GTTTCACTCA CTATATACTT CCCGGTTGTA 9720

GTCTTAGTGT TTCTATTCAT ATATAGAACC ATACCTTTTG ATTTCATACG TTCCCCTTTA 9780

GGTTGAACAA CCATTTCAGA ACCAATAATC CATGTACCTT TATCATTTTT ATCAAATTCG 9840

TCATCACGAT AACCTTCTTT ATCGTATAAA TCCTCTAGAT TTTTAATCGG ATACATACTC 9900

AATGTTTTTT CAAAGCTTTT CTTAACTTCC GCTTCTTTAC CTATGCCACA ACCAGCAGTG 9960

AAACTAATGA CTAATATCAA AAAACTAATA TACAATACCA ATTTGTTTAA TCGTTTCATA 10020

ATTTCACAAT CCTATTCTTC TTATTATCTT TCCTGGATTG ATTTCATATT TTGATCGAGT 10080

CATGATTATT TATCCTCACT TGGTTTAAAA ATTAACCCAT CACTAAAGTA AATGTTCTCT 10140

TCTTTTTTCT CTACAAACGT AAATTCAATG TCTTTATATC CAACTGATGA ACCTTTTAAA 10200

TTCCCTGTAC CyTTCAACAA CArCTTCGGy GCTTTATTTG TTGGTATGTC ATATCTTTTA 10260

ACCTCTGGAT TATATGATAT ATCTCCATCT TTATAATTCA TTAAATCTTT AAAATTGCTA 10380

TATTGCGCAA AAAACTTAAA GTTTTCGATT TCTTTTTTTA TGTtTTCTTC TTTAACTTCC 10440

TCAGTAGAAA TGAATTTATT ATTAATCATT TTAACTGGAT ATTTTTTTTG ATTATCCTGA 10500

GCTACTTCGT ATTTCTCCGT CTTTAtTTCA TTAGTATAGT AAAAtCCTTT TGCACTTCTT 10560

GTATTTCTAT CTATCTTCAA AAGCATGCCT TTTATTTTTA GAGCTTCTCC TTTATTTTGA 10620

ATTGCCATTT GAGAATTTAC AATCCATGTT CCCTTATCAT TTTTATCAAA TTGATCATCA 10680

CGATATCCTT CTTTATCGTA TAAATCCTCT AGATTTTTAA TCGGATACAT ACTCAATGTT 10740

TTTTCAAAAC TTTTCTTT 10758

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

nTaTCaACTT TGGaATTTAA AgTCAATAAC TTTTTTAAAA ACTTTTTGTG TTCACAACCC 60

GCTTCTTTTT CAACGCGTTT ATTGCTTAAC ACAAGAACTT ATTTTACCAG CATTCCAAAA 120

CAAATCAACA TAAAAACGTA CAAAATAAAA GTAATTTTGT ACGTTTAGCA TATATTATAC 180

CTATTTATTT GTAGCAGCTA TAACTTTTTG TGCAATCGAG CTATAAATTT TACCTAGACG 240

ATCATCTGAT TGATATATTG ACGGTGCAAA ATCTTTTGGA TTCCAAGATG GTTGCTCTAA 300

AGGTAATTCC CCAAGTAATT GAGTATTAAG TTCATCAGCT AACTTAGTAC CGCCACCTTT 360

GCCAAAGACA TATTCTTTAT TACCCGTCTC TTTACTTTCA AAATAACTCA TGTTTTCAAT 420

TACGCCAAGA ATAGAATGAT CCGTATGTTT TGCCATCGCA CCTGCGCGAg CTGCAACAAA 480

TGCTGCTGTA GGATGAGGTG TCGTTACAAT AATTTCCTTA CTTGAAGGTA ACATCGTATG 540

AACATCTAAA GCTACATCTC CTGTTCCAGG TGGAAGATCG AGTATTAAAT ATTCAATGTC 600

TCCCCATTTA ACTTCTGTAA AGAAATTCGT CAACATTTTA CCTAACATTG GCCCTCTCCA 660

TATAACTGGC GCATTTTCTT CCACAAAAAA GGCCATTGAT ATAACTTTAA CGCCATGACG 720

TTCAACTGGA ATTACTTCCT TCCCTTTAAT TCCAGGCTTT TCATCAATAC CCATCATATC 780

TGGTACACTA AATCCATATA TATCGGCATC TACTAATCCG ACTTTTTTCC CTTCACGAGC 840

TAAGGCAACG GCTAAATTTA CTGCAACAGT AGATTTACCG ACACCACCTT TACCGGAGGC 900

ATTTTCTTCT TTTGGTTTAA ATTGATTTAC TTTTTCTTCC GGCAATGTTT CAAATCGTAT 1020

ACCGACCGTT TTCGCACCGT TTTCTTTTAA TGCATTAACA ACAGCCATCT GTAAATCTAA 1080

aTTGCGtGCA CCACCTAATT GTGCCATTG 1109

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3997 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

TCTTTATTTA AAAAAATGAT TGTCTAGTTT GTATCTCTCT GAAGATTTGG CAATAAATAA 60

AAGCCGATAA CCGTATAATG ATTATCGACT TAAAGTTTAT GTGGCATTTT TTACTTTTGT 120

AATTTCAGGT GAGTTAGATG ATTATTATCA GATAGATTAT TGCTTATAAT CATATGATGT 180

TTGAATGATA TCTTTGATTT CACTGATTAG TGCTTCTTTA GGATTAGCAG TTGTACATTG 240

ATCTTCAAAT GCGAGCTCTG CCATTCTATC AATTGACTCA TTTAATTCTT CTTCAGACAC 300

ACCTTGTGAT TTCAAATTCA TTTCAATTCC GACTGATTGA CCTAATTCGT AGACAGCTTT 360

AgCTAATGAT TCTACGAGTG CTTCTGTCGT ATTACCTTTT AATCCTAAGA ATTTGGCAAT 420

ATCTGCATAA TCTGTATCTG CTCTGAAGAA CTCATATTTA GGGAATAATG CATGTTTTTG 480

CGGGTCTTTG GCATTATAAC GGATAATATG CGGTAGTAAT ATCGCATTCG CTCTACCATG 540

CGGAATACCA TATTCGCCAC CAATTTTATG CGCAATTGAG TGTGCAATGC CTAAGAATGC 600

ATTTGCAAAT GCCATACCAG CCAAAGTTGA TGCGTTATGC ATTTTCTCTC TTGAAACTTT 660

ATCACCCTTT TCAACAGATG ATTTTAAATA TTCGAACGTC AATTTAATCG CTTGTAGACT 720

CAAACCTCTT GTGTAGTCTG AAGCCATTAC AGATACATAT GATTCCATTG CATGCGTTAG 780

TACATCCATT CCTGTATCTG CTGTAACGCT TTTTGGCACA CTCATCACAA ATTGAGGGTC 840

AATAATTGCA ACGTCAGGTG TTAAAGCAAA ATCAGCCAAC GGATATTTTA CATTTGTTTC 900

ACTATCTGTG ATAACTGCAA ATGGTGTTAC TTCTGAACCT GTACCTGATG TCGTAGGGAT 960

ACAAATGAAC GTCGCATTTT CAGGCATGCC TATTTTATAA GTACGTTTAC CGATGTCTAG 1020

GAACTTTTGT TTAGCACCGA AGAATGATGT CTCAGGGTGT TCAAAGAACA TCCACATTGC 1080

TTTTGCAGCA TCCATCGCTG AACCACCACC AAGTGCAATG ATTGTATCCG GTTGGAAATC 1140

AACCATCATT TCCAGACCTT TATATACTGT ATTAGTTGAT GGGTTCGGTT CGACTTCGCT 1200

ATAACCGAAT TCTACCATAC CAGGGTCACA GACAATCATC ACTTTTTCAA TCTTGTCCAT 1320

TGTTGTTAGA CTCATGATTG CATTTTCTTC AAAATAAATT TGAGCAGGCA CCTTGAAAAT 1380

TTGAGTATTA TTACGTCGTT TAGCAATCGT TTTAATGTTT AATAAATCTG TCGCACTAAC 1440

ATTATGTGAA ATTGAGTTTC TACCGTAGaA CCACAACCTA ATGTTAAAGA CGGAATCAAT 1500

TCGTTATACA TATCACCAAT ACCTCCAACC GCTGATGGTG TATTTACAAG TACACGACAA 1560

GCTTTCATTC TTAGTCCAAA ATCTTTTTGT AATGTTTCAT CTTCTGTATG GATAACGGCT 1620

GTGTGTCCTA ATCCACCAAA ATGTAGTGTG TCTTCACAAA TTTGAAATGC TTGTTTTGTA 1680

GATTGGGCTT TTACTAAGGC TAATACTGGA GATAATTTTT CACGAGATAA CGGATAGTCT 1740

GAACCTACAC CGCTAATTTC GGCTATGATA AGTTTTGTAT TTTCGGGGAC AGGTATACCT 1800

GCTAATTCAG CTATTTCAAC TGCAGATTTA CCGACAATAT CAGGCTTAAT ACCTGTTTTT 1860

TGTTCATTcA TAATTGCATT TTCTAAGCGT TGTAATTCAT CTTTTTTAAC AAAGTATGCT 1920

TGATGTGCTT TAAATTCATT AGTAACATCT TTATAAATTT CTTTATCAAT GACTACAACT 1980

TGTTCAGAAG CACAAATCAT ACCATTATCA AATGTTTTTG AACCAATGAT ATCATTTACT 2040

GCACGTTTAA TGTGTGCTGT TTTTTCAATG TAAGACGGCA CGTTACCTGG TCCCACACCT 2100

AATGCCGGTT TGCCAGTTGA ATATGCAGAC TTAACCATGC CCGAACCACC TGTTGCTAGA 2160

ACTAATGCAA TACCTTTGTG ATTCATTAAT TGTTTTGTTG CTTCGATAGA AGGCACTTCA 2220

ATCCACTGAA TAATATCTTT AGGTGCACCT GCCTTCATTG CCGCTTCTAA TACAACTTCT 2280

GCTGCACGCT TCGACGATTC TTGTGCACTT GGATGGAATG CAAAAATGAT TGGATTTCCT 2340

GTCTTAATTG CAATCATCGC TTTAAAAATA GTTGTCGACG TAGGATTTGT TGTTGGCGTA 2400

ACACCACAAA TAACACCAAT TGGTTCCGCT ACATACGTTA ATCCTTTTTC TTTATCTTCA 2460

CCAATAATCC CTACTGTCTT ATTGTCTTTT ATTGAATTCC ATATATATTC AGAAGCGTAT 2520

AAATTTTTAA TCGCTTTATC TTCGTATATA CCTCTTCCAG TTTCTTCATG TGCTAATTTT 2580

GCTAGCACCA TATGTTGATC AACAGCTGCT AAGCTCaTTT GATGAACAAT ATGATCAATT 2640

TCTTCTTGTG ACTTTTTAGA TAATGCTTCT AATGCTTTTT TCCCTTTGTC AGCTAGAGCA 2700

TCAATCATAA TTGCCACTTC TTGTTCTTTC GATCCACGAT TTTCTTTTTC AGGTATAGTT 2760

AACATATACA ACCACTCCTT TATACTTTGT GAATTATTTC ACAAACATTA TAGTACATGT 2820

CTCTCAGGAT ATAAAGAAAA TTCTATACAA AAAAGTTTAA TTTCGAATAT TATTTGAACA 2880

AATATCAAAT TTTAAAATAA ATGTTTTCAT GAAATCATTG TTATTTCGGT GTTTTTAGAA 2940

TGATTTTATA ATCATAATTT TTTCAATGAC ATAATTTATT CATAATTATA TATTTAATTC 3000

TCCTTGTCGA TACCTATCAA CAGATGTTAC AAATAAAAAC CaCCCGTGTG AACGGGTGGT 3120

TTGTTCTGCG gCTATAAGCC TTCCTTACTG GCCaGCCCTA AAAGGGCACT GACAAGTCAG 3180

CCAACTGCAC TACTATTCCA GCAATCCTAA AGGTTTACTC TTTTTTCTTT CTTTTTTTAT 3240

TTTTCTCTCC AGTGAAAGGA TCTAAATATT CTTCCATTGA AATTTCATCT GCAACGATAT 3300

CCTCTTGTAA TTGATTACGA ATATAATTTT CAATCACTTT TTTATTTCTA CCTACTGTAT 3360

CCACATAAAA TCCTTTACAC CAAAACTTTC TATTTCCATA TCTATACTTT AAGTTAGCAT 3420

GTCTATCAAA TATCATTAAA TTACTTTTCC TTTTAAATAG CCAACAAATG ATGATACCCC 3480

AAGTTTGGGT GGTATACTTA CTAACATATG GATATGATCT TTACATACCT CTGCTTCAAT 3540

TATCTCTACA CCTTTTCTTT CATATAATTG ACGTAATATA ATCCCTATAT CTTTTTTTAT 3600

TTTTCCATAT ATCGCTTGTC TTCTGTATTT AGGTGCAAAG ACAATATGTT ACTTACAATT 3660

CCATTTCGTA TGTGCTAAAC TGTTTGTGTC AGATGACATT AAATAGCATC TCCTCGTGTT 3720

GATTATTTTG GTTGGCTGAC CAATATTTAC TCTAACATGT AGAGATGCAT TTTTTTGACA 3780

ATGGTAGAAC CTTTTCTGGG GAGTGGGACA GAAATGATAT TTTCGCAAAA TTTATTTCGC 3840

CGTCCCACCC CAACTTGCAT TGTCTGTAGA AATTGGGAAT CCAATTTCTC TTTGTTGGGG 3900

CCCCGCCCCA ACTCGCATTG CCTGTAGAAT TTCTTTTCGA AATTCTCTGT GTTGGGGCCC 3960

CTGACTaGAA TTGAAAAAAG CTTaTTaCAA GCGCATT 3997

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

GnGCGAGACA AACACACtTA TTGGTGCCAT TATmCcTAGA ATGaATTCaT ATGCAGTAGA 60

TGAaaCAATC AAAGGATTGG CAAAACAATG CCAAAAATAT GAATCaCAAT TAATTTTAAA 120

TTACACAGGT TTAAATATCG AAGCAGAAAT ACAAGCGCTT GAAACATTAG CACGCaGTAA 180

AGTAGATGGT ATTGTTTTAA TGGCTACAGA CATAACAGAG AGACATATTG AAGTCATTAA 240

TAAAATGAAT GTACCAATCG TTATTGTTGG TCAACAACAT GAACAACTTC ATAGTATTGT 300

GCATGATGAT TATAAAGCAG GTCAAATTAT AGGCGAATGG ATTGGTCAAC AGGGATATCA 360

ACAAGTTGAA GTGTTTAGTG TAAGTGAAAA AGATATTGCA GTTGGTATAC ATAGAAAACG 420

TACTTATGTG GAAGCACAAA AAGATGTTGC AAATGTTTTG GAAAATGTGG AGCAAGTAGA 540

TGCGGTTGTT GGAGCAACTG ATACGATTGC ATTAGCTGCC TATAAATATT ATTCTGATAA 600

AAAAGATGTT ATGAAACCAC ATCAAATATA TGGTTTTGGT GGTGACCCAA TGACACAATT 660

AGTGTCTCCA TCGATAAAAA CAATTCATTA TAATTATTTT GAAGCTGGCC AATGCGCGAT 720

GGaAGAGATA CAACAGATGC TTAAAAAGCA AGATATGCCA TATAGCGTCA CAGTAGATGT 780

TAATATTTAG ACGCTGTATT TTTTAAAATA AATGTGGAAC CGATACCATA TAACTATAAA 840

TGGATAGGTT AAAAGTTAAA GAACGTAGGT AAAATTTGCT ATAATAGAAT ATAAATTGTT 900

AACAGCATAA ATTATAAAAG GAGGACTGGG TAAATATTAT GACCGAATGG ACTAGAGAAG 960

AACGTTATCA ACGAATCGAG GACGTTGATA CTGAGTATTT TAAAACATTA AAACAACAAG 1020

TTGATCAATC AAAATTTCGT CAACAATTTC ATATACAACC AGAAACAGGC TTATTAAATG 1080

ACCCCAACGG ACTTATTTTT TATAAAGGGA AGTATTATGT TTCACATCAA TGGTTCCCAT 1140

TAGGCGCAGT ACATGGCTTA AAGTATTGGT ATAACTACAC GAGTGATGAC TTAATAAACT 1200

TTAAAGCTGA AGGGCCAATT TTAAATCCAG ATACTAAATA TGACAGCCAT GGTGTATATA 1260

GCGGTAGCGC TTTTGAATAT AACGGGCATT TATATTATAT GTACACAGGA AATCATCGAG 1320

ATAATCATTG GCAACGACAT GCGAGTACAG ATGATCGCAC GATTGAAAGA AGACGGTTnC 1380

AGTTGGnAAA A 1391

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 930 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

ATTTATTTTA ATGTTTATAT TTTCTAACAC TTTTTTATGA TCATAGTAGT AATTGACATT 60

TTTCAATTCA AAGACTGGTG TCATCGTATc TCACCTCGCA TTCAACTATA CAACTCCTAG 120

TAACATATGT AAACAGTAAT GTTTACGACT CAAAATTAGA CAAAATAAAG AGATATGCCC 180

CCTTCAAGTT TTATTTATCG CATTTCTTGA AGAGAGCATT ATCATTTTAT TGTTGCATAA 240

CCTTATTTTT TAATTCTGGG TCAAATTGCT GTTGTTTTAA CATTTCAATT TCAAGTTTAT 300

ATGGCGGTTT TTTATTTTTC TTATCTTCAC CAACATAAGG TGTTTCTAAG ATTTTCGGAA 360

TATCTTTAAA ACTATCATGA TGCACAATGT AATTTAATGC ATCAAAACCA ATGTAACCGA 420

GAACAACTTT GATTCTGTCG ACTCCAATGA TTTTATCAAA TTCATTTAAT ACGCCATCAA 540

AGTCCTCTTT AACATTATAT CCAGCATCAT GCGTATGACA TGTATCAAAA CATACTGATA 600

AACGTTCGTT ATTATGAACT CCATCAATAA TACGTGCTAA CTCTTCAAAT GAGCGACCAA 660

TCTCTGTACC TTTACCTGCC ATCGTTTCAA GCGCAATACG TACATTATTG TCATTCGTTA 720

AAACTTCATT TAATCCTTCA ATAATCTTAT TAATTCCGGC ATCAACACCA GCTCCAACAT 780

GCGCACCTGG ATGTAATACa ATATCTTTAG CCCCTATAGC TTGCGTTCTk TCaATTTCTT 840

GTTGCAAGAA ATCTACACCA AGATTAAACG TTTCTGGTTT GGTTGTAttG CAATaTTaAT 900

GATGTATGGT GGCATGAACA ACAATATTAG 930

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1984 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

TGACGCACCA ATTTATAACG CAATTGACAA AACAATTAGA TATACCTGTG AAATTTGTAC 60

CTGGAAACCA TGATTTATGG GAAGTTGAAA GTATGACTAC GCAAGACATT TGGAATAATT 120

ATAAGAGTAT GTCACAGTGC TTGGTAGGAA AACCATTTAT AGTAAATGAA GAATGGGCAA 180

TCATAGGACA TACTGGCTGG TATGATTATA GCTTTGCAGC ACAACGATTT TCATTAGATG 240

AGTTACAAAA AGGAAAACAT TATGGTGCGA CTTGGCAAGA TAAAGAACGA ATATCTTGGG 300

GCATATCAGA TCAAAATTTA TCTAAAATAG CGGCTGAACA AGTGAAGAAA GATATATTAG 360

AAGTAGGAAA TAGACGAGTG ATTTTAGTCA CACATGTTGT GACGCACCCT GATTTCATTG 420

TTCCTATGCC GCATCGTATA TTCGATTTTT ATAATGCATT TATTGGGACA AGTGATTTCA 480

ATCCTTTGTA TGCGATGTTC GATATACCAT ATAGTATTAT GGGCCATGTT CATTTTCGTA 540

AAAGTGTGAT AGATGATGGC AGATGTTATC TCTGTCCGTG TCTAGGCTAT CCAAGACAAT 600

GGCGTTCAGA AGATATTTAC CAGGAAATAA ATGAGACGAT ACAAATAATA GAAATTTAAA 660

ATGCGCAAAC CTGACCCAGT TTGCGCATTT TATGTTTTAC ACACGCGAGT AATGTGTTTA 720

CTTACGTGTG TTTATTTTGT TGCTGATTTT CAATTGTATA TGAATGTGGT TGCACATAAA 780

TGCACTTTCT TCCTGGTGAA TTAAAGCTGT ATTCCATTTT CTCTTTACGA ATTTTAATAA 840

TTTGTTTGCG ATTTGGAATG ATGGCAGGTA AAACTAGGCC ACGACGAATA TGACTCCAAA 900

TTGAAACTTG TTTCGCTGGC TTGTTATCAA AGCGGAAAAC ACGTAGTAAT GGTTTAGAAC 1020

CAAGATTAGT ATGGTATATT AACACAGGTT GACCTTGATC GATAATACCT TTAAGATCTT 1080

CTAACGATTT ACCAGTGCCG TCTACGATAT TAGGATTGTA TTTTTGTAAA AATGGTACAT 1140

ATGCTTCTGG AAATATCGTT TGATGATAAT TGCCAAGCTT AATGAATAAG TGATGTCCAA 1200

CATAACCTTT ATGTGGATTG TTCGGATGTG TCGGCCAATG TCTCATAATT TCTGTAGCAG 1260

GGATATGTTG GTTGTTGTAT TGCAACATCA TGGCTGCGGA AACACCTTCA CACCCCATGA 1320

CCATAGGGAT AGGAAATAGC TGACTGATAG GTTTAACTGG TAATATTTTT CGGTTCATAA 1380

TATAGTCCTC GCATTGATTC AATAAATATT TAATATAATT ATATAGCGTC AATGCAAAAT 1440

GTCCTAAACA TATGTTTTAC ATGAGTGAAT AAAATTAATG GAGTGATAAA ATGGAATATC 1500

AATTACAACA ACTTGCGTCG TTAACGTTAG TAGGTATTAA AGAAACGTAT GAAAATGGAC 1560

GACAGGCTCA GCAACATATA GCAGGGTTTT GGCAAAGATG TTATCAAGAG GGAGTAATTG 1620

CGGATTTACA GTTAAAAAAT AATGGTGATT TAGCCGGGAT ACTTGGCTTA TGTATACCTG 1680

AATTAGACGG TAAGATGTCA TATATGATTG CAGTTACCGG AGATAATAGT GCTGATATTG 1740

AAAAATATGA TGTCATAACA TTAGCAAGTT CAAAGTATAT GGTATTTGAA GCACAGGGCG 1800

CAGTACCTAA AGCAGTTCAA CAAAAAATGG AAGAGGTTCA TCACTACATA CATCAATATC 1860

AAGCAGATAC GGTAAAATCA GCACCATTTT TTGAGTTGTA TCAGGATGGT GATACTACAA 1920

GTGGAAAATT AATATTACCA GAAATTTGGG ATnCCTGTTA AAGGGGTGAT TGAAATAnGA 1980

AnTG 1984

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

GATTCCACGT GTGTTAAAAG AAGTTACAcC TTCAATGATG GTATTTACTA ATTTCTTTAG 60

AGATCAAATG GATCGCTTCG GTGAAATTGA TATTATGGTT AATAACATTG CAGAGACAAT 120

TAGTAATAAA GGCATCAAAT TATTGCTAAA TGCTGATGAT CCATTTGTGA GTCGTTTGAA 180

AATCGCAAGT GATACGATTG TGTACTATGG TATGAAAGCA CATGCCCATG AATTTGAACA 240

AAGTACGATG AATGAAAGTA GATATTGTCC AAACTGTGGT CGCTTATTGC AATACGATTA 300

AAAATATGAA ATATCAAGTT TTGATGTGGC ACCGTTTTTA TATTTAAATA TCAATGATGA 420

AAAATATGAT ATGAAAATTG CAGGTGACTT TAACGCTTAT AACGCGTTAC AGCATATACT 480

GTTTTAAGAG AGCTAGGGTT AAATGAACAA ACAATTAAAA ATGGCTTTGA AACGTATACA 540

TCAGACAATG GTCGTATGCA GTACTTTAAA AAAGAACGAA AAGAAGCGAT GATCAATTTA 600

GCTAAAAATC CTGCAGGAAT GAATGCAAGT TTATCAGTTG GTGAACAATT AGAAGGCGAA 660

AAAGTGTATG TTATTTCGCT AAATGATAAC GCTGCAGATG GTCGAGATAC TTCATGGATT 720

TATGATGCAG ATTTTGAAAA ATTATCTAAG CAACAAATTG AAGCTATCAT CGTGACAGGT 780

ACACGAGCAG AAGAACTTCA ATTGCGATTG AAGTTAGCAG AGGTTGAAGT ACCAATTATA 840

GTTGAGCGTG ATATTTATAA AGCAACGGCA AAGACTATGG ATTATAAAGG TTTCACAGTT 900

GCAATACCAA ACTATACATC ATTAGCGCCT ATGCTTGAAC AATTAAACCG TTCGTTTGAA 960

GGAGGTCAAT CATAATATGC ATGAATTGAC TATTTATCAT TTTATGTCAG ATAAATTGAA 1020

TTTATACAGT GATATAGGAA ATATTATTGC TTTAAGACAA CGTGCTAAAA AACGAAATAT 1080

TAAAGTTAAT GTCGTAGAAA TCAATGAAAC AGAAGGTATT ACCTTTGATG AATGTGATAT 1140

TTTCTTTATC GGTGGTGGAA GTGATAGAGA ACAAGCATTA GCAACAAAAG AATTAAGTAA 1200

AATTAAGACA CCACTTAAAG AAGCGATTGA AGATGGTATG CCGGGATTAA CGATTTGTGG 1260

AGGCTATCAA TTTTTAGGGA AAAAATATAT CACGCCTGAT GGTACAGAAT TAGAAGGGTT 1320

AGGTATTTTA GATTTTTATA CTGAATCAAA GACAAACCGA TTAACAGGAG ATATTGTTAT 1380

CGAAAGTGAT ACTTTTGGAA CTATTGTAGG TTTTGAAAAT CACGGTGGTA GAACATATCA 1440

TGATTTCGGT ACACTTGGTC ATGTTACTTT TGGTTATGGT AATAATGATG AAGATAAAAA 1500

AGAAGGCATT CATTATAAAA ATTTATTAGG TACTTATTTA CATGGACCAA TTTTACCTAA 1560

AAATTACGAA ATCACTGATT ATCTGTTAGA AAAAGCTTGT GAACGTAAGG GTATTCCGTT 1620

TGAGCCTAAA GAAATAGATA ATGAAGCGGA AATACAAGCG AAACAAGTAT TAATAGACAG 1680

AGCAAATAGA CAGAAGAAAT CTCGTTAACT CTGAACATCG CATCAATGGA TTTAATATTG 1740

ATAAACGATG AAGTTTAGTA ATTAATCATA TATGTATAAA CACACACATT ATTTTGGATG 1800

GAAACAACCA AATTGATGTG TGTTTTtTTG TTCTAGTGAA TAATTATTAT ACAATGAGTA 1860

TCTATCCTAG AATTATCAAT AGTAATGGTG ATTATGCAAC ATGAAAAAAT GAATGATGAA 1920

AGGAATTTGA CGATGAAGCC TACTAAAGTG ATATTAAAAG ATGCATCTTA TTTACATAGC 1980

AAAACATCGA TAACATTTAT TTTAAAAGAT GTAGTTATCG AAGAAGATAA TAAAATTTAT 2040

TATTTCGACA CTAGTGCAcT TTCGAAGATC AAGAAGTTAA ATTTGAATTT GCACTCTTTG 2100

TTATAGAACC TGATTTACAT TTTACAATTA TTGATTTTAA TCAAGAACTG CTTTGTATTT 2220

ATATTGATTT TGATTCTGGT TTAAGGCATT CAAACATGGC AACAGAATCT GGTATTTCAT 2280

TAAGGATAAA TGTTGCTAAA TCAGATTTTA CTAAATTTAT TAATGAATTA GCCTCTTTAC 2340

ATTAATGATT TAAATCTGAT ATGTAATTAC AATCAAAAAA GACAGCCACA TCCCTCCGTA 2400

GTTTAGGCGT GTGGCTATAT TTGAGTCTGA ATATTTATGC TTGTAATTTT AAAAAGGGAC 2460

ATGCTATATA CGATAAAAAG AGGCGGGGAC ATAAATCAAT GTTCTATGCT CTACGAAGTT 2520

ATATTGGCAG TAGTTGACTG AACGAAAATG CGCTTGTAAC AAGCTTTTTT CAATTCTAGT 2580

CAGGGGCCCC AACAAAGAGA AATTGGATTC CCAATTTCTA CAGACAATGC AAGTTGGGGT 2640

GTGGGCCCCA ACACAGAGAA TTTCGAAAAG AAATTCTACA GGCAAAGCGA GTTGGGGTGG 2700

GACGACGAAA TAAATTTTAT GAAAATATCA TTTCTGTCCC ACTCCCATGG TGCCAATTAG 2760

CATAAGGTAC TTAAATTAAG CATATCTGCT GTCTAGCAGT CGATAAATCA TTAGAACTTC 2820

GTATAGTATA TGACTTTTAA TTTGATTTTC ACCACTAATT TCAAGTGCTT TTATAGTCGA 2880

ACGTAAAGTT TCTACAGAAT CATCTTCTCT CTTAAAAGAA CCATCATAAA ATATATCTTT 2940

GATGCTACTA CTAATTTTTA GCAATGCCAT TTTTTCGTCA CCTGAAAAGT TAACACGAGT 3000

ATTTTTAGGC AAGTAAATGA TATTTGATAA ATGAGTGATA AACAAACGAT TCGTATATGC 3060

ACGTTTAGTT AATTGATTGA GTAATTTCCA ATCACATTCT TTTTTCTTAT GATAGCTTAA 3120

TTCATCACGT TGATAACTTA TTAACGTTTC AACTTGATTA TTTAAATTGA AAATATTTTT 3180

ATATGCTTTT TCGCTTTTAT CAGATTGCAG TCTTGATAAG ATAAGTTCTT GGCAGCGATT 3240

GTAAAATAAT TTATACATCA AGGCATCTGT CTTACTTAAT TTTTCTTCGA CCTGACCATA 3300

ATACTTAGGT GGAAACACCA TGAAGTTAAT TAAACCTGAT GTCACGAGTC CAATAATTGC 3360

TGTCAATGTT CGAGACAAAA AGTTGAATAT GTAGGCATCA TGAATACCTG GAATCATAGC 3420

TAATGATGTT AGTACAGCGA CATTCGTACC AACTTGCAAT TTGAGTTTTG TACAGAATAA 3480

AATCGTGAAC GTTGCACTCA ATGCATATGT AAAAGGTGAT TGATCGCCGA ATAAATATGT 3540

AAATAATACT GCAAAGCCTG CACCAATTAC CGTAGCAGGT AATCTACGAT AACCTTTAAT 3600

AAGTGATGCC TTGGCAGTTG GTTCAATTGT GACTACAGCT GTTAAAATGG CATAGATGGG 3660

TGTTAAATCT AGTGCCATAC AAAAGACAGC TGTTAAAAAA ATGGCAATAC CAGTTTTAAT 3720

TGTTCTGGCA CCAATTAAAT GTTTATACCA TTGATCGTTC ATTTTTTAAC CTCTAATCAT 3780

CGTAAAATCT TAGCGAGCGC TTTATAATAA TAGTATCGTA CATTGGAAAA GTTCATGTAT 3840

GTAAAATATT TGAAATAATC ATACATAAGC ATTACTTTGA TTTTCATATA CATTAATCAA 3900

CAAGCATTTT TCAATTATAG TCCGGGGCCC CAACATAGAG AATTTCAAAA AAGAAATTCT 4020

ACAGGCAATG CAGGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC AGCTTACgAT 4080

AATGTGCAGG TTGGCGGGGC CCCAACATAG AGAAATTGGA TCTACAATTT CTACAGGCAA 4140

TGCAAGTTGG GGTACAACGA TAAAGAAATA TTTTTTCTTT ATCACACTAT GTCTCACTCA 4200

CTTTCCAAAA TACTAAAGTA ACATCTTTAG TATATCAAAG AATTTTTGCT ATAATAAGTT 4260

ATAATTATAT AAAAAAGGAA CGGGATAAAA TGATTGTAAA AACAGAAGAA GAATTACAAG 4320

CGTTAAAAGA AATTGGATAC ATATGCGCTA AAGTGCGCAA TACAATGCAA GCTGCAACCA 4380

AACCAGGTAT CACTACGAAA GAGCTTGATA ATATTGCGAA AGAGTTATTT GAAGAATACG 4440

GTGCTATTTC TGCGCCAATT CATGATGAAA ATTTTCCTGG TCAAACGTGT ATTAGTGTCA 4500

ATGAAGAGGT GGCACATGGG ATTCCAAGTA AGCGTGTCAT TCGTGAAGGA GATTTAGTAA 4560

ATATTGATGT ATCGGCTTTG AAGAATGGCT ATTATGCAGA TACAGGCATT TCATTTGTCG 4620

TTGGAGAATC AGATGATCCA ATGAAACAAA AAGTATGTGA CGTAGCAACG ATGGCATTTG 4680

AGAATGCAAT TGCAAAAGTA AAACCGGGTA CTAAGTTAAG TAACATTGGT AAAGCGGTGC 4740

ATAATACAGC TAGACAAAAT GATTTGAAAG TCATTAAAAA CTTAACAGGT CATGGTGTTG 4800

GTTTATCATT ACATGAAGCA CCAGCACATG TACTTAATTA CTTTGATCCA AAAGACAAAA 4860

CATTATTAAC TGAAGGTATG GTATTAGCTA TTGAACCGTT TATCTCATCA AATGCATCAT 4920

TTGTTACAGA AGGTAAAAAT GAATGGGCTT TTGAAACGAG CGATAAAAGT TTTGTTGCTC 4980

AAATTGAGCA TACGGTTATC GTGACTAAGG ATGGTCCGAT TTTAACGACA AAGATTGAAG 5040

AAGAATAGTT CAACATATAC TAAGACTAAA GTATGAACAT CATTTAGTTC CGGAGCCTAT 5100

TCATATTGGT TTCGGAACTG TTTTATAATA ATTAAGAACA CAATCAATGC GTCATTTCAA 5160

AAATATGTTG TAACAAAGTA GTTTTTAAGC AAACATATCA TCGACATCAA CGAAGATACA 5220

TAGCGCATTT GGTATTTTAA AACTTATTAT AAAAGGTGAT AGTTATGAAC TATGTTGAAC 5280

GTTATATTGA ACAGTTTTTG AGAGCAACAG TAAGAAATAA TATCAAGCAC TACCTTTTAA 5340

TGCTAGATGA AAAAATGAAA AATTTAGATG ATTATATGCG TTATTTAATT ACTAAAAAAG 5400

AACAACTTAG CAAGTTAATT GACAGTCTAA TGCTAACATT AGAAAATAAA TATATTGATA 5460

TTGCTGAAGC ATTTCAAATT CAATGTGCAA GAGAAATCAA TAATCAAGAA ATTGAAAATA 5520

TTAAATCAGA GTTGAATAAA GTTGAAGCAT ATTATGCACA AATTGAAACT CAAATTCAAC 5580

AAACTTCAAC TGAAAAAATA GCAACAGAAA AAACATCGTA TCTAATAAAT TATATGAACG 5640

CTGTGGCATA GAAAGGCGGC GAAACATGAC ACACAAATAT ATATCAACGC AAATGTTGAT 5700

CTTTTTACTC GTTCTATTAT TGGGATGTGT ATTAGTTTAT GTAGGATATC TTTATTTTCA 5820

TAAAATACGT GGCCTTTTGG CGTTTTGGAT AGGCGCGCTA TTAATTGCAT TCACATTATT 5880

GTCTAATAAG TATACAATCA TCATCTTGTT CGTCTTTTTA TTATTACTTA TTGTGCGTTA 5940

TTTAATACAC AAGTTTAAAC CAAAAAAAGT AGTTGCGACG GATGAGGTTA TGACTTCACC 6000

ATCTTTTATT AAACAAAAGT GGTTTGGTGA GCAACGTACA CCAGTTTATG TATATAAGTG 6060

GGAAGATGTA CAAATTCAAC ATGGAATTGG CGACCTACAT ATTGACTTAA CAAAAGCTGC 6120

AAATATTAAG GAAAATAATA CCATTGTTGT TAGACACATT TTAGGTAAAG TGCAGGTTAT 6180

ATTGCCGGTT AATTACAATA TTAATTTACA TGTAGCTGCT TTTTATGGAA GTACTTACGT 6240

GAATGAAAAA TCATATAAAG TTGAAAATAA CAATATTCAT ATTGAAGAAA TGATGAAACC 6300

GGATAACTAT ACAGTTAATA TCTACGTATC AACGTTTATC GGAGACGTAG AGGTGATTyA 6360

TCGATGAAyC ACT 6373

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

ATAGnGAAAG CGTTTTACAC TTAATAACTC CCTCTTAAAT GCATCCAGGT TCTATGTAGT 60

AAATCATGAA nATAACATAT AAATnTAGAG GAGATTTACC TTTGAATACA GAGAACAACA 120

AGAATCAAAA CCAATCTGTT AAAAATTCTG AAAGaCGCGG CATGTTAAAA GGATGCGGCG 180

GTTGCCTTAT TTCTTTTATT TTATTAATAA TCTTATTATC AGCCTGTTCA ATGATGTTTA 240

GTAATAATGA CAATTCCACT AATAATCAAT CATCAAAAAC GCAATTAACT CAAAAAGATG 300

AAAATAAAAA TGAAGATAAG CCTGAGGAAA AATCAGAAAC AGCAACAGAT GAGGATTTAC 360

AATCAACCGA AGAAGTACCT GCAAATGAAA ATACTGAAAA TAATCAACAT GAAATTGATG 420

AAATAACAAC AAAAGATCAA TCAGACGATG ATATTAACAC ACCAAACGTT GCAGAAGATA 480

AATCACAAGA CGACTTGAAA GATGATTTAA AAGAAAAGCA ACAATCAAGT AACCATCATC 540

AATCCACGCA ACCTAAGACC TCACCATCAA CTGAAACAAA CACGCAACAA TCATTTGCTA 600

ATTGTAAGCA ACTTAGACAA GTATATCCGA ATGGTGTCAC TGCCGATCAT CCAGCATATC 660

GACCACATTT AGATAGAGAT AAAGATAAAC GTGCATGTGA ACCTGATAAA TATTAAACAA 720

GGGAGATTTT TTAGGCATGA GCAATCAATT CAAAAGCGAA GAAGAGCGAA GACAATGGGA 840

ACAATTCCAA GCTTTCCAAA ATCAACAAAA CCAACAGAAC CAGCAATACG GACAAAAGAA 900

ATCTAAAAAA GGATGGTTCT GGGGCTGTGG TGGTTGTCTA GTATTATTTA TTTTAATTAT 960

CATCGGTATT TCAGCTTGTA CAGCTGGTAT TACAGGTAAC CTTGGCGGAA ATAGTTCTAA 1020

AGAAACGAAC AAAACCCATA AAATCGGTGa AACTGTTAAA AATGGCGACC TTGAAGTCAC 1080

TGTAAATTCA GTGGAAACTA TGAAATCTGT AGGACCATCT CTTGCACCAA CAAACGCTAA 1140

AGGTATATTT GTCGTTGCTG ATGTGACGAT TAAAAACAAA GGTAAAGAAG CGTTAACAAT 1200

TGATAGTTCA ATGTTTAAGC TAAAATCCGG TGATAAAACA TTTGAAGCAG ATAATACAGG 1260

TTCAATGTCT GCTAATCAAA GTGACAATGG TAGTATAGAA AATTCATTTT TCTTACAGCG 1320

TATAAATCCA GATAGCACTG CTCAAGGTAA AATTGTTTcG ATGTGTCAGA AAACATAGCC 1380

AACGCAAAaG ATAAAAAATT AGAAGTTATT TCTAGTTTAT TTAGCGTCAA GAAGATTACA 1440

TTTGATTTAT CCGATGCTAA AAAAACATCA AAAGCTAAAA AAGACAAGCA AGATACAGAA 1500

GTAGCTGTTG CGAGTTCAAA TAGCGATAAT GTAAGTTATG AAGCTTCGGC TACTACACCT 1560

GcTACAACTT CTAGTGCGGA TACTGATTCT GAAGATAGCG AAAAGTCTAG TAAAGATGAG 1620

GATAAGCAGA ATGCGTCTAA AAgTGATAAA TCTAGTGTAG AAAAAAGTGA ATCTAATGAG 1680

GAAACTGCTC CTGTAGAGCC CATGCCCCAT AGCAAACCTA CCACTAGTGA aGCACCACCT 1740

AGCCAAAATA TTCACAaTGa AGATAGCmTG TACGACGCTT CAACAGAATA AAATtnyCAG 1800

tAGCTCGGCT ACCCTTCTTT TACGGAAAAA TTAATTATAC ATAATCaAAT CaAGGAGATA 1860

AAAAAATGAA ATTCAAAGCT ATCGTTGCAA TCACATTATC aTTGTCACTA TTAACTGCCT 1920

GTGGTGCTAA TCAACATAAA GAAAATAGTA GTAAATCAAA TGACACTAAT AAAAAGACGC 1980

AACAAACTGA CAACACTACA CAGTCAAATA CAGAAAAGCA AATGACACCA CAAGAAGCCG 2040

AAGATATAGT TCGAAACGAT TACAAAGCAA GAGGCGTTAA TGAATATCAA ACATTAAATT 2100

ATAAAACAAA TCTTGAACGA AGCAATGAAC ATGAATATTA TGTTGAACAT CTAGTCCGCG 2160

ATGCAGTTGG CACACCATTA AAACGTTGTG CTATTGTTAA TCGACACAAT GGCACAATTA 2220

TTAATATTTT TGATGATATG TCAGAAAAAG ACAAAGAAGA ATTTGAAGCA TTTAAAAAGA 2280

GAAGCCCTAA ATACAATCCA GGTATGAACA ATCATGATGA AACAGATGGT GAGTCAGAAG 2340

ACATTCAACA TCATGACATT GATAATAACA AAGCAATTCA AAATGACATA CCAGATCAAA 2400

AAGTCGACGA TAAAAATGAT AAAAATGCTG TTAATAAAGA AGAAAAACAT GATAATGGGG 2460

CAAATAATTC TGAAGAAACT AAAGTTAAAT AATGGCATAC TTTGATTAAT CGTAATTTTT 2520

ACTATGCATG GTCTTTTTAA TCAACTTAAA CTCGGCATTA TTTCAATCGA AAACGCAGAG 2640

CATACGCTTT TTACACCTTA TATGTTGGAA ACGCTCTCTT CCCTAGGCGT GAAAGACAGC 2700

ATTGTCGATT TAATTCATAA AGGGACTGAA TTAGAAGACT TTGCGGCATT TAATTTATCA 2760

ATTGAAGACA CAGTTACAGT CTGTTTACAA AGAACTGAAG AACTATTAAA ACAATACAAA 2820

AATGTGGAAT TCAATGACAA AATATTAATC AATTGGCGTA TTATACAAGA GAAATAGACA 2880

TATAAAAGTC GAATGTAACt ACGTGAGTAT TGATTTTATT CTTTGTAAAT TACAAGCATT 2940

TCATATTATA AAGTTTGAAA AGAGGTATAT TGAAATGGAG AAAAATGAAT ATATAGCTAA 3000

ATATAATGAA TATAGTCAAT TATTAGACGC TACATACTCG CAAGCTGTAG CATmCCTTTT 3060

AAGtAAATaT GGCGCTGTAA CCGATGATTA TTATAAAGaA AAATCATACA CGCGATTTTT 3120

AAAtGGAGnA ATCAAAAGTA TTTCAAAAGG AAAATACACT AGAGCTAGCG AaGGATTATA 3180

TTGCCATCAT ATAAGCGAGG ACAAATTCCA AAATCTATCT GATCTAAGAT TCATtTCCAA 3240

ATTTAAGTAC TCATACGACG TTCAAAAGAA AGAAAACTTA GTGTACTGTG ATCTAATCGA 3300

GCATTTAATT TTACATGCAA TTATTACAAA AGAATCCCAT GGCCAATTTG GTGTAGCTGG 3360

ATTATGTCAA ATGATCAAAC CAACAGTCAT TGATTGGTAC ATTGGCGAAT ATAATCCAAA 3420

ACCAGCATGG ATGCAAGCCA CCAAAGCACG TGCCTATTTG CCTGGAATAT TAGTAGAGAA 3480

ATTACTCATT AAAATTGACG ATATGTTAAA AGGAATAGAA ATATAAGATT TCCTTGAGTC 3540

TAGATAAATG ATTAATGTAG ATTTATTTTT TGCTGTTGAG ATTTTGTTAT AGATGTTTAA 3600

ACCTGTAATT AAATATATTT TATAAAATAG ACCACGCATA CCTATCTATA AACGGrCAAT 3660

GTTTATAAAT GAGTTTGCAT GGtCTTGAAT TGTATTAAAT TTCTTTTGGT TTTAATAAAT 3720

CGACTAGATT TTCACAATAT TTATCAAATA TGTATTCCTA AATTATACAG CCTTAATCCA 3780

GCAGCTACTT TCGAAACTTC CAACTTAGTT GATATAAGGT TCAATAGTTT GTTTCGTTCT 3840

TTTTCAGATA AACCAGAACT TAAATTGATA TTATTGACTT CATAAAAATT ATAGACTAAT 3900

GCCTCTATTT GCTTTTTAGG CATAAGTAAG TCGACTGAAA ACTGATTTAC GTCGCTTTCA 3960

TAAATCATTT CATGTAAATT CTTTAGACTA TTATCGTTAC TATCTCTCAT TAAGTCTGTA 4020

TTTTTAAATA AATAACGGCC CAATTCACGA GCTATTGAAA ATCTTGTATT ATTAATCGAG 4080

TGATTATTAT TAATATAGAT TGTTCTTCCA CTTAAATAAC CCGAAGTATT ACCCTCCATT 4140

TTAATATATC TAACATTTAA ATTAAGTTGA AATAATAGCT TGTCTATGTC AATAGCAAAG 4200

TGTTCAGAAG TAATAAAAAG TTGATCCATT TTGTCCTTTA TAAATGCCTG AAATAATCGA 4260

ACTATTTTTG ATTCTAAAAT ATCTTCATAA TGAACTTTCT CAATAACTTT CAATTGATTC 4320

AACATTATTA AAATAAAACC CCTCTACTAC TATATGTAAC GAAGGGACAT GATTTCAAAA 4440

TAAAATACCT TTTTTATAAA TnTATTATAA TATCCCCCAC TATACnAC 4488

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

TATGGCGCCA TATTAGTTGT AACTGGTTTA AGAGGTCcAa GAAaTATCaA ATAAAGTTGT 60

tCCTGGGCTT GGTACTGTTA TCTCaATATT GmwTGCaTTT GGTGGTCTAG CTTTTAATAT 120

TGGTAATATT GCTGGTGCCG GTTTAGGTTT AAATGCAATT TTTGGATTAG ATGTAAAATG 180

GGGCGCAGCT ATTACTGCAA TCTTTGCAAT ATTAATCTTT GTAAGTAAAA GTGGCCAAAA 240

AATTATGGAC GTTGTTTCAA TGATTCTTGG TATTGTGATG ATTTTAGTTG TGGCATATGT 300

GATGTTTGTT TCTAATCCAC CTTATGGTGA TGCTTTTGTG CATACATTTG CGCCAGAACA 360

TCCAATGAAA TTAGTCTTGC CCATCATTAC GTTAGTTGGT GGAAcTGTar GTGGTTATAT 420

TACCTTTGCA GGTGCACATC GTATATTAGA CTCTGGCATT AAAGGTAAGC AATATTTACC 480

ATTTGTAAAT CAATCAGCAA TTGCTGGTAT TTTAACTACA GGTATTATGA GAACGTTACT 540

ATTCCTAGCG GTATTAGGAG TTGTTGTAAC AGGTGTGACA CTAAGTTCTG AAAATCCACC 600

AGCGTCAGTT TTTGAACACG CAATTGGACC AATTGGAAAG AATATTTTTG GTATTGTGTT 660

ATTTGCTGCA GCTATGTCAT CAGTAATTGG CTCAGCATAC ACAAGCGCAA CATTTTTAAA 720

AACACTTCAT AAATCACTTA ACGAAAGAAG TAATTTAATT GTGATTGTGT TTATCGTTAT 780

TTCAACAATG ATTTTCTTAT TTATTGGAAA ACCAATCAGC CTTTTAATTA TAGCAGGCGC 840

GATAAA 846

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2072 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

TCTTTTTAAA AGGTACTAAT ATTTCTTTAG TGAAAATTGA ATCACGGTCG TTTATTGGTG 120

CCTTGAGTAT ATTATTATAG ACGGAATCTG ATCTAATAAT ATTGATTTTA TACATGATAA 180

ACCTCCTTAT GTTGTCAGCA TAAAGGATAA CGTAACGTGA TTTTCAAGCA GTAATTGTAA 240

CTAATTGAmA AAAATTAAGA AAAGTATGTG AGTGTTCCTA AwTAATATGa TTAAAATGAT 300

GGCGAATAAG TGTCTaAAAG CATCTTAAAG GGACATTGTA TAGGGTAAAT CACTTCATAA 360

ATAAGGGaAA ATCCTTATGT TCACTTTTTC ACAATCATnA TAAAATATAT ATGTAGTCAA 420

TACTTTGTCT ATATTGAATG TTTTCATATA AATGAAAGCA TTTTTAAATA ACATTGACCT 480

CTAATATATA GGCAGAGTAT TGATATCTAT TAAAAAATAA ATGATTTTGA TGAAGGTGAA 540

ACGTATGTAC AAAACAAAAG GTGGCTTTCA ACTTACATTA CAAACATTAA GTTTAGTGGT 600

TGGGTTTATG GCTTGGAGTA TAATTGCGCC ATTAATGCCC TTTATTAAAC AAGATGTCAA 660

TGTTACTGAA GGTCAAATAT CAATCATTTT AGCGATACCA GTTATTTTGG GATCGGTGCT 720

CCGTGTGCCA TTTGGTTATT TAACAAACAT TGTTGGCGCT AAATGGGTAT TCTTTACTAG 780

TTTTATCGTA TTGTTATTCC CGATATTTTT CTTAAGCCAA GCACAAACAC CGGGTATGTT 840

AATGGCTTCA GGATTTTTCC TTGGTGTAGG TGGTGCAATT TTCTCAGTTG GTGTTACATC 900

AGTTCCTAAA TATTTCCCTA AAGAAAAAGT AGGTCTAGCA AATGGTATTT ATGGTATGGG 960

AAATATCGGT ACAGCAGTTT CTTCATTTTT AGCACCACCG ATAGCGGGTA TTATTGGTTG 1020

GCAAACAACA GTTAGAAGTT ACTTAATTAT TATCGCTTTA TTTGCATTAA TTATGTTCAT 1080

TTTTGGTGAC ACACAAGAAC GTAAAATTAA AGTACCATTA ATGGCtCAAA TGAAAmCATT 1140

ATCTAAAAAC TACAAATTAT ATTACTTAAG TTATTGGTAT TTTATTACTT TTGGTGCTTT 1200

TGTAGCATTT GGTATTTTCT TACCTAACTA CTTAGTAAAT CATTTTGGAA TTGACAAAGT 1260

AGATGCTGGT ATTCGATCAG GTGTATTCAT TGCGCTGGCA ACATTCTTAA GACCAATAGG 1320

TGGCATTTTA GGTGATAAAT TTAATGCAGT TAAAGTATTG ATGATTGATT TTGTTGTTAT 1380

GATTATCGGT GCCATTATTT TAGGTATTTC AGACCATATC GCATTATTCA CTGTAGGCTG 1440

TTTAACAATA AGTATTTGTG CAGGTATTGG TAACGGCTTA ATCTTCAAAT TAGTACCATC 1500

ATACTTCTTA AATGAAGCGG GATCCGCAAA TGGTATCGTA TCAATGATGG GTGGTTTAGG 1560

AGGATTCTTC CCACCACTAG TAATCACGTA CGTAGCTAAT TTAACAGGAT CAAGTCATTT 1620

AGCATTTATT TTCTTAGCGG TATTnGGAnG TATTGCATTA TTTACCATGC GTCATTTATA 1680

CCAAAAAGAA TATGGCTCAT TGAAaAACGG TTGATATGTA ATACATGCCA TTcATTTAGT 1740

TAAATACAAA GCCTTaATAT CATGCGCAAT ATTCGTAGCA TGACATTAAG GCTTTAGTAG 1800

CTTGGTTTGA TTTTAGGCAA GGTAATGGTT AATAACCCAT TTTCAAAACT AGCAGTAATA 1920

TGTTGCTTAT CAACAGCTTC AAAATCAAAT TGACGCATTA ATGATTCGAA GTTACGCTCA 1980

TCTAAAATGA GTTGTTCAGA TTTGTATTTT GCGCTTCTAG TAGCTTGAAT AGTGAGCGwA 2040

TTAttATTGA AATCgATACT AATAtCTccC TG 2072

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

CGTCTTCTCT TGGTTATTCT CTGTGTTTTG TCTTTGTTCA AATTCGATTT TTTGTTGTTC 60

GAATGAATGT AATACTTTAT TTTTTTTTGG CACATAATCC AAGTnATTTT TAGGAATTAA 120

TATACGGTCT TTAAATGCTT CTTGTATTTT GCTCACAATC AATTGGTATA GTTGCTCTTC 180

TTTTGATAAA CGCACTTCTA GTTTTGTTGG ATGAACATTT ACGTCTACTA AGATTGGATC 240

CATTTCAATA TTAATATAAC AAATCGGGAA CCTACCTATT GTTAAGAGTG TATGATAGCC 300

TTCTAAAATC GCTTTATTTA GCATAAAGTT TTTAATGTAT CGTCCATTAA TAAAAATAGA 360

AATATAGTGC TTATTACTTC TAGAATGTTC AGGCTTTGCA ACAAAACCTT CAATGTGATA 420

ATCACTTGTA TCTCCAGATA TATGTACTAA ATCTCGTGCA ACTTTCATCC CATAAATCTC 480

TGCCATCACT TCATTAGTTC GTCCTGAACC ATTTGTACTT AACATTGTTT TGCCATCTGA 540

AATGAGTGCT ATTCGAATGT CCGGATGGCT CATTGCCATT CTGTTGACAA TATCTGTTAT 600

TTTACCTAGT TCAGTGTATA AACTTTTAAT ATATTTTAAA CGTGCTGGTG TATTATAAAA 660

TAATGATTCT ACAAGTATAT CTGTTCCTTT TTTCGCTTTT GCAGGCTTAT GATTTAATAT 720

TTCACCATTT TCTACATATA TTTCATTTCC ATTAGCATTA TCCGTGCAAG TCTTCAATGT 780

TACTTTAGCA ACTGATGAAA TACTGGCTAG TGCTTCACCA CGGAATCCTA ATGTCCTAAT 840

ATGAAATAAA TCTTCATCTT GATCTAATTT ACTAGTCGCA TGTCTATGAA ATACTAATCC 900

TAAGTCTTCC GCTTCAATTC CGCTTCCATT ATCGACTACG CGAATAGATT GGACGCCAGA 960

tTCCTCTACT TCAATGCTTA TTTCTGTAGC GCCTGCATCT ATAGCATTTT CCAACAGTTC 1020

TTTCACAACA GAACTCGGTC TTTCAACTAC TTCACCTGCT GCGATTTTAT TTGCTAATGA 1080

GGTTTGGAGT TCTTTAATTT TCCCCATTTT GCAACACCTC TATTTTAATT GATTTTGTAA 1140

TTGTAGTTCA ATCTCGCTTT TTTGATCATT TTCAAACAAA TcAAATGATG CyTGTTCAAA 1260

GTCTTTTTGA GATAAAGTAT CaGTTGTTTC TTCaACACTT aAGTTTAAAT TTTCTTGATT 1320

AATTTCCAGG TTCATTTTCG ACCATTTTTA AATTTGATAT CGATGATtTT TCACCAGCAG 1380

ACGCTTCAAA CTCGCTTAGA ATCACTTGTG CTCTGCTAAT AACTTTTTCA GGTAAATCAG 1440

CTAATTTCGC AACTTGAATA CCATAAtATC GTCAACTGCA CCATCTTTGA CTTTATGCAA 1500

GAATATAAGT TCACCTTTAT ATTCATTAGC AGCGACGTGA ACATTTTTTA GACTTGGTAA 1560

TGCTTGATCT AATGTTGTCA ATTCATGATA ATGTGTTGAA AATAACGTTT TAGCATGTGA 1620

TGTTTCAGCT ACATACTCTA TCATTGCCTG CGCTAAAGCT AAACCGTCAT ACGTTGAAGT 1680

ACCACGTCCA ATTTCATCGA AAATAATCAA ACTATCCTCT GTTGCATAAG TTAATGCCTT 1740

TTGTGCTTCT AGCATTTCTA CCATAAACGT ACTCTTACCT GAAACCAAAT CATCTGCCGC 1800

ACCTATTCTA GTGAATATTT GATCAAATAT AGGTAACACT GCCTCTTTAC AAGGGACATA 1860

AGCTCCCATT TGGGCCATTA TACTAATTAT GGCAACTTGT CTCATATATG TCGATTTACC 1920

AGACATATTC GGACCTGTAA TTAAATATAT AAATGTTTCA TTATCTAATC GACAATTATT 1980

AGGCACATAG TCATTATAAT CCATTACTCT TTCCACTACT GGGTGCCTAG ATTCCACTAA 2040

TTCTAATGTT TTATTTTCAC TAAATGAAGG CCTAGTGTAA TTATATTTTT GAGCAATTTC 2100

TGCAAAGCTC TGTAAACAAT CTAGCTCTGA AATAATTTTA GCTTGTTGTT GTAAACGTTC 2160

AGTATATTTT TTAACTTCTT CACGTAGCTG AACAAATAAT TGATATTCTA ATTCGATGGC 2220

TTTGTCTTCC GCACCTAAAA TGATATCTTC TTTTTCTTTA AGTTCATCAG TTATAAAACG 2280

TTCAGCATTC GATAACGTTT GCTTCCTCAT ATAACCAAAT TCACTTGGTT CAAAATTTTG 2340

CAAGTTGGCA CGTGTTATTT CTATAAAATA ACCAAACACT TTATTAAAGC TTATTTTCAA 2400

TGATTTTATT CCTGTACGTT GTCTTTCTTT GGCTTGTAAT TCTGCTAACC ATGTTTTTCC 2460

GTTTTTTGAA GCTTCAAGAT ATTCATCTAA TTGCGTATTA AAACCAACTT TGAATAGTCC 2520

GCCATCTTTA ACTGAAATTG GTGGTTCTTC TACTAAACTC TGTTCTAATA TATCAAGTAA 2580

ATCATCaAGG GGTTCTAGTT GATTAACTTG TACAAGAGTA TTCTGATTCA TAGAATTTAG 2640

TAATGCTTTA ATATTCGGTA TTTCAGAAAT GGAATGTTTA AGTTGAATTA AATCTCTCGC 2700

ATTAACATTT CCGTAACTAA CACGCCCAAC AAGACGTTCA ATATCATACA CTTGATTAAG 2760

ATATGTTCTT AAGGTGTCTC TTTCTATGAA ATGAGCACTA AATTCATCAA CGATATCTAA 2820

TCGTGCTTCA ATTTGTTCTT TACTTATTAG TGGTCTATCT ATCCATTGTT TTAAGCGGCG 2880

TGCTCCCATT GGTGTTTTCG TTTCGTCCAT TAGCCAAAGT AGCGTTCCTT TTTTTGATTT 2940

ATCTATAGCT GCATATTGAA CAACATCCTC GATATGCGAT AAATCACGTT TTTGTGTATG 3060

ATGAATATAA TCTAGCAATA ATTGTGTCGC TTGATACaTT AATTTATGTT CAGTTTGATT 3120

CACACTATAG ATTtCTGATG ATAACGTTTC CCTGACTGT 3159

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

TAAGCGAGAA GCAATTGGTG TTATGTATGC TAGTGATAAA CCAACAGGTG AAAGTACAAG 60

GTCATTTGCT GTTTATTTCT CTCCTGAAAT TAAGAAATTT ATTGCAGATA ATTTAGATAA 120

ATAAATCATC CATCCATACA TTGATAAATG ATTTTyAGAA ATTAACAACA AAATCAACAA 180

TTTTAAACAT CTCTGTGATT CTATTTATTC GAAATGATTT AAAAAATAAA ACTTCAAAAA 240

CCTAACCTTA TATTTATACG AATACTTAGA GGAGCACAAA AATGAATAAA AATATAATCA 300

TCAAAAGTAT TGCAGCATTG ACGATTTTAA CATCAGTGAC TGGCGTCGGC ACAACAGTGG 360

TTGAGGGTAT TCAACAAACG GCTAAAGCTG AACATAATGT GAAACTAATC AAAAATACTA 420

ATGTAGCACC ATACAATGGT GTCGTTTCGA TAGGATCTGG AACAGGTTTC ATTGTCGGTA 480

AAAATACAAT TGTTACCAAC AAGCATGTCG TTGCAGGTAT GGAAATTGGT GCACATATTA 540

TAGCGCATCC CAATGGTGAA TATAATAATG GCGGATTTTA TAAAGTTAAA AAAATTGTCC 600

GTTATTCAGG TCAAGAAGAT ATTGCCATTC TACATGTGGA AGATAAAGCT GTTCATCCAA 660

AAAACAGGAA TTTTAAAGAT TACACAGGCA TTTTAAAAAT AGCATCAGAA GCTAAAGAAA 720

ATGAACGCAT TTCAATTGTT GGCTATCCAG AACCATATAT AAATAAATTT CAAATGTATG 780

AGTCAACAGG AAAAGTGCTG TCAGTTAAAG GCAACATGAT TATTACTGAT GCTTTCGTAG 840

AACCAGGCAA CTCAGGTTCA GCTGTATTTA ACAGTAAATA CGAaGTtGTA GGTGTTCACT 900

TTGGTGGAAA CGGCCCTGGA AATAAAAGTA CAAAAGGATA TGGTGTTTAT TTCTCTCCTG 960

AAATTAAGAA ATTCATTGCA GATAACACAG ATAAATAAAT CCTTACATAG ATAAATGATT 1020

TTAAAAATTA ACAACAAACT CAACaATTCA AATCATCTCT GTGATTCCAT TTATTCGAAA 1080

TGATTAAAAA AAATAAAACT TCAAAAAGCT AACATTATAA TTATACAAAT ACTTAGAGGA 1140

GCAGAAAAAT GaATAAAAAT ATAATCATCA AAAGTATTGC AGCATTGGAC GATTTTTAAC 1200

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6444 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

TGATAAGTCA TTTAAATTGT CACCTATTGA CATGACTTCT TTCATTTCAA TCCCTAATCT 60

TTCGGCAATT GTTTCTAGCG CAATACCTTT TTGTGCATCT GAATGCGTTA TTTCTATATT 120

TCCTCTCGAA GATGATGATA TAGCTAAATT CGGAGAkTCA GCTAAAATTT TACTAGCTTT 180

GTCAATTTTT TCTAAATTTC CATCAAATGC TAATATTTTC ATAATTAATT CACCAGGTAT 240

GTTTTCAATA GCATCATAAT TATCAACAAC TyTCAACGTA CCATTATCTA TGCGTCTTTG 300

AATACCATTT TTAATACGCT CAACGTTTGC ATGTTGACCT GCACGCTCAG CAATATCTAT 360

GTAAATGTCT AAATCTCTTT GTGGATCTTC AGTATAAATC GCACGACTCG TGTATACTTG 420

ATAATAAATA CCTGCATCTT TTAAAACATT TGTAATTTTG TGTACTAACG ATTTATTAAG 480

GTGTGAAGTG CTCATTACAT TGAAAGTTTC ATCACGTACT TCAGCACCAT TCAAACAAAT 540

ATATGGTACT GTTAAATCTG TGTCAGCAAC TGGTGCTTGk GCTTCATAAA ATGCTCGACC 600

TGTCGCGATA ACAACCGTTA TCCCTTGTTC TTGAGCGTAT TTAATCGCAT CAATATTAGG 660

TTGAGAAATT TCATGTGCTG CATTAAGTAG CGTGCCATCC ATATCAGTGG CTATTAGTTT 720

TATCATTATG TnACCTCGTT TCGTAAATnT AAAATCTTGT TCTTAAATAA GrATATATAC 780

TCAGCGCACA TACTTTtCTA TTAmCATTTA TATkGTCATT aATTTATCAT ATAATGTAAT 840

TCTaACAAAT nTTAAtTAGT ATGTACTATC GTCTAATTGG TGGATTTCTT ATTGGCTCTT 900

AAgTTTTTAA AAAATGTTGT TAATAATGTG CTACATGCTT CTTTAAGTAC ACCTTTATCA 960

ACAATTGCAC GATGATTAAA ATTAGATTGT TGCAATAAAT TCATTAAACT GCcACTACAA 1020

CCACCTTTAG GATCATCTGC GCCATAGACG ACTCTTGGAA TGCGACTCAT TACAATTGTT 1080

CCTGCGCACA TGACACATGG TTCTAAGGTT ACATATAATG TGCAACCTTC TAAACGCCAA 1140

CTACCTAACA CTTTGGCTGC ACGTTCAATT GCAATATGTT CAGCATGCGC CGTTGGTTGT 1200

TGTAGTGTTT CTCTTaAATT ATGTGCTCTA GCGATAACTT CATCATCTTT AGTGATGATA 1260

GCACCTATAG GTACTTCGCC TAGTTGAGCT GCTTTTTTAG CTTCTTCAAT CGCTAATGTC 1320

ATAAAATATA TATCATTTGT CATTTATGTC CAGATACCTC ACTTATGGTA CAATACTCAA 1380

CTATTGGCGT AGGTAAATCT TCACTTGCAC ACAAATTAAG TCAAACTTTA GATTTTTATG 1500

AAGAAAAAGA AATCATCACA GAAAATCCAT TTTTATCAGA CTTTTATGAA GATATCTCTA 1560

AATGGAGTTT TCAAACTGAA ATGTTCTTTT TATGCAATAG ATATAAGCAA TTTCAAGATG 1620

TAACACAACT AAATCAAGGT GTAGTTAGTG ATTATCATAT ACATAAAAAT AAGATATTTG 1680

CTAAAAATAC TTTGAGTTCT GTTGAATTTC AGAAATTCAG TAAAATTTAT GATATTTTAA 1740

CTGAAGATAT GATTATGCCG AATATGATTA TCTTTTTAGA TGCAGACCTT GATGTGTTAA 1800

AATCTAGAAT TGCTAAACGT AACCGTAGTT TTGAGCATCA AATAGAaGtG AtAcTGTaAg 1860

TTAAAAAAAG ATTATCGTGA GTATTATGAG TCCTTACAAA GTAATGGTTC AAATGTAGTT 1920

TTAATCGATA CnACTTCTAT TGATTTTCTT AAAAATGAAC AAGATTACGA AGATATATTA 1980

CATATTATAT TACCTATGAT AGGAGATATT ACCAATGAAT AATTACGGTA TTCCACAAAA 2040

TGCCATTATA ACCATTGCAG GTACAGTTGG TGTTGGAAAA TCAACACTAA sGCAAGCACT 2100

TGCAGATAAA TTAAACTTTA AAACGTCTTT TGAAAATGTC GAACATAATC CATATTTAGA 2160

TAAATTTTAC AGCGATTTTG AACGATGGAG TTTCCATTTG CAAATTTACT TCTTAGCTGA 2220

ACGTTTTAAA GAACAAAAGC GTATGTTTGA ATATGGTGGT GGCTTTGTCC AAGATCGATC 2280

AATTTATGAA GATGTTGATA TTTTTGCAAA AATGCATGAA GAAGAAGGCA CAATGAGTAA 2340

AGAAGATTTC AAAACATATT CAGACTTATT TAATGCCATG GTCATGACAC CTTATTTTCC 2400

TAAACCTGAT GTAATGATTT ATTTAgAATG TAACTATGAT GAGGTCATTG ATCGTATTAT 2460

TGAACGTGGT CGCGAAATGG AAATTAATAC AGACCCTGAA TACTGGAAAA AGCTATTTAA 2520

ACGCTATGAC GATTGGATTA ATAGCTTTAA TGCATGTCCA GTTGTACGTA TCAATATTAA 2580

TGAATATGAT ATCCATAAGG ACCCCGAATC TTTAAATCCT ATGATAAACA AAATTGCTCG 2640

AATTATTCAA ACATATCGAC AAGTAGATAC ACGATAAAAG ACTAAAGACA TAGCGTATAT 2700

GTTTATATTC AATGTATATT CCATAGATAT TATCGATTAT TTTATCAATT CTATCGAATA 2760

CATTAATTCA CATATACACT ATGTCTTTCT TTTTAATTTA AAGCTTCTAA AATATCTGCC 2820

GCACTATTTA AAATAATATC AGCTTCATGT AATTCTTCTT TTGTTGCAAT ACCTGTTAAT 2880

ACACCTATTG CCATACCTAA ATTTGCATTA CTTGCTGTCT TCATATCATT AGCAGTGTCT 2940

CCTACTATAG CTACTTTCTG AGGATCTACA TTATATTGCT CAAATAAAGG CGATAATACT 3000

TTAGGATTTG GCTTCTCATA GGCATCCGCT TCGGTAGAAA TGATCAAATC GAACAACGAG 3060

GTAGCATTGG TATGTGCTAA AAATTGTTCT ACACCTTTTT TAGTATCACT CGTAACAATA 3120

CCAAGTTGAT AGCCTTTTGC TTTCAAATCG ATAAGTGCTT CTTTAACACC TTCTACCCAA 3180

GTATCTTGTC CCGTCACATC ATTAAATGCC TGGATAATTT GTTGTAAAGA TCCTGAACCC 3300

ATCACTGATT TTGGATCAAT AGATTCTTTA ATGACACCGA GTTGTCTTAA AGCAGCTTCT 3360

TTATTATGTA CTGGGAAAGT CTCAAGCAAT GATTGTACAA ATCGTACCCC TATTTTTTCC 3420

CAACTTCTAT CAAATTCAAT TAACGTACCA TCTTTATCAA ATAATATCCA TTCCATTGaT 3480

ATCAATACTC CTATTTATTT ATTTCGTATT ATGCTGATTC TATGATATTC GTTATCCCCT 3540

GAAAATGAAC TCGTAGTATT GTTCTATTTA AATATTGaAT TAAATATAAT AATAAGTGAA 3600

ATCCCCTTCA ATACTTAACA ATAAACATTG TAAACTTAAT TTATTACCAT GCTTCGCTTC 3660

ATTGAAAGGG ATTTTAGTCA TGATTAACTT TTGCATATTG TTTTCATGAT TATATTCAAT 3720

TTTTATTAAT ATTTTGGTAC AACGACTCTC CAACCATTTT TATCTTCTAA AGTACCATTT 3780

TGAATACCAG TATAGACGTC GTATAATTTT TGAGTAATTT CACCAGTCTC ATTATTATTA 3840

ATAACGATTT CACGATCTTC GTATCTCAAT GTACCCACAG GTGAAATAAC TGCTGCAGTA 3900

CCACTACCAA ATACTTCTGT TAACTCACCT TTATCATATG ATTCGAATAA TTCATCGATT 3960

GAAACGCGGC GCTCTTCGAC TTCATATCCT AAGTTTTTAG CTAATTCGAT AATAGATTTA 4020

CGTGTAATAC CAGGTAAAAT ACTGCCATTC AACTCTGGTG TAATTACTTT GCCATTTTCA 4080

ACGAAGAAAA TGTTCATGCT ACCAACTTCT TCGATATATT TCTGTTCAAC ACCATCAAGC 4140

CATAATACTT GGTCATAACC TAATTTATTT GCATTAGTTT GTGCTAATAA ACTTGcCGCA 4200

TAGTTACCTG CAACTTTTGC AAAGCCTACA CCGCCACGaA CAGCACGCAC ATATTCATCT 4260

TCTACATAGA TTTTAGTTGG TTTTAAAGTT TCACCACCAT AATATGCACC TGAAGGAGAT 4320

AAAATAATTA ATAATTTATA CTGATGTGAT GCACCAACGC CAAGTGCCCC TTCTGTTGCA 4380

AAAACAAATG GACGAATATA TAATGATTGA CCTTCCCCTT CAGGAATCCA ATCTCTTTCA 4440

ATATCAACTA ATTGTTTTAG CCCCTCTAAC AATTCTGCTT CGTCTACTTG AGGCATTTCT 4500

AATCGTGCTA ACGAGTTATT AAGACGCTTA AAATTTTCTT CAGGACGGAA AAGTGCAACT 4560

TCCCCATCTC TTTTATATGC TTTTAATCCT TCGAATACCG ATTGACCATA ATGAACACCT 4620

TGTGCAGCAG GTGAAATTTC AATAGGACCA TAAGGTACTA TCTTCAAATC ATGCCATCCT 4680

TTATCTGCAT CATAATCATA ACTCAACATA TAATCAGTAA AATATTTACC AAAACCTAGT 4740

TGAGATGTAT TTGGTTTTTG TTTTAATGTT TCTCGTCGTT CAACTTTAAC TGCTTGTGAC 4800

ATGGTGATTG CCTCCTAATA ATATTGTATA AGAATTTGTT TAACTTAAAT TATAACAATC 4860

CaTATTTTGC TGTTCAACAA ATTTTCTAAA AATTCAAAAT TAATTAACAG ATTTCTAGAA 4920

AGACTATATC TTTTAGTATA AACGTATTAA TTTCACAGAG ACAAGTAATC TGTGTTTTAC 4980

TAAGTATAAT GAATAATATT AGAATTCATG CACTAGTTTA TTAAAATAAA GAGTAATTTA 5100

AAATATCATT CCGTGTATTA AAGTGAATGG AAATGATTAG TTATTATTTT TAACAGTATC 5160

TTTTTGTTCA ATAGCTTCTA ACATTAATTT AGTCATGCTC GCTAAATCAT ATTTAGGATC 5220

AAATCCCCAT TCGCCACGTG AACAGCTTGT ATCAATAGAA TCCGGCCAAC TATTAGCGAT 5280

ACCTTGTCTA ATAGGATCAA CATCGTAATC TAATGTAAAA TTGGGATAGT ATTCTTGAAT 5340

TGCTTCTTTT ACCATCTCTG GATCAAAACT CATTGCGCTC AAATTATAAC CATTTCTAGT 5400

TTCTAATTTA GCGTCGTCTG CTTCCATAAG TTTAATAATT GCTTCAATTG CATCATCCAT 5460

ATACATCATA TCCATATACG TGCCTTTATC TATGAAGCTT GTATAATGAC CCTCTCTTAC 5520

TGCTTTGAAG TATATTTCAA CAGCATAGTC TGTAGTACCG CCACCTGGCT CTTTAACATG 5580

CGAGATTAAA CCTGGGAATC TAACACTTCT TGTATCTACA CCAAAACGTT TGAAATAGTA 5640

TTGACACAAT AATTCTCCAG CTACTTTATT TACACCATAC ATTGTCGTAG GTTGCTGAAT 5700

CGTTACTTGT GGCGTATTAA CTTTAGGAGT TGAGTCTCCA AATGCACCAA TTGAACTTGG 5760

TGTGAAAAAG TGCAAATTAT AAGTTCTTGC AGCTTCTAAT GCATTCATTA ATCCACCCAT 5820

ATTTAAATCC CAAGCTAGAA TTGGATTTTT CTCAGCAGTT GCTGATAATA ATGCTGCCAT 5880

ATGCATTAGA CTATCCGCTT CAAAGTCCCT AACTAACTCA AACATACGGT CACGATCTGT 5940

TACGTCTAAG ATTTCAAATG GTCCATTTTG TACAGGTGAG TCTGCTTCAG GTTCCCTAAT 6000

ATCTGTAGCA AGAACATTAT CTGTCCCATA AATTTCTCTG CACTTAACAA CTAATTCTGT 6060

ACCAATTTGT CCTAATGCAC CAGTAATCAT AATTTTTTTC ATAGAAATAT CTCCTTTGtC 6120

TCTTCTATAT AGCTATAGTC CATCACAAGC GGaCATAATA TTCATTTTCA TAATAATTAT 6180

AATATAAAAG CGCTTTCTTG TATATATGAC ATGTACATGT TGCTGATATk TCTGTAAATG 6240

GAAATTCTAG TTGTATTAAT TGATTTTAGT AATTTATAGC GTTTATTATT GCTAATTACT 6300

GtCAAATTAA ATTTTTTATC CCTCAACTCT TAAACTCTGG ATATCTTTCA TTATATTAGC 6360

TTTTTTATAA CCATGGATAT CATGTAAAGC CTTATAAGCn TTAAATAATG TTTCATACCT 6420

TTGTACTTnT TCCGCTTCTG GATT 6444

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4721 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GCCCATGAGA CAATTTTACT TGCTTTTCCC ATTGGTTATC ACGTTCTTAT TACATAGATT 60

TAAACCGAGA AATATTATTC AAACGCTATT TATTGTATCG TTGATTTCTT TAGGACTTAT 120

GATAGTGATT CATTTCATCA CTGGAGATAA TTCACGTGTG TATTTTGGGA CAGATACACG 180

ACTGCAAACT TTATTGCTTG GTTGTATATT AGCATTTATT TGGCCTCCGT TTGCTTTGAA 240

AAAAGATATT TCTAAAAAGA TTGTCGTATC ATTAGATATT ATAGGGATAT CTGGTTTTGC 300

GGTTCTAATG ACTTTGTTCT TTATAGTTGG AGACCAAGAT CAATGGATCT ATAATGGAGG 360

ATTTTACATT ATATCATTTG CAACTTTATT CATTATTGCA ATTGCGGTAC ATCCTTCTAG 420

TTTATTTGCT AAATTTTTAA GTATGAAACC TTTACTAATT ATAGGTAAAC GATCATATAG 480

CTTATACTTA TGGCATTATC CTATCATTGT TTTTGTGAAC AGTTATTACG TACAAGGACA 540

AATACCGGTA TACGTTTATA TTATAGAAAT TTTGTTAACA GCGTTAATGG CTGAAATTTC 600

GTATCGCTTT ATTGAAACAC CTATACGTAA AAAAGGATTT AAAGCTTTTG CATTTTTACC 660

TAAAAAGAAG GGGCAATTTG CTAGAACAGT GTTAGTTATC CTATTATTGG TTCCGTCTAT 720

CGTTGTGCTC AGTGGACAGT TTGATGCACT TGGCAAACAA CATGAAGCCG AGAAGAAAGA 780

GAAGAAGACG GAATTTAAAA CAACGAAGAA AAAAGTCGTT AAAAAAGATA AGCAAGAGGA 840

TAAGCAGACA GCGAATAGCA AAGAGGATAT TAAAAAGTCA TCACCACTAT TAATTGGTGA 900

CTCGGTCATG GTGGATATTG GTAATGTCTT TACTAAGAAA ATACCAAATG CACAAATTGA 960

TGGTAAAGTT GGACGGCAAC TCGTTGATGC TACACCAATT GTGAAATCGC AATATAAAGA 1020

CTATGCTAAA AAAGGTCAAA AAGTTGTAGT AGAGCTTGGT ACAAATGGGG CATTTACGAA 1080

AGATCAATTA AATGAACTAT TGGATAGTTT TGGAAAAGCA GACATATATT TAGTTTCTAT 1140

TAGAGTACCT AGAGATTATG AAGGTAGAAT AAATAAATTA ATTTATGAGG CAGCTGAAAA 1200

GCGCTcTAAT GTACATCTAG TCGATTGGTA TAAAGCTTCT GCAGGTCATC CGGAATACTT 1260

TGCATATGAC GGTATTCACT TAGAATATGC AGGTAGTAAA GCGCTGACTG ATTTGATTGT 1320

AAAAACGATG GAAACACATG CTACAAATAA GAAATAATTT GATGCACTAA ACTTTTGAAA 1380

TATTACATTA CTTCTGATAT TTATTATCAA AAATGATGTA TTTCATTAAA AGTTTAGTGC 1440

TTTTTTATTT TCAAATCCCA TAGTAACGGT GCAGAAAAAG TGTTGTAAAC ATTCTAATTG 1500

GTATATTACA TTCAATGAAG CTTTATTAGG AACAGATTAC ATTATGATAA CAAAGCCCGC 1560

AAGACACCTA ATCTCTGTTA TAGTTTGTTT TGTCGCAAAA CTATAAAAGT TATAATTGTT 1620

TGCATACTAA AAAAATAAAA AATATAAAAT TTAAAATAAT TGAGTCGCTA ATGACTATAT 1680

GTATAGAGTG TTTTGATTAT TGGGAGGATA TTTAATTATG AAAAAAATCG TTACAGCTAC 1740

ACAAAATAAC AATGGATATA ATTCTAATGA CGCTCAATCA TACAGCTATA CGTATACAAT 1860

TGATGCACAA GGTAATTATC ATTACACTTG GACAGGAAAT TGGAATCCAA GTCAATTAAC 1920

GCAAAACAAC ACATACTACT ACAACAACTA CAATACTTAT AGTTATAACA ATGCATCTTA 1980

CAATAACTAC TATAATCATT CATATCAATA CAATAACTAT ACAAACAATA GTCAAACAGC 2040

AACAAATAAC TATTATACTG GTGGTTCAGG TGCAAGTTAT AGCACAACAA GTAATAATGT 2100

TCATGTGACT ACAACTGCAG CGCCATCTTC AAATGGTCGT TCAATTTCTA ATGGTTATGC 2160

ATCAGGAAGT AACTTATATA CTTCAGGACA ATGTACTTAT TATGTATTTG ATCGTGTTGG 2220

TGGGAAAATT GGTTCAACAT GGGGTAACGC AAGTAATTGG GctAACGCAG CTGCATCATC 2280

TGGCTATACA GTGAACAATA CACCAAAAGT TGGTGCTATC ATGCAAACAA CACAAGGCTA 2340

TTACGGTCAT GTTGCTTACG TTGAAGGCGT TAACAGCAAC GGTTCTGTTC GTGTTTCAGA 2400

AATGAACTAT GGACATGGTG CTGGTGTGGT TACGTCTCGT ACAATTTCAG CAAACCAAGC 2460

AGGTTCATAT AATTTCATTC ATTAATCAAA TGTAAATCAA ATGACGTCAA TATTCTCTAA 2520

CATGAGAGTA TTGGCGTTTT TGTTTTATAT AAATATAAAT GAGAGCGGTT TATTCACTGA 2580

TCTTTAGGGA ACTAAGTAAT AAAGTGATAA TTTATACTAT GTCAGTATGA TTGAGAGTGA 2640

TTCAATTTAG ATGAAAACCA TGAAAAAATA TATTAAAACA GCATTTTTTT GTAGTATGTA 2700

TTGGTTAATT GTTCAACTAA ATATAGCAAA TTTAGGTACA AGAATTCCTG ATAAGTATTT 2760

TCGTCAGAAG TACATAATAT TTAAATCATT TAACTTTGAG AAGCATGGAA AATTTTGGAA 2820

CAAATGGTTT TACGTAAGAA AATGGAAACA TAAGATTTTA GATGGTCATC AGCTTAATCA 2880

AAATATATAT GATCAGCGTC ATTTAATGAC AATCAATACT GATGAAATTG AAAAAATGAT 2940

TATAGAGACA AAGAGGGCAG AGTTGATTCA TTGGATATCG ATACTTCCAG TCATCATATT 3000

CAATAAAGGC CCTCGTTTAG TAAAGTATAT AAATATTTTC TATGCAATGA TAGCTAATGT 3060

TCCAATCATT ATTGTGCAAC GCTATAATCG ACCGAGATTA ACGCAGTTAC TACGCATATT 3120

AAAACGAAGA GGTGAACGTC ATGACTAAAC ATATCATCGT TATTGGTGGT GGCTTAGGTG 3180

GGATTTCTGC AGCAATTCGA ATGGCACAAA GTGGCTATTC GGTCTCATTA TATGAACAAA 3240

ATAATCATAT AGGAGGCAAA GTGAATCGTC ATGAATCAGA TGGCTTTGGC TTTGATTTAG 3300

GTCCATCTAT TTTAACGATG CCTTATATTT TTGAAAAATT ATTCGAATAT AGCAAGAAGC 3360

AAATGTCAGA CTACGTTACA ATCAAGCGAT TGCCACATCA ATGGCGTAgC TTTTTTCCAG 3420

ATGGAACGAC TATCGATTTG TATGAAGGTA TTAAAGAAAC AGGTCAGCAT AATGCGATAT 3480

TGTCGAAACA GGATATAGAG GAACTGCAAA ATTATTTGAA TTATACAAGA CGAATCGATC 3540

TTCATGGGCC ATTAAATGCT CTTATTAATT ATGATTATGT ACATACTATG CAACAGGCCA 3660

TAGACAAGCG TATCTCGAAT CCATACTTGC GACAAATGTT AGGCTATTTT ATCAAATATG 3720

TAGGTTCTTC ATCATACGAT GCGCCAgCTG TATTATCTAT GTTATTCCAT ATGCAACAAG 3780

AGCAAGGCCT TTGGTATGTA GAAGGTGGAA TCCATCATTT AGCCAATGCC TTGGAAAAGc 3840

tAGCGCGTGA AGAAGGTGTC ACAATTCATA CAGGTGCACG TGTGGACAAT ATTAAAACAT 3900

ATCAAAGACG TGTGACGGGT GTCAGATTAG ATACAGGTGA GTTTGTAAAG GCAGATTATA 3960

TTATTTCAAA TATGGAAGTC ATACCTACTT ATAAATATTT AATTCACCTT GATACTCAAC 4020

GATTAAACAA ATTAGAGAGG GAATTTGAGC CGGCAAGCTC AGGATATGTG ATGCATTTAG 4080

GTGTTGCTTG CCAATACCCG CAATTAGCAC ATCATAATTT CTTTTTTACG GAAAATGCTT 4140

ATCTCAATTA TcAACAAGTT TTTCATGAAA AGGTATTGCC AGATGATCCG ACCATTTATC 4200

TAGTAAATAC GAATAAAACT GATCACACAC AAGCGCCAGT AGGTTATGAA AATATCAAAG 4260

TCTTACCACA TATTCCATAT ATTCAAGATC AGCCTTTTAC CACTGAAGAT TATGCGAAGT 4320

TTAGGGATAA AATTTTGGAT AAATTAGAAA AAATGGGACT TACTGATTTA AGAAAACACA 4380

TTATTTATGA AGATGTTTGG ACACCGGAGg ATATTGAAAA AAATTATCGT TCTAATCGTG 4440

GTGCAATATA TGGTGTTGTA GCAGATAAAA AGAAAAACAA AGGATTTAAA TTTCCTAAAG 4500

AAAGTCAGTA TTTTGAAAAC TTGTACTTTG TAGGTGGATC AGTAAATCCT GGTGGTGGCA 4560

TGCCAATGGT TACATTAAGT GGGCAACAAG TCGCAGcAAg ATAAACGCGC GAGAAGCGAA 4620

GAATAGGAAG TGATATCTAT GAAATGGTTA TCACGAATAT TAACAGTAAT AGTGACCATG 4680

TCTATGGCGT GTGGTGCaTT GATATTTaAT CgTAGACATC A 4721

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

TATTCGTGCG CAATGGGCTA AATTAGGTCT AGGTTTAGAT TATAGTAGAG AACGTTTTAC 60

TTTAGATGAA GGTTTAAGTA AAGCAGTTAA AAAAGTTTTT GTTGATTTAT ACAATAAAGG 120

AATTATTTAT CGTGGCGAAC GTATTATAAA TtGGGATCCn AAAGCACGTA CAGCTTTATC 180

TGaTATTGAA GTAATACATG AAGATGTTCA AGGTGCGTTT TATCATTTTA AATATCCTTA 240

TACAGCGATT GTTGTTAACC CTAATGACGA ACGATACAAA GATGTAATCG GTAAAACTGT 360

TATATTACCA ATCGTAGGAC GCGAACTGCC TATTTTAGCA GATGAGTATG TTGATATAGA 420

CTTCGGTTCT GGTGCTATGA AAGTGACACC AGCACATGAC CCTAATGATT TTGAAATTGG 480

TCAAAGACAT CAATTAGAAA ATATTATCGT TATGGATGAA AATGGTAAAA TGAACGACAA 540

AGCGGGTAAA TATGAAGGTA TGGACCGTTT TGATTGTCGT AAACAGCTAG TTAAAGATTT 600

AAAAGAACAA GATTTAGTTA TCAAGATTGA AGATCATGTT CATTCTGTAG GTCATTCAGA 660

ACGATCTGGC GCTGTTGTTG AACCATATTT ATCAACACAA TGGTTTGTGC GCATGGAAGA 720

CTTAGCGAAA CGTTCATTAG ATAACCAAAA AACAGATGAT CGTATTGATT TTTATCCGCA 780

ACGTTTCGAA CATACATTTA ACCAATGGAT GGAAAATATT AGAGATTGGA CGATTTCAAG 840

ACAATTATGG TGGGGTCATC AAATTCCGGC TTGGTATCAT AAAGAAACAG GCGAAATATA 900

TGTTGGAGAA GAAGCGCCAA CTGATATTGA AAATTGGCAA CAAGATGAAG ATGTATTAGA 960

TACGTGGTTC TCaAGTGCTT TATGGCCtTT CTCyACGTTA GGTTGGCCTG ATTTAGAAAG 1020

TGAAGACTTT AAACGATACT ACCCAACAAA TGCCTTAGTT ACAGGTTACG ATATTATCTT 1080

TTTCTGGGTA GCACGCATGA TATTCCAAGG CTTAGAATTT ACAGATCGTC GTCCATTTAA 1140

TGATGTATTA TTACACGGTT TAGTTCGTGC TGAAGACGGG CGTAAGATGA GTAAATCATT 1200

AGGTAATGGT GTGGATCCAA TGGATGTTAT TGACGAATAC GGTGCTGATA GCTTGCGTTA 1260

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ACGTTCAGTA TTGAGTTATA CTTTAGACAA TATTATGAGA ATGCTACATC CATTCATGCC 1680

ATTTGTAACA GAGAAAATAT GGCAAAGTTT ACCACATGAA GGTGACACAA TTGTTAAAGC 1740

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GTTATGAAGT AGGTACATTT ACGTCGCCGT TTATTGAAAC ATTTAATGAA CGAATTAGTC 2520

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GAGAAATTGT TGTTGTATCG CAAAATGATG AATTTACTTA CCGTTATAAA GATTATGAAT 3000

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AATTAGTAGA TGACTACGTT GAATTTATAA AAAATTATCA AGGTGATACA TTAGTAATTA 3480

CCGGTAGTCT GTATTTCATA AGTGAAGTTA AATCAA 3516

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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TGAGTGATAG AATCAAAAAA GCCATCTCAA AAATTAATCA AGCAAACAAC ATTCCAAACA      60
ATGsTCGCAA ATCACCAATG TATCACTCTC CAATTACGTA ACTATGATTT AATTTAAGCA     120
TAGTTATTGA GGTTTTGTGA TATATAGTAT AAAATTAATG AGAATTAAAT TTAATAATGT     180
AAAATTCATm TTCgGGGTCG GGTGTAATTC CCAACCGGCA GTAAATAAAG CCTGCGACCT     240
GCTAGTATGT ATCATATTAG TGGCTGATCT AGTGAGATTC TAGAGCCGAC AGTATAGTCT     300
GGATGGGAGA AGATGGAGGT TTTTTGTTGT GCAATAATCC TCCTATTCTT ACGAGATGAA     360
TGGAAGGAGA AAATTGAATA TGCAACAAAA TAAACGTCTT ATCACAATAA GTATGTTGAG     420
CGCGATTGCG TTTGTGTTAA CTTTTATCAA GTTTCCTATA CCATTTTTGC CACCATACTT     480
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CGGTATCGTA GTTGCACTGG TTAAAAATTT ATTGAACTAC TTATTTAGTA TGGGCGATCC     600
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CATATATATC TGGCGCTGCT GCACCGcATG CACCACATGC AATACAAGTA TCCATATCAA    1260
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TATACATTTG aAAGCATGGG GCAAACATTT CAAGCAATTC AACTATTAGT GCAAaCCATG    1680
TCTAATACCA AACAACATGT TTTTCATTTT GTACCAATCT CTCAAAATAA TAAGATACAm    1740
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CCTAGCGGAC CATGATTTGG ACTTTGAAAT GTGTTTGTAT TAGACGTATG TGTTTTGGTA 7320

ACATTACGCG CCGTATGAAT TTCATCATTA AaTACAACCA TCACGCCTTT ATGACGGGCC 7380

TTTTCATCAG AGGCAACGCG AATAGCGGAA ATATAATTAT ATAATCCGTC AGAACCAATT 7440

TCATTAGACG AGCGCATTGG CCAAGAAnTA ACAACAGGTT G 7481

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

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CGTTGTGACA CCACCTCAAC CTAATGGTGT GTCTCAAGAA GTATTAGCAG CATGCTATAT 180

TACGCAAGTT GATCAAGTAT TTCAAGTTGG TGGTGCTCAA AGTATTGCTG CGTTAACTTA 240

TGGCACAGAA ACGATACCTA AAGTTGATAA GATTGTAGGT CCAGGCAATC AATTTGTTGC 300

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ACAAGCAGAA CATGATGAAT TAGCACGTAC ATATGCCATT AGTGAAGATG CGCAAGTCCT 480

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CATTGCTTCT GGTGGTGGTG GCAATGCACA ACACTTTGTA GAATTATTTG ATCAGACGGA 4440

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AAAGATATTC ATGTAGATTG CGACAATGAC ACTATTTTAA TTGATGTCAT ACCAAATGGA 4800

CCAACATGTC ATACAGGCAG TCAAAGTTGT TTCAACACAG AAGTTCCATT TTCAGTGCAA 4860

ACATTAGCGC AGACAGTTCA AGATAGTGCC CAATCCAATA ATGAAAAGTC ATATACAAAA 4920

TATTTATTAA CAGAAGGTAT AGAAAAGATT ACAAAAAAAT ACGGTGAAGA AGCTTTTGAA 4980

GTCGTAATTG AAGCAATTAA AGGTGACAAA AAAGCATTTG TAAGTGAAGT AGCAGATGAA 5040

CTTTATCATT TATTTGTCTT GATGCATGCG CTTGGCGTCG ATTTTTCAGA AATTGAGGCG 5100

GAATTAGCGC GTAGACATCA TAAGCGCAAT AACTTTAAAG GTGAACGACA AAATATCGAA 5160

CAGTGGTAAA GCAAGTATGG ACTAAGATAT AAGGAAAAGG ATCATGGCTT ATACACTTAC 5220

AAATATTGTG GAAAACGTGA CATTTTCAAG TTTAAAATAC GACACCAACA TATTTTAACT 5280

ATGAATGCTG TGATGGTACT AAAGTTGCGA ACTCGTTATA GATAAGTAGT GGATAATCAC 5340

AATACGAAAT CAAAAATAAT TATAAAAAGT AAATTGAGCA ACTCAGGAAT AGATGTCACT 5400

GTTAAAGATG TCGAAAAGTA TATGAATCGA TATAATGAAG TTATGAAGGG AAAAAATGGC 5460

GAAAAAGCTA AAGAGTTATG TTTGTCGTTA CTACCTATTA ATATCATAGT TGTCTTTACA 5520

TTCTTTGTAT TTATACTATA AATACAAATA TATCTAGCCT GAAATAGAAA TGTCATAGCC 5580

TATTTAAAAG ACAATCTCCA TTAGAACTAA GATATGCATC CCGAAAGTTA GACTAAAAAA 5640

CTAACTTTAT GGGATGTATT TTTATGCTAA TCATCATAAA TTCGAGATTA AGTTAAAGGT 5700

AGTTCAAGAG TAATTAAACA ATAAATwAAA AATAGTAGGA TACTTACTTT GAGGGAAGAA 5760

AATTAACTGT ATATATTTAG TTTAGGAACA AGTATTACGG TTTATCCTGA TACAATTATT 5820

GTGGATGGGA TGATATTTTT AGGTTTAAAA TACGACACCA GCAAACATAA TAACTGTAAT 5880

AGCTCATAAA TCTCCCCATA TAGCTAATCT AAAAAAATAA TACATCATTG GAATTAAGCC 5940

CCAAGCATGT AAATATTAAA AATCAAAAmA GATATmTGTA AAAaAGTTAC AATTtGCATA 6000

ATTAAATTGT GTCTAATTAT TGACTAATTA AATTTTGCCA AATATAATAT TAATTAATAA 6060

TTTGaAATGA TTAGCGTATA CACTTTAAAT TCTCTTTGGA GAATATATTT TTTAAATACA 6120

AATGTAAACG CTTTCTCGTC AAATTAAACA ATAGAAAGGA TGGTCATTAT GAGTGCTTGG 6180

TTAAGTAAAT TATTTGAGTT TATTCCTCGA ATAATTATCA ATTTGTTTAT CTAAAATAAA 6240

AAAATAGAGG TGCTGACAAT GATGAAAAGT CAAAATAAGT ATAGTATTCG TAAATTTAGT 6300

GTAGGTGCAT CTTCCATTTT AATAGCTACA TTACTATTTT TAAGTG 6346

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3775 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

TGATAATGAT TCTCATTGTC ATACATCACG AAGGAGGCTA ATTAGTCAAT GAATAAAGTA 60

ATTAAAATGC TTGTTGTTAC GCTTGCTTTC CTACTTGTTT TAGCAGGATG TAGTGGGAAT 120

TCAAATAAAC AATCATCTGA TAACAAAGAT AAGGAAACAA CTTCAATTAA ACATGCAATG 180

GGtACAACTG AAATTAAAGG GAAACCAAAG CGTGTTGTTA CGCTATATCA AGGTGCCACT 240

GACGTCGCTG TATCTTTAGG TGTTAAACCT GTAGGTGCTG TAGAATCATG GACACAAAAA 300

CCGAAATTCG AATACATAAA AAATGATTTA AAAGATACTA AGATTGTAGG TCAAGAACCT 360

GCACCTAACT TAGAGGAAAT CTCTAAATTA AAACCGGACT TAATTGTCGC GTCAAAAGTT 420

AGAAATGAAA AAGTTTACGA TCAATTATCT AAAATCGCAC CAACAGTTTC TACTGATACA 480

GTTTTCAAAT TCAAAGATAC AACTAAGTTA ATGGGGAAAG CTTTAGGGAA AGAAAAAGAA 540

GCTGAAGATT TACTTAAAAA GTACGATGAT AAAGTAGCTG CATTCCAAAA AGATGCAAAA 600

GCAAAGTATA AAGATGCATG GCCATTGAAA GCTTCAGTTG TTAACTTCCG TGCTGATCAT 660

ACAAGAATTT ATGCTGGTGG ATATGCTGGT GAAATCTTAA ATGATTTAGG ATTCAAACGT 720

AATAAAGACT TACAAAAACA AGTTGATAAT GGTAAAGATA TTATCCAACT TACATCTAAA 780

GAAAGCATTC CATTAATGAA CGCTGATCAT ATTTTTGTAG TAAAATCAGA TCCAAATGCG 840

AAAGATGCTG CATTAGTTAA AAAGACTGAA AGCGAATGGA CTTCAAGTAA AGAGTGGAAA 900

AATTTAGACG CaGTTAAAAA CAACCAAGTA TCTGATGATT TAGATGAAAT CACTTGGAAC 960

TTAGCTGGCG GATATAAATC TTCATTAAAA CTTATTGACG ATTTATATGA AAAGTTAAAT 1020

ATTGAAAAAC AATCAAAATA ATTAAGGAGT TTTACGATGC TACTTAAACC AAAATACCAA 1080

ATCGTTATTG CTGGTTTATG TCTTGCAATA GTAGCTATCT TAAGTTTAAT GATTGGAAAT 1140

ACGCTTGTGT CACCAGGTAC GGTGATACAG GCGTTATTCA ACTTTGATAG TGAAAACGAT 1200

TTACATGATG TTGTCACTGG TGCACGGGCG TCGAGAACAA TCATTGCGTT ATTGACTGGT 1260

GCTGCCCTTG CTGTCTCAGG TTTGTTGATG CAAGCACTTA CACGAAACCC AATAGCCTCA 1320

CCAGGGCTTT TCGGTGTCAA TGCAGGCGCA GTATTTTTTG TCATTTTTAG TATTACATTT 1380

ATCCAAATTC AATCTTTTAA AATGATTGTA GTTATTGCAT TTTTGGGGGC TATTGTTGTT 1440

ACTGTATTAG TTGTTGCACT AGGTATGTTT AGACAAACAC TATTCTCACC TCACCGTGTC 1500

ATTTTGGCAG GTGCTGCGAT TGCGATGCTA TTTACAGCCT TTACTCAAGG CATACTTATT 1560

AATATTTGGG ATATCCCATG GATTATTCCG CTTGTATTGA TACTTATTTT AATTGCATTT 1680

AGCATGGCTG CACACATCAA CATCTTGATG ACAAGTGACG ACATTGCAAC CGGCCTCGGT 1740

CAAAACATAA AATTAATCAA ATGGATGATT ATTATGCTCA TCAGTATGTT AGCCGGTATT 1800

TCGGTAGCCG TAGCTGGATC AATCGTCTTT GTGGGTCTTA TCGTACCGAA TATTAGCAAA 1860

CGATTATTAC CACCAAACTA TAAGTATTTA ATTCCTTTTA CTGCATTAGC TGGAGCAATC 1920

CTAATGATCA TTTCAGACAT TGTTGCTCGT ATAATAATTA AGCCACTAGA GTTGCCTATC 1980

GGTGTCGTTA CCGCTGTCAT TGGCGCTATT GTCTTAATCT ATATTATGAA GAAAGGACGT 2040

CAACGCTTAT GACCGAAAAG ATTAATAAAA AAGACAATTA CCATCTCATC TTCGCGTTAA 2100

TCTTTTTAGC CATCGTTTCA GTGGTAAGTA TGATGATTGG TTCAAGCTTT ATACCATTAC 2160

AACGCGTACT GATGTACTTT ATAAATCCAA ATGACAGTAT GGATCAATTC ACTTTAGAAG 2220

TATTACGCTT ACCTCGCATT ACACTTGCGA TTTTAGCAGG TGCCGCACTA GGAATGAGTG 2280

GTTTAATGTT GCAAAATGTA TTAAAAAATC CAATTGCCTC ACCTGATATT ATCGGTATCA 2340

CAGGTGGTGC TAGCTTAAGT GCTGTTGTCT TTATTGCATT TTTCAGCCAT TTAACAATAC 2400

ATTTACTTCC ACTATTTGCA GTATTAGGTG GCGCAGTTGC AATGATGATA CTATTAGTGT 2460

TTCAAACGAA AGGACAAATA CGCCCGACAA CACTCATAAT CATCGGTATT TCGATGCAAA 2520

CGTTGTTTAT TGCGCTTGTC CAAGGATTAC TCATTACAAC GAAGCAATTA TCTGCTGCCA 2580

AAGCTTATAC ATGGCTAGTC GGAAGTCTTT ACGGTGCTAC GTTTAAAGAT ACAATCATTT 2640

TGGGTATGGT TATTTTAGCT GTTGTGCCGT TGTTATTTCT TGTTATACCA AAAATGAAAA 2700

TATCTATACT TGATGACCCT GTAGCGATTG GCTTAGGCTT ACATGTACAA CGTATGAAAC 2760

TAATCCAATT AATCACTTCT ACTATACTCG TATCTATGGC AATCAGTTTA GTAGGTAACA 2820

TTGGGTTTGT CGGTTTAATC GCACCACATA TCGCGAAAAC AATCGTTCGC GGAAGTTATG 2880

CTAAAAAGTT ACTAATGTCA GCAATGATTG GTGCCATATC AATTGTTATT GCAGACTTAA 2940

TTGGGCGTAC CTTATTCTTG CCTAAAGAAG TGCCAGCAGG TGTATTTATT GCTGCTTTTG 3000

GTGCCCCATT CTTCATATAC TTATTATTAA CCGTGAAAAA GTTATAACGA TATTATTAAA 3060

ACAAAATGAC CTCACAACGA AGTTAGCTAA ATGATTCAGT TAACTAACCG TTGCGAGGTT 3120

TTTTTATACA TATAGTTGTT GTTATTGTTA ACAAGCGTCG ACTTTCTTAA TTACATATTA 3180

ATACTTTATA TACAAATAAC ACCGACTCAT ATTCTATAAT ATCAATCAAT ATTCTTCGAT 3240

TTTTCAAATA TCGATAACTA TTTCTTATTT AAATATAGTG TTTGATAATG TCATTTATTC 3300

AAAAACACAA ATTTTAATAA AAATATCATA TTATTTTTAA TTGTAAATTA TGGATTATTT 3360

ATATAATAAC CATGACAAAA TTAGAGATTT TATAATCATT GAAGCATATA TGTnTCGTTT 3480

TAAGAAAAAA GTCAAGCCTG AAGTCGATAT GACTATAAAA GAATTTATAT TACTGACTTA 3540

TTTATTTCAT CAGCAAGAAA ACACACTTCC ATTTAAGAAG ATTGTTTCAG ATTTATGTTA 3600

TAAACAATCG GATTTAGTAC AGCATATAAA AGTACTTGTG AAACATTCAT ATATTAGTAA 3660

AGTTCGAAGT AAAATTGATG AGCGTAATAC TTACATTTCA ATATCTGAAG AACAACnAGA 3720

nAAAATTGCA GAACnTGTTA CATTGTTTGA TCAAATCATT AAACAATTTA ACCTT 3775

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

AGAAAAATTA GCCTACCTAT GCAAGTTGTT ATTGCATTAG TGTTAGGTGT TGTCGTAGGA 60

CTTTTATTAT ATGGACAAGA AAACGTAGCA AATTACATTA AACCATTTGG TGACGTATTT 120

TTAAATTTAA TTAAAATGAT CGTTATACCA GTTGTATTTT GCTCACTAGC GCTTTCTATT 180

TCGAACGTTG GGGAATCGAA AACTGTAGGG CGTTATGGCT GGaAAACAAT TTTATACTTT 240

GAAATTATTA CAACAATCGC AATAGGTTTA GGGATTATCT TCGGTAACCT ATTTAAACCA 300

GGTGCTGGAT TAGACCCAAC AAAATTACCT AAAGGTGATA TTTCTAAATA TCAATCAACT 360

GCACATGCAG CAGAACAATC TACATATGGa AATCATTTTA TTGATACCAT TGTACATATT 420

ATTCCGACAA ACTTTTTTGA AGCTTTAAAT AAGGGTGAAT TATTACCTAT TATCTTCTTC 480

GCAGTATTCT TTGGATTAGG ATTAGCTGCT GTAGGTAAAA AAGCAGAACC AGTTAAAGAA 540

TTTTTAAGCG GATCGCTTGA AGCTGTGTTC TGGATGATTA ATAAAATTTT AAAATTAGCA 600

CCACTTGGAG TGTTTGCATT CATTTGTACT ACAATTATTA CATTTGGTGC ATCCGCATTA 660

TTACCACTAT TAAAATTAGT ATTAGTTGTT GTCTTTGCAA TGGTGTTCTT TGTATTCGCT 720

ATACTAGGAC TAGTTGCATG GATGTGTGGT ATTAATATCA TGAATATTAT TAGAATCTTG 780

AAAAGTGAAT TGCTTTTAGC ATTTTCTACA TCAAGTTCGG AAGCTGTACT TCCTGTAATG 840

ATGAAGAAAA TGGAAAACTT CGGTTCTCCA AAAGAAATTA CTTCTTTTGT TATACCAATT 900

GGTTATACGT TTAACTTAGA TGGATCAGCA CTTTATCAAT CTATTGCAGC ATTATTCGTT 960

GCACAGATGT ATGGAATGCA CTTAACATTA TCAGAGCAAA TTGTGTTGAT GTTAACATTA 1020

ACATTAGGTG CCATGGGCTT ACCGGCACAA GGTTTAGCAT TAATTATTGG TGTTGACCGT 1140

ATCTTAGATA TGGTACGTAC ATGTGTAAAC GTTATTGGTA ATGCATTATC AACAATCGTT 1200

ATAGCTAAAT GGGAAAACGT ATATGACAAA GCAAAAGGTC AAGAATATTT AAAATCAATT 1260

TAAAAAATAC TATCTGACAT TTAArGnCCC TTACAACCTT TGGTTgTnAG GGCTnTTTTA 1320

TGTCATGCGT CTTAAAGCCA GGCCGTATAn CGGTAAGCGT A 1361

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

TCAATATGTA AATCGGCGAT TGTCCCTATC tTCATACCCT TACCTTCTTT ACTCAAATTA 60

AAATGTTATT TATTATGCCA TaGCTTATCT AATATATATA GTTAACTGCT TCATTTAGAT 120

GATTATTTTA TATTTTTGCA TAAAAACTTA TATCTTTTCA AAAAAATCGA TAAGTTTTAG 180

TTATCATACC CTTACCTATC AAATGTTTTT TCTTATATTT AAAAAAATAA TTGCTTTATT 240

AAATGGATTT CTTTAGTATT TATAATTAAG AAAACGCTTA CACACAACTT TTTTATTTGC 300

TTTATCCTGA GGAGGAAAAT TATGGCAAGA AAATTGCATA GAGAGTTGAA TAACAGACAC 360

ATCCAATTAA TAGCAATTGG GGGCGCAATT GGAACTGGGT TATTCCTAGG ATCAGGTCAA 420

ACAATATCTT TAACTGGTCC ATCACTGTTA TTCACATACA TGATTATTGG GGTTGTACTA 480

TTCGCTTTTA TGCGCGCATT AGGCGAATTG TTGTTGAGCA ATACAAGATT TAATTCATTT 540

GTTGATATTG CAAATGAATA TTTAGGCCCT TTTGGTGGCT TTGTCATTGG CTGGACTTAC 600

TGGTTATGTT GGATTGTATC AAGTATGTCA GACCTAACTG CGATGGGACA ATACTTTGCA 660

TTTTGGTATC CACAAGTCCC AAATTGGATT ACCGTGCTAT TTATTGTTTT AATCTTGATT 720

AGCTTCAACT TATTAGGTGC CAGATTATTT GGTGAACTGG AGTTTTGGTT CTCGATTATT 780

AAAGTTGTCA CAATTATTGC GATGGTTATC GTTGGTCTTG TATTAATCTT TTTCTCATTT 840

AAAACACATT ATGGACATGC ATCATTCACA AACTTAATCA GTCACGGTGG CATGTTCCCT 900

GGTGGAaCAT TTGGTTTCTT AATGTCATTC CAAATTGCTG TATATTCATT CATTGGTATT 960

GAACTTATAG GTGTAaCTGC TGGTGAAaCG AAAGATCCTG AAAAAACCTT ACCGAAAGCA 1020

ATTAATAATG TACCTATCCG TATTTTATTA TTCTATATCG GTGGTCTATT AGTAATTATG 1080

TTAATCGGCG TACCATTTGC AGCAGGTGTC GTTAACTTTG TCGTGCTAAC TGCCGCGGCC 1200

TCTGCTACAA ATAGTGGTAT CTATTCGAAT AGTCGTATCT TATTCGGACT GTCACAACAA 1260

GGGTTAGGTC CTAAAGTTTT AAATAAAACG AATAGTCATG GCGTGCCTTA TTTATCAATG 1320

TTAGTTTCAT CAATTGCATT ACTTATAGCA GCCTTGTTAA ACTACATTTT CCCTAATGCA 1380

ATTCAACTAT TCATATACGT TACAACGTTA tCAACTGTGT TGTTTTTAGT TGTtTGGGCA 1440

ATGATnATTG TCGCTTATCn AATGTATTTG GAAAAAGCAT CCTGAGGCA 1489

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5000 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

TTTTCCATCA TrATcACCAT TTAAGACAAT AGCTGTATGA CCATATCCTC CACCAAATCT 60

TCCACTAAAA ACCACTAAGT CCCCAGGTTC AGCTTTGAAA GTTGGTGTGT TGTGATAAAT 120

TTTAGCTTCA CTATTAAAAT TATTTGCATA TGGTATATCT TTAGCTCCAT ATCCTTTtAA 180

TCCAkGACCA TAAAGAkGAT TCCAATATAC ATTAACTAAA TCGAAACATT GCCATCCATA 240

ACTACCGTCG AAATCCCATC CTCTATTCTC TAATGTTTTC AAATAATTTA ATGTACTGCT 300

ATTACTATTA CTTTTATTAT TTGAAGACAC TGTTTTTGGT TTTGGTTCTA CTAATGGTGT 360

CATTGGCACT TTTAATTTTT GACCAATAAA TATTAAATTA GGATTTGCTA TATTATTTGT 420

ATTTTGAATA TTTGAAACTG TAGTTTTGTA TTTTAATGCT ATAGCACTAA GTGTGTCTCC 480

TTTTTTTACA GTATAGATTT GTGTTTTTGG AGCTTCTCTA AAACTGTAGT AACCAAAGTA 540

ATTATTAGTA ACTTTATTCG TTTTCTTCTG ATTAGAATTT TGAGCTTCCA AGTTTGCAAT 600

TTTAATTTCT TTAGTAAGTT CATTGTTATT AATAACTAGA TTGTTACCTT GGCTTGAGTT 660

TTTCGGAGTA TTTGAAATCT TTATATCTTG ATTAATTTCA TTTCCGTTTG AAATTGCTGA 720

TTTGTTGTCT AACTTTAAAC TTGTGTCCGA TGTTTTAACA GCACCTTCAT TTTTTATTTT 780

GTCTTTTGTC GTATTTTTAT TAGCATTTAA CTCTGATTTC GCGAATACAT TTTGCTCATA 840

CCCTCTTGTA AAATCTTTAG ATTTATCAAT TTCATCTGCA TATGCTTTGT TCGACATACC 900

CAATGCCAAA AACATACCTA TTGAAATTGA CAAAATTCCA ATACTAACTT TTCTAATTGA 960

ATAGCGTACT TTACTTTGTT GTTTATTCAT GATGAAACAC TCCTTACAAT AATATACAAA 1020

GTAGGAGGTA AAATAATTAA CTTGTCTTTC CAAAATATGA AAAGTGTACT AAAaTTCATC 1140

GCACGACAAA TAGCCCATTT CCGATACTTT TATAAAGTAT GGAaTGGGCT ATAGCCATTT 1200

ATATCATCTT TTAACTTTAT TTATTAACAG TTAATAATGA TTCATAAATA CCTGCTTCTT 1260

TAGCAGCTTC AATTAATGTT GAACCAATTT CTGAAGGTGT TGCCGCTGTT TTCACACCAC 1320

AACTATTTAA TGTTTTAATT TTCTCTTCAG CAGTACCTTT ACCACCTGAA ATGATTGCAC 1380

CAGCATGTCC CATACGTTTT CCAGGAGGTG CTGTTTGTCC ACCGATAAAG CCTACAACTG 1440

GTTTTGTCAT ATTCGCTTTA ATCCATTCAG CTGCTTCTTC TTCAGCCGTA CCACCGATTT 1500

CACCAATCAT AACAACTGCT TTCGTTTCGT CATCTTCATT GAATGCTTTT AAAACATCAA 1560

TAAAGTTTGT TCCGTTGACT GGGTCTCCAC CAATACCAAC AGCTGTAGTT TGACCAATAC 1620

CTTCTTCAGT CAATTGGTGC ACTGCTTCAT ATGTTAATGT ACCTGAACGA GATACTACAC 1680

CAACATGACC TTTTTTGTGA ATATAGCCAG GCATAATACC AATTTTACAT TCATCTGCTG 1740

TAATCACACC TGGACAGTTC GGACCAACTA AACGTGTTTT TCTACCTTGT AAGTAGCGTT 1800

TAACTTTAAC CATGTCTAAT ACAGGAATAT GTTCAGTGAT ACAAATAACC ATATCTAAGT 1860

CTGCATCAGC TGCTTCTAAA ATTGAGTCTG CAGCAAATGG TGCTGGAACG TAAATGACTG 1920

AAACCGTTGC CCCAGTTTCA TTTTTAGCTT CTTCAACAGT GTTGAAAACA GGAACGCCTT 1980

CAACAACTTG ACCACCTTTA CCAGGCGTCA CACCTGCTAC TATTTTCGTA CCATAATCAA 2040

GCATTTGTTT TGTATGGAAA AGGGCAGTAG ACCCTGTAAT ACCTTGTACC ATTACTTTAG 2100

TATTCTTATC TATAAATACA CTCATCTTAG TGCTCCCATC CTTTCCTTAT GCTTCTTTGA 2160

CTAGTTTAAC AATTTTTTGT GCACCTTCAG CCATTGTTGC TGCTGGTTCA ATTGCTAATC 2220

CTGAGTCTTT TAAGATTTTT TTACCTAACT CAACATTTGT ACCTTCTAGG CGTACAACTA 2280

GTGGTAAAGT TAAATCTACT TCTTTTACAG CTTCAACGAT ACCTTCTGCG ATAACATCAC 2340

ATTTCATAAT GCCACCGAAA ATGTTTACAA AAATACCTTT AACATTTTCA TCACCTAAAA 2400

TGATTTTAAA TGCTTCAGTT ACTTTTTCTC TAGTAGCGCT TCCGCCTGCA TCTAAGAAAT 2460

TGGCTGGGTT TCCACCGAAA TGATTAATCG TATCCATTGT TGCCATGGCT AAACCTGCAC 2520

CATTAACCAT ACATCCGATG TCACCATCTA ATGCAATGTA TGATAAATCA TGTTTAGACG 2580

CTTCAATCTC TTTCGGATCT TCTTCTTCTA AATCACGTAA TTCTACAACA TCTTTATGTC 2640

TGAATAATGC ATTATCATCA AAATTAATTT TAGCATCTAA TGCCAATACA TCACCATCAG 2700

CTGTTGTAAC TAATGGGTTG ATTTCTACGA TTGAACAATC TTTTTCAATG AATACATTAT 2760

AAAGTGCTAA TAAGAATTTA GCAGCTTTGT TAACAGATTC TTTAGGAATA TTAATATTAA 2820

AGATCTTTTC AGGAGTCTTC GCAGCAACTT CTTCAATCTC AGTGCCCCCT TCTTCAGACG 2940

CCATCAATGT TACTTGGTCA GTCGCACGAT CAATAACGAA TCCAACGTAA TATTCTTTTT 3000

GAATAGCACA ACCTTCTTCG ATATATAAAC GCTTAATTTC TTTACCTTCT GGACCAGTTT 3060

GATGTGTCAC CAAAGTTTTC CCTAATAATT CTTTTGCATA TGTTTCTACC TCAGATAAAG 3120

ATTTAGCAAT TTTTACTCCG CCTGCTTTAC CTCTACCTCC AGCATGAATT TGTGCTTTTA 3180

CAACATAAAC ATCAGAATTT AATTCTTTTG CTTTCTCCAC CGCTTCTTCA GCAGTAAATG 3240

CTACTCGTCC TTCTGGAACT GCAACGCCCA TTGAACGAAA TATTTCTTTA CCTTGATACT 3300

CGTGGATATT CATCTTCCAT CCTCCTGTTA CTTAGGTTAA GTTCCCTTAC AATTATAAAA 3360

AATGTAAGCG CTATTGTAAA CTTAAATGCT ACTTTTTTAT CATTTAATTG AATTTTACGA 3420

TTTACAGTAA CGATTTTATA GGTTCAAAGC TTTTTCTATG CTCTTTCATA ATGCCAATAT 3480

CATCGATTGC TAGTAAATGT TGTTTGGTAC CGTAACCCGC GTTTTTTTCA AAACCATATT 3540

CAGGATAATC TTTAGATAAC TGTGTCATAT AATCATCACG AAAAACCTTT GCCATGATAC 3600

TTGCAGCTGC AATGGACACA CTTCTTGCAT CACCCTTGAT TAAAGATACT TGAGGCAGTG 3660

CATTATCAAG CGTCATCGCG TCTATCAATA AATGCGTTGG TTGTACTGAT AATCCATCAA 3720

TAGCTCGCTG CATGGCGATT TGAGTAGCTT TATAAATATT AAATTCATCT ATTTCTTnCA 3780

GtGTCGCGAT CCCATATGCA AAAGCAGTAA CTTCATTTTT TAGTGCTTCA TTTAATTCTA 3840

GACGTTTCGT AACAGGTACT TTTTTCGAGT CATCAAGGCC CAAATAATTG TGATTTGAAT 3900

TTAAAATTGT TGCGCATGCA ACGACTGGAC CTGCTAAAGG TCCTCTTCCA ACTTCATCAA 3960

TCCCACAAAT AATAGCATTA GGATGCTCTT TTAATATTTC ATTTTCAAAG TAAGTCATTT 4020

CAACATACTT TTCTTTTAAA GCTTGTTCTT TTTCTAACGC TTTTCTGCGC CTAGCTATGG 4080

CATTTTGAAC ACCTTTTCGC TCATCTAAAA AGCATTCATG ATTTTCTAAT TCTTCTATTG 4140

TATTAACCGC ATTAATCAAC TGCGTAACTT CTTTAATTGT TAGCGTCATT TGCTAATTCC 4200

TCAGTCATAT CTTTAAAAAT ATCAAAACAA TAATTTCCTA TTTTAGCATT TCGAATATCA 4260

TAAATAATCA GTTCAATGAC TGCTTCGTAA TCAATTTCAT TACCACGTCG AATTAAGCCc 4320

ACGTTTTTTC CCTATCGCAT CAAACCACGC TATGATTTCT GCAtCTTCAG GAACTTCAAT 4380

ATTATAATGT GACTTTAATC GCGCTAAATC ATTTTGAATT AAAAAGTTTA ATCCATAGAT 4440

GGCAACTTCA TCTAAGTGCA CAATACTATC TTTTATCGCA CCAGTTAAAC TCAACTTCTT 4500

ACCGACTTCT TCATCTTCAA ATTTAGGCCA AAGTATCCCT GGTGTGTCTA ATAGTTGTAA 4560

TGCATTACCA ACTTTAATCC ATTGTTGTTG TTTGGTCACA CCTGGTTTAT TACCAGTCTG 4620

AACGATCATT GCTCTTATCG CTCTAGGTTT AAGTCCTTTC GCTTTTTCGC GTTCAAATTT 4740

TTCAGCAGTC GCCTTAATTG CTGCAGCTTC CACTTTCTTT AAATTTTTAC CGTGCTTAGC 4800

ATCCACTGAT ACAGGATAgT AtCCTTTATC AATAAAAAAT tGTTCCCATT TTGACATCTC 4860

ATTTAAATTA GACATATCTT TTTTATTTAA TATAACAACA CGTGGTTTTT GGTTAATAAC 4920

TTCATCTATC ATAGGGTTTC TTGAACTATA TGGAATTCTT GCATCTACTA GTTCAAACAC 4980

TACATCTACT TTTTTTAATT 5000

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1700 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

AACCCGnAGA CGAAACTnCA TAGTTGCCTG TTATGTTGAT TAGTGCGTTT GTAGCTATTT 60

nAAATCAAAC ATTATTAAAT ACAGCGTTaC CTAGTATAAT GAGAGAATTA AATATCAATG 120

AAAGTACATC GCAATGGCTA GTTACTGGGT TTATGCTTGT TAATGGCGTC ATGATACCTC 180

TGACGGCATA TCTAATGGAT AGAATTAAAA CTAGACCTTT ATACTTAGCG GCGATGGGGA 240

CATTTTTATT AGGTTCTATT GTTGCAGCCT TAGCTCCGAA TTTTGGAGTT TTAATGTTAG 300

CTCGTGTAAT TCAAGCGATG GGTGCAGGCG TACTTATGCC CTTAATGCAA TTTACGTTAT 360

TTACATTGTT CAGTAAAGAA CATCGAGGTy TtGCAATGGG ACTAGCAGGT TTAGTAATTC 420

AATTTGCACC AGCAATAGGA CCTACAGTTA CAGGATTAAT TATTGATCAA GCGAGTTGGC 480

GAGTTCCATT TATTATAATT GTAGGAATTG CTATACTTGC CTTTGTTTTC GGTTTGGTTT 540

CAATCTCGAG TTACAATGAA GTGAAATATA CGAAATTAGA TAAGCGTTCA GTAATGTATT 600

CAACTATTGG GTTCGGGTTA ATGCTATACG CATTTAGTAG TGCAGGAGAT TTAGGATTTA 660

CAAGTCCAAT AGTAATAGGT GCGTTGATAT TAAGTATGGT TATTATCTAT TTATTTATAC 720

GTAGACAATT TAATATTACT AATGCACTTT TAAATTTAAG GGTTTTTAAA AATAGAACAT 780

TTGCATTATG TACGATTAGT TCAATGATTA TAATGATGTC AATGGTTGGA CCTGCGCTGC 840

TTATACCGCT ATATGTTCAA AACAGTTTAT CTTTATCTGC CTTGTTATCA GGACTTGTTA 900

TCATGCCTGG TGCAATAATA AATGGTATTA TGTCAGTTTT TACAGGTAAA TTTTATGATA 960

AGTATGGTCC TAGACCATTG ATTTATACTG GTTTTACAAT TTTAACAATT ACTACAATTA 1020

GAATGTTTTC AGTTTCTTTA CTCATGATGC CGATAAATAC TACAGGAATT AATTCTTTGA 1140

GAAATGAAGA AATCTCACAT GGCACGGCTA TTATGAACTT TGGTCGTGTA ATGGCTGGTT 1200

CACTAGGCAC AGCTTTAATG GTTACATTAA TGAGTTTTGG TGCAAAAATA TTTTTATCTA 1260

CATCGCCATC GCATTTAACT GCAACTGAAA TTAAACAGCA ATCCATTGCT ATAGGGGTGG 1320

ATATCTCATT TGCTTTTGTA GCTGTGCTTG TTATGGCAGC TTATGTGATA GCACTTTTTA 1380

TAAGAGAACC TAAAGAAATA GAAAGTAATA GAAGGAAATT TTAAAATAAT TATAGTAGTT 1440

GGTCTATTTA AAATAATAGG CTAACTGCTT TTTTTATTTA ATAAAAAGTT TTATACTTTT 1500

AGTGATAGAC TAAGCAAAAA TTGTTATTTG CTATGATGTA GATGTCTTAA AATGATTAAG 1560

GGGGATTTGC TTTGTTAACG GTAGATCAAG TGAAAGAATT GGTAGGAGAA ATTAAAGATC 1620

CTATTATAGA TGTGCCTTTA AAAGAAACAG AAGGTATTGT TGAnGTTTCT ATTAAGGGAG 1680

AAnAAGAACA TGTGAGTGTT 1700

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

TGCATCAACT TTCAAACAAT AAATCATCAC AATAACCACA CCTAATTCAA CACTTTTCAA 60

ACATAAGTAT TGACACATTG AGCAAAATGA TTTTTAATTG TAACTAATAC AGTTACAATT 120

ATGAGGTGAG AAACATTGAA TTTAGAATTT AACATTGCCG TGCATGTATT AGCTTTTTTA 180

ACTAAGCATC aTTCAGAAAA ATTCAATAGT AGTTCATTAG CAGAaTTAaC TTGTTTAAAT 240

CCTGTTCAAT TACGACGCGT GACGACTCAA CTTGTCGATT TAAAAATGAT TGACACAATA 300

CGAGGTAAAG ATGGCGGTTA TTTAGCAAAT GATCAAAGTG CTGATGTCTC TCTAGCAACA 360

TTATaTAAAC ATTTTGTCTT AGAGAAAGAA CACCACACAC GTCTATTTAC TGGCGACGAA 420

GGCAGTCACT GTCAAATTGC TCGTAATATT GCAACTACCA TGTCACATTA TCAGCAAGAC 480

GAACAGAATA TCATTATTAA TTTTTATAAT GGAAAAACAA TCAAAGATGT CATTGAAGAC 540

ATTCAAAAGG AGGATTTATG TCATGAAAAC ATATGATTTA ATTGTAATAG GATTTGGGAA 600

AGCTGGTAAA ACTTTAGCGA AATACGCTGC ATCAACAGGT CAACACGTCG CAGTTATCGA 660

ACAATCTCCG AAAATGTATG GAGGCACTTG TATAAACATA GGATGTATAC CTTCGAAGAC 720

TGTTGTCAAT GCGCTAAACA ATAAAAATTA CCACTTATTA GCAGACGATA ACAACATTGA 840

TGTACTGGAT TTTAAAGCGC AGTTTAAATC TAATACTGAA GTGAATTTAT TAGATCAACA 900

TGACGATATC GTCGATAGTA TTACTGCACC TCATATCATT ATTAATACCG GTGCTACCTC 960

TGTCATTCCT AACATTAAAG GCCTTGATCA AGCTAAACAC GTCTTCGATT CGACAGGTTT 1020

ATTAAACATT AGCTATCAAC CTAAGCACCT CGTTATTGTA GGTGGCGGTT ATATCGCCTT 1080

AGAATTTGCT TCAATGTTTG CGAATTTAGG TAGTAAGGTA ACAGTATTAG AACGTGGCGA 1140

ATCATTTATG CCACGCGAAG ATCAAGATGT CGTTGCATAT GGTATTACTG ACTTAGAAAA 1200

TAAAGGCATT GCATTGCATA CAAATGTTGA AACGACTGAA TTGTCATCTG ACAATCATCA 1260

TACAACAGTC CATACCAACG TTGGTAACTT TGAGGCTGAT GCAGTACTTT TGGCTATCGG 1320

GCGCAAACCG AATACGGATT TAGCTTTAGA AAATACTGAT ATCGAATTAG GCGACAGAGG 1380

CGAAATTAAA GTCAATGCTC ATCTTCAAAC AACTGTGCCG CATATTTATG CTGCAGGTGA 1440

TGTTAAAGGC GGACTTCAAT TTACGTATAT ATCTTTAGAT GATTATCGAA TTATCAAATC 1500

AGCGTTATAT GGTAATCAGT CACGTACGAC TGACAATAGA GGCAGCGTGC CTTATACAGT 1560

ATTTATAGAT CCACCATTAT CACGTGTTGG ATTAACTAGT AAAGAAGCTG CCGCTCAACA 1620

TTATGATTAC ACTGAACATC AACTTTTAGT AAGTGCTATA CCTCGTCATA AAATTAACAA 1680

TGATCCAAGA GGTTTATTTA AAGTAGTCAT TAATAATGAA AATAATATGA TTTTAGGTGC 1740

TACATTATAT GGTAAGCAAT CTGAAGAATT AATTAATATA ATTAAACTTG CGATTGATCA 1800

AAACATTCCA TATACCGTAT TACGAGATAA TATTTATACG CATCCTACGA TGGCCGAATC 1860

ATTTAATGAT TTATTTAATT TCTAGACAAA ACATAAAAAC CTGGTGGCAC GCATTGAATG 1920

ATGCTGCCAT CAGGCTTTAT TGTTGTGCTT TTCGCTTTTC TAATTTTTCT TTAAGCTTTC 1980

TATCTTGTTC TTCTTTACGA CGTTTACGTT CTTCATGTCG TTTTCTTAAA CGCTCTTCTT 2040

CTTCAGGATC ACGTGGTTTC TTTAATTGTT GAGAAACTTT TTCGATTAAT TCTTCTTCAG 2100

TAAGCGCagc CAGTGGGCGG TTATTAACAA AAGTGAATGT TTTTCGGCGT CCAGGTCCAC 2160

AATAAGATTG ACAACCTATC ACGATTTCAG CATCGGGATC TAATTTTTCC AACTTCTTTT 2220

GTAACGTTCT TATATTGACT GCCTGACATT CATCACAAAT AAGGAATGTA TTTTTCATAT 2280

TGCTACCCAC CTTTCTTTAT CATATCTATA TCGTCGATTT CATTAATTTT TTCGTTAACT 2340

CTATCTATTT TACTCTTTTT AATATTTTTT TCAAGATACG TAACACGGCT GaCAATAAAA 2400

AATGGAGCAT TTATCTTCTA ATTAAATTAG ATGaTTGCTC CCCTATCAAA TCATTTATTG 2460

CCCATGATAA ATATTAAATT TTAATGGTTT AATACCATGT TTTGTCCATT CATCATAAAT 2520

TGATGTTTTA GATGCGCCGT GATACTTTTC AGCAATATCA CACAAATATT TTAGCTTTTC 2640

AGTTTCTATA TCAACTGTAG CTTCTTTATC CATACGTTGA ATAATTGTAC GATTCTGACG 2700

CACCATCTTT TGCACACCTT TAATGTTATT TGTTTTAAAA GCATGAATAA GTTTTTCAAC 2760

ACAACGATGT GAATCTTCTA AGAAGTCACC GTAAAATGAA GGATCTGATT TCAAACGTTT 2820

CACTTCGCTA ACAAAGTGTG GTGATGACGC CGGTGAGCCA GTCCAACCGA TAAGTACTTC 2880

CATATTTTCA GGTGCTTGTA ATGGTTCGAT GTGCAATCCA GGCCAGTTTT TGATTAAAAC 2940

TTCTTCAACC GTAGTATCTT CAATTTGATG CTTAACCCAT TCATGATCAA AAGTACTATA 3000

CGCTAGCCAT CCACTATATA CACTCACAGC AATATCTCCG CATGAACTTA AACTTTGTAA 3060

CTTCATATTT GCAATCACTG CTAGTTTATA AATGTATAAA TTAGATAACT TCATATCATA 3120

AAATTCATTT AATACTTTTA TAACTGACAC AAGTACTGCT GCACTTGAAC CTAATCCATA 3180

TTTATGACCA TTTGAATCAT CTAAATTACT ATCAATAGTC AGATGAAAAT GCTTCATCGC 3240

TATATCGCAA CTTTTCGCGT ATTGTTCAAA TATTTCAATA GCTGTGaCCA CATAATTTAA 3300

TTGTTTTGCT GcATGTGGAT CTGAAATGAC AATACTATCT TCATCTCTAC TAAATGTAAC 3360

TGGGTTATGA TGTAATGCTT TTGAATGAAT GGTACCTTTA TATTGGTCTG CTTCTTCAAT 3420

AGTAGCAGTT ACAAAACGAT CTAACGCAAT AAGTACAGAT TTATATCCTG GTTCTGTTAC 3480

AGCATATTCT CCAGCAATAT AAAGTTTTCC GGGTGCTTTG ACCTGAATCA TTTTATCTCT 3540

TCCTTACTCA ATTATTTCAA TTCCTGTGGC AATAATGTCA CTATCAATAA TTTGGTTATT 3600

ATCAAACTGT GTTAATAATT TATCTATAAT CTGTTGCTTG TTTTTCTTTT CTACAAGTAT 3660

TTTCACATTA GGTCCCGCAT CCATTGTAAA ATAACACGGA TACCCCGCTT CTCGGCATTC 3720

GTGAACAAGC GCCATGACAT CATAACTTTC TTGCACAAGA TATGTGAACG GCGGTGTTGA 3780

TCCTAGATTC GTGGCATGCA TACGCAAACC ATTTTCTTCA ATTACTTCAC CAAGGCGTTT 3840

AAAATCTTTG TCTTGAATCG CTGCTTTTGC TTCAGCTAAA TCTTCATCAA TATGATCTAA 3900

CCAATATTGA TAAAACCTTG ATGTGTTTCG TGTCAATGAC ATACCATATC GACTAGGTAC 3960

CTTTTTAGAA TGTTGATTAA TCACAACAAA TATCATGGCA AGGTCATCTT CAAAATGATT 4020

CGATTCAAGT GGAACGGCAT ATGACGTCTC ATCACTATAC CCTTTTTCCC ATTCTGCAAA 4080

TCCACCATAA ATACTACGCG ACGCAGAACC CGAACCAATT CGCGCCAATC TCGATAAATC 4140

CTTATCTGAC AGCTGCATGT CTAGCGCTTG ATTACAAGCT GCTGCTAAAG CTGCATATGC 4200

GCTTGCCGAT GAAGCCAACC CTGCTGCTGT TGGTACAAAA TTGTCGCTTT CAATTTCTGC 4260

ATACCAATCG ATGCCAGCTC TATTTCTGAC AATATCCATA TATTTTGAAA TTTTCTCTAA 4320

AAAAGTGACT TTCGTTTCAG TGTAAAATTT TTCTAATGTA ACAGATATGC TATTATTCAT 4440

TGGAATGATT AGTGCTTCAT CTTTTTTACC CCAATATTTT ATAAGTGCAA TATTCGTATG 4500

TGCACGTGCT TTGCCACTTT TAATCAACGC ATTAACCTCC TAAATTCTCA ATCCAAGTAT 4560

GTGCTGCACC AGCTTTTTCT ACAGCTTTTA CAATATTTTT CGCTGTTGGT AAATCTTTGG 4620

CAAGCAATAA CATACTTCCA CCACGACCAG CGCCAGTAAG TTTTCCAGCA ATCGCACCAT 4680

TTTCTTTACC AATTTTCATT AATTGTTCTA TTTTATCATG ACTAACTGTC AACGCCTTTA 4740

AATCCGCATG ACATTCATTA AAAATATCCG CTAAGGCTTC AAAGTTATGA TGTTCAATCA 4800

CATCACTCGC ACGTAAAACT AACTTACCGA TATGTTTTAC ATGTGACATG TACTGAGGGT 4860

CCTCACAAAG TTTATGAACA TCTTCTACTG CTTGTCTTGT TGAACCTTTC ACACCAGTAT 4920

CTATAACAAC CATATAGCCG TCTAAACTTA ACGTTTTCAA CGTTTCAGCA TGACCTTTTT 4980

GGAACCAAAC TGGTTTGCCT GATACAATCG TTTGCGTATC AATACCACTT GGTTTACCAT 5040

GTGCAATTTG CTCTGCCCAA TTAGCCTTTT CAATGAGTTC TTCTTTCGTT AATGATTTCC 5100

CTAAAAAATC ATAACTTGCA CGAACAAAAG CAACCGCGAC AGCTGCACTC GATCCTAATC 5160

CACGTGATGG TGGTAAATTC GTTTGGATCG TTACTGCTAG CGGCTCTGTA ATATTATTTA 5220

ATTCTACAAA ACGGTTCACC AAAGACTTAA GATGGTCAGG CGCATCATAT AACATACCAT 5280

CGTAAACATC GCTTTTAATA GACGAATAGT TCCCGCTCTC TAAGGCTTCT ATTAAAACTT 5340

TGATTTTACC TGCGTTAAAC GGTACTGCAA TAGCAGGCTC TCCAAATGTA ACAGCATGTT 5400

CTCCTATTAA AATAATCTTA CCTGTCGATT CCCCATATCC TTTTCTTGTC ATGTCAATAT 5460

CACCTTTTAT ATTTATCCTA TACTTGATTC ATTATTTTTA TTTATTAGTA AAAGACATCA 5520

TATTCTAAGT TGCAtngCAT TCGCGTTAAA TTTCATTGCA GTCTTTATCT CACATTATTC 5580

ATATTATGTA TAATCTTTAT TTTGAATTTA TATTTGACTT AACTTGATTA GTATAAAACT 5640

AACTTTCGTT TACTTCAAAG TTTAAATCTT ATCGAGTGAT ATTTCAGATT CTTTATCTTT 5700

TTATAAAATA GCCCTACAAT TTATAATTTT CCACCCTAAC TATAATACTA CAAATAATAA 5760

TTGGAATATA TAGATTTACT ACTAAAGTAT TAGAACATTT CAATAGAAGG TCGTTTCTTT 5820

CATAGTCATA CGCATTATAT ATACCCTATT CTCAATCTAT TTAATACGTA AAACATGAAA 5880

TTTTCTTATT AAATTTATTA TTTCCATCAT ATCATTACTT TTAATTTAAT GATGTTCAAT 5940

TTAAATATTA GGTCAATAAC ATATTTATGC TTTTTATGGA TACTTTCAAA AATAACAGCC 6000

CCAAACGATA ACTTGAAAGG GGCTGTTAAA TATTTAACTA TTGCATTTGA TCTATCATTT 6060

TCTTGTTTCT TTCAATCATT TTATCAAAAT ACGTATCGTA TCTTTGCCAT TCTTCTTGAG 6120

TTACATCTTG AACAGTAATC GTTTTGTTAA GCAATGTCTC TAATGAGGCC ATACAAGATG 6240

GTTCAATTTC AGGATATTTA AATTTAGTCA CTTCACCTTT TAAAGCATGT TCATAAAATG 6300

TTTGCATCAT CAATGCACGT TCTGAACCAG AGCCTTCAAC ACAAAGATAA ATTTGTACAG 6360

CAATACCGCC TCTAACTCTT CGTTGCGATA TGCCTGCAAA TTTCTTACCA TCGATACTTA 6420

AGTCAAATTT TCCTGGGCAA TAAGAATGTT CAATTTCCAT CGTATCAATA TCAACATTCT 6480

CATTTTCGAA CATTTTGCTA ATTAAGAGGT ACATCACAGT AAACGCTTCA TCAATCGTTG 6540

TTTCTGTTTG TCCTTTGAAC ATCAGCGATA TATTTAATAC ACCTTGATCT AGAACGACAC 6600

CTAAGCCACC AGAATTTCTA ACAATGGCAT TATAACCAAT CTCATTCGTT AAATAATCAA 6660

TGCCATCTTT TAAAAACGGC AATCTTGAAT CATGAATACC AAGAATAACA GTATGTTGAT 6720

GAATCCAAGT ACGCACAACA TTATCTGATA TATCTTTGCC CACACTTTCG CAAAATGTAT 6780

CATCGAATGC GAAAGATTGC ATAGGTTCTA ATCCAGAAGA ATGATCGATA TATCGCCAGT 6840

TGACGCCATT AAAATATTTA CTCGCTAAAT CCATCGTTAT TGTAAGGCTT GCGCTGCTGT 6900

AATAATTGAA AGATTGTATA CATCTTCAAT TGAGCAGCCA CGTGATAAGT CATTTACTGG 6960

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TAATTTAGCA CCTGGCGCTT TTTTCTCAGC AACACCTGGT ACAATCGCAG CATCAAATTG 7140

GAATTCGCCA TCAATGATTG CTTCTAATTT TtCTTCTTCA GCTTTTtGTT GTGCTAATTT 7200

GACAGCTTCT TGAACTTTTG TCACGTCGTC TGATTTAGCA GACCCTTTTG TTGAAAAGCT 7260

TAACATTGCA ACTTTTGGAT CCATGCCAAA GCTTAATGCT GATTTTGCAC TTTCTACTGC 7320

AATTTCTGCA AGTCCTTGTG AATCAAGTTC TGGATTGATT GCACAATCAC CAAAGATGTA 7380

TTGTTCATCA CCTTTAATCA TAAAGAAGAT ACCTGATGTT CTTGATACAC CTGGTTTCGT 7440

TTTGATGATT TGTAAAGCTG GACGCACAGT GTCGCCTGTT GAATGTGCTG CACCACTAAC 7500

TAAACCATCT GCTTTACCAG CATAAACAAG CATTGTACCG AAGTAGTTCA CATTGTTTAA 7560

TAATTCTTGT GCTTGTTCTT CAGTCGCTTT ACCTTTACGT CGTTCAACAA ATGATTGAAC 7620

TAATTCAGCT TTCAATTCAC TTGTCGCAGG ATTAATTAAT TCAATATTAG AAATATCAAG 7680

ATCAAGTTTT TGCGCTAAAG ATTGAACCTT AGTCTCATCA CCTAACACGA TTGGTGTAAC 7740

ATAATCTGTT GCTTGTAATT GTGTTGCAGC TGTTAGAACA CGTTCGTCCT CTCCTTCAGG 7800

TAATACGATT TTAACGTTTT TACCAGAAAG TTTGTCTTTT AATACATTTA ATAAATCAGC 7860

CATAATGTCC TCCTGTAATA TAAATCTTAT TAATCATTCA CGGTATAATT ATACGCCATT 7920

TATGATAAAA TTTATAAAGA ACTGATGATT TTTGAAAAGG AGCGATAAAC ATGAGTCAAG 8040

CAGCCGAAAC ATTAGATGGT TGGTATAGTC TACATTTATT TTATGCAGTT GATTGGGCAT 8100

CATTACGTAT AGTTCCAAAG GACGAACGCG ATGCACTTGT CACTGAATTT CAATCATTTT 8160

TAGAAAATAC AGCAACTGTA AGATCATCAA AATCTGGTGA TCAAGCTATT TATAATATAA 8220

CTGGTCAAAA AGCAGATTTG TTATTATGGT TCTTACGTCC TGAAATGAAG TCTTTAAATC 8280

ATATTGAAAA TGAATTTAAC AAATTGCGCA TTGCTGACTT CCTAATCCCT ACATATTCAT 8340

ATGTATCAGT CATTGAATTG AGCAATTATT TAGCTGGTAA ATCTGATGAA GATCCTTATG 8400

AGAACCCTCA TATCAAAGCA AGATTATACC CAGAATTACC ACATTCTGAT TATATTTGTT 8460

TCTATCCAAT GAACAAACGT CGTAATGAAA CTTATAACTG GTACATGTTA ACTATGGAAG 8520

AACGCCAAAA ATTAATGTAT GACCATGGTA TGATTGGTAG AAAATATGCT GGCAAAATCA 8580

AACAATTTAT TACTGGTTCT GTAGGGTTTG ATGATTTCGA ATGGGGCGTA ACATTGTTCT 8640

CAGATGACGT ATTACAATTC AAAAAAATTG TATACGAAAT GCGCTTTGAT GAAACAACAG 8700

CACGATACGG TGAATTCGGT AGTTTCTTTG TAGGACATAT TATTAACACA AACGAATTCG 8760

ATCAATTCTT TGCGATTTCT TAATACATTG GTACGTTTAT AAATTAATAA AAAAATTCCA 8820

AGCTTATCGG TTTAAGCTTG GAATTTTTCG TTTATCTTCA GTATATTCCC GTATACATAA 8880

GACGTGATTT GGTAAATAGT TGAAATCTGT ATGTTTAAAC TTATATATAT GTGCTAATGT 8940

ATTATCAATA ACAAAGtACA CTTTGCTCAT AGCAAgTsaC CCGAgTAGTC TTCCTTGGGA 9000

GAACTTTAAC TACTATCACT ACATATAAAC GTTAACCTCA ATAGAAATTA TACAGTCGCT 9060

ACTCTATACA ATTTTTGTAA TGGTTAACTA ATATTATTTT AACCTATTTG AAATATTTGA 9120

AACATATTTT TGTCGAATTT TTTTCAATAA TTTTTCCTTT TTATACTTCA AGAGAATTTT 9180

AACTACTAAA AATTCCGATG ATTATTATTA CAATAGTATC AAATATTAGT TTTTTAAAAT 9240

CAATAACAAC TTATCAAAAA GCTCATGTGG TTATTTTATA GTGTATAAAC TATAATGAGT 9300

ATTAAATTCT TATAAACAAT GGTGATGAAA TGGACATAAA TTCAGAAGAA TACAAACAAG 9360

AGGTACTTAT CAAAGACGTT GTCATGCTTG CTGCTCGCAT ACTATTAGAA TCTGGTGCAG 9420

AAGGTACGCG TGTAGAAGAT ACCATGACAC GTATTGCAAA AAAACTTGGT TACAGTGAAA 9480

GTAACAGCTT TGTTACAAAC ACTGTCATCC AGTTTACGTT ACATTCGGAA TCGTTTCCTA 9540

GAATATTTAG AATTACCTCT CGAGATACAA ACTTAATAAA AATTTCTCAA GCTAATAAAA 9600

TTTCGCGTCA AATTACAAAC AATGAAATTT CTTTAGCCGA AGCAAAAACG CAACTTGAAA 9660

AAATATATGT TGCTAAGCGT GACAGCAGTC TTCCCTTTAA AGGTTTTGCT GCAGCAATGA 9720

TAGCAGGTAG TCTAGGATAC CTAGTCACTG AGATTTTAGA TCGTAAGTwA CACGCACAGT 9840

TTATCCCAGA ATTCaTTGGT TCaTTAGTTA tTGGGATTAT CGCCGTTATT GGACATACAC 9900

TTATTCCAAC AGGTGACTTG GCAACTATTA TCATTGCGGC AGTCATGCCT ATTGTTCCTG 9960

GTGTATTAAT AACAAACGCA ATACAAGATT TATTTGGTGG ACACATGTTG ATGTTCACAA 10020

CGAAATCATT AGAAGCATTG GTTTnGCGTT TGGCATCGGT GCTGGCGTTG GTAGCGTATT 10080

AATTTTAGTA TAGGAGTATC AGACTATGTT TTGGATCTTA AACTTTATCT TTAGCTTTTT 10140

AGCTTC 10146

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2022 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

ATTTAATTGG TTGGTGGCGT ATTCTCnTTT CCAAGATTTG CCACGATTGG ATGTTCAGTC 60

GACAAATATG TAACCAGTCC CGATAAATTA CGTTCCTCAA TCATTGATAG TATGTCTGGT 120

GTTTGTAACG ATTTATCGAG TAAGGCATCA AGCAATTGAT AATGTCCCAA TACAACAAAA 180

TGCACGTTGT CTCTCAACTG CTGTTGAATA AACTGAATAA AGAGCTTTAA GCTCTGTTGC 240

ACATTCGCTA ATGATGGTGC ATAGTTTTCC AAACCAACTT GTACAGCCGC TTCATTATTC 300

CGAATGATTA AACCTGTGTA TGCCACTTTT GTTGCTGCAG TTGGATACAT TGAGTAATAA 360

CGCAATAATT GATCTGTAAA ATCATTTCGA AGTGCATAAA TTTGATGCTC ATGTTGCCAA 420

AAATTTCGCT CACCCATCTG CTgCAAATCC TCATGGTTCA ATTGTTTCCA GTCCAACTTT 480

TCAACCACAC TAAAATCAAC TAACTCATAA TCCGCTTTAT TAAAATATTT TAAAAATGCT 540

GTTTCCGATT CTTTTAACGC AATTAATTGT TCTGnATTAT TCACTCGACC ACCCTTTACT 600

TTCAATACTG TATTTAAAAT CACTTGGTAT TTTCGTTGTT TGCTTTACTT CTCTACCACG 660

CTAAAGTGTA ATATGATTAA TAACTTATCA TTTTTAGCAA TACATTACAA CCTTTTTCAG 720

AAAATTCGGT GTATTGATTT TAAAATTTTT TAAAATAnAA AAGGCAAGAC ATTTGTGCCT 780

ATAAAAATGC TTAACCAAGA TTTTTATATT GaAGTTGTAC TTCTTGCACA TATTGTCCTT 840

GCCTTATTAT GTAAAGTTAT TTTCTTTCTA TCTTTTTATT AAATTTAACT ATTCTTCATA 900

ATCCCGATTC CCTTTAAAGT AACGTCTATC TTGTTTACTA TATACATTTT CAGGATTAAA 960

TTGGTAAACG TTCGTTGCTG ATATATCTGT AAAATTGTTT GGACCGACAC CTGCAATAAA 1080

CTTAAACTCT GCTTCATCTA CCAAATAATC ATACGCTTGT GTATGTCTAT CCTGTGCGCC 1140

ATGTGGAAAT ACAAACATAT CTGTTTTACC TACAATTGGT TCAACTTCAT CTTTCCATCT 1200

TTTAGTATCA CGTTTAATAC CTTCTAAAGA TGTTTTTTCA AAATTAATGT GACCATATGA 1260

ATGACTCGCA AATGACCATC CATCCCGTTT CATTGCGCGA ACAACTTCCT CAGCTGCCTT 1320

TTTATTCTTT GTATAATCTT TACTCGTTAA TTCATTCGTG CGATAACCTA ATACGCCCTC 1380

ATAACCGGTT AAAGCAACAA CACCTTTTTC ACCATTTAAA GAAAAATCTG GATGCTCTTT 1440

TACAAATTTA TTTAAAATTG GCACGATATC ATTGTCATCA GAATAAGTAG CATGGCCTTT 1500

TTTGTCTGTA GTTTCAGAAA CAACATGTTT ATTTTTATCG AGTACTAAAC GGTCAGCATA 1560

ACCATGGTGT CTCATGTAAC TATAGTAATT CATATCATCA ATTGAGATGA TTAGTGGCTT 1620

TTTACCTTTC GGCAATTTTA TTTTTTTGGC TTTTACATGA TGAGATGATA AGTCGTATAC 1680

ATCATGTGGA TTAACGATGA TGTAATTATT TTTATATAAT TCGTTCAATG ATTTTTTAAA 1740

TTCACTTACA GTAATCATCC AATCATTGTT GCCCTTAGCT TGGTGTGTAT CTCCTGTAAA 1800

CGCAACTTTT GGGTCTGTAA TTAATGGGTG ATAAAACACA TGATAAACTT GGCCGTGATA 1860

TGTTTCCCAA TGTTCATCCA TTTTcGATTT aTGCTTTGCA TACTCATTTG GATTAACAGA 1920

TTTATTkTGA GCTTTCTCAT TTTGCTTGGA ACAGCTATAT mACAATGCAA CTGATAATAA 1980

CAGAAAAAAT AGCAATAAAT ATTTTTTATG CATTAAACAT TC 2022

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

ATAGAGTGAT AAAGGATGGT TGTCATATGA TAAATGCAGT AGTAATAGCA GTAATTTTAA 60

TGATTGTGCT ATGTTTATGT CGATTAAACG TnTTATTAAG CTTATTTATC AGTGCGCTAG 120

TTGGTGGCTT AATTTCAGGC ATGAGCATTG AAAAAGTTAT AAATGTATTT GGGAAAAATA 180

TAGTCGATGG TGCTGAGGTA GCATTAAGCT ATGCTTTATT AGGTGGATTT GCAGCATTAA 240

TTTCATACAG TGGTATCACA GACTATTTAG TAGGAAAAAT TATAAATGCA ATTCACGCTG 300

AAAATAGTCG ATGGTCAAGA GTTAAAGTCA AAGTGACAAT AATCATTGCA TTATTAGCTA 360

CACCATTGTT AAGTCTGTTT AATGACTTAA AAATAGATAG ACGTTTAATC GGTTTGATTA 480

TCGGTTTTGG TTTATGTTTC CCGTATGTGT TATTACCATA TGGATTCGGT CAAATTTTCC 540

AGCAAATTAT TCAAAGTGGC TTTGCAAAGG CAAATCACCC AATTGAGTTT AATATGATTT 600

GGAAAGCAAT GCTTATTCCT TCAATGGGGT ATATTGTTGG CTTACTTATC GGTTTATATG 660

TATATCGTAA ACCACGTGAA TATGAAACAC GTAAAATTTC AGATAGTGAC AATGTTACAG 720

AGTTAAAACC ATATATCTTA ATAGTAACAA TTGTAGCAAT ACTAGCTACA TTTTTAGTAC 780

AAACATTTAC AGATTCAATG ATTTTTGGTG CACTGGCAGG GGTACTCGTA TTCTTTATTT 840

CACGTGCATA TAATTGGTAT GAATTAGATG CTAAGTTTGT TGAAGGTATT AAAATTATGG 900

CTTATATTGG TGTAGTTATT TTAACAGCAA ATGGATTTGC TGGTGTAATG AATGCTACTG 960

GTGATATAGA TGAATTAGTT AAAACTTTAA CAAGTATTAC TGGTGATAAT AAATTATTTA 1020

GCATTATCAT GATGTATGTG ATAGGTTTAA TTGTCACTTT AGGTATTGGA TCATCATTTG 1080

CAACAATTCC TATTATCGCA TCATTATTCA TTCCTTTTGG AGCGTCAATT GGACTAGATA 1140

CAATGGCATT AATCGCATTG ATTGGAACAG CGAGTGCATT AGGTGACTCA GGTTCGCCTG 1200

CAAGTGATTC AACATTAGGA CCAACTGCGG GATTAAATGT TGATGGCCAm CATGATCATA 1260

TACGTGATAC ATGTGTACCA AACTTCTTGT TTTATAATAT TCCTTTAAAT GATTTTCGGT 1320

ACTATTGCTG CTATGGTACT 1340

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

CAAAATCTAA GAGAATAAnA TTTGTTAATT TnAAATAGCA AGCAATTCAA AGTTATATGT 60

GTAATAGATA AAATAGATAT CCCTATAGTG ATGCGTTACT AGCTAAACAT AATAACACAT 120

TAGAAGATAA TGAAGTTAAG GAGTTACTGG ATTGTTTCGA CTATGTAATT AAGTATAAAA 180

ATATCCAACG ACAAAACGTA ATTATAAAAT GGTAAAAGCT ATGGTACAGT TTCAAATTGC 240

TAATGACATG CGTATCGGTG AGCTACTTGC AATAAAGAGA GTAAATATAA ACTATGAAGA 300

TAAAACGCTA GATATCGACG GTAAAGTTAA TTGGATAACT GAAAAAAGAC GGGAGCATTC 360

GGAGTAAAGG AGACAACTGA AAGAAGTAAT AGCTATAAGG CCACAGGGCT CACTACCCAA 420

TATTCACAAA TACGTCTGGT AGCCCTATCG ACTCGAACAA AATTAGCCAC ATTATTAAAG 540

GGGGGCGCTG ATATTAGTTC TATTAAGAAA CCTATAACGA CGCATACATT ACATCATTCG 600

CATATATCTA CACTTGCTCA ATTAGGAATT AACTTAAAAG CAATGCAAGA GCATGTAGGT 660

CATTCAGATT ATAAAArAAA TCTAGAGATA TACACACATG TTACTAATCA GATGGCGAAA 720

GATATGATGA ATAAATTTGA ACGATTGGGG AGTTAAAATT GGAAAAAGAT GaTACACTAG 780

CAGAAATTAA GCCTATGCTC AATTTTGATG AGCAAATAGC AAAATTAAAA CAGATGAATA 840

TATTTTTTAA TATTATTGAC ACCGAAAAAG CAAATGAAAT TCTTAGAAAA AATAATTACT 900

TCTTCAAACT wGcTTATTTC CGaAAAAATT TCGrAAAAAA GaATGGCGGC TATTTCATAG 960

AATTTGCTTA TTTATCAGAT TTAGCAACTA TAGATATGaA ATTAAGATAC ACAATGTTGC 1020

ATTTAACTTT AGATATTGAA CATAGTTTAA AGTATCTAGT CTTAAAACTA ATAACAGAAA 1080

ATAACCAAGA AGATGGTTAT AAAATAATAG ATGAGTTCTT ATGTATTGaT AAATCATATA 1140

GCAATTCAAA TTTTGACACA AATTCAAGAA CACCAGAAGA AGTTATGGAA ACCAAAATCA 1200

AAAATAAAAA CGAAATATTC AAGCATATGA ATAAACGAGG ACAACTACCC GAGAAGTTGa 1260

ATAAATACTA TCmAAATCCA CCCGCnnGGk TTTGCaTTGr ATTCATGCAA CTAGGTCAAT 1320

TCGTTTCGTT TCTCAACTTC TATTACAAGA AGTACAATGA CGAAGAATTG AGAGTTGCTA 1380

ATATTTTAAT GCCTTTAGTT AAAAATATAA GAAaCAAATC AGCTCATAAC CAACCCATCA 1440

TAGCAAATCT AAATTATGAC AGTAGATTAC CTCAATATTT ATTTGAAAAA GGGAATAATA 1500

TAGGCATATC TAGAAACATG TTCGGAATAA AAAATTTCAT AGATACTkTC ksTACGCTAG 1560

AATTACATAA TCAAGTTTGT AGTAATGCAA TTATCCAAGC AAGATATCAC GATTTGGACC 1620

AACTTCAAAA GCGATATAAA AGrAACGrAA GCTATTATAA TAATGCATTA GCTATCAAAA 1680

GATTTTTTAT AGCTTTAGAT AAAATTATTG ACTTCAACAG ACCAAAAGTA TAAACTATCT 1740

AGTGAGGAAA GAGACTTATA GGTCTCGCGA GTTATTTTAA TTCGTATGCA AGAAAAAGAA 1800

GAGCTATGCA TTTTATTTAA AATGCGTAGT TCTTtTTTTA TGCATCTAAA TTCATATTAT 1860

TTTTGCAATA TAAACATATC TTTGTGCAAA TTCCGAACAC AAAACATTCA CATCATCCTT 1920

TTTtGCCCTT TTTCTATACC CCAAAACACA AAAAGCCCCG TAAGCCTATG CcTACGGGgT 1980

TTGACAATAA ATTATATATT ATTGTTCTTC TTTAACATAT GGTAATAATG CCATATGACG 2040

AGAACGTTTG ATAGCTGTAG TCAaCATACG TTGATATTTA GCTGAAGTAC CAGTTACACG 2100

ACGTGGTAAA ATTTTACCGC GTTCTGAGAT AAAACGTTTT AATAATTCAG TGTCTTTGTA 2160

GTCGATATGT GTAATACCAT TTGCTGTGAA ATAGCATACT TTTTTACGAC GACGTCCGCC 2220

CGTTAATTTT TATTAGAATG GTAAGTCATC ATCACTTATA TCAATCGGTC CGTTTGCATT 2340

TGCAAATGGA TTATCAGATT GTTTCGTGTT TGATGAATTA TTGTACGAAT TGTTTTGTCC 2400

TGATTGTTGA CCACCGAATC CTTGACCGTA ATCTTGGAAT TCATTTTGTT GACGTTGGCC 2460

ACCATTTTGT TGCGCATTTT TAGGTTCAAG GAATTGAACG CTATCACACA CAACTTCAGT 2520

AACAAACACA CGACGACCTT CTTGATTTTC ATAATTACGG GATTGTAAGC GACCATCTAC 2580

ACCAGCTAAA CTACCTTTAG ATAAATAGTT ATTTACATTA TCTGCTTGTC TTCTAAAAAC 2640

AACACAGTTA ATAAAATctG ctTCGCGCTC CCCTTGAGCA TTCGTGAACG TACGATTTAC 2700

TGCAAGAGTG AATGtCGCTA CACTCACACC TGAGGGAGTG GTTCTGTATT CCGGATCTTT 2760

CGTTAAACGA CCTACTAATA CAACTCTATT TAGCATTTAA ACGCCCCCTC TAATTATTAC 2820

TTGTCTTCGT CTTCACGAAT AACCATGTAA CGAATGATAT CGTCACTGAT TTTAGCTAGA 2880

CGTTGGAATT CGTCAGTAGC TTTGTTGTTA TCAGATTTAA CACGTACGAT GTTGTAGAAG 2940

CCATCTTTGA AATCATTGAT TTCATAAGCT AGGCGACGTT TACCCCAGTC TTTTGCTTCT 3000

AAAACTTCTG CACCTTCAGT AGCTAAGATA CCGTTGAAAC GTTCAACTAA CGCTTTTTTA 3060

GCATCTTCCT CAATGTTTGG GCGTACGATG TACATAACTT CATATGTTCT CATTTTATAT 3120

TTGCACCTCC TTGTGGTCTA TACGGCTTAT CAATCTTAAA ACAGATAAGC AAGGaATAAT 3180

TTTCATTACT CACAATAAAG AATTaTATCA TGCGCCATTA CTTTTTACAA TaATAATTcA 3240

AACTACTCTT CATATCATTT TTGATATTaA TTCATTTGaA ACTTTCnATG ATATTTTnAA 3300

AAATACACTT CACAAAAGCG AACATATGTn CTATAAnAGT TGTGAGGTGG TAAGGAATGA 3360

ATTTA 3365

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1032 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

GTTAAAAGTA ATTGGTGGTA TTGATGATGA TTTTACAGCC AATGTTATGC ATCCAAATCA 60

ATATCGAATT CGATATTCGT CTCAGAAACA GGACCTTAAT GAAGATATGA CAGTTTTTGA 120

TGCAGTATTA AGTTCTGATA CAACAACTTT ACGCATCATC AAGCAATATG AGCAGGCAGT 180

ACAAGCTTAT GCGGATGACC AAAGTGATAA ATTGTTCAAG CGAATGATGG ATGCGCAAGA 240

ACTAGGTATA CATGATACTA CTAAATACAT TAAAGAATTA TCCGGCGGAC AACAAAAACG 360

TGTTGTACTT GCTAAAACAT TAATAGAACA ACCAGATTTA TTGTTATTAG ATGAACCTAC 420

GAACCATTTA GACTTCGAAT CAATCAGCTG GTTGATCAAT TATGTGAAGC AATATCCTCA 480

TACTGTTTTA TTCGTAACCC ATGATCGATA TTTTTTAAAT GAAGTTTCCA CTAGAATTAT 540

TGAACTAAAC AGAGGTAAGT TAGCGTCATA TCCTGGTAAC TATGAATCTT ATATTGAAAT 600

GCGCGCTGAA AGAGAAGTAA CACTTCAAAA GCAACAACAA AAGCAACGAG CTTTATATAA 660

GGAAGAACTT GCTTGGATGA GGGCTGGgAG CTAaGGCTCG TACTACAAAG cAACAAGCTA 720

GAATTAATCG ATTTAATGAC CTAGAmAATG AAGTTaACCA GCAATATAAA GACGATAAAG 780

GTGAATTGAA TCTTGCTTAT TCaAGATTAG GTAAGCAAGT GTTCGAATTA GAAGACTTAT 840

CAAAGGCTAT TAATGATAAA GTATTATTTG AACATCTGAC GGAAATTATT CAAAAmGGTG 900

AGCGTATTGG TGTTGTTGGG CCAAATGGAG CTGGTAAAAC AACACTCTTA AATATTTTGA 960

GTGGAGAAGA CCAACAATTC GAAGGTAAAT TGAAGACTGG GCAGACGGTT AAAGTAGCTT 1020

ATTTTAAGCA AA 1032

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 852 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

TGTGATTAAC GAAGCTTATT TTCGTACACC TTCAACAACT GATTACAACG GCGTTTATCA 60

AGGTTATTAT ATTGATTTTG AAGCAAAGGA AACTAAAAAC AAGACGTCCT TTCCTTTAAA 120

TAATATTCAT GACCATCAAG TCGAACATAT GAAAAATGCA TATCAACAAA AAGGTATTGT 180

GTTTTTAATG ATTCGTTTTA AAACGCTAGA TGAAGTTTAT CTTTTACCCT ATTCAAAATT 240

CGAAGTATTT TGGAAGAGAT ATAAAGATAA TATTAAAAAG TCTATAACAG TTGATGAAAT 300

ACGAAAAAAT GGTTACCATA TTCCTTATCA GTATCAACCA AGATTAGACT ATCTAAAAGC 360

AGTTGATAAG TTGATATTAG ATGAAAGTGA GGACCGCGTA TGACGGAAAA CAAAGGATCT 420

TCTCAGCCTA AGAAAAACGG TAATAATGGT GGGAAATCCA ACTCAAAAAA GAATAGAAAT 480

GTGAAGAGAA CGATTATTAA GATTATTGGC TTCATGATTA TTGCATTTTT CGTTGTTCTT 540

TTACTAGGTA TCTTATTGTT TGCTTATTAT GCTTGGAAAG CACCTGCTTT TACCGAAGCT 600

TTAGATAATG GCCAAAGACA TGAGCATGTA AATTTAAAAG ACGTGCCGAA ATCAATGAAA 720

GACGCAGTAC TTGCAACTGA AGACAATCGT TTCTACGAAC ATGGCGCACT TGATTATAAA 780

CGTTTATTCG GTGCAATTGG TAAGAACTTG ACTGGTGGAT TTGGkTCtGA AGGtGCCTCA 840

ACATTAACAC AA 852

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5804 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

CACTTTTTTC ATTAAAAATC TCATATTTAT ACACTGAACG TAATCTCGAA TATTTTTCAA 60

CCCAAGTTTT AACTTTAACT TTTTCTGGAT AAAAAATAGA CTTTTTATAA TTGACATTGA 120

GGTCAGTCAC AGGTGAAATG ATTCCTTGTT TTTCCATATC AGCATAACTA AAACCTAACT 180

TCGATATATA ATCCAACCGC GCAACTTCAA ACCAAGTTGC ATAATTCCCG TGATAAATTA 240

CACCCATCTT ATCAGTTTCA GCATAACGCG CTTCTATTTC TGTAATACTA TATATCATTT 300

TAAGCCTTCT TTCAGTTTAA CTTTATATCT CATTCTAACA TAAAATACAA GAAGAGGCCG 360

GCCAAGAACA CAAAGGkTTT GAACCGACCT ATTATATCAT AAaGTTTATA GAAGTATTTT 420

TGAGCACTAT CAAAGTGCCT CAAATACCGA TTAAAATTTT ACTGTGATAT CTATTTTTTA 480

TTGCGCTAAT TTATTTCTTA AAACCATTTG TAAAATTCCA CCGTGACGAT AGTAATCCAT 540

TTCAACAAGT GAGTCAAAAC GAACCATAGC GTCAAATTCT ACCAAATCAC CATCTTGCTT 600

CTTAGCAGTA ACTTTGACGT AGtCATGTGG TTGAACATTT TCATCAATAT TAACAGrAAT 660

TTCTTCTGTA CCATCTAGAC CAAGAGAATC AGCTGATTCA CCTTTTTTAA ACTCTAATGG 720

TAATACACCC ATCATAACTA AATTTGAACG ATGGATACGT TCATAACTTT GTGCAATAAC 780

TGTTTTAACA CCTAATAAGT TTGTACCTTT TGCTGCCCAG TCACGAGATG AACCCATACC 840

ATAATCGTTA CCAGCTAATA CAACTAAACC TGTACCATCT TCTTTATATT TCATTGCAGC 900

ATCAAAGATA GGCATTACTT CATTTGTTGG CCAATAAGTT GTAAAACCAC CTTCAGTACC 960

TGGCGCTAAT TGGTTTTTAA TACGTATATT AGCAAACGTA CCTCGAACCA TTACTTCGTG 1020

ATTACCACGT CTTGAACCAT ATGAATTAAA TTCACGAATA GGCACTTGAT GATCTTGTAA 1080

ATATTTACCA GCTGGCGTAT CTTTACCAAT TGCACCTGCT GGAGAGATGT GGTCAGTTGT 1140

TTCTTTAGAT AATCCTTGGA AGAATGATGG ATTTTGAATG TATGTTGAAT TAGGATCAAA 1260

GTCATATAGA GGTTGATCAG TTACATCAAT CTCATTCCAT AATTCGTTGT TATTGTATAC 1320

GTTATTATAT TCTTCAATAA ATAATTCAGG TGTTACAACA CTATCAACGG TATCTGAAAC 1380

TTCTTTAATT GATGGCCAAA TATCTTTCAA ATATACATCT TCACCGTCAT TACCTTTACC 1440

AATAGGTTCA TTTTGTAAAT CAATATCAAC CGTTCCAGCT AATGCATAAG CAACAACTAA 1500

CTGTGGTGAA GCTAGGTAAT TGGCTTTAAC AAGAGGATGG ATACGACCTT CAAAGTTACG 1560

GTTACCAGAT AATACAGATG TCACTAATAG GTCCTCATCA GCAATCGCTT TTTCAATTTC 1620

TGGTAATAAA GGACCTGAAT TACCGATACA AGTTGTACAT CCATAACCAA CCAAGTTGAA 1680

GCCTAAATCA TCTAAATAAG GTTGTAAGCC AGCATCTCTT AAATATCCGG TAACAACTTT 1740

TGATCCTGGT GCTAGAGAAG TTTTAACGTA TTCAGGAACT TTCAAGCCTT TTTCAACTGC 1800

TTTTTTAGCA ACTAAACCTG cACCTAACAT TACATAAGGG TTAGATGTAT TTGTACATGA 1860

TGTAATTGCT GCTATTGCAA TATCACCTGT TTTCATTGTA GCTTTTGATC CATCTTTAAA 1920

GTTAATTTCA GCTTTCTTAT CAAATTCACT TTTATCTAAA CCGTGTCCTT GGTTGCCTGC 1980

TGGAGCTGTT ACAGAATTTT CAAATGATGA TTTCATATCA CTTAAGAAAA TTAAATCTTG 2040

AGGACGTTTT GGTCCTGAAA GCGATGCTTC AACTGTTGAT AAATCCAATT CGATAACATC 2100

TGTATAATTA GGATCTTCTT TCTCAACATC AAAGAACATA TGGTTTTGTT TCAAATATTC 2160

TTTTACTAGC GCGATATGTT CGTCTGATCT ACCAGTTAAC TTCATATATT TAAGAGATTC 2220

ATCATCAACT GGGAAGAATC CGCAAGTTGC TCCATACTCT GGTGCCATGT TTGCAATTGT 2280

AGCACGGTCT GCTAGTGGTA AATGTTGTAC ACCTGGACCA AAGAACTCCA CAAATTTACC 2340

AACAACACCT TTTTTACGTA GCTCTTGAGT TACTCTTAAC GCTAAATCAG TTGCTGTTGC 2400

GCCTTGTGGT AATGAATTTA CTAGTCGTAC ACCAATAACC TCTGGAATTG GGAAATAAGA 2460

AGGTTGTCCA AGCATTCCAG CTTCAGCTTC AATACCACCA ACACCCCATC CTAGTACGCC 2520

AATACCATTT ATCATTGTTG TATGTGAATC AGTACCAACT AATGTATCTG GAAATGCAGT 2580

TTTTTCACCA TCTACATCAC GAACATGTAC AACACTTGCT AAATATTCTA AGTTAACTTG 2640

GTGAACTATT CCAGTTGCAG GAGGAACTGC ATTGTAATTA TCAAATGCTT TCGTTGCCCA 2700

ATTTAAAAAC TGATAACGTT CATAGTTACG TTCAAATTCT AATTTCATAT TACGTTCAAG 2760

AGCTTCTGGA TTTGCATAGC TATCCACTTG AACTGAGTGG TCAATAACTA AATCCACCGG 2820

TACTTCTGGA TTAATTTTAG TAATATCTCC CCCAACGTCA TCCATTGCTT TACGTAAAGA 2880

AGCTAAATCA ACTACGGCTG GTACACCTGT GAAATCTTGT AAAATAACAC GAGAAGGTTT 2940

GTCTGTAATT ACAAAATCAT CTTCTTGACG AAGTAAAGAT TCTAACAAAA CACGAATTGA 3060

ATAAGGTAAA TTGGAAACTT TAGTAATACC TTGCTCTTCT ACAGCTTTTA AATCATAGTA 3120

AGTATAACTT TGGCCATTCA AGTCAAAATG TTTTTTTGAT TGCTCTTTAA AATTTGCAGC 3180

CATTTAATGA TCCCCCTTGA TACATTTTTA TATTTATATG CCTTGATTAA ATTGTATTAT 3240

TATATTTATT GATAAACAAC TCATCATGCT TAGAAAACGC TTAATTTAGG TTTTGACTTT 3300

TTAATCAGAG TATATAAGCA AAACTTATCA TACAGGTAAG GTGTAATAAG TATTTTTTAT 3360

TAATTGAGAA TAATTATCAA TTTCGCGAAT GATTCAATTC AATTTTTAAA CGTATTATTT 3420

CATTGAGCAG AAAGAAAATT ATGGCACCAA ACTTTAATAT TTTTTTCAAT GTCATTCTTT 3480

TGATGGGAGT GGGACAGAAA TGATATTTTC GCAAAATTTA TTTCGTCGTC CCACCCCAAC 3540

TTGCATTGTC TGTAGAAATT GGGAATCCAA TTTCTCTTTG TTGGGGCCCA TCCCCAACTT 3600

GCACATTATT GTAAGCTGAC TTTTCGTCAG CTTCTGTGTT GGGGCCCTCA CCCCAACTCG 3660

CATTGCCTGT AGAATTTCTT TTCGAAATTC TCTGTGTTGG GGCCCCTGAC TAGAATTGAA 3720

AAAAGCTTGT TACAAGCGCA TTTTCGTTCA GTCAACTACT GCCAATATAA CTTCGTAGAG 3780

CATAGAATAT TGATTTATGT CCCAGCCTGA GTTAATTTTC TATAAAAGTA TATTTAATTT 3840

GCGTTTATAC CGTCAAACTT CACTTTAGCT TTGTCAAACC CCTTTCTATT AAGTTTTCAG 3900

AAATAAACCT ATCTTAAAAT ATAAAAAAAT CGAGAATTCG TAGTTTAATA ACGAAATTCT 3960

CGTTCTTATC CTTTTGAATA TACTCAATTT TCCACAAAAA CAAACAAGTA GTATATCTGT 4020

TCTAGCTACT AGAATGACAT ACTACTTGTT ATTAAAATAC TTAACTAAAC TTTATTAGTT 4080

ATCTTTTTTC TCTATATTTC TACGTGACTG ACGCTTTTCA AGAATGTCAG ATTCATAATC 4140

TTCTTGTTGA CTCTTGATAT ATTCTTGTAA GCGATGTTTA TTCGGAGTCA ATGTTAAACC 4200

TAGGAATTTA CGTTCCTGGT TCGCATCCTT GTAGAAACTT ACCATCATGA GTATGACGAC 4260

AAAGGAGAAT GGGAATGCAC TTATAATTGC AGCACTTTGA ATCGCATTTA AAGCTTCAGC 4320

GCCGTTACCG CCACCAGCTA ATAAAAGTAC AAATGCTATT AAGGCCTGTG AAATTCCCCA 4380

AACAACTTTT ACCATACTAG ATGGATTTAA TGAACCAAAT GTTGTTTGCA TTCCTAATAC 4440

AAATGTTGCT GAGTCAGCAG ATGTAATAAA GAATGATGCA ATTAATAATA ATGCAATCAA 4500

CGATAAAACA ATGCCAAATG GCACATGATT AAACACTCCA AATAGCTGTG TTTCAGGAGT 4560

CATATCAAAA ATTTCTTTGT GTTTCTTACC TGTCTCGATG CCTAATACAC CAAAGACACT 4620

AAACCAAACA AAACTAACAA TTGCTGGAAC TAGCAAGACA CCAGAAATGA ACTCTCTAAT 4680

TGAACGTCCT TTTGAAACTC GTGCAATAAA CACTCCAACG AATGGACTCC AACTTAACCA 4740

TGCTGTATCA AAACTATTAA ACAAGAATGT GTTTAGTAAA CTACCCGTAG AGCTAGTTAA 4860

CATATTTAAA ATAAGAACAG TTGGTCCAAC AATTAAAGCA GCTACCATTA AAATAGTACC 4920

TAAACCAATG TTCAAGTTAC TTAAGTATTG AATACCTTTA CTTAATCCAG ACCATGCACT 4980

TGCTATAAAT AAGATAGTAA CAACAATGAT GATAATCGCT TGTACAAACG TATTGTTTGG 5040

AACATTGAAC AAGTAATGTA AACCACCATT AATTTGTAGA GCACCCATAC CTAACGAAAC 5100

GGCTACCCCA ACGATTGTCG CAAATACAGA TAAAACGTCA ATAAAAATCC CAATAGGACC 5160

TTCTACTTTA TCACCTAAAA GAGGACGTAA AGTTCTAGAT AATAAACCTG GTTCACCTTT 5220

ACGGAATTGC GAATATGCCA ACGTAACGCA ACAACACCAT AAACAGCCCA AGCATGGAAT 5280

CCCCAATGGA AAAATGTTGA ACGTAGAGCT TCAGTATAAG CTTCAGTAGT TTTGGGATCT 5340

GCTGTAGGTG GCGTAGCAAA GTGCGCCATC GGTTCAGCTG CACCATAAAA CACCAAACCT 5400

ATCCCCATAC CAGCACTAAA CAACATAGCA AACCATGAAA TTGTATTAAA CTCAGGTTTG 5460

TCATTTGGTT TACCTAGTTT AAGTTTTCCA ATAGGACTAA AAATAAGGAA TATACAGAAG 5520

AACACGATAA TCGTAGTAAG AATAAGATAA TACCAACCTA ACTTTTCTGT AATCCACATT 5580

TTAATATTAT TGGTAACATA GTTGAATTGT TCAGGTAAAA ATGCACCAAG TAATACGACT 5640

ATAGCAACAA CAATTGCACT ATAGATGAAG ACTGGTGAAT ACTTCTTTCC ATTTGGATTC 5700

TCTGGTGAAG AAGAATTCAT AATTAATTAC TCCCTTCAAT TCTATATTTA ATTTTATGTA 5760

GTAGAATAAA AATATTATCT AAACATTTTA TTCAATAACT CACG 5804

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

ACCCGCGAAT ATGGTCCATC CTATCGATTT ATTTTTAACT GGTTTGACAA TATTTAATTT 60

TTCATAATCA TTCTTAGTGA TTTTGACATA TGTTTTCGGT ATGAGCCAGT TAATAAATGG 120

AAAGAAGAAG ACAATCCAAT TACTTGCCAA ATCaATCATT AAATATTCAC TATCGTATTT 180

GATTATTCGA TATTTAGGGT TTTTATTAAT AACTTTAGAT TCGCAAAGCA ATGTCTCCAC 240

ATCCCTTTAA TTTTATGTGT AATACATTTT TCGATACTTC AAAAGACATT CAAATACTAT 300

CAAGTTACTG TCATCAAAGG TTTTATTAAC TGATATTtTC ATATTTTTAa TCTGAATTTA 360

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 964 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

CCAGGGTGCG GAAAGCTTTA AAATTTGGAC TAATAAAGAT GCTGATATTA ATTCTATGAA 60

AACAGCAGTT TTACAACAAT TAAAAGGAGA ATAACATATG CTTACTGGcA AACAAAAAAG 120

ATACTTAAGA AGTTTAGCAC ACAATATTGA TCCGATTTTT CAAATTGGAA AAGGCGGTAT 180

CAACGAAAAT ATGATTAAAC AAATAGATGA TACGTTAGAA AACAGAGAAT TGATTAAAGT 240

ACATGTACTA CAAAATAACT TTGATGATAA AAAAGAATTA GCTGAAACAT TAAGCGAAGC 300

TACTCATAGT GAATTAGTGC AAGTGATTGG ATCTATGATA GTGATTTATA GAGAATCTAA 360

AGATAATAAA GAAATTGAAT TGCCATAATA ATGAAAAAGA TAryACTTTA CGGCGGTCAG 420

TTTAACCCTA TCCATACTGC ACATATGATA GTAGCTAGCG AAGTATTTCA TGAATTACAG 480

CCAGATGAAT TTTATTTTTT ACCTAGTTTT ATGTCTCCAT TGAAAAAGCA CCATGATTTT 540

ATAGACGTTC AGCACAGATT AACAATGATA CAGATGATTA TCGACGAGCT TGGTTTTGGA 600

GATATTTGTG ACGATGAAAT TAAACGTGGT GGTCAAAGTT ATACCTATGA CACGATCAAG 660

GCATTCAAGG AGCAACACAA AGACAGTGAG TTGTACTTTG TTATTGGGAC GGATCAGTAT 720

AACCAACTAG AGAAATGGTA TCAAATTGAA TACTTAAAAG AAATGGTTAC TTTTGTAGTT 780

GTAAATCGAG ACAAAAATAG TCAAAATGTT GAAAATGCTA TGATTGCAAT TCAGATACCT 840

AGGGTAGATA TAAGTTCGAC AATGATTCGA CAAAGAGTTA GTGAAGGGAA ATCTATCCAA 900

GTTCTTGTTC CTAAATCCGT TGAAAACTAT ATTAAGGGGG AAGGATTATA TGAACATTGA 960

AAAA 964

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

TTGTCATGAA ATAAATGGGA TGAATATCAC GACTAGAAGT AATGTTACGA ACAGGAGCGT 120

ATAAACTAGA GACGCTAAAT TCGACATAGT ATGTnGCTCA ATTATGGCTG ATGATGAATT 180

TAAAGTATGT GCGTTGGAAC TGTCGGATTT TTGTTCATAA TGTTTTGCAT ATTGCGCCAT 240

GATGAATAGT GTAAAAATAA ATAAAACAAT AAGAGATATA ATGCCCATAA TCAAAAGTAT 300

TTGTTTAGAG CCTTTCATTA TTTCACATCC TTTCTAAAAT ATATTTGTAA CTAAATTTAA 360

AATAGTTATT TTTGTAATTC TAAACCTTTT TCATCGCGAA AACAATTAAA TAGGTCGCGG 420

TATTAATTAT TATATTATTA CCGCTTAATA TGAAAAATAC ATGAaAATTA ATTTTCTAAT 480

ATACTTTTGA AAAATTATTA CAAATTAGCC CCTTCAAAAC GCGAAAACAT AAGGATTCTA 540

GTTTCAAAAG GGCTGATAAG CATAAAATGA AATGTAATAT TTCGATGTAT AAAATTTTTA 600

ATTAGCTAAA AATCATCGCA TTAATTTTTT GAGCTACATC ATCAAAATTC GGACATTTTA 660

ACGACACATA TAATTTAATT TTAGGTTCAG TACCAGAAGG ACGTAAAGCG ATAAATCCTT 720

CGTCAAATAA GACACGAATA ACATTTGATT TAGGAGAATT AATCTGCGAC GTTGTATCTT 780

TATCCAAATG ATAAACCTCG CTAGTTAAAT AATCTTCAAT TGCTTTCACT TTGAGTCCTT 840

GAATCTCTTG CGGTGGATTT GAACGGAATT TGGTCATTAT TGCATTAATT TTCTTTTTCC 900

CTTCAAATCC TTCTAGCGTA TGCGgAATAA TGTATCCTCA TGTCTACCAA CAGTTTGATA 960

AATCTGTTCT AATTCATCTT TCAATGTTTT GCCATATAAT TTTAACTCAG AAGCGTATTT 1020

TATAATGAGT GGCACAATTT GTACGGCATC TTTATCACGT ACAAAAGGCT CTGATAGAAA 1080

ACCGTAACTC TCTTCAAATG CGAAAATCAT ATTTGATGAT CATCCAGTTG TCTTATTTCC 1140

TGAGCAATAA ATTTAAGCCC GTCAGCACCT CTTTGGTATT CAACATTATT ATA 1193

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1098 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

TATCAGGATG ATTATGnCGG GGTTTTATTA AGTCTGAGCG TATATnCCTT TTATTCTCCT 60

AAATGGTTTG GAATTCAAGG AGAAGACGAT GAAATGGTAT CCAAAAACCA AnGAATATAT 120

nGCATTAAGT CTGAGGATGA TAGTGCGGTG GCAATTCGTT CATTAATTTT GCATAAAGAT 180

GAACCTATGT ATTTAAAAAA ACGTACATGT GTACCTACTT TGTTAATTAA TGGGGAACAT 240

AAAAAAATCT TCGAACATTC AGGACATGCA CCGCATATTG AAGAACCAGA AGCATTTATG 360

AATTATTATT TAAAATTTTT AAAAAGCGTA TCATAATATG TGATATATAA ACCTAGGGCA 420

TAAAGTCCTT AGGCAATGTG AAAAAGCTGA TTACTATTCA TTATTTGATA GAAATCAGCT 480

TTTTTTGAAA TGTATTTGAT ATATACTGCT CGTTATGCGG CTATCTTCCT TATATTAAGT 540

GCCATTAGTG CAAAACCTCT TAACAATTAG GTAAAAAGAG CATAAAAAAA GGAAGTTTAA 600

TAGAATGTAT CATCTATCAA ACTTCACCAA ATTGCGCTAA ACAAAATTAT AGTTCAATTT 660

CGTTGTTTGC TTCAGTGATT CGTTTATTTA CTCGACTCAA TAATGATTCG ATTTTTTTAC 720

GTTGTTGTGC ATTAACAAGA ATTAATACAG TTCTTTCATC ATGCTCATTA CGTTTTTTAT 780

CGAAGTAATC TTCTTGAGAT AAAATTTTAA CTGCTTTAAC AACTTGTGGT TGTTTGTAGT 840

TTAAATGATT AATAATATCt TTAAGATAGT ATTCTTTCTC TTTGTTTTCG CTGATGTATG 900

TCAATACAGC GAATTCTTCA AAGCTAATTG AnAATTCCTT TTTAATTAAA CTTTTTAATT 960

TGTCAGCATA AGTGACCATT GATAACAACT CAAAGCAATC ATTGATTTTT GTAATTGCCA 1020

TGTTTAAAAC CTCCCTATTT GATGCATCTT GCTCGATACA TTTGCCCCGA TAATATAnTG 1080

TATCTAATCT TTATGnAT 1098

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2881 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

CCAGGTAAAA TTGTGCAATC ATTTGACGCA TTAATGGACG CCTTGGACAA TGAAGATTAT 60

GAAGGAGAAA AAGTCATTCC ATTCTTAGAT AAACATTTTA AATATCAAGA TGGCCGATCA 120

AGTGAGCGTT TAGTCAGAAA TTTATTTGGT AGCTAAGTTT ATATAGTAGT CAAAGTGGGA 180

GAGGTATAAT GATGAAATTT TCAGTAATAG TTCCAACATr CAATTCAGAA AAGTATATAA 240

CAGAATTACT TAATAGCCTT GCGAAACAAG ATTTTCCGAA AACTGAATTT GAAGTGGTTG 300

TAGTTGATGA CTGTTCAACA GATCAAACGT TACAAATAGT TGAAAAGTAT CGCAATAAAT 360

TGAACTTGAA AGTAAGTCAA CTCGAAACAA ATTCTGGTGG TCCAGGTAAA CCTAGAAATG 420

kGGCGTTAAA ACAAGCAGAA GGTGAATTTG TATTATTTGT GGACTCCGAT GACTATATAA 480

ACAAAGAGAC TTTAAAGGAT GCAGCAGCAT TTATTGATGA ACATCACTCA GATGTCTTAT 540

CACCTGAAGT TACTTTGTTA AATTCAAGAA TTATCTATAC TTTAAGCCCG ACTAAAATCT 660

ATAGAACAGC ATTACTAAAA GATAATGACA TTTATTTTCC AGAAGAATTA AAGAGTGCAG 720

AAGATCAATT ATTTACAATG AAAGCATATT TAAATGCAAA TCGAATCAGT GTGTTAAGTG 780

ATAAAGCGTA TTATTATGCT ACAAAGCGTG AAGGTGAACA TATGAGTAGT GCGTATGTTT 840

CACCTGAAGA CTTTTATGAA GTCATGAGAT TGATTGCTGT AGAAATATTA AATGCAGATT 900

TAGAAGAAGC CCATAAAAAT CAAATCTTAG CAGAATTTTT AAATCGTCAT TTTAGTTTTT 960

CTCGTACGAA TGGCTTCTCA CTTAAAGTTA AACTAGAAGA TCAACCACAA TGGATTAATG 1020

CTCTAGGAGA CTTTATACAA GCAGTTCCAG AACGTGTAGA TGCATTGGTG ATGAGTAAAT 1080

TACGACCATT GTTGCACTAC GCGAGAGCGA AAGATATAGA CAACTATAGA ACTGTGGAAG 1140

AAAGTTACCG TCAAGGTCAA TACTACCGTT TTGATATTGT AGATGGTAAA TTAAACATTC 1200

AATTCAATGA AGGCGAACCA TACTTTAAAG GCATTGATAT CGCTAAGCCA AAAGTGAAAA 1260

TGACAGCATT TAAATTTGAT AATCATAAAA TTGTTACAGA GCTAACGTTA AATGAATTTA 1320

TGATTGGCGA AGGACATTAT GATGTCAGAC TTAAATTACA TTCACGAAAC AAGAAGCACA 1380

CAATGTATGT ACCTTTAAGT GTCAATGCGA ATAAACAATA TCGTTTTAAC ATTATGTTAG 1440

AAGATATTAA AGCGTATTTA CCTAAAGAAA AAATTTGGGA TGTTTTCTTA GAAGTCCAAA 1500

TAGGTACGGA AGTATTTGAA GTGCGTGTTG GTAATCAACG TAATAAATAT GCATATACTG 1560

CAGAAACAAG TGCATTAATT CATTTGAATA ATGATTTTTA TAGATTAACA CCGTATTTCA 1620

CAAAAGACTT TAATAACATT TCGTTATACT TTACAGCTAT TACATTAACG GATTCAATCT 1680

CATTGAAGTT AAAAGGTAAA AACAAAATCA TTTTAACTGG TCTGGATCGT GGTTATGTAT 1740

TTGAAGAAGG TATGGCTAGT GTCGTACTAA AAGACGACAT GGTGATGGGA ATGTTAAGCC 1800

AAACATCAGA AAACGAAGTG CnAAATCTTA CTTAGCAAAG ATATTAAAAA GCGAGACTTC 1860

AAAAATATTG TTAAGTTAAA CACTGCACAT ATCACTTATC CACTAAATAA ATAATAAATG 1920

CCCTCAAATC ATTGTGAGCC AACATGATTT GAGGGCTTTA TTTTGCTGTT TATGACATGA 1980

TTATGACATT TCCCTGATTT TCATTTTCAT ATACATTAAA TTGTATACAC TGGAAATGAG 2040

GAGGTTATCT ATAATGATAA ATAAAAATGA CATAGTAGCA GATGTAGTAA CTGATTATCC 2100

GAAAGCAGCG GATATTTTTA GAAGTGTGGG AATAGATTTT TGTTGTGGCG GACAAGTAAG 2160

TATAGAAGCA GCAGCCTTAG AAAAGAAAAA TGTAGATTTG AACGAATTAT TACAGCGTCT 2220

CAACGACGTT GAACAAACGA ATACACCAGG TTCGTTAAAT CCTAAATTTT TAAATGTTTC 2280

ATCACTTATT CAATATATTC AATCAGCATA TCATGAACCT CTAAGAGAAG AATTTAAAAA 2340

TGAGTTAAAA GAAACATACG ATACATTTAA AAATGGCATG TTAGAGCATA TGCAAAAAGA 2460

AGACGATGTC GATTTTCCAA AACTCATTAA ATATGAGCAA GGTGAGGTAG TAGACGATAT 2520

TAATACTGTG ATAGATGATT TAGTTTCAGA CCACATTGCA ACGGGAGAAT TGTTAGTAAA 2580

AATGAGCGAA TTAACATCTA GTTATGAACC TCCGATAGAA GCGTGTGGTA CTTGGCGACT 2640

TGTTTATCAG AGATTAAAAG CACTTGAAGT GTTAACACAT GAACACGTAC ATTTAGAGAA 2700

TCACGTATTA TTTAAAAAAG TATCATAAAT AACGCGATTA GAAACTGTTG GCAAAAATAA 2760

GTCCAGCAGT TTTTCGCTAT GTATAAAAGT CATAATAGTG ACATAAACAG CATTATTTGA 2820

AAAGAAnAAT GGTCAACTTA GCATAAAAAT TGATATGAAn ATTTAATGGT ATAGATAATT 2880

A 2881

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1056 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

ACCGTCGAAT ATCGCTTGTG ATTTACAATT TGTGTATTAA GATGCTCAAC TAATTTGGGT 60

ACATATTCCG AATTTAGATT TGCAAGTACA ACAATTCCAT AATTTTGTTT TGGATTTAGT 120

AAAATAAATG ATGAAAAGTT ATCTAGCGTT CCTGAATGAA ACACTAAATG TTCATCATTA 180

TTGGTAAACC AGCCGGAAGC ATATGCATTG GCATTAGGTT CACCAATTGT TGAAGATAAA 240

TTTTTATGTG ATTGTTGAAC TAATGATTTG TATTTATCAG GTGGATTAAG TTGGAATTTT 300

ATCGAATGTT CCAAATCTTC AGTTGATGTC ATCATATATG CTGATGGTGT ATCCCAAAGG 360

TTAAATTCAG GTTTAGAGAC GACAGGTGTC GAACCTTGTA ATTCATAGCC AATAGCATCA 420

TGTTTTGATT TGTAATTGGT TTGTTTGAAT GATGTATGTG TCATATGCAA AGGCTTGAGC 480

CATGAATTTG TAATATATTT TGTATAGGAT TGCTTCGTAA CGTTTTGGAT AATTAAACCT 540

AATAAATCAT AGTTCATATT TGAGTATTCA AATTCTTCTC CGGGCTTATG ATGTAATTCA 600

TCACCCATAA TTGCATGGGT TACATCATTT AAACGATTAT TTTTGCTTGT CACAGAATCT 660

tCGCTTGTAA TAtCACTAGG TATACCACTT GTTTGAGCCA AAAGTTGCTT AATCGTAATA 720

GTTTCATTTT GACCATTATA GTTCATTTTA AAATGAGGCA CATGTTTGGA TACGGCATCA 780

TTTAAGTTTA ATCGACCTTC TTGAGCTAAT TTTAAAATTG CAAGACCTGT GAAAGCTTTC 840

TGATAACCAT AACCTTTATT TAAAAAAACT TTGCCATTTT TTACTAyTAA AATTGATGCT 960

CCAGGAATGT GTCCCTTTTG TAAATCATGC TCGATAATTG TATCTATTTG TTGTTGCGAA 1020

TCATTGGTTA ACCGTGTCTT CGTATTGCTA TTTAAT 1056

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

ATGCCaCACT TATTGGTGGC AGGATCGACG GGTAGTGGTA AATCTGTTTG TATAAATGGT 60

ATTATTACAA GTATTTTATT AAATGCTAAG CCGCATGAAG TTAAACTTAT GTTAATCGAT 120

CCGAAAATGG TTGAACTAAA TGTTTATAAC GGAATTCCAC ACTTATTAAT TCCGGTTGTT 180

ACAAATCCTC ATAAAGCTGC TCAAGCTTTA GAAAAAATTG TAGCTGAGAT GGAAAGACGT 240

TATGATTTAT TCCAACATTC ATCAACTAGA AACATTAAAG GTTATAACGA ATTAATCCGT 300

AAGCAAAATC AAGAATTAGA TGAGAAGCAA CCAGAATTAC CTTATATCGT TGTTATTGTA 360

GATGAGCTTG CAGATTTAAT GATGGTAGCT GGTAAAGAAG TTGAAAATGC GATTCAACGT 420

ATTACACAAA TGGCACGTGC AGCAGGTATA CATTTAATTG TAGCGACACA AAGACCTTCT 480

GTGGATGTAA TTACAGGTAT CATTAAAAAT AATATTCCAT CTAGAATAGC TTTTGCTGTG 540

AGTTCTCAAA CAGATTCAAG AACTATTATT GGTACTGGCG GCGCAGAAAA GTkACTTGGT 600

AAAGGTGACA TGTTATACGT TGGAAATGGT GACTCATCAC AAACACGTAT TCAAGGGGCG 660

TTTTTAAGTG ACCAAGAGGT GCAAGATGTT GTAAATTATG TAGTAGAACA ACAACAGGCA 720

AATTATGTAA AAGAAATGGA ACCAGATGCA CCAGTGGATA AATCGGAAAT GAAAAGTGAA 780

GATGCTTTAT ATGaTGAAGC GTATTTGTTT GTTGTTGaAC AACAAAAGGC aAGTACATCA 840

TTGTTACAAC GCCAATTTaG AATTGGtTAT AATAGAGCAT CTAGGTTGAT GGATGATTTA 900

GAACGCAATC AGGTAATCGG TCCACAAAAA GGAAGCAAGC CTAGACAAGT TTTAATAGAT 960

CTTAATAATG ACGAGGTGTA AAAAAATGTC AGAAATGAAT GCGGTATATA ACGTTAAACA 1020

ATaCATTTtA AATTTgATTA AGCAAAATAA ATTGGAATAT GGTGACCAAC TTCCAAGTAA 1080

TTTATCAATT GCCAGAGAAT TAAATGTAAA AACCGACGAT GTTTATGAAG CAATTCAGcA 1140

TTGATTACTG AACAAGTCAT TAAAGATAtT TTGAAGAGGG CACAAGTGTT AAGTCACTGC 1200

GrtTTGAATG CGGAACT 1277

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

TACCGTCGTT TTATGyGTCA AATTTTACAG TAAATTTTGC TTCATCAAAA GAAATAACCT 60

TTAACAAGTA TAGTAATTTT ACATTTTACA ATGTTACAAA ATATAATTTT TTATAATTAG 120

TTAAAATCAC TAAAACGCTT TTATACACTA TCAAATCAGC ATTTATAAAA ATATGAACCG 180

ATATCCTAAA ATGTTAATAA TATTACAAGA TAATAACArA CCACACAAAG CTACTTATTT 240

TTGATAATAT GGAAATCGTA ATATAAAACn AAAACTTAAT TTACTATATA AATTGTCTTA 300

ATAATTTTTA AAAGTAGTAA AACATAATTT TAAGGAGGAG TCCCTTTGAA AAAATTAGCA 360

TTTGCAATAA CAGCAACATC TGGTGCAGCT GCATTTTTAA CGCATCATGA TGCACAAGCT 420

TCTACACAAC ATACAGTACA ATCTGGTGAA TCATTATGGA GTATTGCTCA AAAATACAAC 480

ACTTCAGTAG AGAGTATTAA ACAAAATAAC CAATTAGATA ACAACTTGGT ATTCCCTGGT 540

CAAGTTATCT CAGTAGGTGG AAGTGATGCA CAAAATACGT CAAACACTTC TCCACAAGCT 600

GGTTCAGCAT CATCTCATAC TGTACAAGCT GGTGAATCAT TAAATATCAT TGCTAGCAGA 660

TATGGTGTTT CAGTTGATCA ATTAATGGCA GCCAATAACT TACGTGGTTA TTTAATTATG 720

CCTAACCAAA CATTACAAAT TCCTAATGGT GGATCAGGTG GTACAACACC AACAGCTACA 780

ACAGGTAGCA ATGGCAATGC ATCATCTTTT AATCACCAAA ATTTATACAC TGCTGGTCAA 840

TGTACATGGT ACGTATTTGA CCGTCGTGCT CAAGCTGGTA GTCCAATTAG CACATATTGG 900

TCAGACGCTA AGTATTGGGC TGGTAACGCA GCTAATGATG GTTACCAAGT AAACAACACA 960

CCATCAGTTG GTTCAATTAT GCAAAGCACA CCTGGTCCAT ATGGTCATGT TGCTTATGTT 1020

GAACGTGTCA ATGGTGATGG TAGTATCTTG ATTTCTGAAA TGAATTACAC ATATGGTCCA 1080

TACAATATGA ACTACCGTAC AATTCCAGCT TCAGAAGTTT CTAGCTATGC ATTCATCCAT 1140

TAATTAAATA AATTGTACTG ATATATACTA GCAATTCACA TCATGTGAGA TTGCTAGTTT 1200

TTTATTTTTG AAAAAAATTT TCATTTTGGT ACAAAAAATT ATCTCACCCT TCCCTATCAT 1260

ACATATTTAT ATTTTGTATG AATGGTAGTT AGGTAAAAAT TAACAACCTA CCTATTTGAT 1320

ATTTAATTTG TTATACCAGT ATTTTACGCT TTTTCGTCTA CATATACAAA TTTATATTAA 1440

ATAAAGCCCA ATACAATTTA GGTTAATTAA ACAAGTTGAT AACTATTTAA TTATTCCTTC 1500

ATTGAAGAAT ATAAACTATT AAATCATTAT TTTGCTCTTA CATATATTTT AATGACCTAA 1560

CTGaTTATGT TCCATGGAAT ACATTTATAA TATAGCCTCC TAATTAArAT GCyTTGTCTT 1620

GGTCATTCTA CGTAAATTCT ATAAAATATG TTATCTACTT ACATAArArn CTGrACTTCA 1680

ATACCACCAT ATGTTTGTGA TACTGAAGTT CAGTTTAGTT TTATTTTCAA TTAGAAAAAT 1740

AAGTTAAGTA TATAGAATAG TAAACCTGCT AACAATGCTG AAATAGGTAA TGTAATCACC 1800

CATGTAATGA TCATTCGTTG CGCAgTGCTC CATTTTACAC CTTTAGCTCG GTTAGAAGCA 1860

CCAACACCTA AGATTGATGA TGACACAACG TGAGTTGTTG ATAATGGGAA ATGTAGCGAT 1920

GATGCAACAA AAATTGTTAA TGCAGATGAT AAATCGGCCG CAGCACCATT TGCTGGACGT 1980

ATTTTCATAA TATTACCACC TACAGTTTTG ATAATTTTCC AGCCACCAAT TGCAGTACCA 2040

AGCCCCATTG cTGTCGCACA GGCAAATTTT ACCCATAACT GTGGTTCAAC ACTGCCATCA 2100

TTCTGTACAT TAGCGACAAT CAATGCCAAC GTAATAATAC CCATTGATTT TTGCGCATCA 2160

TTCGTACCGT GAGAGAATGA TTGTAACGCT GCTGTGAAAA TTTGGAAAAA TCTAAAGTTA 2220

CGATTCGCTC TTGTTAAATT TGCATTTTTA AAGATAACTT TAAAAATTGA ATACATCAAG 2280

AAACCAACAC AAAATGCGAT AATCGGTGAA ACGATTAATA CAATAATAAT TTTTGTGAAA 2340

CCTTGGTAAT GTAACACTCC AAATGAGCCT TCAGATGCGA TTGCTGCACC CGCAATTGAA 2400

CCTATAAGTG CATGTGAAGA CGAACTTGGA ATTCCGTAAA ACCAAGTAGC TAAATTCCAA 2460

ATAATAGCCG CAAGTATTGC AGCTAACACA ACAACTAATC CATTTTCCAA TTTAAATGGA 2520

TCGACAATGT CTTTAGTAAT GGTGCCTGCA ACGCCCGTAA ATGTTAAAGC ACCTATAAAG 2580

TTCATCACTG CTGCCATTAA AATTGCCGTT TTAGGgTTAA CGCTCTAGTA GATACAGCAG 2640

TAGCTACTGC ATTGGcTGTA TCATGGAaTC CcATTGATAA AGTCAAATAT CAGCGAGAAA 2700

ATAACTACAG CTATAGTGAC GATGATTATA TATGACATAA ATATATACTC CCCTTAGCTA 2760

TTTTTCATAA TAATAGTTTC AAAATTATTT GCTACGATTT GACATTTATC AGCGATTTCT 2820

TCCATGCTTT CATAAATATC TTTTATTTTA ATTAAAGTGA TTGGATCTGT TTCGCTATTG 2880

AAAATATGTT TAATTGACTG TCTTAAAATA CCATCACAGT TTGTTTCAAA TTCTTTAATA 2940

TTAATTGAAT GAATACGCAT ATGTGATAAT TTTTTATCGA CTAATAAGCC GACAGCAAGT 3000

TTCATTTCTG CAACTGCTTT TTGAATGTTA TCAACAAACT CAGCCATATA TTCATCTGTG 3060

TATTCGATTG AATACATTTC AAACATrGCT GCCGTTTCTT CAATTGCATC TAAAACATCA 3120

TTTAAATCAG TAATTACTTG ATGTACTAAt tCGcACCATG TGACTCATAA GTTTTAATGT 3240

TGTCTGAGTA TGCTTTTAAA TCTAAATGTG TATTGAAATC CATTTTACCG AATTCAATAG 3300

CAGCACGATC CAGATTGAAA ACCATCTCTT CTAATTGAAC CATAAACTTA TCTTTTTTCT 3360

TACTAAACAT TTAAAATCCT CCATTTAAGC GATTGTCACC AATCACATTC AGTTATAATT 3420

TGTTTCAAAT TAAGACAAGT GAATTTACAA ACTAATGATA CAAATTTGTT ATTATCAATC 3480

GTCAGTATAA TTTTAGTGTA CTGATATTAA TTTCAAAAAT GCCTCACAGT AAACAATTTA 3540

CTGTATTTGC CCTTATA 3557

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1631 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AACTATACAT TTCGAAAAAT TCTTCTAGTG AACCTGCGCC ACCAGGAGCC ATGACAAATG 60

CATCTGCAAG TTCTGCCATT TTATTTTnAC GTTCATGCAT AGAATCAACT AAAATTAATT 120

CAGTTAAACG TTGGCTTGTG ATTTCATGTT CATCTAACAT TTTAGGCATG ACGCCAATAG 180

CTTTGCCGCC ATGATCTAAT ACACCATCTT GaATGGCACC CATAATGCCA ATTGACCCTG 240

CACCAAATAC TAATTCATAA CCTTGTTCAG CAAAATATTT ACCTAAATCG TATGCTTTTT 300

GTACATATGA AGGGTCATGA CCTTTGCTTG CACCACAATA AACTGCGATT CGTTTCATGT 360

TAATCCAGCT CCTTAATTCG ATGAATGACT TTTAATAGTG ATTGTTCAAA CACTTTTTGA 420

TCTTGCTTTG TAAAAGGTGG GGGACCTTTG TGGCGACCAC CTTGTTTTCT AATTTGTGCA 480

TTCATATATC GTTTATCTAA TAGTTGTTGA ATATTTTTGG AATTGTATAT CTTCCCATTA 540

TGATGCATGA CAATTAAGAC TTTGTCGACT AATAAACTTG CGAGTCCATA ATCTTGAGTG 600

ACTACGATAT CATCCTTCGT TGATAATTGA ACAATTTTGT AATCAACTGC ATCTGGTCCA 660

TCATCAACAT ATAATGTTGA TACATGTGGA GGATATAATT GGTTCGAAAA ATGGCTGAAG 720

CTCCGAATAA TTGTCACAAA AATGCCTGTC TCAGTTGTTA AATCTATAAT AGAATCAACA 780

ACAGGACAAG CATCTCCATC AATAATAATA TGTGTCACAA TTATGCCTCT GTATTGTTTT 840

CTTTATTTTG TTGAGAGGCG CTTTTGGCAA CATAATCTTT ATATTTTTTA AATGACTTGA 900

TGCGTGCTTT ATCAGCTTCT TGTTGGCGTT TTTGTTCTTC TTTGTGTCGT TTTTCAATAT 960

CGCCTTTTTT CTCAGTTTTC TCATCTAATT TATTAGGTGT TAAGCCTGCT TTTTCTTCGT 1080

ATTTTTGTGA TTTTTTCATA TCTTTAATAC GTTGTATTTC ATTCTTTTCG CGGGCTTTTT 1140

GCTCTTCTTT ATGACGCTTT TCGATATTTT TTTGAAGTAT TTTATTCATT TTATCAGCGT 1200

CTTTACGATT TTGTTTAGCT AATTTTTCGC CTTTTTTCTC AATATAGGCA GGATCATGTT 1260

CTCTAGCAAA CTTTTTAAGT TCACGTTTAT TTTCAAAATC TTGTTTTTTA TCGCCGACAT 1320

ATTCTTTAAC ATCACTCGCT GTGTTACTGA TTGCTGCAGA TGTTTTTGAA GCAACTTTAC 1380

TTGTAGCATC TGTAACTTTT TGTACGTCCG GATGTTGTTT GATACGTTTA CGTTCAACAA 1440

TTAACGGTAC CAATACAATT GGTAATACAT TAATCATAAA TTTGATGACT TTTTTCTTAT 1500

CCATAGATCT TGcCTCCaTA ATTACTTTAT TAAtTTTACa TACCCtATGa TACATCAATA 1560

TAAACGATGA TAGTAGTGAA TCACTATTAA GTATTTCAGA TGTTTtTTAA AAgaAGaCCC 1620

AATTAnAAAA A 1631

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6645 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

CGAAATCATG ATTTAATGCT TTTTCATATA AGCTTTTCCA ATTAATCTTT CGTCCATGAT 60

ATTCTTCAAC TGTTGCTAGA TATTGTGCAA TTTTAGTTAC TTTAAAGGAG TGTGCTGCAA 120

CaTTGTGkTC mAAATATTTA AATTTTCCaG GtAATCTTAT AAGTCTTTCC aTATCTGATA 180

ATCTtTTAAA ATATTGATGT ACACCCATTT CAATTACCTC CTCCATTAAT TAATCATAAA 240

TTATACTTTC TTTTTACATA TCAATCAATT AAATATCATT TaAATATCTT CTTTaTATAA 300

cTCTGATTAA ATGATACCAA AAAATCCtCT CAACCTGTTA CTTAAACAGG CTAAGAGGAT 360

AGTCTTGTCT TGATATATTA CTTAGTGGAT GTAATTATAT TTTCCTGGAT TTAAAATTGT 420

TCTTGAAGAT TTAACATTAA ATCCAGCATA GTTCATTTCA GAAACAGTAA TTGTTCCATT 480

AGGGTTTACA GATTCAACAA CACCAACATG TCCATATGGA CCAGCAGCTG TTTGGAAAAT 540

AGCGCCAACT TCTGGTGTTT TATCTACTTT AAATCCTGCA ACTTTTGCTG CGTAATTCCA 600

GTTATTTGCA TTGCCCCATA AACTTCCTAT ACTTCTACCT AATTGTGCAC GACGATCGAA 660

AGCATAATAT GTGCAGTTTC CATAAGCATA TAAGTTTCCT CTGTTAGCAA CTGATTTATT 720

TACATTAACT GTCTTAGTTA CTGCTTGCTT AGGTGCTTGC TTAACTACTA CTTTTTTAGA 840

TGCTTGTTGT ACAGGTTGTT TTACTACCTT TTTAGCTTGG CTTGCTTTTC TTACTGGTGA 900

TTTAACCGCT TTAGTTTGTT TCACTTTATT TTGAGGCACA AGTGAAATCA CGTCACCAGG 960

AAAAATTAAA GGTGTTACAC CAGGATTGTA TGAATATAAT TGATTCAACG TTAAGTGATG 1020

CTCTAAAGCA ATCTTATATA ATGAATCGCC AGCAACTACT GTATAAGTTG TCGGTGATTG 1080

CGTTTGTGCT TGAACATTTG ATACATAATT ATGTTGAACA GGTGTTTTTA CTTGTGTGCC 1140

ATGTTGTTGT GCATGTGCTG CATTATTTAA AGCTAAAAAA GCTAACACTG ACGAAACCGT 1200

CACTGTAAGA GATTTTTTCA TCTTGCTGTC ATTCCTTTGC TGTTAGTATT TTAAGTATGC 1260

AAATACTATA GCACAATACA TTTTGTCAAA AGCTATTGTT ATAACGATGT AATCAAATGG 1320

TTAACAATAT AAAAAGAATA CAACCTTTTA TCATAGTGTA AAATGTATTC ATACCATGTA 1380

ATTGAGAACG TTTTCAATAA TTAATTCAAT ACCTTGAAAA TCGCCATAGG TAATATTACT 1440

AAATGCACAC TGCATATGTT GTTTTAACAA ACACAACTTT TAAAAAATAT ATTCTAACTC 1500

TATCTACCGA ATTGTACTTA AATATTCATA AACAAATCAT ATTCCAAAAT CTAATTTACA 1560

ATTTATTTAG CTACCTTTAA AAAAACCAAA AACCGACGCC CTTTTAGAGC CTCGGTTTTA 1620

AAATATATAT TAATCGTGCG ACATTGTCTG TCTTAAATAT GATTCGATAA ATGGTCCAAT 1680

GTCTCCATCC ATCACTGCAT CAACCTTACC TGTTTCTTCG TTCGTACGAT GATCTTTCAC 1740

CATTGAGTAT GGATGGAAAA CATATGATCT AATTTGGCTT CCCCAGCCGA TTTCTTTTTG 1800

TTCGCCACGA ATTTCAGCCA TTTCACGTGC CTGCTCTTCC AATTTTAATT GATATAATTT 1860

AGACTTTAAC ATTTTCATAG CTGCTTCACG GTTTTTAATT TGAGAACGTT CATTTTGGTT 1920

ATTAACAACT ATACCTGAGG GGTGGTGGGT AATTCGTATT GCCGATTCAG TTTTGTTAAT 1980

ATGCTGACCA CCTGCACCAG AAGCTCTGAA TGTATCAACT GTAATATCAT CCGGATTGAT 2040

TTCAATCTCT ATTTCATCAT TATTAAAATC TGGAATAACG TCGCATGATG CAAATGATGT 2100

ATGACGACGT CCTGATGAAT CAAATGGAGA AATTCGTACT AGTCGGTGTA CACCTTTTTC 2160

AGCTTTTAAA TAACCATAAG CATTATGCCC TTTGATGAGC AATGTTACAC TTTTAATCCC 2220

CGCTTCATCC CCAGGTAGAT AATCAACAGT TTCAACTTTA AAGCCTTTCT TCTCACAATA 2280

ACGTTGATAC ATTCTAAATA GCATATTAGC CCAATCTTGA GACTCCGTGC CACCTGCACC 2340

AGGATGTAAC TCTAGAATTG CGTTATTGGC ATCGTGAGGC CCATCTAATA ATAATTGCAA 2400

TTCGTATTCA TCCACTTTAG CCTTAAAATT AATGACCTCT TGCTCTAAGT CTTCTTTCAT 2460

TTCTTCATCA AATTCTTCTT GTAATAAATC CCAAGTAGCA TCCATGTCAT CTACTTCTGC 2520

TTGCGCTTTC GTTTGGTTAT CCCAAAAATT AGGTTCTGCC ATCATTTCTT CATATTCTTG 2640

AATATTAGTT TCTTTGTTCT CTAAGTCAAA GAGACCCCCT AATTTGTGTT AAATCTTGAT 2700

TATACTTATC TATATTTCGT TTGATTTCTG ATAATTCCAT AGcATTCGCT CCTATTTATA 2760

TTTCAATTCA AGTCATTGAT TTGCATCTTT TATAATGCTA AATTTTAACA TAATTTTGTT 2820

AAATAACAAT GTTAAGAAAT ATAAGCACAC TGACAATTAG TTTATGCATT TATTGTTAAA 2880

AATCAGTACA TTTATCATCG ACATATGCCT AAACCGATTT TTTAAAACTA AGTACATAAC 2940

AACGTTTAAC AACTTCTTCA CATTTTTTAA AGTATTTAAC GCTTGTAAAA TAAAAAGACT 3000

CCTCCCATAA CACAAACTAT AGGTGTTTAA TTGGAAGGAG TTATTTTATA TCATTTATTT 3060

TCCATGGCAA TTTTTGAATT TTTTACCACT ACCACATGGA CAATCATCGT TACGACCAAC 3120

TTGATCGCCT TTAACGATTG GTTTCGGTTT CACTTTTTCT TTACCATCTT CAGCTGAAAC 3180

GTGcTTCGCT TCACCAAACT CTGTTGTTTT TTCACGTTCA ATATTATCTT CAACTTGTAC 3240

TACAGATTTT AAAATGAATT TACAAGTATC TTCTTCAATA TTTTGCATCA TGATATCAAA 3300

TAATTCATGA CCTTCATTTT GATAGTCACG TAATGGATTT TGTTGTGCAT AAGAACGTAA 3360

GTGAATACCT TGACGTAATT GATCCATTGT GTCGATATGA TCAGTCCAAT GGCTATCAAT 3420

AGAACGAaGT AAAATCATAC GCTCAAACTC ATTCATTTGT TCTTCTAAGA TATCTTTTTG 3480

ACTTTGATAT GCTGCTTCAA TCTTAGCCCA AACGACTTCG AAAATATCTT CAGCATCTTT 3540

ACCTTTGATA TCATCCTCTG TAATGTCACC TTCTTGTAAG AAGATGTCAT TAATGTAGTC 3600

GATGAATGGT TGATATTCAG GCTCGTCATC TGCTGTATTA ATATAGTAAT TGATACTACG 3660

TTGTAACGTT GAACGTAGCA TTGCATCTAC AACTTGAGAG CTGTCTTCTT CATCAATAAT 3720

ACTATTTCTT TCGTTATAGA TAATTTCACG TTGTTTACGT AATACTTCAT CGTATTCTAA 3780

GATACGTTTA CGCGCGTCGA AGTTATTACC TTCTACACGT TTTTGTGCTG ATTCTACAGC 3840

TCTTGATACC ATTTTTGATT CAATTGGTGT AGAGTCATCT AAACCTAGTC GGCTCATCAT 3900

TTTCTGTAAA CGTTCAGAAC CAAAACGAAT CATTAATTCA TCTTGTAATG ATAAATAGAA 3960

GCGACTATCC CCTTTATCAC CTTGACGTCC AGAACGACCA CGTAACTGGT CATCAATACG 4020

ACGAGATTCA TGTCGCTCTG TACCTATTAC TGCTAAACCG CCTAATTCCT CTACGCCTTC 4080

ACCTAATTTG ATATCTGTAC CACGACCAGC CATGTTAGTG GCAATAGTAA CGGCACCTTT 4140

TTGTCCAGCG CCTGCAACAA TTTCAGCTTC ACGTTCATGA TTTTTCGCAT TTAACACATC 4200

ATGACGGATA CCACGTTTTT TAAGTAAATT TGAAATATAT TCAGAAGTCT CAACTGCAAC 4260

AGTACCTAAT AGCACTGGTT GCCCTGCCTT GTGTTTTTCA ACAACATCTT CTACTACTGC 4320

TTTATTTGTC GGAATTTGAG TTACTGTCAT GTTATAAATA TTTCTAAATT CTTCTTCTTC 4440

AGTTTTAGCT GTACCTGTCA TACCCGCAAG TTTATTGTAC ATTCTGAAAT AGTTTTGGAA 4500

TGTAATAGAC GCCATAGTTT TAGATTCATT TTGAATTTGA ACGCCTTCCT TCGCTTCAAT 4560

AGCTTGGTGT AAACCTTCCG AGAAACGACG GCCTGGCATT GTACGTCCTG TAAATTGATC 4620

GACAATTAAT ACTTCGCCAT CAACAACCAT ATAGTCTACG TCACGTTGTA ATGTAACGTG 4680

CGCACGTAAA GCTGTGTTGA TATGACTAAT AACATCAACA TTTTGTACAT CATATAAGTT 4740

TTCAACTTTG AACATACGTT CAGCTTTATC CGCACCTTGT TCTGTTAAAT GTACAGCTTT 4800

CGTTTTTTCA TCGTATTTAT AATCTTCGTC CTGTTTTAAC ATTTTCGCAA AAACATTTGC 4860

TTGTGTATAA AGTGACGTTG ACTTTTCAGC TTCACCAGAA ATAATTAATG GCGTACGTGC 4920

CTCGTCGATT AAAATTGAGT CAACCTCATC AATGATTGCA AAATGTAATG GACGCATTAC 4980

TCTATCTTCA GAATAATTCA CCATGTTATC TCGTAAGTAA TCAAAACCTA GCTCATTATT 5040

AGTACTGTAA GTAATGTCTT GTGCGTATGC TTCACGTTTT TCTTCTGTCG TCTTACTGTT 5100

TAAGTTTAAT CCGACAGTCA AACCTAAGAA GTTATATAAC TCAGCCATTT CTTCACTTTG 5160

AACACTTGAT AAGTATTCAT TGACTGTAAT AACGTGAACA CCTCTACCAG CTAATGCATT 5220

TAAGTATGTT GGCATTGTCG CTGTTAATGT TTTACCTTCA CCTGTTCTCA TCTCAGCGAT 5280

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AGCAAGTTTA CCTAACTGTT TAATTTCTTT ATTATTGCCA TCAAGAATTT TTGATAAAAA 5580

TCCCATTTCG TTCGCTCCTT TAGCTAAAAA ACTGTTTGGC CTACAACAAT ATATCTTATC 5640

ATTTATAGTT AGAAAATTAT ACTTATTTAC TCATTTGTAG AATCAATATA AATATATTTA 5700

TGACATACTT CATTCACATT CTGTTGTCAA CAAGTTTATC ACTAATAAAT ATATTCTCAA 5760

TACGCAATTA TACTTCCTAA TAAATTATAT TATAAATATT TTACGATTTT CGACTCGGAC 5820

TATACAATAG ACTGACATAC TATTATTAAC TTAACATTCA AATATATACA TCCATTAACA 5880

TTAGCATAGT CACTATGTTT CATTCAACAA ATTACATTAT CGAACTATGA AATAGTCATA 5940

ATTTGCTTTT GGAGTATAAA AAAGCACTTG TGCAAAAACA CAAGTGCTTT AAACTTAATT 6000

TATTGTTCAC TAGTTTGAAT CAAGCCATAT TTACCGTCTT TACGGCGGTA AACGATACTT 6060

GTTCCATCAG TTTCTCTGTC TGTGAATACA AAGAAGTCAT GACCTAATAG ATTCATTTGT 6120

ATCTCGTTAT CATCGTAAGC GTCATTATCA ACTTGTGTTT CTTGCATTTC TTGTAATTCG 6240

GCAACAAACA CTTCTTGATC TCCTCGATCA CGGCTCTTAC GATTAATACG TGTTTTATAT 6300

TTTCGAACTT GTCTTTCAAG TTTATTATTA ATTAAATcAA TACCTGCGTA TAAATCATCG 6360

TTTCGCTCTT CAGCTCTTAA CGTAACATTT TTCAATGGAA TTGTTACTTC AATTTTAGTA 6420

GCTGAATTTG AATAAGTTTT AACTTTAACA TGCGCCACTG CATTTGGTAC GTCATTAAAA 6480

TAACGTTCCA ACTTACCAAT TTTTTCCkCA ATATAGTTGC GAATAGCATC TGTGATAGTG 6540

AGGTTATCTC CATGAATTTC AAATCTAATC ATAGTAAATC TCTCCTTAAA CCTCTTTATn 6600

GGnAACTCnT TATTATATTT AACATTTTTA CGCCAATCGT GCAAA 6645

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7430 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

CAGTTCCAGC ACAtCTATTG GGGATCAACA AACTAGGGAA AATGCTAATT ATCAACGTGA 60

AAACGGTGTT GACGAACAGC AACATACTGA AAATTTAACT AAGAACTTGC ATAATGATAA 120

AACAATATCA GAAGAAAATC ATCGTAAAAC AGATGATTTG AATAAAGATC AACTAAAGGA 180

TGATAAAAAA TCATCGCTTA ATAATAAAAA TATTCAACGT GATACAACAA AAAATAACAA 240

TGCTAATCCT AGCGATGTAA ATCAAGGGTT AGAACAGGCT ATTAATGATG GTAAACAAAG 300

TAAAGTGGCG TCACAGCAAC AGTCAAAAGA GGCAGATAAT AGTCAAGATT CAAACGCTAA 360

TAACAATCTA CCTTCACAAA GTCGAATAAA GGAAGCACCA TCATTAAATA AGTTAGATCA 420

AACAAGTCAA CGAGAAATTG TTAATGAGAC AGAAATAGAG AAAGTACAAC CACAACAAAA 480

TAATCAAGCG AATGATAAAA TTACTAACTA CAATTTTAAC AATGAACAAG AAGTGAAaCC 540

TCAAAAAGAC GAAAAAACAC TATCAGTTTC AGATTTAAAA AACAATCAAA AATCACCAGT 600

AGAACCAACA AAGGACAATG ACAAGAAAAA TGGATTAAAT TTATTAAAAA GTAGTGCAGT 660

AGCAACGTTA CCAAACAAAG GGACAAAGGA ACTTACTGCA AAAGCGAAAG ATGATCAAAC 720

GAATAAAGTT GCCAAACAAG GGCAGTATAA AAATCAGGAT CCTATCGTTT TAGTGCATGG 780

TTTCAATGGG TTTACAGATG ATATTAATCC TTCAGTGTTA GCTCATTATT GGGGCGGTAA 840

TAAAATGAAC ATTCGCCAAG ATTTAGAAGA AAATGGTTAC AAAGCTTATG AAGCAAGTAT 900

TCGTGTAGAT TATGGTGCAG CACATGCAGC AAAATATGGA CATGAACGTT ATGGAAAAAC 1020

ATACGAaGGA ATTTACAAAG ACTGGAAACC AGGACAGAAG GTACACCTAG TTGGACATAG 1080

TATGGGCGGT CAAACGATAC GTCAACTAGA AGAATTACTG CGTAATGGTA ATCGTGAAGA 1140

AATAGAGTAT CAAAAGAAAC ATGGTGGcGA AATTTCTCCA CTATTCAAAG GTAATCATGA 1200

CAATATGATT TCATCAATTA CTACTTTAGG AACACCACAT AATGGTACAC ACGCATCAGA 1260

TTTAGCTGGT AATGAAGCTT TAGTGAGACA AATCGTATTT GATATCGGTA AAATGTTTGG 1320

TAATAAAAAT TCAAGAGTAG ACTTCGGGTT GGCTCAATGG GGTCTAAAAC AGAAGCCAAA 1380

TGAATCATAT ATTGATTATG TCAAACGCGT TAAACAATCT AATTTATGGA AATCAAAAGA 1440

TAATGGATTT TACGATCTGA CGCGTGAGGG TGCAnCAGAT TTAAATCGTA AAACGTCGTT 1500

GAACCCTAAC ATTGTGTATA AAACATACAC TGGTGAAGCA ACGCACAAAG CATTAAATAG 1560

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TCAACATCCA TTTAATCAAG CTTATACAAA AGCGACAGAT AAAATTCAAA AAGGCATTTG 1740

GCAAGTGACG CCTACAAAAC ATGATTGGGA TCATGTTGAC TTTGTAGGAC AAGACAGTTC 1800

TGATACAGTG CGCACAAGAG AAGAATTACA AGATTTTTGG CATCATTTAG CAGACGATTT 1860

AGTGAAAACT GAAAAGCTGA CTGATACTAA GCAAGCATAA TTTATAAAGT AAAGGGAGGA 1920

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ATTATTCAAG TAAAACATTG GCGAGGCCCC AACATAAAGA ATTTCGAAAA GAAATTCTAC 2040

AAACAATGCA AGTTGGCGGG GCCCCAACAA AGAAGCTGGC GGAAAGTCAG CTTACAATAA 2100

TGTGCAAGTT GGCGGGGCCC CAACATAGAA GCTGGCGGAA AGTCAGGTTA CAATAATGTG 2160

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TGATATCGCT AGAAAGACCA TTGTATTATC CTCAAATATA TTTGTATATG CAAACAATGA 2520

GTCTAGAATG ATTGGATGTA ATAAATAAAT AAAGAATGAG AAAGCACTAA TCATTTGAAT 2580

CGTATTAAAT AACATTGTTT TAAAATGCGT GCAAATACCC AAGATAACAA TAAACATAAT 2640

ACTATTATAT GGTGTTAATG AATATGAAAA GCTGGTAACG TTCCAATAGT CTCCaTTTGT 2700

TCTAAGAAAT TTAATACACG TTCGTAGTTA TAACCCATAT ATGCACCTAA GAAGAAATAA 2820

AAAATCCATC CGAATATTAT AGTATTTTCA CTTAATGGAT AATAGTGTAG CACGGTATCG 2880

TGAAACGCTG TGTTGTTCGT AAAGTAATAT AAAAATGATT GCTGTAAAAT AAAAGATAAC 2940

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AATCCCATTA ATATGTAAGG AATAAGTATA TATTTTACGC GTGTAGTTAA GTATCTATAG 3180

GTGACTTTTT GGTAATTCAA GGTTGTCAGT AACTGTGACA AGATAATAAA GCAAGGTGTA 3240

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TCATGTTTTA AAGTAATTTG TGTAAGTAAA TGTGTGATAA TAATAATTGC ACATATAATA 3360

GCACGTAAAT ATACGAGTTC AAGTCTAATC TTTTTCATGG AATCCGTCCC ATCTCTTAAT 3420

TAAATGCTCA AAAGCATCAT CACTAATTAA TATTCTAGGG ATGTAATAAT CATTGGAGTT 3480

CGGAGTGACT GCTTTTTCCT CTAATGAAAA ACCGTATTTT AACCCAGCTT TTTTGATTAC 3540

CGGTAATTTA TCGTCATTCA TCAAGCCATA AGGATAGGCT ATAGTTTTCT GCGACTTTTT 3600

AAAGTTTTTA GTTAGATATT TTTCACTTTT GTTTAAATCT TTTATGATTG TAGCTTCAGA 3660

AGCTTTCATT AATTTTGACT TATTATTTTT AGATAAGTTA TGCAAATCGT GGGTATGTGT 3720

TTCAAATTCC CATAACCCAG TTTTATACAT TTCTTTTAGT TCTTTTTTAC TAATCATATC 3780

GAGGTTGTGA AAGTTTTCTT CCCCAACATG ACCTGTGATA ATAAACCCAG TTGCCGGTAT 3840

TTTATATTTT TTTAAGATTG GATAAGCATT TTCATAAATA GTTTCATCCA TATCATCAAA 3900

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CAAGGTTAAA AATTTAGCAT CATGTGATTT TAGCCATTTT ATTTGAGATT CAAATTGTGA 4020

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TACAGGCAAT ATGATCAAGA TACTCAACAC TAAAATTATA AATTTTCTAT ACTTCACGAT 4260

TCTCTTCCTC TCTGCCATTT TTGAATCAAT ATGCTAATTG TAAAAAATAC AAAAATGATA 4320

ATCGCGAAAA TGCCCATAGT TTCAAATATA TCTAAAATTT CAGTATTTTC AATGTTTAAA 4380

GCAACACGTA TTGTATTGAT ACTTTCGTCA TGAATTTCAA ATATAGTACC AATATAAACG 4440

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CGTTAATAAT CCAGTATACT GTCGGATACC AACTTACAAA TATGAGTCCA GCCATATTCT 4680

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TAGTATTGAc TGCGCCAGCA AGTGTCTGAC TtCGCTTAAT ACAGCCAATT AAACTTGCAT 5220

ATTCTATCGT TTGAATTTTA CCTAAAATAG AACTCTTATT TCGAATTCTA GGATTACCTG 5280

TAACTGCACC AAGTTTTGGA TCATGTTTGA AATTCTCAAT CATATAATAT GGTGCATCTT 5340

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TATTTTCTTT GATTTTATAG ATGAGTTCTG CTGTATTATC TGAACTTCCA TCATTAATGA 5520

TAATAATTTC TTTCTTCTCG TATTTGAGTG CAAGAACATT AGACAACGTA TCTTCAAyCG 5580

TTTCACTTTC GTTATAACAG GCAAGTAAAA ATGTAATGCC TTCTAATTCA TCCACATTTA 5640

TGTCAGGCTT CTTGTTCAAT GAATATCTAA TTTCTCTGGT AAAATAGAAA TAAATTGAAC 5700

CGACAATCCA GTAAATAGAC ATAAATACAG GATAAAAAAG CAAAAAGTTA AAAAATTGCA 5760

ATTTCTTTAC CTACCTTTCG TTAGTTAGGT TGTAAGCCAT ATGGTAATTG ATAGTATTTT 5820

AATTTGCAAT AGATTGTTGT TATAATTAAA CGGAAATATT TGTAATTGCA ACTTAATTTT 5880

CCTGTAACAT AGTGTGATTA ATTTTCAGTA GGGGGTTATA AAAATTGAAG GATAAGATTA 5940

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TCGACATCGA AGAAAGGTAT ATTAGAATGT ACGTTCAATT ATCTAATACG CCTGAGGAAT 6240

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TGCTGTTTCT TGAAAGTTGG TATTTGAAAG CATCCTTTTC GCAAAAATTT GGAGCAGTGG 6420

AAGAAAGTAA AAGTCAATTC AAAGATGAAG TGTATTCGCT ACTAAATATA TTTTTGAAGA 6480

AATAATTTTT GTTACTAGTT TGTAATAATT AACTTACTTT TGTAAAAAAA GACATGAGAT 6540

TATTTTTTTA AATCTATATA AAGTTGACAA TACAAATCGA TATTGAGAAT ATTAAGATGT 6600

ATATGAATTT TATAAATTAA ATGCAATACA TTAATATAAA TATCAATTGT TGCAAAATAC 6660

GATTTGTTCA ATGATTTGAT AATATTATTC TTTATATTTG TGAATGGTTA AGTTTGTCTT 6720

TGAACATATT ATAAAAGTGT AATGTTCCCC TGAAAAGAAT AAGTTGTCAT CTAATTACAG 6780

GAAATCCGCA TAAATTAGAT GAAATGGAAA GTAATAAGTA ATAATTTATT GATAAGCGCC 6840

TATGTGATGG TAAATCATGA CATAGGCGCT TTTTTTTATA AGTTAAAAAT GTAAATAAAA 6900

ATTATATAAA TTACCCACAT CTTTTTAAAA GGTGTGGGCT TTATTATCAT TAACCCAACT 6960

CACAGTGACG GGTTACGCAA GGTATTGAAT TACCGAGTAC GGGCACGCTC GGTGTTGTAA 7020

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AACGATAAAA TATTTATATA AATAATTAGA GaAAATGTAG TTGTGTATGT yTTGTGGtCG 7260

TTAAACTAGA TATAATTGTC CGATTTATAA AACATACATA ATGAATACaA TGATTGATTA 7320

TGTGGAGGAA ACCATGAmAG AmAAGTTTgA TTTAGTAAAA CTATTAAATA TTCTAAAGAA 7380

GAATATTAAA TTATTGCTTA TTTTACCGGC AATATGTCTT GTAGTAAGTG 7430

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4082 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

ATTGTTACTC ATTATTTTTT CATATTCACA CAAATGATCT TGTTTATATT TAGCTAATTG 60

ATTTTTATCT AGCATTTTAT CCTCCTGCTG AGTTTGTAAC CTTTAATAAT TTATTTTCTA 120

TAAAAACTTA GTATTCCAGT TGCTTATTAT ATCATTGATG AAAGGCTGAA ATAAAACATA 180

AACTGTTCCG ACCATTAACG CTGTAGCTAA AGATAAGTCT ACAAGTCCAC CTGTTTTAAA 240

TTGAATCGGT GTCTTCACAT TAAACGGTAA gGAknAAAAT AATTTCACGC CTTTTGGTGT 300

AGGCGTCTGA ATAATTTGCA ATAAAAATGC TATGATTGCG ATAAATAATA TTGAATGCGT 420

AAAGGTTCGA TGTCCAAAGA TCAATCTCAC AAAAAAACTA ATTACCTTAA ACCTTCTGCC 480

AATCTTACTT TGAGTGTGAC ATATATCGGG TAATAAGCTA GCTAGAGTTG CTAGAATGAT 540

AACCGTAACC GACGAAAAAA TATCCGTTTG AAAATATTGT GTTGTTAGCG CTCCAACGAG 600

CATGCCGCAT GAAGCATGTG TTTTACCTGT CATATTTGTT CTCCTTTAAT ACTCACATTT 660

TACCACATCC CTAACAAAAA CACGAACATA TTTTCGGGTT AAAATTCATT AGTATGACAC 720

AATTTAAAAA AGTATCACAT AACTCTTGAA AACGATTACA AAATCGTTTA TGATGTATTT 780

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TTACACAAGA CCAAGATATT CATGCAGTTC CTAAATTAGA CAGCAAAGAT GTATCTAGAA 960

TCGGCTCAAC GTTTGGTAAA ACGAATCGCG TTATTATCGA TACTGAAGAC CACGAATACA 1020

TTATTTATAC TCAAAATGAT CAAAAGGTTT ACAATGAATT AACTAAATAA ATTGTATAAA 1080

AaAATCATTC ATGGTGAGGG CTTCATGAAT GATTTTTTTA ATTGATTCAA CACCCAGCAT 1140

AAACAAATAC AAAAGGACAA CTGTTCCCAT AATTTTAACA GTTGTCCTTT TTCACATATA 1200

TTTATAACAA AAGATGTGCC ATCAAAGAAA TAATTGGTAG TGTAATGATT GTTCTAATCA 1260

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CTACTTCAGA CAAGTATATT AACTGCGATA TACTAAGTGC CCCAATAACA AAACGAGTTA 1380

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CAACGAGGCA GGATACTATC ACTGATAAAT AGAAAGCAAA AAATTGATTT TGCATGTGCA 1860

CTGTTTCAGC AACTACAATT GCAAAGGTGA TAGAAACTAC ACTAAATGTC GTTGAAATAA 1920

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CACCTAATAC ATCTTTAAGC ACGCCTGCTA AAAATGCCAC GGGCAACGTT GTTTGCTTCT 2460

GTCCATCTTG TTCGACTGGA ATTGGTACTA AAAATAATAA GATACCAATT AAAGACATCG 2520

TAATAAACTT AAGTCTCCCA ATAACTATCT CTTTCCTTGA AAAGCTATCC ATAAAATCAA 2580

TCCATTTCTC TATGTATTCG TTTTAAGTAT ATACAGAATT CTATTCAGTT AACAAACATA 2640

TTCCTTATCA TTCTATCTTT CAAAATGTTT ATGTATGCAA AATAATGAAT AATTACAGTT 2700

ATTAAATATA CGCTATTTCT TGTAATTTTT CAAGATGAAT TCAAAAAAGG TTAAGTACAA 2760

TTACTGATTT CGTACTTAAC CTTTTTTAAA CTCTAATCAT ATGTTAGTTA TTTCATTCTT 2820

CGTAATAATA TTAAGAAGTA TGGTGCACCG ATAATTGCAA TGATAACCCC AACAGGAATA 2880

TCCAGTGGCG GATGAATGCC ACGGGCTAAA CCATCTCCAA ATGTTAACAA TATAGCACCA 2940

ATTAACCCCG ACATGATAAT AACGTGTAAT GTTTTATTTC CTATTAATTG TCTCGCAATA 3000

TGAGGTGCAA TTAATCCTAA AAAGCTAATA CCACCGACAA CTGAAATTGC GGATCCTGCT 3060

AATATTACTG CTAAAATTAA CAATAGCATT TTAATAGTTT TAACTTTTAA ACCGAGTGCG 3120

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CTTATTACAG CTTGTATAAT TGCACCTGAA ATAGCCAAGC TACTACCGAT AATAATACCA 3600

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ACAATTAAAA GGATTGTGAT TAAACTATAA CGACGTATAA TTTTCGTTGT CATCATATTC 3780

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TCCCTACTGG TGATTCATAA GGATATGTAA TTAAACGACT TAATACATCT GATAGTAGTA 3900

AGCGTTTGAC TATATGCGGT ACGATTAAGC CAACAAATCC AATTGGTCCT GCCACTGACA 4020

CCGACATACC TGTAAGAATA ATGACTAATA GTCCAATGAT AATTCTAACT TTATTTATAT 4080

TT 4082

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

TATTAGAAGG TCGTTCGGAT GAACAATTAA AAAATTTAGT TAGCGAAGTA ACTGACGCCG 60

TAGAAAAAAC AACGGGGGCA AATAGACAAG CAATTCACGT TGTTATAGAA GAAATGAAAC 120

CAAACCATTA TGGTGTGGCT GGCGTAAGAA AGTCAGATCA ATAATTCTTC ATAAGATGCA 180

TGCCAATTAA TTCTTTGAAA ACGAACAAGG CGACTTCTAT CTGaGTATGA TAGAAATCGC 240

CTTGTTTATT TTTAATCTTC ATCTAAAAAG TCTTTAATAG CTTGTTTATT TGTGTTTTTA 300

TTAATCTGTA ATGCACTACC ATCAGTATTT GTATTGACAT CyTCGTATGA GTTCTTGATT 360

GGCaCAGTCA ATGACTTAAC ATCTTTTTCA CCTCGGATAC CaAAACTCAA ACCTGTTTGG 420

AAAATCCCTG AATCAGGAAT GTTTGTATTC ACATAGCCTC TTAAAATACC TGCAACTTTT 480

GGTAATTTAA CAACTGTTCT AAAATTAACC ATTTCTTTTT TCAATGTTTG CATCACTTGT 540

TGCTGACGTC GCACGCGTCC GAAGTCACCT TCAGGGTCGT GACGGAATCT TGCATAACCA 600

AGTAATTCTT TACCATTCAA CCTATGGTTA CCCTTTTTCA AAGATACACC AATATTTTTC 660

GACATATCTT TTTCGACATT AATTGGTACA CCTTCAGGCA TTAATTCATC AATCATTTTC 720

TCAAATCCAG TAAAATCAAC TACTGCATAA TATTCAGGAT TAATTCCTAA ATTTTTATCA 780

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TTGATAAAGT CATATTGAAC AACCATGATA GAATCTGTTC TTGATTGTCC ACCTTGTGCT 960

TTATCTGCAC CGAGTACAAG AATAGAAATT nTACCATCAT TTTTTACTGG TCCATTAAAT 1020

TGATGTACTT TAACATCTTT CGCATGTTTC TTGGCATATT CTACACCGCT ATTGTAACTA 1080

TGTACAATAT ATACAACTAA TGCCGATAAG TAAAATTACA ACAATCAGAA GAATGATAGG 1140

TAATT 1145

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7075 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

TATGGCTCAT CATTAATGCA CGTATCGGGT AGCGTTTACC ATTGATAAGT GCTTCATGTT 60

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TGTTTTTAGT CACTTCAAAG GCAAAGCTAT AACCGCAATA ATCACCAGCT TGTACTTCGC 180

GCACTTGAAT AACATGTGCT TTTAAAGTTA ATGACTGAAC TATATCATGT TGATTCAGTG 240

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GTAATAyyyg TCCTTCCCGA TAAAAACTCG CACTATTTTG AGCATGGATT AGGTCGAACT 360

GATAACCTTC AGATAAAAGT GCTTCAACAA TTTCCATCCA TTGTGAACGT TCAACATTAT 420

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TGACCATAAA AACTAAAATC TTCCCCAAAT AAGAATGGCG TTGGTTTGTC ATAGACATTT 1140

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GGGGGATAAC CTTCTGCAAA TTTAACTTCA CAATCTACAT TAAACAGAAG CTTGACACTT 1260

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GTTTCTTCTG CAGGTTGGAA AATGAAAACG ACATTTTGCG GTAATTGACC TGCATCTTGC 1740

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GCATGCATCA CATGATCAGA TTGACTGCGA TAAGGCACAT CATTTTCCTC TAAAATAGGT 1860

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AACGCTTTAA TATCTTCTGC TGTTGTTTCT TTGTCAAGCG TTACATCAAT TTCAACACTA 4860

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ACAACAGATT GAATCGTAGA GCAGTTTGGA TTGGCAATGA TACCTCTTGT AAATGTAGGT  5220
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AGTAGCTGAT TGTCAGGTAG GGGATAACTA ATTGTTACAT GCATCATATG TTTATCCAAA  6060
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TTCACGTTCG ATAAAGTTTT TCCTAAATAT AAAGGGATAT TATAGTTTTT AGCTAATTCA  6180
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TCAACGTCGG TATAAATTTC ACAAGGTATT TGATTACTAA CAGCAAGTGC CACAGCGGTC  6360
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GATACATTCG TCATTAATTG ATCTGTTGTG TTACCCATAG CACTTACAAC GACAATTAAa  6720
TTGTTCATCT TGATTGACTC GCTCCTTTAA CATTTCAGCG ATCCTTTTTA TTTTTGTAAA  6780
ATCACTGACG GATGATCCGC CAAATTTCAA CACACTTCTT GTTACCATAT AATCCTCCTA  6840
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TAATCTATAT ACAAGTGATG CACTCCATTA TTTTTAAATA ATGACAAACT CTCAGCTCTT 6960

AACCAAAAAG TCCAACAAAT TATAACTGCT ATTATAATTG CTTCGGCATC GCACCCTTTC 7020

AAATTTAGCT GTTAGCAGAC AGTAATCTAa ACTTTACTCA TGATTGATGC GCCTC 7075

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

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TGAACCTGAT TGACTAGTAC TTTGTGATAA TGACTTACTA TCAGAATCAG ATGTACTTTG 120

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TCTTGTTACT TCATATTTAA AAGTTGTCGT CGTTTTGTTA CCGCTCGCAT CTGTAGAAAC 1080

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CCTCCACCAG CTACATTAGA TGGGTCAGCA TTCGCCTTTG CAGCTGAATT TGGTTTAGAT 2160

GTATTGTGAT ACGTATCCAA TTTGAAGCCA AATGCGTTAC TTAAGCCACC AATACCTACT 2220

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GTATTTCCAT C 5171

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3589 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

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TTTGGTTTCT TAACATAAAA TGAGTTGAAG CTAATTCATA TTCAAATTTA CCAGTTTGAT 1320

CATAATTCAG TGTTACTATA CATGGTACTG CTTCTCGTAG TTCGACACGC CCGATATCAT 1380

AAATGACGTC TCTAACAGCA CCGCTATAGG CGCGAATTAA ACCGCCACCA CCTAATTTAA 1440

TACCACCAAA ATATCTTGTT ACTACGACAC ACGCATTATG aACATCGrGC TTTTTTaATA 1500

TGTCTAACAT TGGGaCACCG GcAGTTCCtG TCGGTTCACC ATCATCATTC GCnTTTTGAA 1560

TATTCATTtC AGGTCCAATA GTATATGCAG AACAATTATG AGTGGCATCT TTATGTTCTT 1620

TTTTTATTGC AGCAATAAAT GCTTTaGCTT CATCTTCATT TTGAACAGGT TTGATATGAG 1680

CAATGAATCT TGATTTACTA ATCACATTTT CAATAATGTG TTCTTTTTTA ACAGTAATGA 1740

TATTTTGTGT CATAATAACT CCTTAATTCA TAAGCTTAAG ATTATTTAAT CTTCATTATA 1800

CACTGAAAAT GACATGACTA TAAATCGTTT GATTGCCATT TTCTTTTTAA CTGAAATATT 1860

GTATCATTGC TATGAGTATA TTTTAGGAGG ACGACTATGA AAATTGCTGT GATGACCGAT 1920

TCTACAAGTT ATCTGTCGCA GGACTTAATC GATAAATATA ATATTcAAAT AGCGCCATTA 1980

AGTGTGACTT TTGAAGATGG CAAGATTATA CCAGAAGAAA AAGTTCGTAC TAAAAAGCGT 2040

GCCATTCAAA CATTAGAAAA GAAAGTATTA GATATTGTAA AAGACTTTGA AGAAGTAACT 2100

TTATTTGTCA TAAATGGAGA TCATTTCGAA GATGGTCAAG CGTTATACAA AAAGTTACAA 2160

GATGATTGTC CTTCAGCTTA TCAAGTAGCA TACTCTGAGT TTGGTCCAGT TGTTGCAGCA 2220

CATTTAGGTT CTGGTGGATT AGGTTTAGGC TATGTTGGCA GAAAAATAAG ATTAACATAA 2280

TTATAAAATT TTAATAAAAG AGTCTATATT GTAATTGGAA ATTATCTCTC GTATACATGG 2340

CTTTAAATGT TCATCATTTG AAAGCCAAAA TGCTAAAGAT ATAAGAAAAT CATTATAATA 2400

TTAGGCTCTT TTTTACGTTG AAATGAGGTT TTAAGCATTA AACATTACGG GAAATTAATT 2460

CATCCTCATA CTTCACTTAC TAATGAAAAA ATTAAAAAAG AAGTAACAGG TGTCATCAAA 2520

CAAAATTCAA ACTATTATTG TGTTCAATGT GAAAGTACAA ATCCAAAGCA TTTTTATCAG 2580

TATGATTCCT CAGTACATTC CAAGAAAATT GTATATTGCA GAAATTGTAT ATCACTGGGT 2640

CGAATGGATA ATGTAACAAG ATATAAAATA ACAGAGAGTT CGCAAAGTTC ATCACAAGCA 2700

TATTATCATC TCTCATTTGA ATTGTCGGAA CAGCAGTCTT ATGCCTCAGA ACATATTGTT 2760

CGAGCCATTA GAAAGAGACA AACGATTTTG TTATATGCCG TAACAGGTGC AGGTAAGACA 2820

TCACCACGTG TAGATGTTGT TGTAGAAATT AGTAAACGTA TTAAAGACGC ATTTCTTAAT 2940

GAAGATATAG ACATACTACA CCAGCAATCA AGACAACAAT TTGAAGGGCA TTTTGTTGTA 3000

TGCACAGTGC ATCAACTTTA CCGATTCAAA CAGCACTTTG ATACTATTTT TATTGATGAA 3060

GTCGATGCCT TTCCTTTATC AATGGATAAA AATTTACAAC AAGCATTGAA GTCATCTTCT 3120

AAAGTTGAAC ATGCAACAAT TTATATGACA GCAACACCAC CGAAACAACT TCTGTCAGAG 3180

ATTCCCCACG AAAATATAAT TAAATTGCCA GCTCGCTTTC ATAAAAAATC ACTTCCAGTT 3240

CCTAAATATC GTTATTTCAA ACTTAATAAT AAGAAGATTC AGAAAATGTT ATACCGAATT 3300

TTACAAGATC AAATTAATAA TCAACGTTAT ACACTGGTGT TTTTTAACAA TATAGAAACA 3360

ATGATTAAAA CATTTTCGGT TTATAAGCAG AAAATTACTA AATTAACATA CGTCCATAGC 3420

GAGGATGTTT TTCGCTTTGA AAAAGTTGAA CAATTAAGGA ATGGACATTT CGATGTCATT 3480

TTTACTACGA CAATATTAGA ACGTGGATTT ACAATGGCAA ATTTGGATGT TGTTGTTATC 3540

GATGCACATC AATATACTCA AGAGGCTTTA ATACAAATTG CTGGACGTG 3589

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1017 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

TTTCCAAGAA GGcTTgAAAA AtGTTwCaAG TGGTGCGAmC CCAGTTGGTT TACGACAAGG 60

TATCGACAAA GCAGTTAAAG TTGCTGTTGA AGCGTTACAT GAAAATTCTC AAAAAGTTGA 120

AAATAAAAAT GAAATTGCGC AAGTAGGTGC GATTTCAGCA GCAGATGAAG AAATTGGACG 180

TTATATTTCT GAAGCTATGG AAAAAGTAGG TAACGATGGT GTCATTACAA TTGAAGAATC 240

AAATGGACTA AACACTGAAC TAGAAGTGGT TGAAGGTATG CAATTTGATC GTGGTTATCA 300

ATCACCGTAT ATGGTTACTG ATTCAGATAA AATGGTTGCT GAATTAGAAC GCCCATACAT 360

TTTAGTAACA GATAAGAAAA TCTCGTCTTT CCAAGATATC TTACCTTTAT TAGAACAAGT 420

GGTTCAATCT AATCGTCCAA TCTTAATTGT AGCTGATGAA GTTGAAGGCG ATGCATTAAC 480

AAATATCGTG CTAAACCGTA TGCGTGGCAC ATTTACAGCT GTTGCAGTAA AAGCACCTGG 540

TTTTGGTGAT CGTAGAAAAG CGATGCTTGA AGATTTAGCT ATTTTAACTG GTGCGCAAGT 600

GATTACTGAT GATTTAGGCT TAGATTTAAA AGATGCATCA ATTGATATGT TAGGTACTGC 660

CAGCATTGAT GCACGTGTTA GCCAATTGAA ATCTCAAATT GAAGAAACTG AATCTGACTT 780

TGATCGTGAA AAATTACAAG AGCGCTTAGC TAAATTAGCA GGTGGTGTTG CAGTTATCAA 840

AgTAgGTGCA GCAAGTGAAA CAGAGCTTAA AGAACGTAAA TTACGTATTG AAGATGCATT 900

AAATTCTACA CGTGCAGCAG TTGAAGAAGG TATTGTTGCA GGTGGTGGTA CTGCATTAGT 960

AAATGTTTAC CAAAAAGTAA GTGAAATTGA AGCTGAAGGT GACATTGAAA CAGGTGT 1017

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1409 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

TTAATCCAGC GTTAACTGTA TTTGCATTTA TTATGATTAT TTCGATTCTT TTAGCGTATG 60

TATTTAAATG GCTTGGATTA GTGGATGATG TGTTATTAAT GGTCATTATC ATTTCAACTA 120

TTTCCTTAGG CGTAGTTGTT CCAACTTTAA AAGAAATGAA TATTATGAGA ACAACTATAG 180

GGCAATTTAT CCTATTAGTA GCAGTACTTG CGGACTTAGT AACTATGATT TTATTAACGG 240

TCTATGGCGC AATCAATGGT CAAGGCGGCA GTACAATATG GTTAATAGGT ATATTAGTTG 300

TTTTCACAGC AATTTCATAT ATTTTAGGTG TTCAATTTAA AAGAATGTCA TTTTTACAAA 360

AATTGATGGA TGGTACGACG CAAATCGGTA TTCGTGCGGT ATTTGCATTA ATAATATTAT 420

TAGTAGCCCT AGCAGAGGGA GTTGGCGCAG AAAATATATT AGGTGCATTC TTAGCAGGTG 480

TCGTTGTTTC ATTATTAAAT CCAGATGAAG AAATGGTTGA AAAGTTAGAC TCATTTGGTT 540

ATGGGTTCTT TATTCCTATT TTCTTTATAA TGGnTGGTGT AGATTTAAAC ATACCTTCAT 600

TAATTAAAGA ACCGAAATTA CTAATTATCA TACCGATTTT AATCGTnGCA TTTATCATTT 660

CAAAATTAAT TCCAGTCATG TTTATTCGAC GTTGGTTTGA TATGAAAACA ACGATTGCAT 720

CAGCATTTTT ATTAACATCA ACATTATCGC TCGTGATAGC TGCAGCCAAA ATTTCAGAAA 780

GATTAAATGC TATTTCAGCT GAAACGTCAG GTATATTAAT TTTAAGCGCA GTCATTACAT 840

GTGTATTCGT TCCGATTATT TTCAAAAAAC TGTTTCCAGT TCCAGATGAG TTTAACCGTA 900

AAATTGAAGT TAGTTTAATT GGTAAAAATC AATTAACGAT TCCTATAGCG CAAAATTTAA 960

CATCTCAGTT ATATGACGTG ACATTATATT ATCGCAAAGA CTTGAGTGAT CGTCGTCAAT 1020

TGTCAGATGA TATCACGATG ATAGAAATTG CTGATTATGA ACAAGATGTT TTAGAACGAC 1080

AAGTTGCTAA ATTAGCCAAA GCACATCAAG TTGAGCGTGT CATTTGCAGA CTTGAAAGCA 1200

CAACGGACGA TACAGAGTTA GTTGATTCAG GTATTGAAAT TTTCAGTAGC TACTTAAGTA 1260

ATAAAATCTT ATTAAAAGGT TTAATTGAAA CACCTAACAT GTTGAATTTA TTAAGTAATG 1320

TTGAAACGTC ACTATATGAA ATTCAAATGT TAAATTATAA ATATGAAAAT ATTCAATTAC 1380

GTAATTTCCC ATTCGGAGGA GACATCATC 1409

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4702 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

AAAGAGGGTT TTTTACTACT ATAATCCATC CTTTAATGGA ATTCCATTTG TCCCTTTGGC 60

CCGTTCATAA CCATAGGAAA ATATATGCnG nAATCATTGA TAGTAAATAC ATCAATAATA 120

CGAATAATGT CGGTGAAATC ACGTCCGTAT TACCATTATT AGCTAAAACA TTTTCCAAGT 180

TTTCTTTTGA ACCGGATACT CATAAATGCT TTTAATGCnT GGTTTTGTCT GTCGCCATCT 240

TTAGAATTTG TAATACTTTT TTAAATTCTT TAGCGAACAA CTCATTATCT TTATCGTTTT 300

TAGCCATTTG ACGATTCAAA TCGTTAGCTC TTACGCCTAA TGCTCGACCT GTCGCATGTA 360

GCTTATTCAC ATTATTGTCG ACTTGATTTA ATTGGCCACT AACAGAATCT GCAATTGATT 420

TTGATTCTTG TGTATCTGAT AGCAATTGCG TACTCTTTTC AGAAATTCTA CTAATTTCTT 480

TATCTAAATT TGAAGACATC GTATTAAATT CATCATTTTT GCCTTTATCA ATTTTTGGTT 540

CTTGTGGCTC TTCAGCAAAA GTCTTTTTAA CGTTTTCTAA CTGATCAATC AGCTTGGAAA 600

TATCTTCTTk ATTTTTTGTT gTATTCTTTT TGTTATTTAA AATGTCATCA ATCAGTTTGT 660

CTGAGTTTTC TTCCATTGAA TCAATTTGaT GTAACACAGC TACTTTATCG TCTTTGAAAC 720

TTTCCATGTC ATTGATAACT TGGTCAACCA TCATATCAAT TAAACGTTTG TTGTCGAATG 780

GTTTATCTTC tCTGCCTTTT GTATCTGTGT ACATTTTATA ATGCGCATCA AACCTAGATA 840

ATGCACTCAA TTGCTGGCTT AATGCATCTT TCGATAAGCG ACCATCaAGG TTATGATTCA 900

ATGTTACATC CACAACACTC GTTGCTTTCT TATCATTTGG TTCATCTTGA CGATTTGCTT 960

GTCCAAATAA CAATTGTAAA TGCATTGTTT TATCTTTTAA GAAATCTTTC TCAGCATCCT 1020

TTTTCAATTT AGCAACGCCA TTGACTTCAA CTTTATATTC CTTGTTAGAT GTATCGAGTT 1080

TAAAATGAGG AtCTGTTGCA ACAGTTAATT GATTAATATC ATTACTTTTA ATCGTTTCAG 1200

TACGTTGCAC TTTGACACCA TCATTAATCA AACTACTTGT GTCTTGCGCA ACTTGGTTAT 1260

CGTAATCTGT TAAATTAATG TGTTCTGCTA ACGGTTTTTT CAAATTATAT TCATTTTTAT 1320

AACGTTTTGC TTCTTTGACA ATTGCTTCGT ATTTATTAGC TTCATCCTCA TTTAAACCTG 1380

CAGCTATAAA GTCTTGTTTA GACATGTTAT AGATAAATGT TGTATCTGTA TCAGGTTCTT 1440

TGACAATATC ATCATGAAGT TGTTTCTCTA AGTTTTCAGC GAATTGAGCA TTGTTCATTT 1500

TAATGCTATT TAGCGCATCT TGTAAGTCTT TGTTATTTGC AAGCTCATCT TGCAGTGATT 1560

CTGTTAATTG CTTACGATAn TCTTCAATCA TACCTTTTGA AAATGGTGAC TCTTGTGATT 1620

GAATGATTTC TCTTAATTTA TCTAAGTTTT CTTTAACAGT TTGTTTATAT TCTTCTTTAC 1680

CTGTATCTTG CATACTTGAT TGTTGATCAA TTTGGCTGTC CATCTGTTTT AATGCATTGA 1740

TATAGTTATC AAGTTCCACG CTATCTTTTT GCGATTTATA ATCTTGTAAC ATTTTATCCA 1800

TCGCTGTATT GTGCTCGTCA AATAATGAAT TTTGTTTTTC AATTAAAGTC GAAACATTAT 1860

AATCTGTGTT CACTCTGAAC GTATCTGAAT TCGCACTCAA TAATGATTTA TTGTATGTTT 1920

GGAACCATTT TGTAATGTCT TTGTTTGCAG AAATTGAATT TACAAGCGTA TCTGTAAATA 1980

ATTCCGGGAA GTCGTTAATT GGATTTAATA AGTAATTCGA GAATTTACTA TTCACACCAT 2040

GTTCACGCGT CATAATAGCG CCAACATTTT TTTGTGCATT ATGTAAATTA TCAATGATGC 2100

TTGTTAAATA AATTTCGACT AAGTTTTTGT TAAAGTCGTT AAGTACATTA CTTACAACTT 2160

TTTCTGTGTT TTTAGCTACT TCTTCTTTTT GTCCTACAGC TGTTTTATAC TGTAGCGATA 2220

TTTTCGATGG TGTTTTAGCG TCTAATTGCA TTGCCAATTT TGAAAAGTTT TCTGGGATAA 2280

CAATCATGAC TTGGTATCCA CCATTTTTCA AACCAGACTC AGCAACGTTT CTTGTTACTG 2340

TTTCAAATTT ATAGTTTTTC TCATTTGCTA ACCTTTTAAT AAATGCTTGA CCCAGCTCAA 2400

CTTTTTTACC GTTATATGTC GTTGGTTGAT CCTCGTTAAC AATTGCGATA TGTATTTTAT 2460

TATTTTTATT ACTTACACTT TGGGATCCTT TTTCTGATTG ATCTCCATAT TTTGTTTGAA 2520

CAAAAAATAT CATACTAACT ATGGCAATTA TAATAATTAA AGTGACAATT AATGCATAAA 2580

TCCAATTTTT CTTTTTCATG CTTATTTCCT TTCAGTTGTT TTCTTAAAAA AATGATAAGC 2640

AAAGCCACAT TAGAAAATGT GACTTTGCCA ATTTCAGAAT GCTTATTGCA AACCGAAATT 2700

ATTAGAAAGT TGTTGGTCTT GTTCTTGAAC GGCATCAGCA GTGCtATTcA ATTGTTGTTT 2760

AATTTCTTCT AATAATTGTG CAAATTTTTC TACTTTAGGA CTAAGTTGTT GGAATTGCTC 2820

TTCGAAACGG CTGAAAGCTT GACCTTCCCA GTTCGCTGCA ATTTCACCTt GTGCACGkGT 2880

TCTGATTTCC TCTGGACTCA TCTTAATCAT TGCCATAACT AGAAACCTCC TGAATATTTT 3000

AAGTTTATCa AAACTTTTTA GGGACACTAT TTTTTGAAAA AGTGCTCCTT ACTCAAATAA 3060

TATATAAATT ATTAGTATAT GTATATAGTt TTTTAAGTAT TTTTAGCTTT TTTAAAATAA 3120

ATATATTGAA TATAACCATA TATTTTTAAT TAACCATTCA TTTTTGTAAT ATAAATGTGT 3180

ATACTAAAAT TAAATTAAAT ACATAAAGGA TTAAATGGTT ATTATGAAGA AAACAATTTT 3240

ACTGACGATG ACAACTCTTA CTTTATTTAG TATGTCGCCT AACTCGGCTC AAGCATATAC 3300

GAATGATAGC AAAACATTAG AAGAAGCAAA GAAAGCACAC CCAAACGCAC AGTTCAAAGT 3360

GAATAAAGAC ACCGGCGCGT ATACTTATAC ATATGACAAA AACAACACGC CAAACAACAA 3420

TCATCAAAAC CAGTCACGTA CAAACGACAA TCATCAACAC GCAAATCAAC GTGATCTTAA 3480

CAACAATCAG TACCATTCTT CATTAAGTGG TCAGTATACG CACATTAATG ACGCAATTGA 3540

TTCACACACA CCGCCTCAAA CGTCACCAAG CAATCCTTTG ACACCAGCAA TACCGAATGT 3600

CGAAGACAAT GACGATGAAT TAAATAACGC TTTTTCAAAA GATAACAAAG GGCTTATTAC 3660

AGGCATCGAT TTAGACGAAT TGTATGACGA ATTACAAATC GCCGAATTTA ATGACAAAGC 3720

AAAGACCGCT GACGGTAAAC CTTTAGCATT AGGTAACGGT AAAATCATTG ATCAGCCTCT 3780

TATCACAAGT AAGAACAACT TATATACTGC TGGACAATGT ACATGGTATG TCTTTGATAA 3840

ACGTGCCAAA GATGGACACA CGATTAGTAC ATTTTGGGGA GATGCTAAAA ACTGGGCAGG 3900

CCAAGCTTCA AGCAATGGCT TCAAAGTAGA TAGACACCCA ACACGAGGAT CAATTTTACA 3960

AACAGTAAAT GGTCCATTTG GTCATGTAGC CTACGTTGrA AAAGTTAATA TTGATGGAAG 4020

TATTCTAATT TCAGAAATGA ACTGGATTGG TGAATATATC GTTTCATCAA GAACCATCTC 4080

TGCTTCAGAA GTTTCATCAT ATAATTACAT CCATTAAATT AATCATGACA TCAATAAAAA 4140

GCGACCAGTT CGCAGTTTAC AATTCGTAAC ACTGCAAAAT TGGTCGCTTT ATTTTGTATG 4200

TTATTCGATT ATAAAATTAC AAAGAAATGT TCTCTACATT CCCCATTAAT CAAAATCGTT 4260

TACGAAAGTA TAATTGTAGC TATAATAATC CAAGTCGTAA CAACTAGTGG CACTATCGTC 4320

TTGAATAAGA ATATACCGTA TTTTTTCTTG CGATATATAT CCAGTACTAG CCAAATTAAA 4380

ATGATTATAA CACCAACAAA AATAAATACA GGATTCATCG ATATAGCATC TGCCTGTAAC 4440

TCAGGTTGCA TTCTTAATTT AGTGATAATT AACATCACTA CTGAAATAAT GAAAAAGTAG 4500

ATACCTCTTA TCTTTGATGT CTGTAAATCT AATTCCTGCT CTTCAATGAC CTCTTTAGAT 4560

TCACCCAATT CTTTTGCAAT CAAATAATTT ACTACCTTAG GTTTCACCCA TAAACACTTA 4620

ATTGCAAAGT ACATAAAAAT ATATGATCCA GTATCCATAA ACATTAAAAA GTTGCTTAAA 4680

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2004 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ACAAAAAATT CACCCTCATT AATATTGAAA CTAATGTTAT CGACAGCAAC ATGTTTGCCA 60

TAACGCTTAG TTACATTTTT AAACTTAATC ACTTTGCCAC CTCTTTTTTT CTCATAGCAT 120

AAAACCGAGA TTATATGTAT GTATTCCCTA TTTAACCACG TTTATTACAA TTTTCAAATT 180

TAAATGATTT ATCCTTGAAC TTTTTTAATA AAATAATGAA TAAwAGGwAA TCwCCAGTTA 240

AGAAATAGTG TTATTTTACC TTGAATTCAA AAAAACACCC AGTAAAACAA GGAATGCTTA 300

CTAGGTGTCT TCACTATACT TTGGCTTTAT AATTTTGAAT CGTTtCTAAA AATGCTGGAC 360

AATAATGTTT TAATTTGTAA CTACCTACGC CATCmATATT AATCATATCT TGTTTCGAAG 420

CAGGCTTACG TTTAGCAAAT TCCTCCAACG TGTAATCAGA AAATATACTT ACAGGTGCTA 480

TCGTTAATTT GTCACTTAAC TTTTTACGAA CTTCTACCAA CTGACTGAAT AATACTCGGT 540

CAACCCCTTC AACCGTATTT ATAAATACTT TTTCAGTCGC TTTTTGCTTA AATGGTGTTG 600

TGAATACTTC TACTTCATTA CTGAGTAATT TTTTAATTGA AGTATCACAC ATTAATATTT 660

CGTCATTTTC ATTTAAGAAC CCTTTGAATC TTAATTCATC TATTAAGTGA CTTAATTCTG 720

ATGTTGTGTA ACCTTTCATT AAACCATGGG TTGAAATTTG GTCATAACCT TTATACTTAA 780

TATAATCTGk TGACTCTCCT CTTAACACTT GAATGATAAC ACTATAACTC TCTTGTTGTT 840

TCATACGAGC GATGCAACTA ATAATCATCT TAGCTTCTTG TGTCATATTA TATGATTTAT 900

CTTGTTGAAC ACAATTACTA CATTGTTCAC ATTCTTCTAA TTTTTCATTC GGTTCAAAAT 960

AATGGACAAT TGTTGCTTCT AGACATTTTT TTGTTTTTGT ATATTGAATC ATTTTAGTTA 1020

ACTTTTCGCC CATTTTATCT TTATAGTCAT CATCAGCTTG AGAGACTGTT ATAAAATACT 1080

CGTGTAAATT GATAtCGCGT TCGCTAAATA ACAAAATACA TTCACTTTTC AACCCGTCAC 1140

GACCTGCACG ACCCGCTTCT TGATAATAAG ATTCTAAATC TCCAGGCATA TTATAATGAA 1200

TAACAAAGCG TACATTGGAT TTATCAATAC CCATACCAAA AGCATTTGTA GCAACGACTA 1260

CTTTAACACG ATCAAATAAG AAATCATTCT GCGCTTCTTC TCTTTCTTTA TTGCTCAAAC 1320

CTGCATGATA TATAACACTT TCAATTTTCT GACTTTCTAA GGCTTCTTGA AGCTCTTCAA 1380

CCAATATAAA TTTTTGACGT TGATAAGTAG GATTTACTTT AAAAATTAAG TTTCTACGCT 1500

TAGTACTCGT TTTAATTTGA TCAGTTTGAG CGATATTTAA CTTTTCTCTA ATATCTTGCT 1560

GTACTTCAAC CGTGGCAGTT GCTGTCAACG CTATTATTGT AAAATCTTGA GGTAACGTAA 1620

ATACTTTTGA AATAACATTT TGGTAACTCG GCCTGAAATC ATGACCCCAT TTAGAAATAC 1680

AATGCGCTTC ATCAAACGCG ACTAAGTGAA TCTTTATACG CTGAAGCATA TTTAAAAAAT 1740

ATCGGTTTTC AAATCGTTCT GGTGCAACAT ACAAAAATTG AATTTCTCCA TTTGATAATG 1800

CTTTTTCAAT ACGTTGTTGC TCTTTTTGAG TCAAACTACT ATTTAAAAAA GCAGCTTGAA 1860

TTCCCATCGC TTTTAATTGA TCCACTTGAT CTTTCATTAA TGATATTAGT GGACTTATTA 1920

CAATTGTTGT ACCACCTAAC mATAAACCTG GTACTTGrTA GCmTATAGAC yTACCTCCAC 1980

CAGTtGGkAA GrCACCAAGC ACAT 2004

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

AAAGATTGCT TGCCTTGAGG GTTTATATAT CTGACTCAAT TGCCACATTT TTATCAAGAG 60

TAGTTGATAA TACTCATCAT AATTATAGCT AATATTATAT TTTTTTAAAA GATAGTGTAT 120

GATTTTCTGG TGTTTGTTGT ATACGTCATT AAATTTCAAG TAGTCATTCT CCAAGTTATA 180

CGTATAACAA ATATTTCCGG ATAAAGTTAG AATAAAATAT TTAGAAAAAT CATTCATTTG 240

CGTAATCGCT AAATTAAGTG TTAAATATAA GACATAAGTA ATTAATTTAA TGTGATATGA 300

TGTATTATTA CTTTGCTAAA TAGTAGATAG AACAAAATTT GTAATCGGGA GGTAACAATG 360

GATTACGCAC ATTTAAATTT AGAACATTTT TTTGCACGAA ACGACGATTT AGATGTTATA 420

AGAGATCGCG CTGATTTCGT GATGATAAAT AACTTCACTA ATGAAATGAT GTATCGTGAT 480

GGTCAAATTG AAGGCACGAT TGATTTAAAT CAGTACTATT ATAAAAATAG ATCAAATGCA 540

GCAAGTTTTA TTATGATGGA TTATAAAAAA GAAACTAAGT AAACGAACAA AAGAATTTTT 600

TGTTTTTTAA TACGTGAATA ATAAGATTAT TGATATAAAG GTTTTCAAAG GTTATACAAA 660

AAGATAAAAC ATTTATGATT CGTAGATCAA CGTAAAGTAA TGTTGATAAA TGGTTTAAAA 720

CGTTTCATTT ACATTACTGT TTATTTATGA ATATGTAACA ATGCATAGAT AAAATTGTTA 780

ACCTAAGAGG TGTGGATATG AATAAACACA AGAAAGGTTC TATTTTTGGA ATAATAGGAC 900

TTGTTGTCAT ATTTGCTGTT GTCyCaTTTT TATTTTTCTC AATGATATCC GATCAGATAT 960

TTTTCAAACA TGTTAAATCC GACATTAAGA TTGAAAAGTT AAATGTTACA TTAAACGATG 1020

CAGCAAAGAA ACAAATAAAT AATTATACGA GTCAACAGGT ATCAAATAAA AAGAATGATG 1080

CATGGAGAGA TGCATCTGCA ACTGAAATTA AAAGTGCAAT GGATAGCGGT ACTTTTATCG 1140

ATAATGAAAA GCAAAAATAT CAATTTTTAG ATTTATCAAA GTATCAAGGG ATTGATAAAA 1200

ATAGAATTAA ACGTATGTTA GTAGATAGAC CAACGTTATT GAAACATACG GATGATTTCT 1260

TAAAAGCTGC TAAAGATAAG CACGTTAACG AAGTTTATTT AATTTCACAT GCATTATTAG 1320

AAACTGGCGC AGTTAAAAGT GAATTAGCTA ATGGAGTCGA AATTGATGGC AAAAAGTACT 1380

ACAATTTCTA TGGAGTAGGA GCCCTTGATA AAGACCCAAT TAAAACAGGT GCAGAATATG 1440

CTAAAAAGCA TGGTTGGGAT ACACCTGAAA AAGCTATTTC AGGCGGTGCT GATTTCATTC 1500

ATAAGCACTT CTTATCAAGC ACAGATCAAA ATACATTGTA TAGTATGAGA TGGAATCCAA 1560

AAAATCCAGG AGAACATCAA TATGCTACAG ATATTAAGTG GGCAGAAAGT AATGCAACAA 1620

TTATCGCTGA CTTTTATAAG AACATGAAGA CTGAAGGAAA ATACTTCAAA TACTTTGTGT 1680

ATAAAGATGA CAGTAAACAT TTGAATAAGT AATTTGATAA GCTACGAGTT GTTTTTATGA 1740

CTCGGACATA CTAAAAAGAC GCTTTCTATC TTGTTTTGAT AGAAAGCGTC TTTTTGCATT 1800

AGAGAAAACA CATTGATkGA TAAtCCCaCC aATGCAAgTG GGGcAGGACa TCGATAAAGA 1860

ATTACTTTTT CTTTAGAAAT TAGTATTTCT TATGCATGAG TTTTACTCAT GTATTCCTAT 1920

TTTTAAGTAC ACATTAGTTA TAGCTAATGA TAAAGAACCA CTACATAATA AATCATTAGT 1980

GTTTTTTTAT CATTTCTGTC CCaCTCTCAT CGTGATTTGA AATTTTCAAT TGCGATTTTA 2040

ATTTCATCTC TTACACGTTG GAACTCTGAC CAAGGCTTGC CTGCAGGATC ATCAAATCCC 2100

CAATGTTCTT TCTTAACATT TGTTGGTAAA GAAGGGCAAT TTACGTCTGC ATCACTACAT 2160

AATGTAACAA CTAAATTTGA ATTTnTAATA ATATTATTAT CGGATTAAAA TCTGATGGAT 2220

GATTTGATAT ATCAATGCCT ACTT 2244

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATAAGCAATT TAATTTTGAG TCTACAATGG AGGAATTATC ATCTTTATCA GAGACTTGCC 60

AACTTGAAGT GTTGGGTCAA ATTACTCAAA ACAGAGATCG TGTAGATCGC AAATATTATG 120

TTGGTAAAGG TAAAATTGAA GAAATTCAAG CATTTATTGA GTTCAAAGAT ATTGATGTAG 180

TCATCACAAA TGATGAATTA ACGACTGCAC AATCCAAATC ACTAAATGAA GCTTTAGGTG 240

TAAAAATTAT TGATAGAACT CAGTTGATTC TTGAAATATT TGCATTAAGA GCAAGAAGTA 300

AAGAAGGTAA ATTGCAAGTA GAGCTAGCAC AACTTGATTA TTTATTACCT AGATTGCAAG 360

GCCATGGTAA AAGCCTTTCT CGTTTAGGTG GCGGTATTGG AACTAGAGGC CCTGGTGAAA 420

CGAAGTTAGA GATGGATCGC AGACATATTC GAACTCGTAT GAATGAAATT AAACATCAAT 480

TGCGGACGGT AGAAGAACAT CGCGAAAGAT ATCGAAATAA AAGAAATCAA AATCAGGTGT 540

TTCAAGTAGC TTTAGTTGGT TATACAAATG CTGGTAAATC ATCATGGTTT AATGTTTTAG 600

CAAATGAAGA GACGTATGAA AAAGATCAAT TATTTGCAAC GTTAGATCCT AAAACACGAC 660

AAATTCAAAT AAATGATGGA TTTAATTTAA TTATTTCAGA TACTGTTGGT TTTATACAGA 720

AACTACCTAC GACGTTAATT GCAGCTTTTA AATCAACTTT AGAAGAGGCT AAAGGTGCAG 780

ATTTATTAGT ACATGTCGTA GATAGTAGCC ATCCTGAATA CCGTACGCAG TATGACACAG 840

TTAATGATTT AATCAAACAA TTAGATATGA GTCATATTTC TCAAATAGTT ATTTTTAATA 900

AAAAGGACTT ATGTGATCAT GCATCAAATC GTCCAGCAAG TGATTTGCCT AATGTTTTTG 960

TTTCTTCTAA AAATGATGGT GATAAATTAC TTGTTAAGAC GTTATTTATT GATGAAATCA 1020

AAAGGCAATT AACTTATTAT GATGAGACAA TTGCGACGAA TAATGCAGAT CGATTATATT 1080

TTCTAAAACA ACATACATTA GTGACTGAAC TTAAATATGA TGAAATTGAA AATGTTTATC 1140

GTATAAAAGG ATTTAAAAAA TAATAAAAGG ACGAAATTCA AATGAAAGAT ATAAGTAAGA 1200

TAGTAGCTGA CGTCGAATCA ACGTTAGCAC CATATTTTAA AGAAATTGAA GAAACAGCAT 1260

ATATTAATCA AGAAAAAGTA TTAAATGCAT TTCATCATGT CAAAGCAACC GAAAGTGATC 1320

TACAAGGATC AACAGGATAC GGGTATGATG ACTTTGGACG TGATCATTTA G 1371

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6035 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CGTAAAcCTA TGCGTTTTAA TATTCTGAAG TTACTTAGTT CATCCTCAGT TTCATCCATT 120

TGTTTAATAT AAATAATACA TCCAGCTGCT ACTAAAAATG CTAATCCTAA AAATGATGTA 180

ACAAATATTA GAATACCGTT AGTAGCATcG ACCTCTTTTT TCATTTCATC ATACGTGATG 240

ACTTTGTCTC CAAACTGTTT TGCAATTGCT TGAGCTTTTT CCTTTTGTGA TGTTTGTTTA 300

ATATCATATC CATAAAAAGT ATGAACGTTA TTTTGTGTTT TCAACTGCTG ATACTTTTCA 360

GGACTTACTT CGATGACAGG TGAGTTGAAG CTTAGATTTA AAGGATAAAC CTTACCTTTG 420

TCTTCTTGTG TAcACGGAAA GTTTCATTCT TAGTACCTTT TACTACTAAA TCTTTGTTTA 480

AATGGATATT AATAATGTTA GGCAGCGATT TTGTATTTGT AATGATGGCA TTGTTGCCTG 540

TtAACTTGTT ATTTGCACTT AAAATAGAAT TCGTGCGACC TGAATCACTA CCATTTTCCA 600

AAGTAATAAC CTGATCATTA ACATTATCTA CAGTAATAGT TTCGTAAGCA TTTTTAGAAA 660

ATGTAATTTG TTGTTGGCTT AGTTTAGTTT CAAATTGTTT AGCATCTTGA GTAGCGACCA 720

CGTTAAATTC ATTTGGTGCC ATAGATGTAA GGGTTTGATC TGTATTTGAT TTAGATAATG 780

CCGCAAAACA CAATACAGTT ACTGTAACTG CAGAAATAAT TGCAATGATA GTTAAAGACA 840

TGGCATTTTT CTTCATTCTG TACATAATAG ACGATGTGAA TACAACATCG GTAATAGATA 900

CGCGTCCATT TTTTGATTTT TTCAATGTTT TAAAAATAAG TGACACGGAA CTTCTGAAGA 960

ATAAATAGGC GCCTACAACC GTTAAAAATA AAATGATAAA CGGTGATGTC ATAGCCATAG 1020

TTAGTGCTTT GAACGTACCA AACATTTCTG TCGCCATATA ATAGCCTAGT GCAATCATAG 1080

CAATACCTAA TACGCCTGAA ATAACCTCTG CAGTCGTTAC TTTAGCAGTT GTGGCATCAG 1140

TTTTAATTGA ATCTTTCATC ATTGATAAGA TACTACGTCT TTTTAGAAAT AAAGCACTTT 1200

GAAATAAAAT CAGTACATAC GCAATAATTA GCATGAAAAT AGTTAAAACA AGGGCCATAG 1260

GTTCGAAATG TATCGATAAG TTAATCGATA ACGACATCAA TTTAGATACT ATGGAAAGCA 1320

ATAaTTGTGC ACCTGCAATG CCACATAATA CACCGACAAC ACCTGTGATT AAAAATACGA 1380

TCATTtGTTC AAGTGCTAAC ATTTnCAAAA TGTTTTGTCG TGTTAAACCA ATCaACTGAA 1440

ATAGCGCAAA TTCACGTGTA CGGCGTTTTA CGrmTAAATG ATTGGCATAC ATTAAAAAGA 1500

TGACAATAAT GATAAATAAA AATATTGATC CGACTAAAGC ACCTTTCTTA ATGATGGCCA 1560

TCGAGTCGTC ATTATTTACA CCTTTAGTAA ACTGTAAGGT TGTAAAACTG AAATATAAGA 1620

CGATGCTAAA AAATAATGAA AATAAATACA TTGCATAATG TTTTAAGTTT TGTCGTAAGT 1680

TTTTGAAAAC GATATGGTTA AATGTCATTT GAGACACCAC CTAATACTGA TTGAAGATGT 1740

ACAATGTCTT CATAAAAGGC CTGTTTAGAA CGTCCTTCCT GATAAAGTTG TGTATGAATT 1800

ACCATGACAA TAGTTGTATC AAACGATTTA TTCATTTCTT CCAAACGTTG TAATAGGTCA 1920

TTTGCACTTT TCGAGTCGAG TGCGCCTGTT GGCTCATCTG CAAATATGAT TTGTGGTTTG 1980

TGAACAAATG CTCTCGCTGC TGCAGTTCTT TGTTGTTGAC CACCAGATAA TTCGCTAGGG 2040

TATTTATTTC CTAGGTCATA AATACCTAAT GCTGTCGTGA TCGCTTTATA ATTTTCTTCC 2100

ATTGTTGCCT TCGACATTTT TTGAACAGAT AAAGGTAACA TAATGTTTTC TTTAACGGTT 2160

AATGTCGGCA GAATACTGTA ATCTTGGAAG ATGAAACCTA ATGATTCTTT GCGGAATTTG 2220

GCAAGTGCTT TTTGATTAAG TTTATTAAGC TCTTGTCCGT TAGCAATCcg cTACCGCTAG 2280

AAATTTGGTC AATTGAACTT AGTACATTTA ATAAGGTTGT CTTACCTGAT CCAGAAGGCC 2340

CCATAATCGC AACGAATTCG CCTTTTTGTA TGTCAAAGTT AATATCTTTA AGTGCTTGAA 2400

ATGTGTGCTT TTTACCGTAT GTTTTTGAAA CATGTgCACT GATAATATCG TCATAGTCTC 2460

ACTCCTTtTG TATTTAATTT CATTTTAAAT AATGTTTGGA GTAGTAGCCT TTATCTAAAC 2520

TTACAATTCA ATGAATGAAC CTTACAGAGT TGAAArcTAT CGCTACTTAG TAGATTTTTG 2580

AGTGAGGATA CAGATTCATC GTACATATTA GACAAAAGCA ATGGTGCTTT CTAAGTGATG 2640

ATGTTTGTGT AAATTGAGAA AAGGGAATTT AATTATTGTA TAATAAATTT TTTGTAAAAA 2700

TTAAAAGAGG GTTTTATTTG AAAGGAATTG ATTGTTATGG AAAAAGGAAA TCAAGGTATT 2760

AAATGGTCTA GTTTAATAAT GGGTGTATTA TTATTAATGT TGGCAGTCGT TATTTTTACA 2820

TTTCCAATTG AAAATTTTTA TGCTATTACC TGGTTGATTG GACTGTTTGT ATTAATTAAC 2880

GGTGTGATTC AAATCGTTTA CCGTAGAAAA GCAAAAGCTT TAGTAGGTGG TAACCAAAAT 2940

TGGATTCTGT TTATGGGGAT TGTAGATATT CTATTTGGTC TATTAGTTAT TTTTAATGTT 3000

GGCGCAAGTT CAGCATTCTT TATTTATATG TTTGCTTTTT GGTTTATTTT TAGTTCTATC 3060

TCTGGATTAT TTACGTTTTC GGGTAGTGGT AGCTTAAAAC TAATTTCAGT GATTTTTAAT 3120

TTATTAGGTA TTGTTTTCGG TGTCATTTTA TTATTTAATC CATTAATGGG TATCGTCTTT 3180

ATTTCGACGA TGATTGCTAT TGCATTTGTA TTCGTAGGTG TCATTTATGT TGTAGATGCA 3240

CTTGCTTAAG TAAAATGAAG CGGTTCAAAA GAAGGGTGTG ACATGAAGTT TGTGTCATAT 3300

CCTTTTTGTT GTGTTTATGA AGCATAAAAA AGGGGCGCTA CCTACAATAA GTAAGATACG 3360

CCCATATTTT TATATTTTAC TATTATTGTT TTTCAATACG ATTAATAGTT ACATTTAGTC 3420

CAAAATATTT TTCTAAAAAA TGTTTATAGT TATCTTTAGT GACATCAAAT TTTTCTGAGC 3480

TACCATTCCT TGTTAAAGTT AAATGATTTT CAGACATTGT AGCACGGCCA AATGATTGTG 3540

GCATTGTAAT TAATAAATGC TGTACAAATA TTGAATCTGG ATGCGTTTGA TTATATTCGA 3600

AATGATCATT TTCGAATTTT TGAACATAGA AAATATCCTT GTCTTCGTTG TTAAAAATAG 3720

CGCGGAATGT ACCACTGATA TCAGTAATTG GTTGTGTATG CTCAGATGAA GTAATAGGAA 3780

TGGCATGTAG AGGTAAGTCT CCAAAGCCAA CATCAGTTAC ATAGAATACA TCATTTATAG 3840

AAACAACAAG TGAAGCATGT GAACCGTTCA GACTACGACC GCCACCGGGw GTGTGAATAG 3900

TAGCTGACAT TAATTCAGGA TTAAATCCTT TTTGTTGTAA ATAGGCTTTG AAAAATGTAT 3960

TTAATTCATA ACAAAAACCA CCACGTTTAT CATGAACAAT TTTATTAAAA AGTGCATCGA 4020

TATTTATAGA TATCGGCTTA CTATTTTGAA CATCAATATT TTCAAAAGGT ACAGTTAACA 4080

TAAAACGTGT TGCATAATAA TTTAATGCTT CAATACTCGG TCGATTATAA CGAGATGAAT 4140

CAATTTGTAA ATAATTCTCT AACTTCGCAA TATTCATAAG CATAGCGCCT CCTGTATTAA 4200

AGATTATAAT TAAATTTTAA ACAGAAATAC TGAAATTTTA AATTCGAAAG CATTGAATTT 4260

TGGATAAATA CATTTTAAAT AGAAAAATAC GCTCTCAAAA TGAAGTCATC TCTAAAAGAA 4320

ACGATTTAAA GATGACTACT GAGAGCGTAg CATAATGGAA GAAGTGTGCA GGGTGTCTAA 4380

AAATGCAACA ATACAAAGGT AGTTGCAAGA CAAGTTGCCT TATCTAGACC ATTTGTGTTC 4440

TATGCGACCA AACTTCCAAA TTAAACTTGA AATAAGCCAA GTAATTAAAA ATAATGCAAC 4500

TAAAATATAG CCTAAATAAT CAAATTCGAT CGAACCAATG AATGCCCAAA ACGCACCATG 4560

TAAATCTAAC TTATCAGCAA GAATTTGTAG CAATTCAATC ATCCCAATCA CTAATGCTGC 4620

CATGACTGAT ATCGCAGTAA TCGTTATATT GTAATAGATT TTGCGAATAG GATTGAAGAA 4680

TGCCCAATTA TAGGCATACT TCATTACAAC ACCATCTAAT GTATCCAATA AACTCATACC 4740

TGATGCGAAT AAAATTGGTA AAGATAAGAT TCCGATAAAT GAAATGGCTT GTTGTGATGC 4800

GCCTGAAGAA AGAGCGAGTA ACGCAATTTC ACTAGCTGTA TCAAAACCAA GTCCAAATAA 4860

AAAGCCAAGT GGCAATACGT GCCAACTACG CGTGATTAAT TTGAAATAAG GTCCTACAAA 4920

TCGAGAAACC AATCCTCTAG ATTCAAGTAA TGCATCGACT TCAGCTTCTT CAATGTGTTC 4980

ACGACGTAAT TTAGCGAACA AGTTAATTAA AGAGATTAAA ATAATTAGAT TCAACACACC 5040

GATAAGCACT AAAAAGAAAC CTGAAACTAG TGTACCAATC GTTCCACCAA TATCTTGGAA 5100

ATGCGGTAAT TCATCTTTAG CCCATTTTAC AGATACCCCT AAAAAAACAG CCATTAAAAA 5160

TACGACAGAT GAATGTCCAA TTGAAAAATA GAAACCCACA CCAGATGGAT CTTTGCGTTG 5220

CTGTAATAAT TTGCGaACCG TATTATCTAT TGCAGCAATG TGATCTGCAT CAAATGCATG 5280

ACGCAAACCT AATGTATATG CAAGAATCCC CaTACCAAAT AAGATATGAT GGTCTTTTCC 5340

AGCAATCCAT AAAAAACTAA ACCCAATAAC GTGTAACAAA ATGACAATAG CTATGTATGG 5400

ATATTTAATC ATACTGTATG TTCAATGGGC ACTCTAGTAA TAAGTGTTCA TATAACAAAA 5520

ATGTTATGCC AAATTATTTG TTATATAAAA ATATACATGT AACCACAAAA GATTTTTTGC 5580

GATATATATA ATTTGATAAA TTAACCAACA ACAATGTAAG ATGTCACTTT GCTTAACTTG 5640

GCATCCTTTT TATGATTTTC AAATTCAAAA AAATGAGCAA AATGAATCTC TTTAcCAGTT 5700

TTTAATATTT CaATACCATG CATGGAACCT AAGCACCCAT GTGTGATGCT GGAATGGATA 5760

TTGAGACTAG CAACCTGATT GTAATGATTA GATAGTTCTT GAATTAATAT TTGAGGTCCG 5820

TATATGTCAA AGCGGCCAGG GACAGACCAA ATAAATTCTG TTGTAACCAG TGAACGTAAT 5880

AATTCAATAT CTAATGCTGC TGTAACAACT ATAAAATCTA TCATTTGTTG ACGTTTAGGC 5940

GCATGATTGC ATGACACATC TCCTGTTAAC TTAAAAGGTA ATGATGACTG AACTTCCGTT 6000

TTAAAATGTA GTTGGTGCTG AAATAAAGCT TGTTC 6035

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1039 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

TTTTGAACAG CCATATTTAT TCACCCTCAA CATCATTATA ATGGTATTAG TCGCATTACC 60

TTCACTTGTT TTAGCTATAT ATGATTATAT GAGTTTTAGA ATTTCTTCTG CTATTTTACA 120

ATTTCTAGGG GCTATCTCTT GGTTCTTTTT ATCATTGATA TTATCGCTCA CACAATTTAC 180

ACCTTTTACA TTAGCGTCAT TTATAACTTC AATTATTTTG TTCACAAGCA CAATTATCAC 240

ATTAGCCATT GGTGGTAAGT CTGTTGAAAA GAATGATTCC CCTTAAATTC CAAATGAAAA 300

AAAGGTTCTG AAGGCCGCTA TAAAACACAG TTTTTCAGAA CCTCTATACT TCTATTCAAT 360

GATATATGGT TTGCAATTTT CTACCTTTAA ATCCACAGCT TCTGCCCTTG AAACTTTGTT 420

AAAATAAACC ATCAAACAAC GAATGACAAC TTGATGTGCA ACAATGACAA TATCATCTTT 480

TTGTGTATCT TCATTGACAA CATGATTCAT AAAATGTTCT ACGCGTTGAT ATACATCTTC 540

ATAACTTTCT CCTTCAGGCG CTTTTTGTGA AAAACTATGA CGAAAGTCTT TAAAGTTTGG 600

ATCATTGAAA TATTTTTCAT ATTTCGGATT CGCACTGATT TCATCTTTAT ATTCACCCTC 660

AAATACGCCA AGTGAACGTT CTCTTAATAG AGGGGTAGTC GTTGATGCAA TGTCATATGG 720

AAAAATATGT TCAAACGTTT GCTGTGTTCT TAATAAGTCT GAAACATATA CATGTTTAAT 780

CGGCACATCT AATTGTCCAC AAAAATAAGA TCGAAAATGT TTATTATCAT AATTCGATTT 900

TGATTCGCCA TGTCTAACTA AATAAATCGT CATAATATTA CTCCTTACCT TATGTATTTC 960

ATATCTACCA TAACACTTTG ACTACTAATT CGATATCAAT CTTAATATTC TATTCTAAAA 1020

AAAGAATTAA TTCATATnT 1039

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

GAGAGAATnT GCAATTAGTT ATTCAATTAG TTGATTTAAG ACATGATCCA ACACAAGATG 60

ATATCTTAAT GTACAATTAT TTGAAACATT TTGATATTCC TACTTTAGTT ATATGCACTA 120

ArGAaGACAA AATTCCaAAA GGTAAGGTyC AAAAGCATAT TAAAAATATT AAGACACAAT 180

TAGATATGGA CCCAGACGAT ACAATTGTAA GTTATTCATC AATTCAAAAT AATAmaCAAC 240

AACAAATATG GAATTTAATT GAACCGTATA TTTCATAGTT TTTGTACGTC AAAACTTATA 300

CAAAAATTTT AAAAATAATG TAAGCACGAA ACTTTTAATT AGTACACAAT TGATAACATT 360

TTTCAACGTT CATCATTTTG TCAAAAACTC AAAAGTAAAT TAGAAAGATT ATAATTTATT 420

TAAGCATCGT ACTTAATTGG ATTTTAAATT ATGTTATAAT ATTTGTATTG TTAGTATATA 480

TGGGGGCTTT TCAAATGCAT TTTATTGCAA TTAGTATAAA TCATCGCACA GCTGATGTgC 540

ACTAAGAGAG CAAGTTACTT TTAGAGATGA TGCCTTACGA ATTGCCCATG AAGATTTATA 600

TGAAACTAAA TCTAyTTTAG AAAATGgTCA TATTaTCAAC ATGTAATCGA ACTGAAGTAT 660

ATGCTGTTGT TGATCAAATT CACACAGGTC GTTACTATAT TCAACGATTT CTAGCTCGTG 720

CATTTGGATT TGAAGTAGAT GATATTAAAG CAATGTCAGA AGTAAAAGTG GGGGACGAAG 780

CaGTAGAACA TTTATTGCGT GTCACTTCTG GTTTAGATTC AATCGTACTT GGAGAAACTC 840

AAATTTTAGG TCAAATAAGA GATGCATTTT TCTTAGCGCA AAGCACAGGT ACGACAGGrA 900

CAATTTTTAA TCATCTATTT AAACAGGCAA TTACTTTTGC AAAAAGAGCA CATAATGAAA 960

CAGATATAGC TGATAATGCT GTAAGTGTGT CTTATGCTGC GGTCGAGTTG GCGAAAAAAG 1020

TATTTGGCAA ATTGAAAAGT AAGCAAGCTA TCATTATTGG TGCAGGGGAA ATGAGTGAAT 1080

TATCACTATT AAATCTTCTT GGTTCTGGAA TTACTGaTAT TACAGTAGTA AATAGAACAA 1140

TACCAAATTT ACTTGAAAGT GCAGATATTG TGATTAGTTC AACGAGTGCA CAATCTTATA 1260

TCATTACAAA TGAAATGATA GAAAGAATTG CAGAAAATAG AAAGCAAGAT TCACTAGTAT 1320

TGATTGATAT TGCAGTTCCT CGAGATATTG AACCTGGTAT TAGTGCCATC ACAAACATCT 1380

TTAATTATGA TGTTGATGAC TTAAAAGGTT TAGTTGATGC AAACTTACGT GAGCGACAAT 1440

TAGCGGCTGC AACAATTTCG GAACAAATTC CTACAGAAAT ACATGCACAC AATGAG 1496

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4826 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

CTTGATTTTT TCCCtTTAGT ATTTTCCaTt TGanTGTCGC AGCTTCTAAA TCCTGCTTTG 60

GTTCTCTAGT GAACTTCATA ATTAAAGCAG CTACAACGAA TGATACAAGT GCAGCAAGGA 120

AGACACCGAG TAACATGTGC AAGAATTCAC CTCTAGGTGC ATTTAAACAG TAAACTATAA 180

ATGAACCTGG TGACGCGGGA CTTTTAAATC CAAATCCTGT TGCTTGATAA GTTGCAACAC 240

CAGTCATTCC ACCTAAAATA ACAGCGATAA ATAATAAAGG ACGCATTAAT ACATATGGGA 300

AATAAATTTC ATGAATACCA CCTAAGAAGT GGATAATTCC AGCACCATAT GACGTTGCTT 360

TTGCAGTGCC TTTTCCAAAA ATCATATAAG CAAGTAAGAT ACCTAAACCT GGTCCAGGGT 420

TAGATTCAAT TGTGTATAAA ATTGATTGAC CAGCTTTTGC AGCTTGATCT GCACCAAGCG 480

GTGTGAATAC ACCATGGTTA ATCGCATTGT TTAAAAATAC AATTTTTGCA GGCTCTACTA 540

AAATACTTAC AAGTGGAAGT AGGTGTGCAT GTACTAATGC TTCAACTGCC ACTGATAAAA 600

TATGCATAAT AAATTTCATA AGTGGTGCTA AAATTTTAAA TCCTGCAATC GTCATGATAA 660

ATCCTAAAAT ACCAGCAGAA AAGTTATTAA ATAACATTTC AAAACCTTGC GGCGTTCTAG 720

GTTGAATCAA TTGGTCGGTC TTCTTCATTA ACCAACCAAC AAGTGGACCC ATAATCATTG 780

CACCAAGTAA CATTGGTGTA TCAGGTAATG CAACGATGAC CCCCATAGTT GCTGTTGCTG 840

CGATGATACC ACCACGTAAA TCATAAATTA AACGACCACC ACTAAATGCG ATCAATAATG 900

GGATTAAATA AGTAATCATT GGTCCTGCTA AAGTAGCTAA ATCTTTGTTA GGTAACCATC 960

CATTATCTAT AAAAATGGCC GCGATAAAAC CCCAAGCGAT GAAAGCGCCA ATGTTTGGCA 1020

TGATCATACT ACTTAAGAAT GATCCAAATG CTTGAACACG ACGACCAATT CCTTTTTTCT 1080

GAGAGGTTAC TTGTTACTCA ATATAAACAA AAATCAACTT TGTCAAAATA AATGTGACAA 1200

AATTAAATAA AGTGTCATCA ATGTGACAGT ATAGATATTT TGAAAAAGTA AAACAAAAAA 1260

ATTGTTTTAG GATTTTTAAA ATTTTATTGT GAAAATATTT GCAAAACAAA ACAACACCGT 1320

gTACAATAAT GATTAATGGA AAGGGGGAAA GTTCGGCAGT ACAGTTAAAG CGCCTGTGCA 1380

AATAAATATT TGTATTTGAA GATTAAAGGT TAATATATGA GTGGCCTTTA TAGAGTGCAA 1440

TATATGTATT TGTAGACGAG GAGGATAGTG ATCGAATAGA TCGGCGGATG CTATCCCGGA 1500

TGTGGCTCAT TCGTTAGCTT ATTAAGTAAA ACATTAGGGT GACTTAATGG ACAAAGTTAA 1560

TAAGATCGCC AGAAATTGAA TATAAAAAAT ATTAATATGG AAAGTACAGT GTGAGCAATT 1620

TGTATAGTTG TAAAAATAAC TATGCTTAAT TTGTTATGGA TGAATGCGAT GATAGCATGT 1680

TCCTATTTAT ATTATGAAAG CAGATTGTCA ATCTAAATTA TCGGCAATAA ATCATAATTT 1740

ACGCGTACTA TTCCAATATG GAGGAAAATG TCGTTATGTG TGGAATTGTT GGTTATATTG 1800

GCTATGaTAA TGCCAAAGAA TTATTATTAA AAGGTTTAGA AAAATTAGAA TACAGAGGTT 1860

ATGACTCTGC AGGTATCGCA GTAGTAAATG ATGATAATAC AACTGTATTT AAAGAAAAAG 1920

GTCGTATTGC AGAATTACGT AAAGTTGCTG ATAGTAGCGA TTTTGATGGA CCTGTTGGAA 1980

TCGGTCACAC ACGTTGGGCA ACACACGGTG TACCGAATCA TGAAAACTCT CATCCACATC 2040

AATCATCAAA TGGCCGTTTT ACTCTAGTTC ATAACGGTGT TATTGAAAAC TATGAAGAGT 2100

TAAAAGGTGA ATACTTACAA GGTGTATCAT TCATTTCAGA AACAGATACA GAAGTTATCG 2160

TTCAATTAGT TGAATACTTT TCAAATCAAG GACTTTCAAC TGAAGAAGCA TTTACAAAAG 2220

TTGTGTCATT ATTACATGGT TCATATGCAT TAGGTTTATT AGATGCTGAA GACAAAGACA 2280

CAATCTATGT TGCTAAAAAT AAATCACCAT TATTATTAGG TGTTGGTGAA GGTTTCAATG 2340

TTATCGCATC AGACGCACTT GCAATGTTAC AAGTGACAAG CGAATATAAA GAAATCCATG 2400

ACCATGAAAT CGTTATTGTT AAAAAAGATG AAGTTATTAT TAAAGATGCA GATGGAAACG 2460

TTGTAGAACG TGATTCATAT ATTGCTGAAA TTGATGCATC AGATGCTGAA AAAGGTGTTT 2520

ATGCACACTA CATGTTAAAA GAAATTCATG AACAACCAGC AGTAATGCGT CGTATTATTC 2580

AAGAATATCA AGATGCAGAA GGTAACTTGA AAATTGATCA AGACATCATC AATGATGTTA 2640

AAGAAGCAGA CCGCATTTAC GTTATTGCAG CAGGTACAAG CTACCATGCA GGTTTAGTAG 2700

GTAAAGAATT TTTAGAAAAA TGGGCTGGCG TACCAACTGA AGTACACGTT GCATCAGAGT 2760

TTGTCTACAA CATGCCATTA TTATCTGAAA AACCATTGTT CGTTTATATT TCTCAATCAG 2820

GTGAAACTGC AGATAGCCGC GCCGTATTAG TTGAAACTAA TAAATTAGGT CATAAATCAT 2880

TACACGCGGG TCCTGAAATC GCAGTTGCAT CTACAAAAGC ATATACTGCA CAAATTGCAG 3000

TATTATCAAT CTTGTCTCAA ATCGTTGCAA AAGAGCaTGG TCGTGAAGCA GATATTGATT 3060

TATTGAGAGA ATTAGCAAAA GTAACAACAG CAATAGAAGC AATTGTTGAC GATGCACCAA 3120

TTATGGAACA AATTGCTACA GATTTCTTAG AAACAACACG CAATGCATTC TTTATCGGAC 3180

GTACTATTGA CTATAACGTA AGTTTAGAAG GTGCGTTAAA ACTTAAAGAA ATTTCTTACA 3240

TTCaAGCAGA AGGTTTTGCT GGTGGAGAAC TTAAACATGG TACAATTGCC TTAATCGAAG 3300

AAGGTACACC AGTTGTAGGT TTAGCAACAC AAGAGAAAGT TAATTTATCA ATTCGTGGTA 3360

ACGTTAAAGA GGTAGTAGCA CGTGGTGCAC ATCCATGTAT TATTTCTATG GAGGGTCTTG 3420

AAAAAGAAGG CGACACTTAT GTCATTCCTC ATGTACATGA ATTGTTAACG CCATTAGTAT 3480

CAGTGGTTGC ATTACAATTA ATTTCATACT ATGCAGCATT ACACAGAGAT TTAGATGTTG 3540

ATAAACCACG TAACCTTGCT AAATCAGTTA CTGTGGAATA ATTCACTTTT TTAGAATCAA 3600

TCATGTATTA AAATTAAAGT ATATGGCACC CTTTTAGATT AATCGACTAG AAGGGTGCTT 3660

TTTTAGGTCG ACTTaGCTTT TACTTCATCT TAATTTGGCA GAAATGCGTa AAAATGAAGT 3720

GTTTTATTTA TTTAAATAGT CTGACAATTA AGGGTGTTAT GTTAATATGA TTTTATGAGA 3780

AGTATGGAGT AGCAATAAAG GGGTGACCTC GCATGTTAAT TCAATTAGAT CAAATTGGGC 3840

GAATGAAGCA AGGAAAAACA ATTTTAAAAA AGATTTCTTG GCAAATTGCT AAAGGTGATA 3900

AATGGATATT ATATGGGTTG AATGGTGCTG GCAAGACAAC ACTTCTAAAT ATTTTAAATG 3960

CGTATGAGCC TGCAACATCT GGAACTGTTA ACCTTTTCGG TAAAATGCCA GGCAAGGTAG 4020

GGTATTCTGC AGAGACTGTA CGACAACATA TAGGTTTTGT ATCTCATAGT TTACTGGAAA 4080

AGTTTCAAGA GGGTGAAAGA GTAATCGATG TGGTGATAAG CGGTGCCTTT AAATCAATTG 4140

GTGTTTATCA AGATATTGAT GATGAGATAC GTAATGAAGC ACATCAATTA CTTAAATTAG 4200

TTGGAATGTC TGCTAAAGCG CAACAATATA TTGGTTATTT ATCTACCGGT GAAAAACAAC 4260

GAGTGATGAT TGCACGAGCT TTAATGGGGC AACCCCAGGT TTTAATTTTA GATGAGCCAG 4320

CAGCTGGTTT AGACTTTATT GCACGAGAAT CGTTGTTAAG TATACTTGAC TCATTGTCAG 4380

ATTCATATCC AACGCTTGCG ATGATTTATG TGACGCACTT TATTGAAGAA ATAACTGCTA 4440

ACTTTTCCAA AATTTTACTG CTAAAAGATG GCCAAAGTAT TCAACAAGGC GCTGTAGAAG 4500

ACATATTAAC TTCTGAAAAC ATGTCACGAT TTTTCCAGAA AAATGTAGCA GTTCAAAGAT 4560

GGAATAATCG ATTTTCTATG GCAATGTTAG AGTAAATATT TTGCAAATAA TAAGTAATAA 4620

TGACAAAATT TAATTAAGAT AAAATGGACA GTGGAGGGCA ATATGGATAA CGTAAAAGCA 4680

AAAGATGTCA TTAATCAATT GAGAGAGAAA GGATATAAAG TATTTTTGGC AACAGGACGT 4800

TCGCATTCTG AAAATACATC AACTTG 4826

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

GAATAAAAAG TAAAATTACT CGCCTTTGTT ACCTTTTACT TTATCAATaA AATCAGTTGC 60

TTTTTCTTTT GCATTTTCAA CGAATTCTTT CGCTTTACCA GAAGCTTTAT CTTCTTTACC 120

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ATTTTTACGC CTTTTTTGAT TTTAATTAAA CCTGCATCAA CGAAGAATTT TAAGAAACGT 960

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CTTTTATACT TTTTAGAGTA TACAGCCATA GGTTCTAAGT GAACATCACC GGCACTTACG 1080

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CAGTCCTTGA CCATAACAAA TTAAAATGTT GGAAGATCAT ACTTACTTTT TGTCTTTTTG 2880

CTCTTAATCC ATTTTTGGAC AATTGACCTA TATGGTCTCC ATCTATAATA ACTTCACCTG 2940

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AGATACTACA CTTATTAAAG TAATATATTT TTATGATTCT CTTAGCTGCA ATCCCATGAA 4800

TACATGTAAT CATCAAACTT CATAGCCTCA AGGTCAGTAG ATTTCA 4846

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

AACAAAGACA CAATCGAACA TGAACCATCA GTAAAAGCTG AAGATATATC AAAAAAGGAG 60

GATACACCAA AAGAAGTAGC TGATGTTGCT GAAGTTCAGC CGAAATCGTC AGTCACTCAT 120

AACGCAGAGA CACCTAAGGT TAGAAAAGCT CGTTCTGTTG ATGAAGGCTC TTTTGATATT 180

ACAAGAGATT CTAAAAATGT AGTTGAATCT ACCCCAATTA CAATTCAAGG TAAAGAACAT 240

TTTGAAGGTT ACGGAAGTGT TGATATACAA AAAAAACCAA CAGATTTAGG GGTATCAGAG 300

GTAACCAGGT TTAATGTTGG TAATGAAAGT AATGGTTTGA TAGGAGCTTT ACAATTAAAA 360

AATAAAATAG ATTTTAGTAA GGATTTCAAT TTTAAAGTTA GAGTGGCAAA TAACCATCAA 420

TCAAATACCA CAGGTGCTGA TGGTTGGGGG TTCTTATTTA GTAAAGGAAA TGCAGAAGAA 480

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GGAGAAAATA TTGATAAATC AAAAACTAAT TTTTTAAACT ATGCGGACAA TTCAACTAAT 720

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ACTTTTACAC CAGAAGCGCC AAAAACAATA ACAGAATTAG AAAAAAAAGT TGAAGAGATT 1020

CCATTCAAGA AAGAACGTAA ATTTAATCCG GATTTAGCAC CAGGGACAGA AAAAGTAACA 1080

AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACrCCAA CACTAAAAAA TCCATTAACT 1140

GGAGwAATTA TTAGTAAAGG TGAAyCgAAA GAAGAAATCA CAAAAGATCC GATTAATGAA 1200

TTAACAGAAT ACGGACCAGA AACGATAACA CCAGGTCATC GAGACGAATT TGATCCGAAG 1260

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AAATATGGgA CCTGTaAAAG GAGACTCgAT TgTaGGAAAA AGarGAATTc CaTTCaGGAA 1800

AGAcGTaATT TaTCCTGTTT AGCACCCGGG GCAGAAAAGT TAC 1843

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8536 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

TAAACAGCGC GTGTACTTGT GATTCCCCCT TCTTCTATTT TACCCACCCG GGAAATAATA 60

CTTTTCGCGA TTCCTTACTT GaACAAGCAA TATTTTATCa GCTGTTTCTT CAACTAAACA 120

GACACATTTA ATCATCTTTG ACACCCCAAC TTTGTGAAAT CAATTTTTCA AATTATACTG 180

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CTATAAATAT CATGCTAAAA ATAAAAAATT AGTATATCTT TCATTAGGTT TAAGCACTGT 420

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GTTCTGTAAG TTAAAATACC TGGTGCAGCT GAATAGTTCA TTTCTGAAAC TAAAATACTA 840

CCATCGTTAT TTACACGTTC TACAAACATA ACATGACCAT AGTAACCTAC ATCTGTTTGA 900

GCGATAGAAC CTACAGTAGG TCTATTGTCG ATAGTGTAAC CATCTGCTGC CGCTGCGTTA 960

TCCCAGTTAT TAGCATTCCA CCAATAAGTA CTAATACCTT TACCAATTTC AGCACGACGA 1020

GTATTGTAAC CTCTATTTGT CGTTGTTGCA GATCCTGAGT TCGTAGATGC aTTACCAGTT 1140

ACTTTCAATT TTTGACCCGG ATATATAAAG AAATTATTTA AGCCATTTAA GCTCATAATT 1200

TTTTGATAAG TTGTACCATA TTTTGATGCA ATTAATGACA ATGAGTCACC TGCTTGTACT 1260

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GTTGCCGCAA CAGCGCTAAT CGCGCTTGTC CCAATAATAG CTGCAATTAC TTTTTTTTGC 1740

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TAACATGACA ATAATCATCG TAGCGAATAT GAATATACCT TGCCCTAGAA CGGTTAACCA 8100

AGGATTTGAT ATTACCGCTT CAAAATTCAT TTCTTGGAGA TGATTGATGC GTTGAAATAT 8160

AACTAATTGC CATAATACTT GTCCGATGTA AATGACAATC CAACCACCGA TAACACTATA 8220

TTTACCAGTT AATTTACTAT ATATTTGTGT TGTATATGTC CGTCCCATTT TCCCAACAGT 8340

GAATTCCATA ATGAGTAATG GCAACCCAAC AAAAATGGTG AATATTAAGA ACATAGCTAG 8400

AAAGGCACCG CCGCCATAAA TCCCTGCCAT ATATGGGAAT TTCCACATGG CACCAAGACC 8460

GATTGCAGAA CcCGCACTAG CTAAAATAAA TCCAGTTGAT GACTTCCATT GTGATTGTTG 8520

TCTTTTCATC ATTCAC 8536

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4328 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

GCTTTGGCCA TTTTATGTGG CGATTGAGAC AATCtGTkGT TGTCTTATTT GATGTTGTAT 60

TTCAACTGGT AATTCTAGTT GCGATTGAAA TAATGGCAAC TTTTCCCAAT CATTAACAAA 120

TAATTCAATA CCTGCTATGT CTAATACTTT AGCACGTGCA TCATCAACAA GACGGCGTTC 180

CAATTGATTT GCTTCTTCTT TAATACCTGG TGACGTACTT TCTAATATCA AATTAGATAT 240

AGGGATGTGA CCATTAATTG CATAATATAA TGCAACACGC CCACCCATTG AATATCCAAA 300

CAATGTTATT GATTTATCTT TATATTTATC TAAAATTCGG TCTAACAACG TCGTAATATA 360

ATCAAAATTC CACGTTTCAT CCATTGAAGA CTGATCTTCG CCATGGCCTG GTAAGTCTAT 420

AGTGATGACA TGATAGTTAT CAGTAAATTT TTCGATGTGA TTATGATAAG TACGGCTGTC 480

GCTAAGAAAT CCATGCAGAA ATACTAAAAC TTGATTGGTC TCAACGTTTG CTTCATAAAA 540

TTTATAATGT GTCATGAATC ATTTCACTCA ATTTCTGGTA TAAAATTTGA TGCTGTTTAA 600

AGTTATCTTC GCGATTCGTT ATCAATTCAT AAATCGTCGA AGTTTCAGAT AACAATGTGG 660

CATTTTTAAA TTCTGAAACA CTGTTAAAAC GTTTAAAATC GAATTGATAT AACTTAGCTG 720

TATACTCGAA ATCCAATCCC GTCGGTGTGC CAAACAACCG TTCAAAATAG TCAGTTGCAC 780

TTTCTTTTTG TGGTAAATAT GAAAAAATAC CGCCACCATC GTTGTTCAAT AATACAATAT 840

TCATCTGAAT ATTATTTAAT TTTGACATTA ATAGTCCATT CATATCATGA TAAAATGATA 900

AATCACCTAT CAATAATGTT ATTCGTTTAT GCACAGCCAT ACCCAGTGCA GTTGAAACGA 960

TACCATCAAT ACCATTCGCA CCACGATTCG CATAGACATC TATATTTTTA TTCAATAACA 1020

AGTTATCTAC ATCTCTGATA GGCATACTAT TACTAATAAA TAATGCATCT TTTTCAGATG 1080

TAATTTCTTT ACGCCCTTTT TTCTCTAAGC ATTGCCATTT TTCTAACCAA CTTACGCGAT 1200

TAACTGTCGT GTCTTCCATT AATGACCTAA AGAAATCATT CGCAGAAATC TCATATGAAA 1260

TATCTGGCGC TATCGGAAAG ACATCAATCT TATCATTGTT TTGCACTAAT ATTTGAAATG 1320

CATCAGTTTT CTTTAACCAT TGATTTAACT TTTTAGAAAT CACTGGTTTC CCAACACGAA 1380

TTACGAAATC CACATTTAAG TCTAAGCCGC TTCTAAACAG CAAATCATAT GTACAGATAA 1440

CATTCGGATG ATCAAATTTT CTTAAATGAC TTAAAGGATC AGCTAAAATA GGCAAATCAT 1500

ATATCGTTGA ATACGTTAGT ATTTGaTCAA CTTCTTGGTG CTGCATATCC CCTACAATAA 1560

TTAAACCTTT TTTCTTATTT AAAATGTGTC TTAATGCCGA TGCATCTATA CTTTTTTGAT 1620

AGTGCGGTAA AATCTTCATC TCAGAAGTTA ACAATTCTGT TGCATTCAAA TCAGGTGTTA 1680

ACGGATCTCT AAATGGCAAG TTAAAATGAA TTGGCCCTTT ATGTGGTCCA TATAAATATT 1740

GACTAGCAAT TTGCATTTGA TAGTAAATTG CATCAATGGT CTCTTTACTA TCATCCGCAA 1800

TAGGCATATC GAACTCATAA CTTACATAAT TATTAAACAT ATTTACTTGA TTAATCGCTT 1860

GTGGTGCGCC TACACTTCTT AATTCATGCG GACGGTCACT TGTTAAAACG ATTAAAGGAA 1920

TTCTACTAAT TTGGCTTTCA GCAATTGCAG GCGTATAATT CGCTGCTGCT GTACCTGACG 1980

TACATAATAT AGCGACAGGT CTTTCACTGC CTTTAATTAA CCCAACTGCA AAAAACGCTG 2040

CACTTCGCTC ATCGGGGTGT ATCCATGTTT TAATATTTGG ATGTGCTTCA AATGCAAGTG 2100

CAAGTGGCGT TGAGCGTGAT CCCGGACTGA TAACTACTTC CCTTACGCCG TACGCATATA 2160

ACTCAGATGC AAATGTAAAA ACTTGCTTCG TTAAAGCTGC TTTATGATTT CCCATTCATA 2220

TCGACTCCTA ATGCATTCAT CATAGGTGTG AACTTAAGGT TCGTTTCTGC CAATTCACTA 2280

TCTGGATCAG AATCTTTAAC AATGCCACAC CCAGCAAATA AAGTTGCTTG TGCTTTCTTA 2340

ATAAGCATCG AACGAATTGC AACAATAAAT TCACAATCAT CGTATATATC TATATAGCCA 2400

ACCGGTGCAC CATATAATCC TCGCGTACCA AATTCTTTCT GCTCAATAAA ATCCATTGCA 2460

AATTCTTTTG GATAGCCACC TAAAGCAGGT GTTGGATGTA AATTATCAAT TAAACTAATA 2520

TACGAATCAT CCTTCAGTGG CGCCTTTATT TCAGTGTACA AGTGATATAA ATGATCATTT 2580

TTTAGAATTT TAGGCGTCTT ATCATAATGT AATTCAGTGA TATAAGGTTT AATATCATGT 2640

AAAATACTGT CAACAACAAA TCGATGTTCG ATTAAGTTTT TATTATCTTT TAAAAATGCT 2700

TCAACATTTT TTGTATCTTC GTCCTCATCT TGTGAACGTT TAATTGTACC TGCTACAGCT 2760

TTAGTCGATA GTATTTTATT ATTGACCTTT ATTAATTGTT CAGGTGTTTG TGAAAAGAAT 2820

ATAGAATCTT GTGATTCTAA CAAGAATATA TAACTGTTTT TTTCTTTAGA ATATGCTTGC 2880

ACAATTTTTT CTTCATTATT AATAGATTCT ATAGCTTCTA CTACAAGTTG ACGCCAGTCA 3000

TCTTTATAAA TATCTTCATT TCTAGTAATT TCCCCAATTT GCTCGTCCAC ATCTATGTCC 3060

GATATATTGT TGAACAAATC CATTAAATCG TTCAATGCCT CAACAGTAAA ACTTTCCCTT 3120

TTAACTGTAT AAGTTAAAAA TGTCCCATTA TTATCAGTTG AAATTAAAAC TTCAGGTAAT 3180

ACAAAATGAT TTAGTCCAAA CTCTCGCCAT TCATCATCTG ATTTATGACT TGAAAATTGG 3240

AACCCTCCAA CAACTCGAAG ATGATGTTTC TCAGATTGCG GATGTATAAA TGTGATGTTA 3300

TGTTTTAATT TTTCCCAGTC TTTAAAAATA GATTGTTTAT TTTTAGAATT ATTTTTGAAT 3360

AATTGAATTG CTTTGTAGCC AAAATATGAC GTTCGATTAT CATTCAAACG CATATAAAAG 3420

CGATCTCCTG CCTCATTGTC AGTGAGATGA AATAATGTGC TCGGGTCTAG TGACTGTGAT 3480

AATTTCACTT CAACTGAAAC CCATTCCTTT GAGCTGCCAT ATATCTCTTT GACAATATCG 3540

TCCTCTAATA CGCCCGTAGC CATCCATTTC ACTTCTTTCT TCGTCTTTTT TCACTCATTA 3600

TTATATTGTA TCATTTTTGG ATAATTGTGT TACAAGAATT GCTTAAACTT ATCTTGCAAT 3660

TTTTCACGTC AATTGACCTT TATGCTACTT TCTATTAAAA TATCTTTGTT ATAAAAAATA 3720

TGATTTAAAG AGGTTTTGTA TTCAATGAGT AATCAATATC AGCAATATTC TACAGTTAAG 3780

AAATATTGGC ATTTAATGCG TCCTCATACA TTAACTGCTT CCGTAGTACC CGTTTTAGTT 3840

GGTACAGCAG CATCTAAAAT ATATTTTCTT GGTAGCGAAG ATCATATTAA AATCAGCCTA 3900

TTCATTGCCA TGTTACTAGC ATGCTTACTT ATTCAAGCAG CAACTAATAT GTTTAATGAA 3960

TACTATGATT ATAAAAAAGG CCTCGATGAT CATGAATCTG TAGGCATTGG TGGTGCCATT 4020

GTTCGCAACG GTATGAGCCC AGAGCTTGTG CTACGATTAG CCATTGCATT TTACATCTTA 4080

GCAGCAATAT TAGGTTTGTT TTTAGCTGCT AACTCTTCAT TTTGGTTATT ACCAGTTGGA 4140

TTAGTATGTA TGGCTGTTGG TTACCTATAT ACAGGTGGCC CTTTCCCTAT TTCATGGACG 4200

CCTTTCGGTG AATTATTCTC AGGCGTATTT ATGGGTATGT TTATTATCGT TATTGCATTC 4260

TTTATTCAAA CTGGCAATAT TCAAAGTTAT GTAATTTGGT TAAGTGTACC TATAGTAATC 4320

ACTATCGG 4328

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GTTCAATACA GAAAAAATAA ATTTAGATGT TGAAGCATCC TACAATTAAT ACAGATCCAT 60

TTCAATATAT TTAAACTAAA ATCTCGGGAT TTCTAAATTT TGAAATTTCG AGGTTTTnAT 120

ATTTTTATTT AAAATAGCAC ATTTATACTT TATAATAGTA AAGATGAACA TATAAGGAGG 180

CCAAATCATG GCAAAACATC CATTCGAACA ATTTAATCTA GAATCTAGTT TAATTGACGC 240

TGTGAAAGAC CTTAATTTTG AAAAACCAAC TGAAATTCAG AATCGAATTA TTCCAAGAAT 300

ACTAAAGAGA ACAAATTTAA TTGGTCAATC TCAAACGGGT ACAGGGAAAT CTCATGCATT 360

TTTATTACCA TTAATGCAGT TAATTGATAG TGAAATAAAA GAACCACAAG CAATCGTAGT 420

TGCACCAACA AGAGAACTTG CACAACAACT ATACGATGCA GCGAACCATT TAAGCCAATT 480

TAAAGCTGGT GTTTCAGTTA AAGTTTTTAT TGGTGGTACA GATATAGAGA AAGATAGACA 540

ACGTTGTAAT GCACAACCAC AATTGATTAT AGGCACCCCT ACTAGAATTA ATGACTTAGC 600

TAAAACGGGA CATTTACATG TGCACTTAGC ATCATATTTA GTTATTGATG AAGCGGATCT 660

TATGATTGAC TTAGGATTAA TTGAAGATGT AGATTACATT GCTGCAAGAT TGGAAGATAA 720

TGCAAATATT GCGGTGTTTA GTGCTACAAT CCCACAACAG TTACAACCAT TTTTAAATAA 780

ATATTTAAGT CATCCAGAAT ATGTAGCTGT CGACAGTAAA AAACAAAATA AAAAGAACAT 840

CGAATTCTAT TTAATACCTA CTAAAGGTGC AGCTAAAGTT GAAAAGACTT TAAATTTAAT 900

TGATATACTA AATCCATACT TATGTATTAT TTTCTGTAAT AGTAGAGATA ATGCAAATGA 960

TTTAGCACGT TCACTAAATG AAGCTGGTAT TAAAGTTGGT ATGATTCATG GTGGCTTAAC 1020

GCCaCGTgAA CGTAAACAAC AAATGarACG TATACGTAAT TTaGAATTCC aATACGTTAT 1080

TGCCaGCGAT TTAGCATCTC GTGGTATTGA TATTGAAGGT GTTAGTCrTG TCATCaATTT 1140

TGATGTGCCA AATGATATTG ACTTCTTTAC GCATAGAGTC GGACGAACTG GTCGTGGGAA 1200

TTATrrAGGT GTAGCAATTA CGCTTTATAG TCCTGATGAA GAACACAATA TTTCATTAAT 1260

AGAAGATCGC GGTTTTGTAT TCAATACTGT TGATATTAAA GATGGTGAGT TAAAAGAAGT 1320

TAAAGCGCAC AATCAGCGTC AAGCAAGAAT GCGCAAAGAT GACCATTTAA CTAATCAAGT 1380

GAAGAACAAA GTTCGAAGTA AAATTAAAAA CAAAGTTAAA CCAGGTTATA AGAAGAAATT 1440

TAAACAAGAA 1450

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

AGTCAGGTAT ATCATGCCaT yCTGAATTGG TCGATATTAA TATCAGTGGT GTTAAAGAAC 60

GAATTGTATA CCAATAGACG CTTTATATTG TAAAATAGTA TTAAATGCaG AATAGAGAGG 120

AGATTTAATG CGATATGACA AATTATAAAG TTGTCGTTTT AGATATGGAT GACACATTGC 180

TAAATTCAGA TAATGTGATA TCAGAAGAAA CTGCAAATTA TTTAACAGCA ATTCAAGATG 240

AAGGTTATTA TGTTGTTCTA GCATCTGGTA GACCTACTGA AGGTATGATT CCAACTGCTA 300

GAGATTTAAA ATTACCTGAA CATCATAGCT ATATTATTAG TTATAACGGT AGTAAAACGA 360

TTAACATGAC TAATGAAGAA GTAGAAGTAA GTAAATCGAT TGGTAAGCAA GATTTCGATG 420

AAATTGTAGA TTATTGTCGA GATAGAGGCT TTTTCGTTCT TACATATCAT GATGGTCAAA 480

TTATTTaCGA CAGCGAACAT GAGTATATGA ATATTGAAGC AGAATTAACA GGTTTACCGA 540

TGAAACGTGT TGATGATATC AAAGCGTATA TTCAAGGCGA TGTACCCAAG GTCATGGGTG 600

TAGATTATGT AGCGAATATT ACAGAAGCTA GAATTGATTT GAATGGTGTG TTCAATGATA 660

ATGTAGATGC TACGACAAGT AAGCCATTCT TCTTAGAATT TATGGCCAAA GACGTTTCAA 720

AAGGTAATGC AATTAAAGCG TTATGTCACA AATTGGGATA TTCGGTGGAT CAAGTCATTG 780

CTTTTGGTGA TAGTATGAAT GATAAATCAA TGTTTGAAGT CGCAGGTCTA GCTATTGCTA 840

TGGGGaATGC ATCAGATGAA CTTAAGCAAT ATGCAAATGA AGTTACGTTG GATCATAATG 900

AAAATGGTAT TCCACATGCG CTCAAAAAAT TGTTATAAAT TTTAAAATAA GCCTTAACAC 960

ATGATATTTG AATAAGATAT CTTGTGGTTA AGGCTTTTTA TTTTTGTGAA AATGACTTCA 1020

GTTATACTAT GGAGGATTTG AAATACATAT TTTAGATTAG TAATGATATC AAACGAATAG 1080

AGTAAATGTA TATTTttTGA ATAAATCAAG TATTAACTAG TCACGGAAGG nAGATAAAT 1139

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2931 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

TCTAAAAATG CTGTGAAATT CTTTTATAAA TATCTAAAAG GAATTAATGT TGATAACATT 60

GCTGTGATAG GAAGTAAGAC AGCGCAATAT TGTGAATCAC TTGGCATTCG AGTTGATTTT 120

AtGCCAAACG ACTTTTCTCA AGAAGGATTT TTAAAATCAT TTAATCAAAC TAACCAAAAA 180

AATGAAGTTG TTAAAATAGA TTTATATACT TCAGTGCCTA ACAAACAAAA TATACAAGAT 300

GTTAAAGAAA TGATAGAACA TCAACAAATC GATGCATTAA CATTTTCAAG TTCGTCGGCA 360

GTACGTTATT ATTTTAATGA AGGATTTGTA CCAAAATTCA AGTCGTATTT TGCTATTGGA 420

GAACAAACAG CACGGACCAT TAAATCATAT CAACAACCAG TAACAATTGC AGAAATTCAA 480

ACACTCGAAT CACTAATTGA AAAGATTTTA GAAAGTAGGG GCTAAAAATG AAATTTGATA 540

GACATAGAAG ATTGAGATCA TCAGCGACAA TGAGAGATAT GGTTAGAGAG AATCATGTAA 600

GAAAAGAAGA TTTAATATAT CCAATTTTTG TAGTTGAAAA AGACGATGTG AAAAAAGAAA 660

TTAAGTCATT GCCAGGTGTA TACCAAATCA GTTTGAATTT ACTTGAAAGT GAATTAAAAG 720

AAGCTTATGA CTTAGGCATA CGTGCCATTA TGTTTTTCGG TGTTCCAAAC TCAAAaGATG 780

ATATAGGTAC TGGTGCATAC ATTCACGATG GTGTTATTCA ACAGGCAACA CGTATTGCTA 840

AAAAAATGTA TGATGACTTA TTAATTGTTG CAGACACTTG TTTATGTGAA TATACTGATC 900

ATGGTCATTG TGGCGTGATT GATGACCATA CACATGACGT TGACAATGAT AAATCATTGC 960

CACTACTTGT TAAAACAGCA ATTTCTCAAG TGGAAGCTGG TGCTGATATT ATTGCGCCAA 1020

GTAATATGAT GGATGGTTTT GTTGCTGAAA TTCGTCGTGG ATTAGATGAA GCCGGCTATT 1080

ACAATATTCC TATAATGAGT TATGGTGTCA AGTATGCATC AAGTTTCTTT GGACCTTTTA 1140

GAGATGCAGC AGATTCAGCG CCATCATTTG GGGATAGAAA AACGTATCAG ATGGACCCTG 1200

CTAACCGTTT GGAAGCACTT CGTGAATTAG AAAGTGATCT TAAAGAAGGG TGCGACATGA 1260

TGATTGTTAA ACCTGCTCTA AGTTATTTAG ATATAGTTCG AGATGTTAAA AATCATACGA 1320

ATGTTCCAGT TGTTGCATAT AATGTGAGTG GAGAATATAG TATGACTAAA GCAGCGGCAC 1380

AAAATGGTTG GATAGATGAA GAACGTGTCG TTATGGAACA AATGGTTTCA ATGAAACGTG 1440

CAGGTGCTGA TATGATTATT ACGTATTTTG CAAAGGACAT TTGTCGCTAT TTAGATAAAT 1500

AAGGTTTTAT ATTTATGATT TTCCATAAAC TGTAGGAGGA ATTTACTTTA TGAGATATAC 1560

GAAATCAGAA GAAGCAATGa AGGTTGCTGA AACTTTAATG CCTGGTGGTG TAAATAGTCC 1620

AGTACGCGCA TTTAAATCAG TAGATACACC AGCAATTTTT ATGGATCACG GTAAAGGTTC 1680

AAAAATTTAT GATATCGATG GTAACGAGTA TATCGACTAT GTACTAAGTT GGGGACCACT 1740

TATTTTAGGA CATAGAGACC CTCAAGTTAT TAGTCATTTA CATGAAGCAA TTGATAAAGG 1800

TACAAGTTTT GGTGCATCAA CATTACTTGA AAATAAATTG GCGCAgcTCG TTATTGACCG 1860

AGTACCTTCA ATAGAAAAAG TGCGTATGGT GTCATCTGGT ACAGAAGCTA CATTGGATAC 1920

TTTAAGATTA GCACGTGGTT ATACTGGCAG AAATAAAATT GTGAAATTTG AAGGTTGCTA 1980

GCCGGATTCT CCTGGTGTGC CTGAAGGTAT TGCTAAAAAT ACAATTACAG TTCCATACAA 2100

TGATTTAGAT GCACTTAAAA TCGCTTTCGA AAAATTTGGa AACGATATTG CTGGTGTAAT 2160

CGTAGAACCT GTTGCTGGTA ATATGGGTGT CGTACCGCCG ATTGAAGGTT TTTTACAGGG 2220

ATTAAGAGAT ATTACGACTG AATACGGCGC ATTGCTAATT TTCGATGAAG TAATGACTGG 2280

TTTCAGAGTC GGTTATCATT GTGCACAAGG TTACTTTGGT GTGACACCAG ATTTAACTTG 2340

CTTAGGAAAA GTTATCGGTG GAGGACTACC TGTAGGTGCA TTTGGTGGTA AAAAAGAAAT 2400

CATGGATCAT ATAGCACCAT TAGGAAATAT TTATCAAGCG GGTACGTTAT CAGGAAATCC 2460

TCTTGCAATG ACAAGTGGTT ATGAAACGTT AAGCCAATTA ACGCCAGAGA CATATGAGTA 2520

TTTTAATATG TTAGGCGATA TACTTGAAGA CGGTTTAAAA CGTGTATTTG CTAAACACAA 2580

TGTACCAATA ACTGTAAATA GAGCAGGTTC AATGATTGGT TATTTCTTAA ATGAAGGACC 2640

TGTAACTAAT TTTGAACAAG CGAATAAAAG TGATTTGAAA TTATTTGCAG AAATGTATCG 2700

AGAAATGGCA AAAGAAGGTG TGTTTTTACC ACCATCTCAA TTTGAAGGTA CATTCTTATC 2760

TACGGCACAC ACGAAAGAAG ATATTGAAAA AACGATTCAA GCATTTGATA CGGCTTTAAG 2820

TCGTATTGTA AAATAAATAT ACGGACAAAT TGAGAGCCTG AACTTTGTTC AGGCTCnTTT 2880

TAAATGTATA TAAGGCATGG GCGGCGACTT GATAGTGAAA GTCCACTACT A 2931

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

AATTATGAAT GCATTACCAG TATTATTACA AAAGAACAAT TAAAAATGTT TGTTTATGAT 60

TATGATACGC ATCTCATTAA AAATGTAaTG GTTGCAGCAG ACGTGTTAAA GGCAAATGAT 120

ATTCAAGGAC ATGAACCATT AATCGTTAAC CTTCAAACGA TTGATGAAAC ATTACATCGT 180

TTACCTATGC ATAATAGAAA AGACATGATG GTTAATGGCG GTGTACTTAT GGCACATTTA 240

AATGCCAAAA GTGGTCCGTG GTTAAAAGAT GTGCTAAGAC AAATTGAGAT AGCGATTGTA 300

ACAGGTAAAG TAAGCAACGA AGAAACTGAA ATTTTGAAAT GGGTGGATAA TCATGTCAAA 360

ATATAGTCAA GATGTACTTC AATTACTCTA TAAAAATAAA CCGAATTATA TATCTGGACA 420

AAGCATTGCG GAATCACTTA ATATTTCACG CACTGCAGTA AAAAAAGTGA TTGACCAATT 480

CCCAGATATT TGGTATCAAG GTATAATAGA CCAATATACA AAAAGTTCTG CTTTGTTTGA 600

TTTTAGTGAA GTATACGATT CAATAGATTC TACACAACTT GCTGCGAAAA AGTCACTTGT 660

TGGAAATCAA TCTTCATTTT TTATCTTGAG TGATGAACAA ACGAAAGGTC GTGGGCGATT 720

TAATAGACAT TGGAGTTCTT CAAAAGGGCA AGGACTTTGG ATGTCTGTCG TGTTAAGACC 780

TAACGTTGCA TTCTCAATGA TATCTAAATT TAATTTATTT ATTGCATTAG GGATAAGAGA 840

TGCGATTCAA CATTTTAGTC AAGATGAAGT CAAAGTGAAA TGGCCGAATG ATATATTTAT 900

TGATAATGGT AAAGTGTGTG GTTTCTTAAC TGAAATGGTT GCTAATAATG ATGGTATAGA 960

AGCAATAATA TGTGGTATAG GTATTAATTT GACGCAACAA CTAGAAAACT TTGATGAAAG 1020

TATTAGACAT AGAGCAACAA GTATACAATT ACATGATAAA AATAAATTAG ATAGATATCA 1080

ATTTTTAGAG ATATTACTTC AAGAAATTGA AAAAAGATAT AATCAATTTT TAACGTTACC 1140

TTTTTCTGAA ATTCGTGAAG AATATACTGC AGCTTCTAAT ATTTGGAATA GAACGTTGCt 1200

ATTTACAGAA AATGATAAAC AGTTTAAAgG ACAAGCAATT GATTTAGATT ACGATGGCTA 1260

TCTAATTGTT AGAGATGAAG CGGGTGAATC ACACCGTTTA ATTAGTGCAG ATATAGATTT 1320

TTAACACTAA AGCAAGGAGA GATAGCTATG GGTATGGCAA CCTATGCCGT TGTGGATTTG 1380

GnAACAACAG GCAACCAATT AGATTTTGAC GATATCATTC A 1421

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

CCAAGTTGCC TAAAATGATT AAGCAAGGTT TATACCCTAT GCnAACGATT GAACAAGAAT 60

CTGGAGCCAT CCGACTGCCA ACGATTTCTA GAGTGAnGCG TTCATTACAA TGGGGTAATG 120

ATGCTTATAC AATGATTTTA GATCGTATGA ATATTGAAAC AAATGAATAA TAAATGAACG 180

ATAAACAATG GTTATCTATC TGCACTAATA AGGTAGATAA TCATTGTTTT TTCACGAAAA 240

AATTTACAGA GTAAAAGAAC TTAAATTTCA TATTAAGTCT TTAGAACTCG ACACTTAAAA 300

ATGCTATAAT CATATGTATG TTAAAAAAGG AGTTTCGGAA AATGTATGAC ATTAAAAAAT 360

GGCGCCATAT TTTTAAATTA GACCCAGCTA AACATATTTC AGATGATGAT TTAGATGCGA 420

TTTGTATGTC TCAAACAGAT GCAATTATGA TTGGTGGAaC TGATGACGTT ACTGAAGATA 480

CAAACATCGA AAGTGTAATG CCTGGTTTTG ATTtTTATTT TGTACCTACA GTACTGAACA 600

GTACAGATGT TGTATTTCAC AATGGTACAT TATTAGAAGC GCTTAAAACA TATGGACATA 660

GTATAGATTT TGAGGAAGTA ATATTTGAAG GGTATGTCGT GTGCAATGCT GATAGCAAAG 720

TGGCAAAACA TACCAAAGCA AATACAGATT TAACAACAGA AGATTTAGAA GCATATGCCC 780

AAATGGTCAA TCATATGTAT CGATTACCGG TTATGTATAT AGAGTATAGT GGCATTTATG 840

GCGACGTATC AAAGGTTCAA GCTGTCTCAG AACATCTAAC AGAAACGCAA CTTTTTTATG 900

GTGGCGGTAT TTCCTCAGAA CAACAAGCGA CAGAGATGGC AGCTATTGCA GATACAATTA 960

TCGTCGGTGA TATTATTTAT AAAGATATTA AAAAAGCTTT AAAAACAGTA AAAATAAAGG 1020

AGTCTAGTAA ATGAATGCGT TATTAAATCA TATGAATACA GAGCAAAGTG AAGCTGTAAA 1080

GACAACAGAA GGACCATTGT TAATTATGGC AGGTGCTGGT TCAGGGAAGA CACGTGTTTT 1140

AACACATAGA ATTGCTTATT TATTAGACGA AAAAGATGTC TCACCATACA ATGTTTTGGC 1200

TATTACTTTT ACAAATAAAG CTGCAAGAGA AATGAAAGAA CGTGTTCAAA AATTAGTAGG 1260

TGATCAAGCA GAAGTTATTT GGATGTCAAC ATTCCACTCA ATGTGTGTTC GTATTTTACG 1320

TCGTGATGCA GATCGAATTG GTATAGAACG CAATTTTACG ATAATTGATC CTACAGACCA 1380

AAAATCTGTT ATTAAAGACG TCTTAAAAAA TGAAAATATT GATAGTAAAA AGTTTGAACC 1440

TCGTATGTTT ATCGGTGCGA TCAGTAATTT GAAAAATGAA CTTAAAACAC CTGCAGATGC 1500

TCAAAAAGAA GCCACAGATT aTCACTCgcA AwTGGTaGCA ACgGTTTaTA GTgGATATCA 1560

ACGCCAATTG TCACGTAATG AAGCGTTAGA TTTTGATGAC CTTATTATGA CAACGATTAA 1620

CTTATTTGAG CGTGTACCAG AAGTTCTAGA ATATTATCAG AACAAATTCC AATATATTCA 1680

TGTAGATGAG TATCAAGATA CTAATAAAGC ACAATACACA TTAGTTAAAT TATTAGCAAG 1740

TAAGTTTAAA AACTTATGTG TTGTAGGTGA CTCAGATCAG TCAATTTATG GTTGGCGTGG 1800

TGCTGATATT CAAAATATCT TATCATTTGA AAAAGACTAT CCAGAAGCGA ATACAATCTT 1860

TTTAGAGCAA AATTATCGTT CGACGAAAAC GATTTTAAAT GCGGCTAACG AAGTGrTTAA 1920

AAATAATTCT GAACGTAAGC CAAAAGGACT GTGGACTGCA AATACGAATG GTGAGAAAAT 1980

TCATTACTAT GAAGCAATGA CGGAACtGAT GAAGCGGAAT TTGTAATACG AGAAATTATG 2040

AAGCATCAAC GTAATGGTAA GAAATATCAA GATATGGCAA TTTTATATAG AACGAATGCA 2100

CAATCACGTG TACTTGAGGA AACATTCATG AAATCTAATA TGCCATACAC AATGGTTGGT 2160

GGCCAAAAGT TCTATGACCG TAAAGnAATC CAAAGATTTA TT 2202

(2) INFORMATION FOR SEQ ID NO: 285:

(A) LENGTH: 785 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

AGTGGTGCAA AGATAGGCAT TGATaATACC GCTAAGCCAG cAAGATGATG GCACGATAAA 60

ACCTAAACAG AAGAAmATAA ATAGTAATAC GATGATAAAT AATGGTCCAC TCATATGTTG 120

AACTAAAGAT GATGAAAAGT GTAAGATTGT ATCTGAAATC ATACCTTCAT TCAACACTAA 180

ATTAATACCT CGAGCTAAAC CAATAATTAA AGATACACCT ACTAAACTTG ATGCACCATT 240

GACAAATGCA TCTACAGTTC CTTTTTCTCC CAATCCAGAT TTACCTGTCC CAGCAATAAA 300

CATTATTATA ATTGTAAATA TTAAAAATGC TGAAGCCATA ACTGGGAACC ACCAACCTTG 360

CGTCATAACT CCCCATACCA TAATTGGAAA TGGTAGTACA AATAATGTAA GGATTATCTT 420

CTTACGCAAA GTAAAATGGG CACTATCGTC ATCTTTTAAT ACAGACCATT GCTGTTCAAA 480

AGCATCTTTG TCTTCATAAG AATATGACGC TTTAGGATCG TTTTTAATTT TTTTACAGTA 540

CCAATATAAA TAACTAATAA CAAAAATCGC ACCGACAATA CAAGCACCTA TTCTCCAATA 600

CAAGCCATCC GTAAAAGTTG TACCAGCGGC ATTAGAGGCA ATTACAACCG AGAACGGGTT 660

AATAGTTGAA AATGTACTAC CGACAGAGCT GGcAAGGAAT ATGGCACCAA CTGGAAACGA 720

TAGAATCGTA TCCTAACGCT AATAAATATA GGGACTAAAA TCGGATAAAA TGCTACAGCT 780

TCTTC 785

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 812 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

CTAACGnGAT AAGGTTGCAA nTTTATCTGA ACATCTGATG ACTGTAATTT TGTtAATGAT 60

AAAATATTTG TCACTAATAG ATATAAATAC TGACTTTCTT GAAAACTATG TACAAGTAAT 120

TGTTCCTTTT CTATGATAGA CATATCTTTA CTATGTGATA CTAAAATATC TAAATkTCCC 180

ATAATTGTTG TTAACGGTGT ACGTATGTCA TGCGAAATTG ATCTTAAAAA ATTTGAATGT 240

GTCAGTTGAC GTTCAGCCTG TAACATGGAT TCTCTCGTTT GTTTAAGTAA CGTCACATTT 300

ATCACTTGAG AACTTTGGTA ATCAATGGCT AGAATGCCTT TAATCGGAGA TGTGCCAATT 420

GGTATCAACC ATTTATTAAT GCCTGGAAAT GTATCTGTTG TTGCACCAGC TTGTCTTTCA 480

TTTTTAATTA CCCAGCTTAA TGCTTGTTCA TGCTGTTGAG TCGTATTATC GATATGGTTT 540

TGCAATGGTA TTGTTTTAAT TACTTTCGAT TGATTGATAA CGTATATAGT AATTGATTGT 600

TGCAATAATT GATTAATTTG GTATCCAGCA TTTATTAGTA AGTTTTCAAC TGTATAAGTT 660

TGTTTAATCG AATCATTAAA TTGAAATAAT AAATCTGTAC GATAAAGTTG CTTTTTAGTA 720

ATGGaGTAwT GGAATTTAAT TTGTnTTAAT AAAGCACTCG TTAAAATACT TGTnAAAATG 780

CTAACGATAA ATGTAATAGG ATAGTCAAAG CG 812

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1732 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

ATnnATTATT ATTACTGCTA TTTTAAATTT TAAAAAATGC TTTTGATTAT ATTCAACAnT 60

TTGTATAAAA TTAAATTTGC TTTTGATTAA AGCATGAAAA TTGTAATCAA ACCATAAATT 120

GTCGTATGAT GTAGTTAGAA TTTTAAAATG CAGGAGGTCa AGTATATGAC TGAAATaACA 180

TTCAAAGGTG GACCAATCCA CTTAAAAGGT CAACAAATTA ATGAAGGTGA TTTTGCACCT 240

GATTTTACAG TGTTAGATAA TGACTTAAAT CAAGTAACAT TAGCAGATTA TGCTGGTAAA 300

AAGAAATTAA TTAgTGTGGT ACCATCAATT GATACAGGTG TTTGTGATCA GCAGACTCGC 360

AAATTCAACT CTGATGCTTC TAAAGAAGAG GGGATTGTGC TTACAATTTC AGCAGACTTA 420

CCATTCGCAC AAAAAAGATG GTGCGCTTCA GCAGGTTTAG ACAATGTCAT TACATTAAGT 480

GACCACCGTG ACTTATCATT TGGTGAAAAC TATGGCGTTG TTATGGAAGA ACTTCGCTTA 540

TTAGCTCGTG CAGTATTTGT ATTAGATGCA GATAATAAAG TTGTTTATAA AGAAATCGTT 600

AGTGAAGGTA CTGATTTCCC AGATTTTGAT GCTGCTTTAG CTGCATACAA AAATATTTAA 660

TCATTAAAGA GATAAATCTT AAAATGTATA CATCGTGTCC ATCGTTGTCA ACAGCATTAA 720

AATAGAATTG TTTTCTATGA TTGCTAAGAC CTATGGGCAC TTTTTATTGG AGAGGGACGA 780

ATATGGCAGA ACAACAAACA ATTATGGAAC GCTTGTTTCA TACATTAGAT GAAAAAGCTA 840

AAACATTAAA TAATGAAAAT GGCCaAAGTT TTATTGAAAA TCTTGGGCTA GCAATGGAAC 900

CATTCCAATT TGCATATTTA AGTTTAATGC aGGAAGAAAA GATAcAAGCA AATCATCAAA 1020

TTACACCAGA TTCAATTGGA TTGATACTAG GATTTTTAGT TGAGCGTTTT ATGAACAACC 1080

AAGAAGAATT ACATATTGTT GATATTGCAA GTGGTGCCGG TCATTTAAGT GCTACTGTAA 1140

AAGAAGTGTT ACCTGraAtT GcGGTTATGc ATcATTTaAT TGaAGTTGAt CCAGTTTTAT 1200

CACGTGTTAG TGTACATTTA GCAAACTTCT TAGAAATTCC TTTCGATGTG TATCCTCAAG 1260

ATGCCATCAT GCCACTACCA TTAGAAGAAG CAGATATCGT TATTGGTGAT TTTCCAGTAG 1320

GCTATTATCC AATTGATGAA AGAAGTAAGG AGTTTAAGCT AGGTTTTGAA GAAGGACATA 1380

GTTATTCACA TTATTTATTA ATAGAACAAG CAATAAATGC ATTAAAAGAT GCTGGATATG 1440

CCTTTCTAGT GGTACCAAGT AATATTTTTA CAGGTGAACA TGTAAAACAG CTTGAAAAAT 1500

ATATTGCAAC AGAGACAGAG ATGCAAGCAT TTTTAAATTT ACCACCAACT TTATTTAAAA 1560

ATGAAAAAGC GCGAAAATCT ATATTAATTT TACAAAAGAA AAAATCGGGT GaAACAAAGC 1620

CAGTTGAAGT ATTATTGGCA AATATTCCTg ATTTCcAAAA TTCCTTCACC AATTTCCAAG 1680

GATTTATGGA CAGAGTTAAA ATCCAGTGGG ATGGGACCAC CAAATCGTCC TA 1732

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2779 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

AAAAGAACTA GCTAAACGCA AGCAAGAAGC TATTAGTAGA ATTAAAGACT TTTCAAATGA 60

AAAAATAAAT AGTATTCGAA ATAGTGAAAT TGGCACAGCT GATGAAAAAC AAGCAGCAAT 120

GAATCAAATT AACGAAATTG TGCTTGAAAC AATTAGAGAT ATTAATAATG CGCATACATT 180

ACAGCAAGTT GAGGCTGCAT TGAACAATGG TATTGCTCGA ATTTCAGCAG TACAAATTGT 240

AACATCTGAT CGTGCTAAAC AATCGTCAAG TACTGGAAAT GAATCTAATA GCCATTTAAC 300

AATTGGTTAT GGAACTGCAA ATCATCCATT TAACAGTTCG ACTATTGGAC ATAAAAAGAA 360

ACTTGATGAA GATGATGACA TTGATCCACT TCATATGCGT CACTTTAGTA ATAATTTCGG 420

TAATGTTATT AAAAACGCTA TTGGTGTGGT GGGTATCTCT GGTTTACTAG CTAGTTTCTG 480

GTTCTTCATT GCCAAACGTC GTCGTAAAGA AGATGAAGAG GAAGAATTAG AAATAAGAGA 540

TAATAATAAA GATTCAATAA AAGAGACTTT AGACGATACA AAACATTTAC CACTTTTATT 600

AAATAATGGC GAGTCACTCG ATAAAGTTAA ACATACGCCG TTCTTCTTAC CAAAACGTCG 720

TCGTAAAGAA GATGAAGAAG ATGTGGAAGT TACAAATGAA AACACAGATG AAAAAGTGTT 780

GAAAGATAAC GAACATTCAC CACTCTTATT CGCAAAACGA CGCAAAGATA AAGAGGAAGA 840

TGTTGAAACA ACAACTAGTA TTGAATCTAA AGATGAGGAC GTTCCTTTAT TATTGGCTAA 900

AAAGAAAAAT CAAAAAGATA ACCAATCCAA AGACAAAAAG TCAGCATCAA AAAATACTTC 960

TAAAAAGGTA GCAGCTAAAA AGAAGAAAAA GAAAGCTAAG AAAAATAAAA AATAATTTGT 1020

TTCTTTGATA AATAGaGGAG CACCGATTGA CATCACATCA GTCGGTGCTC CTTTTATTTA 1080

TTCTTTTTAA TTAATTTATA CAATGCCTGT TGAGCGTGTT GATTCGCTTC TTTGTTTTGT 1140

TCTCTCGGTA TCCATTTAAC AAATAATAAA TCAAAATCTT TTTCAAATAT TTCTATTTGA 1200

TCAAAATAAG GTTTGAAATT TGCGTTTTTC ACATAACCAG CTTCAATGCT ATCTGCAATT 1260

AGCTTTGAGT CTGTATATAA TAGTGCGTTT TGAACATTTA ATTCACGTGC ATGTTCTAGT 1320

GCATAAATAC ATGCAGCCCA TTCTGCAGTG TGGTTATCCA TTTCGCCTAA CTCATGTGTA 1380

TATGTATAAT GCTGCTCATC TTCTTTGATT ACAATGGCAC ATGTACTTAT GCCTGGATTT 1440

cCTTTCGTCG CAGCATCAAA ATTTATTTTC GCCATAATAA ACCTACTTTC TATTCAATAC 1500

TTAGTTAAAG TTACTATTAC TGTAATACAA AATATGTTGG GTAATCCATT AAAAAACACG 1560

CATCACTTAA ATAAGTAACA CGTGTTTAAA ATACTCGCTG ATTCAAAGAT GATTTTCTAA 1620

TACGTAtACT GTaATATACT TCCTAAAAAA ATCATCTTCA GGCTGGGACA TAAATCAATG 1680

TTCTATGCTC TACGATGTTA TATTGGCAGT AGTTGACTGA ACGAAAATGC GCTTGTAACA 1740

AGCTTTTTTC AATTCTAGTC AGGGGCCCCA ACACAGAGAA TTTCGAAAAG AAATTCTACA 1800

GGCAATGCGA GTTGGGGTGT GGGTCCCAAC ACAGAAGATG ACGAAAAGTC AGCTTACAAT 1860

AATGTGCaAG TTTGGGATGG GCCCCAACAA AGAGAAATTG GATTCCCAAT TTCTACAGAC 1920

AATGCAAGTT GGGGTGGGAC GACGAAATAA ATTTTGCGAA AATATTATTT CTGTCCCACT 1980

CCCTTAAAAC TTATTCTTTT GTGTAGTAAG TGCGTTAATA GCCTTGATCT AACTTATCAA 2040

TCTTACCTTT ACGATAAAAT GATTTAGCAA TATATCCAAA TGGTACATTG AAAACTGTTG 2100

AAGCTAATTT TAATACGTAC GTTGTAATAA ATATTTCAAa TACAAmTGTa CCAGGTAAAC 2160

TTCCGATAAA TGCGATAGCT ACAAATAAAG CTGTATCAAT TATTGrGCTT AAAAATGTAC 2220

TACCATATGg CACGGATGAA AAACGTTTTa TCmGaACTAA ATACTTTTTT AATTAGTGAA 2280

AAGATAAATA CATCAATATG TTGACCAATA ATATATGCGA CGATTGAGCC TAAAGCAATG 2340

CGTGGCACAA CATCAAAGAT TGCGTGTAAT GCTTTTTGTG CCATATCTTC TGGTGCAGGA 2400

CAAACTGCTC TTTTTGCAAC TCTACGCCCA TAAATATCGT TTAATATATC TGTTGCTAAA 2520

TAAATAGAAG CAAACATGAC ATTACCTAAA GTTGCTGAAA TACCAAAGAT TTCTACAGTT 2580

TTAATCACTT GTATGTTGGC AATGATTGTG CCAATTGCAA CCCATGCAAT TAAACCTTGT 2640

TTACCAAAAA AGCGATACAT AAGTACCATA AGCACGAACG TTGCAATAAA CGTAACTAGT 2700

CCTAAAATTT CATTATACAT ATTAAAATGT CCTCCTAAAT TTTGATCATG CGGGTGTTTA 2760

GAAACCGCTC AATAAATAA 2779

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1999 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

ACTGATGTGC GTTCATCAAA AACAATATAA TCAAATTCAT TTTCATCAAA TTGCTTAAAA 60

TTATCATCTC TAGATAATGT TTGAATGGTT GCAAATAAAT ATTTGGCATC GACATCTCTA 120

TGTTTTCCTG TCAACAATCC AAAATCACTA TCATTTTTTA TAGGTAATAC TTTTTTAAAT 180

TCTTCCTTAG CTCTATTTAA AATCCCCTCA TTATGAACAA TAAATAAAAA TTTATTAGGG 240

TTTACTTCTC TAACATCTAA TGCACATAAA ATCGTTTTAC CTGTACCAGT TGCAGATATT 300

ATTAACGCCT TATCTTTGGC TTTATCCCTA ATAGCTTTTA ATGACCTTAA TGCTTCTGCT 360

TGCATTAAAT TGGGTACAAT TTCCACTGAT TTTTTCACCT TATCAGCTAG CAGCATTTGA 420

GTTTGTTCAA CCTCCGCTAA TTTTTCTAAG GAACGGTACT CAAATGATTC TTTATATGAA 480

TTAATCCATT GCTCAGTCAG TGGGGTACTC TTTTGCCATA ACAAGTCAAA TTCACTTTTT 540

ACACTATCAA CTAAATCGCC ATTTTTCATA GTAGACAGTA AAACATTATG CTCATAATTA 600

ACCTTTAACG CATTAGATGT TAAATTAGAG CTTCCTATTA CCATAGAACT ATAATCCTTA 660

TGCTCAAAAA TATATCCTTT GGCATGGAAT CCAGCAATAT CAGTTAATCT TACCTCTACA 720

TTTTTTAATT TAAGTAATTC TCCATACATT TTAGGACTAT TAAACCCTAA GTAATTAGAT 780

GTTAATATTT TCCCTTTAAC ACCCTTATTG CTTAAATCTA ATAGTTGAGC CTTTAAGCTG 840

GcTAAACCGC TTTCTGTTAT AAAAGCCACA GAAAAATAAA ACGTTTCACA TTTTTGAAGT 900

TCATCTATAA TTGTTGAAAG AACTTTTTCA TTTTTATTAT TTACTAAAAG CTTCGGTGTA 960

TAATTCCCTT TATGAGAAAT ATGTTTGTCT ATAAACCCTT TATGTAAAGA TTGATTGAAA 1020

CGCTGGGGCC CAATTTAATT TATCAAGTTC GTTTATTGAC AACCATTCAA TACTCTTATG 1140

TTCAGTTAGA GTTGGTAACT CTTTGTTTAA AGTACATTTG TATGTTGTTA ACCTAACAAT 1200

TCCAAAATCA TATTCATGTT CTGTAGTTAT AACTTTGTCT CCAACAATTA AATCACATTT 1260

CATTTCTTCT CTAATTTCTC TAATCAAAGC GTCTTTTTCA GTTTCATTCT TTTCAACCTT 1320

ACnGCCAGGA AATTCCCACA TTAAAGGCAG ACTCATTTTT TCACTTCTCT GTGCACAAAG 1380

AATTTTGTTA TCAGAAAAAA TAATAGCTCC TACTACATTG ATTACTTTTT TCATAAGACT 1440

CACCCTTCAA TTTAAAATCA TCTTAATTGT TATTCTATCA AAAATTACAA AACTATATAT 1500

AAATCAATAT TAAAAATTAA TATTTTACAT TCACATGAAC GCTCTACTCC ATGCATTTTC 1560

ATACACATCT ATTATATAAT ACTTGTGAAA AGTATTGTCT TGGGGCTGTG TTTTTTTACT 1620

TTTGGGGCGT ATTTCTTTAT AATTCATTAC ATAAATGTAA GGGCTTTAGT TTTCATGTTT 1680

TATTAAGTCT AACTGAGATT TTGAAAGGAT GTTTAGCAAC AATGGATAAA GAATTATGGA 1740

TAGAACGAGc TAATGATAGT TTAGTTAAAC ATTTTTATGa GCAGCAATCT GACATTGAAC 1800

AGCGAGAAGG TTTTGAAAGT AAATTAACAT TTGGTACTGC GGGTATACGC GGAAAATTCG 1860

GTCTTGGTGA AGGTCGACTT AATAAGTTTA CTATTGAAAA ATTGGCATTA GGTTTAGCGC 1920

GTTATTTAAA TGCCCAAACA AACAGTCCAA CAATAGTCAT TCATTATGAT ATTAGACATC 1980

TTTCcAACTG AATTCGCCC 1999

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1933 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GATGACTTTT CCCCCTCATA ATCTTCATGG TCCAGGCGTC CATTAATGCG TCAAAGGATG 60

GCACATTTTA CCTGGAACAA ATGATTCATA TGGTTCATAA AAATCACGCG TCGTAATATA 120

ATCTTCTAAA TCAAATGCAT AGAAAATCAT TGGCTTTTTA AATACTGCAT ATTCATATAT 180

TAAAGATGAA TAGTCACTAA TTAATAAATC TGTTATGAAC AGTATATCAT TAACTTCTCT 240

AAAGTCAGAA ACGTCAACAA AATATTGTTT ATGTTTGTCT GCAATATTAA GTCTATTTTT 300

CACAAATGGA TGCATTTTAA ATAATACAAC CGCGTTATTT TTTTCGCAAT ATCTTGCTAA 360

ACGTTCAAAA TCAATTTTGA AAAATGGGTA ATGTGCTGTA CCATGACCAC TACCTCTAAA 420

TTGTTTGATC TGTGTCGCAT AAGCTTCATC AAATAGTACA TCAGTACGTG GAACACCTGT 540

AGGCACTACA TTTTTCTCTT TAATACCAAA TGCTTCAGCG TAGAATGGAA TATCGGTTTC 600

AGATGATACA TAAGCTTTTG TATAGCTACG ATGATTTAAT GAATCAATAA ATGGTCCACC 660

CTTTTTACCA GTACGACTAA AGCCAACTGT TTTAAAGGCA CCAACGGCAT GCCATACTTG 720

AATAACTTCT TGAGAACGTC TAAAACGCAC TGTATAAATC AATGGGTGAA AGTCATCAAC 780

AAAGATGTAG TCTGCCTTCC CAAGTAAATA TGGCAATCTA AACTTGTCGA TGATGCCACG 840

TCTATCTGTA ATATTCGCTT TAAAAACAGT GTGAATATCA TACTTTTTAT CTAAATTTTG 900

ACGTAACATT TCGTTATAGA TGTATTCAAA GTTTCCAGAC ATCGTTGGTC TAGAGTCTGA 960

TGTGAACAAC ACCGTATTCC CTTTTTTCAA GTGGAAAAAT TTCGTCGTAT TAAATATCGC 1020

TTTAAAAATA AATTGTCTTG TATTAAATGA TTGTTTGCGG AAATACTTAC GTAATTCTTT 1080

ATATTTACGA ACGATATAAA TACTTTTAAC TTCCGGAGTC GTTACAACAA CATCAAGGAC 1140

AAATTCATTA ACATCGCTAG AAATTTCAGG TGTAACAGTA TAAACCGTTT TCTTCGAAAT 1200

GCCGCCTTTT CTAAATTCTT TTAGGTAAGT CTGCAATAAG AAATTGATTT TACCATTTTG 1260

TGTTTCTAAT TCGTTGTATT CTTCTTCTTG TTCTGGCTTT AGATTTTGAT ATGCATCATT 1320

AATCACATCT GGGTTTAACT GTGCAATATA ATCAAGTTCT TGCTCATTCA CTAATAAGTA 1380

CTTATCTTCA GGTAAGTAAT AACCATTATC TAAGATAGCT ACATTGAAAC GACAAACGAA 1440

TTGATTCCCA TCTATTTTGA CATCATTCGC CTTCATTGTA CGTGTCTCAG TTAAATTTCT 1500

TAATACAAAA TTACTATCTT CTAAATCTAG GTTTTCACTA TGTCCTTCAA CGAATAACTG 1560

AACACGTTCC CAATAGATTT TATCTATATA TATCTTACTT TTAACCAACG TTAATTCATC 1620

CTTTTCTATT TACATAATCC ATTTTAATAC TGTTTTACCC CAAGATGTAG ACAGGTCTGC 1680

TTCAAAAGCT TCTGTAAGAT CATTAATTGT TGcAATTTCA AATTCTTGAC CTTTTAACAA 1740

CGCTAATTTA nCTACAATAT CTGGGTATTG AATGTATAAG TCTACAACAT CTTGGAAATC 1800

TTTTGAACCA CTTCGACTAC TACCAATCAA CGTTAGTCCT TTTTCCAATA CTAGACGTGT 1860

ATTAACTTCT ACTGGGAACT CACTTACACC TAACAGTnCA ATGCTTCCTT CTGGTGAAAT 1920

GTAATCGATC ATT 1933

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2049 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

nGTnCGGnCA GATATATTGG TGGTCTTTAG TAAGTGTATC AAATTCATCA GATGTCAAGG 60

GCATGTTATC ACCTCCTTAG GTTGATAACA aCATTATACa CGaAAGGAGC ATAAaCAAaT 120

GAACACAaGA TCAGAAGGAT TGCGTATAGG CGTCCCACAA GTTTCTAGCA AAGCTGATGC 180

TTCTTCATCC TATTTAACGG AAAAGGAACG TAACTTAGGA GCGGAAATAT TAGAACTTAT 240

TAAAAAAAGT GATTACAGCT ACTTAGAAAT AAACAAAGTT TTCTATGCAT TAGATAGAGA 300

ACTTCAATAC AGGGCGAATA ATAACAAACT TTAaCATTTA TCTAAAGGAG TGATAGAGAT 360

GCCAAAAATC ATAATACCAC CAACACCAGA AAACACATAT CGAGGCGAAG AAAAATTTGT 420

GAAAAAGTTA TACGCAACAC CTACACAAAT CCATCAATTG TTTGGAGTAT GTAGAAGTAC 480

AGTATACAAC TGGTTGAAAT ATTACCGTGA AGATAATTTA GGTGTAGAAA ATTTATACAT 540

TGATTATTCA GCAACGGGAA CATTGATTAA TATTTCTAAA TTAGAAGAGT ATTTGATCAG 600

AAAGCATAAA AAATGGTATT AGGAGGATTA TCAAATGAGC GACACATATA AAAGCTACCT 660

ATTAGCAGTG TTGTGCTTCA CGGTCTTAGC GATTGTACTC ATGCCATTGC TGTACTTCAC 720

TACAGCATGG TCAATTGCAG GATTCGCAAG TATAGTGACA TTCATATTTT ATAAGGAATA 780

CTTTTATGAA GAATAAAAAA ACTGCTACTT GTTGGAGCAA GTAACAGTGC AAGATGAGCA 840

ATTGTCTTAA ATAATTATAT AAGGAGTTAT TAATATGACC TTACAACAAA AAATACTATC 900

ACATTTTGCA ACATATGACA ATTTCAATTC TGATGATGTT GTTGAAACTT TTGGGATATC 960

TAAAACACAT GCAAAATCCA CACTTTCAAA ACTTAAGAAA AAAGGAAAGA TTGCAATGGA 1020

AAGTTGGGGT GTCTGGCGTG TTATTGAATC GCAATTGCAT TTAAGTGTAG TCGAACGTAA 1080

AAAAGAAATT TTAGAAGAAC AATTTGAATT GTTAGCAAGA TTAAATGAAC AAAGTGATGA 1140

CCCTAGAGAA ATAGAAGAAC GTATCAAGTT AATGATTCGT CTAGCTAACC AATTTTAAGG 1200

AGGAGTTAAT CAATGGCAGT ATTAGAAGGT ATTTTTGAAG AATTAAAACT ATTAAATAAG 1260

AACTTACGTG TGTTAAACAC TGAACTATCA ACTGTAGATT CATCAATTGT ACAAGAGAAA 1320

GTTAAAGAAG CACCAATGCC AAAAGAAGAA ACAGCTCAAC TGGAATCAAT TGAAGAAGTT 1380

AAGGAAACTT CTGCTGATTT GACTAAAGAT TATGTTTTAT CAGTAGGAAA AGAGTTCCTT 1440

AAAAAAGCAG ACACTTCTGA TAAGAAAGAA TTTAGAAATA AACTTAACGA ACTTGGTGCG 1500

GATAAGCTAT CTACTATCAA AGAAGAGCAT TATGAAAAAA TTGTTGATTT TATGAATGCG 1560

AGAATAAATG CATGAAGCTA GATCACTCAA ATAGAGCTCA TGCAAAGCTT AGTGCAAGTG 1620

GAGCAAAACA ATGGCTAAAC TGTCCACCGA GTATTAAGGC AAGTGAAGGT ATTGCAGATA 1680

GTCTTAAATA TGAAGGCCTA ACACAGTTTG AGTTTAATAA AGCTTTTCAA AATTATAAGC 1800

GAAATCAATA TTACAGTGAA GAGTTGCGCG AATATGTTGa AGAGTACGTA GCTAATGTAG 1860

AAGAAAAGTA TAACGAGGCT TTGaGTAGAG ATGACGATGT AATAGCTTTA TTTGAAACAA 1920

AATTGGATyT AGGTAAATAC GTCCCTGAAT CTTTTGGTAy TGGTGATGTC AtTATATTTT 1980

CAGGTGGTGT ACTTGAAATT ATTGACCTTA AATACGGTAA AGGCATTGAA GTTTCAGCTA 2040

TAGATAATC 2049

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 942 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

ATGATGTTTC TATATTCGTA TTAGGAAAAC CTGTTGGTAT TACAACAAAC GCCCTAAAAT 60

TACAATACCG CTGCTCCTAT ACCAATTGCA ACAACAGTTT TAACTGAAAT ATCTTGTTTT 120

TTCATCTTCA TTACTCCTtt ACATAAAAAA TTCATTATAT TGATGGTGCT TTAGATAAAT 180

GAATCGTCCA ATCATTTCCA GTACCAATAT GATATAAATC TGAAAATGAG TCTTGATTGA 240

CTGCTACACC AATATTTACT AGCGAGTTAA CATACACAAG AGGTTCACCC ACATTAACAT 300

CTGCAAACGA TCGCGCAAAT TTAATAATAT TTTGATAGAC TTTCTTATCT TGATGATAAA 360

TTGTTACCAC CAAATTATTA CCATGAACAA TTTCCAAGGA TTTTAAGAAT GCCAATGGAA 420

TATTTGTCCA TAATGACCCA AATCTGATAT CTAAAATATC AATGCTTCCT GTAACAGAAT 480

CCTCATTTTT TGTCACTTCT CTTATTTCTA ATGCCTCAAT ACTATCAACA TTAATTGCCT 540

GACCGAGACG TTCAAACGCT ATCTTATTTG CAGCTAATCT CGCACCATTG TATGCATAAA 600

CATCTCTACC ATGAAAAGTA TGACTTTCTT CCGAATGAGG CAATCGGCTT TTCACTTCAT 660

CAATTTCGAT AACTTTTTTA ATACCTTCGT AATGTTTAAT ATGACTTAAA GAACCATTAT 720

CAGGTGTAAT AATGTAATGA CCTGAATATG TTAAGCAAGC AATGTCCGCC TATCACTACC 780

TACACCCGGG TCTACCACTG ATACAAAraC TGTGCCTTTA GGCCAGTATT TTACAGTTTG 840

ATATAAACGA TATGACGCTA CCCAAATGTC ATACGGTGGT ATATCATGCG TTAAGTTTTC 900

AACACGTATA TCATCATTAC AGTATATGCA ACTCCATACA TT 942

(2) INFORMATION FOR SEQ ID NO: 293:

(A) LENGTH: 1268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

TGTAATAAAA TTTTATGnAA CATGCTGnGA TGCTACCATG AACCTTCTTC ATTTCTTTAT 60

GTGAGATTGT GaAATTAATC AAATAATAAT ACGGTGGATA CTTTCCTAAT TTACGATATT 120

CCATTTCCTG ACGATAAAAT GTTAAATAAT CATTTTTTTG AACATCCAAT ATTGAATAAT 180

GATCTGGATT ATACGTTTGA ATGATGACTT GACCTGCCTT TTCATGACGA CCAGCTCTAC 240

CAGCCACTTG CGTTAATAGT TGATAAGTAC GTTCGCTCGC CCGAAAATCA GGTAAATTTA 300

ACATTGTATC TGCATTCAGC ACACCAACTA AAGTAATATT TGGATAATCT AATCCTTTCG 360

CAATCATCTG AGTACCTAGT AAAATGTCAC CGTTACCTTT TTCGAATTCA GTCAATAACT 420

TTTCATGTGC ACCTTTCTTT GAGGTTGTAT CTACATCCAT CCTAATTATG CGCGCATCTT 480

CAAATTCTTG TTGCAATAGT TCTTCAACTT TCTGAGTACC AGTACCTACT TGTCGAATGT 540

GTTCACTCTC ACAATTTGGA CATTGATTCG GTGGCGTCTC TTGGTAACCA CAATAGTGAC 600

ATTTTAATAA GTCTGTCGTT TTATGATACG TTAATGAAAT ATCACAGTTT GGACATTGCG 660

GTACATATCC ACAATCCCGA CATAACATAA ACGATGCATA ACCACGTCGA TTTAAAAATA 720

AAACAACTTG TTCCTGTCGA TCTAATCTTA ATTGTATGGC TTCACGTAAA TCTTTTGAAA 780

ACATTGACCG ATTACCTTCA CTCAATTCTT CACGCATGTC TACTATATCA ATTTCAGGTA 840

AAGCTTGTTG GTTCACTCTG TTTGGTAATG ATAGCAAATG ATAAACGCCT TTTTCAGCTC 900

GTGCATAACT TTCAAGACAT GGTGTTGCAC TTCCTAAAAT GACTGGACAG TGATGATATT 960

CAcTTCGCCA TTGGGCAATT TCTCTAGCGT GATATCTCGG ATAATCTTCT TGTTTATATG 1020

TAGATTCATG TTCTTCATCA ATGATGATTA ACCCTAAATT TTTGAAAGGT GCGAACACAC 1080

TTGACCTTGC ACCAACACTT ACTCTCGCAC GACCATCCCT AATTTTTTGC CATTCATCAT 1140

AACGTTCCCC ATTAGATAAG CCAGAATGTA ATACAGCAAC GTCATCACCA AATCGACGTT 1200

TGAAGCGTAA AACCATTTGC GGTGTTAGAG CGATTTCAGG AACTAACATC ATCGCCTGTT 1260

TTCCTTGG 1268

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 629 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

TACCACCAAA TAATATATTA GCTGGCATTT TAATAACATT TAnATTTGTC ATGATATCAT 60

CAATAAAATG TTGAAACTTC GTAATTTCAC CTTCATAATC ATCAATTGCT GCTAATTGCG 120

CACTCGATGC TTGCTGATCT AAATTTAAAA TATTCGACAT GCGTTGACTA TAATAAACTA 180

AATGTTCTAT TAAGCCATCG TCACTCTTTT CCTTTGGTGC TGACATGACA GCGATACGTT 240

TCAAAGGATA GTGTTGCGCC AATTTTAATG TCATTAATCC ACCTAAAGAC ACACCCGTTG 300

CACTGATAGA TTCATAACCT TCATTGACTA AAAATTGGTA AGCTTTCTCA ACTTCTTCCC 360

ACCAATCATC TACATTATAT GTCATGAAAT CTTTCAACAA TAAACCATGA CCTGGATAAT 420

TCGGTGCATA ACAACTAAAT CCTTGGTCAT TTAACTCAGC TGCAAGATGC TTCACATCCC 480

GATTTGTACC TGTAAATGAA TGTAATAATA ATATCGCATG TCCATTTGTG CCTTTTAAAT 540

ACGtGGACTC GGTGTTTTAA TTCTCATTTT TCtaTATAcC TCCACTAtGT CTAAAGakGT 600

TkGCTAAACG CGTTGtCGTC GATGATTAA 629

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2817 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

TATGAAAGTA ATGAATGGTA ATATTATTAA ATTTGATGGA AAAGTAGATA TTGATAATGC 60

AGATAATATC GGTTTTTTAA TTGAGCATCC TAAATTATAT GATAATAAAT CAGGATTGTA 120

TAACTTGAAA TTATTTGCAC AAGTATTAGG TAAGGGTTTT GATAAAGCAT ACACAGACAA 180

AATTATAGAT GCATTTGGTA TGAGACCTTA TATTAAAAAG AAAGTTAAGA AATATTCAAT 240

GGGGATGAAG CAAAAGTTAG CAATTGCAGT ATCTTTArTG AATAAACCTA AATTTTTAAT 300

CTTGGATGAG CCTACAAATG GkATGGATCC AGATGGCTCa ATTGATGTGC TGACTACAAT 360

TAAGTCTTTA GkAAATGaAC TTGATATGAG AATTCtAATA TCAAGTCATA AGTTAGAAGA 420

TATTGAATTA ATTTGTGATA GAGCTGTATT TTTAAGAGAC GGnCATTTTG TTCAAGATGT 480

AAACATGGAG GAAGGTGTTG CATCTGACAC AACGATAGTT ACTGTTGATC ATAAAGACTT 540

TGATAGAACT GAAAAATATC TTGCAGAGCA TTTCCAATTA CAAAATGTCG ACAAAGCAGA 600

ATTAGATATT TATCCGAAAT ATATTGAAAC ACGTAAAAGT TCATTGCGTG ATACGTACTT 720

CAATATAAAT CAAAGAGGTG ATAAATAATG AGAATTTTAA ATTTAGTTAA GTATGATTTT 780

TATAGTATAT TTAAaArTCC TTTAACATAT TTAGCGaTAC TAGTCGTATC TAGTTTGATT 840

GCAACTCAAA GTATACTTAT GGCAAATTCG ATGGATAACC CGAAACATAT TATTGTCTAT 900

GGATCTGTAT TTGCTGCAGC AAAATGGTTA TTGTTAATAA TTGGATTAAT GTTTGTTGTT 960

AAGACAATTA CGCGTGATTT TTCACAAGGT ACAaTTCAAC TATATATGAG TAAAGTTAAA 1020

ACACGCGTTG GAtACATTAT TTCGAAAACA ATTTCAATTa TTTTAATTTC AATATTATTT 1080

GCATTAATTC ATTATGTGAT TTTGATTGTT GTGCAGGCAT CTAGTAATGG AAAAAATTTG 1140

GCGTTTTCTA AATATGTAGA TAATTTATGG TTCTTCCTAA TCTTTTTACT ATTCTTTGGC 1200

TTGTTTTTAT TCTTAATCAC ACTTGCATCA CAAAAAACAG CAATGATATT TTCATTAGGT 1260

GTATTTTTAG TACTCATTGT ACCGTTTATT AAACCTTTTA TTACATTTAT CCCAAGATAC 1320

GGTGAAAAAG TTTTAGATGC TTTTGATTAT ATCCCTTTTG CTTACTTAAC TGATAAAATG 1380

ATTAGCTCTA ACTTTGATTT TAGCAATTGG CAATGGGTAA TTTCATTAGG TTCTATAGTG 1440

ATATTCTTCA TTTTGAATAT CTTATATGTC GCTAAAAAAG ACATyTAATA AAAATAATTT 1500

TGAGGTTGGG AATTTTAAAT TTTCCCAACC TCAAAGTTTG TCTTATTGTA AATTTATTTA 1560

TTTTCTAATT TATTTAGGAT GGAATTATAA ACTGCTTTCC AAAATGAAGC GTCAGTTTTA 1620

TAGCGGTTTG ATATAACTAA GTGTGTTTCT TTTTCTAAAT CTGCATAGTC TGGATGATCT 1680

TTGCTCGGTA ATTTATCAGC ACGAACATCA GTTACAAATT TTTGGACTTC ATTTGCTCTT 1740

GGTCCCCAAA CTGTTTCTTG TTCGAATTGA TCATTCAAGA ATACGAAGAT AGGAATTGCA 1800

CGTGATTTAC CATTTGTTAA ATATTGATCG ATCAGTTTTG TATCATCATC TCTATGGAAC 1860

ACGCGTACTT CTAAATTTAA TGCTTCACTG ATGTGTTTTA GAATTGGGAG ATTCATCATT 1920

GCATCTCCAC ACCAGTCTTC AGTAATTACT AATACTTTAG AATAATTCAT CTCTTTTATT 1980

TTTTTGATGC GTGAATCATC TTCTGGTAAC TCAAATGATT GATAGATACT GAGAACGGTA 2040

TCTTGATTTG TCTTCATTCC ATCAATGTAT TCATTTAAGG GTTGGCTATT TTTGAAATAA 2100

GTTTCTAAAT TTGTCATTGT AAAAACCTCC TTTAGCATTT ACAACATTAT ACCAATTTAT 2160

AGTAATAAAA GGTAATGAAA TAAATTAATT GCAAATTCTT TGTTAATTTT TGTTAAGGAT 2220

GAAACGGGAA GCACCTTATG CTATATTTAA ATAAGTACAA AGAAAGGGTG ACATCAGTGC 2280

GTATTCAAAA TCGCTGGGTT GTGTTTATAT TATTTTTAAT CTGTTCTTTT GGTGTATTAA 2340

TTGGTTTATA TCAATATCGT CATACGAAAA CTGTGGATTT GTCTAATCTT GAAATAAACG 2400

TTGATCGTTT TAAATTTTAT AACAGTAAAG CTCACCCTGA TCTTACCGTT AAAGTGAGAG 2520

AAAAGGATAA CATCGTTAAG GGGATAATAT TAGTAAGAGA TGAAAAGATA CATACTAATT 2580

TTGAtGGGGG AATTGGTTCG CCGATAAATA ACGCgATTGA AAATCTTGGa TTCgGATATA 2640

AAAGrACaAA AGTTGGcAAT GrtTkCtCAT CgGTAAAGTA TATTGATAGA GATAACCATT 2700

TAAAATTAAA CTTACTTTAT CAAGATTTAG AAATTAAACG TATTGAATTT TTTAGTAAAT 2760

AGCTTTAGGT CTTAAAGTTw TAAAAAACGA ATGAaTAATT TTATTGGGAT GAGTGAC 2817

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1607 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

TCTGTTAAAA TGATTTTTCT TTTAnAAAGG CCGnAAATCA ATGTTCGATT nTTATTTGCA 60

TTATGGTCTC GATATTGGTA GAATATCAAA TGGTTAAATG AGAAAAACTT GGAGGTGCTC 120

ACATGTCATC AATCGTAGTA GTTGGGACAC AATGGGGAGA CGAAGGAAAA GGAAAAATAA 180

CGGATTTCTT GGcAGAACAG TCAGATGTTA TCGCGCGTTT TTCAGGTGGT AATAATGCAG 240

GCCATACCAT TCAATTTGGC GGAGAAACAT ATAAATTACA TTTAGTACCA TCTGGTATCT 300

TTTACAAAGA CAAATTAGCG GTAATCGGTA ACGGAGTCGT TGTTGATCCA GTTGCACTAT 360

TGAAAGAATT AGACGGATTA AATGAACGTG GCATTCCTAC AAGTAATTTA CGTATATCTA 420

ATCGTGCGCA AGTGATTTTA CCATATCACT TAGCACAAGA TGAATATGAA GAACGTTTAC 480

gTGGtGACAA TAAGATTGGT ACAACTAAAA AAGGTATCGG TCCAGCATAT GTAGACAAAG 540

TTCAACGTAT CGGTATTCGT ATGGCAGATT TACTTGAAAA AGAAACATTC GAAAGATTAT 600

TAAAATCAAA CATTGAATAT AAACAAGCAT ATTTCAAAGG TATGTTTAAC GAAACATGTC 660

CATCATTTGA TGATATCTTT GAAGAATATT ATGCAGCAGG TCAACGTCTA AAAGAATTTG 720

TAACAGACAC ATCAAAAATC TTAGACGATG CATTTGTAGC AGATGAAAAG GTACTTTTCG 780

AAGGTGCGCA AGGTGTAATG TTAGATATCG ACCATGGTAC ATATCCATTC GTTACATCAA 840

GTAATCCAAT TGCAGGTAAC GTTACTGTTG GTACAGGTGT AGGTCCTACA TTCGTTTCAA 900

AGGTAATTGG TGTATGTAAA GCTTATACAT CACGTGTTGG TGATGGTCCA TTCCCTACTG 960

AATTATTCGA TGAAGATGGA CATCATATTA GAGAGGTTGG TCGTGAATAC GGTACAACAA 1020

TAAGTGGTAT TACAGATTTA TCTATTAACT CAATCGATGT TTTAACAGGC CTAGACACAG 1140

TGAAAATCTG TACAGCTTAT GAATTAGACG GTAAAGAAAT TACTGAGTAC CCAGCAAACT 1200

TAGATCAATT AAAACGTTGT AAACCAATCT TTGAAGAGTT ACCAGGTTGG ACAGAAGACG 1260

TAACAAATGT GCGTACTTTA GAAGAATTAC CTGAAAATGC ACGTAAATAT TTAGAGCGTA 1320

TTTCAGAATT ATGTAATGTA CAAATTTCTA TCTTCTCAGT TGGTCCAGAT AGAGAACAAA 1380

CAAACCTATT AAAAGAATTG TGGTAGAACT TTATATAAGT CATACACAAT GATTATAAAT 1440

ACATGAGCCT TCTATCTTTA TTGGTAGGAG GCTTTTGTTA TGCTTGCTTC TGTATCGATT 1500

CGATTATTTA GATAAAAAAT ACTAACGTAA AGGCGATATT TGCTAGTCAT AATTTAGAAG 1560

rTTAgATGAt AtTtAACGAA AAtTAAgATG anATACtTGA ATGGTAA 1607

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3055 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

TTAGAAGTAA GCACTTTAAT ATCTTTACCT ACCCATGTAC CAACACCTTC TTTAGGCTTT 60

GGATTTTCAG CATGGTTATT TGATTTATTC ACCTGTTCAG ATCTATTTAC TTTATTACCT 120

TTATTCGGGT TCTCTAATAC ATCAAATTTT AATCTCGGTG AATAAAAAAG ATATATTAAA 180

AATCCAACTA AAAATAATAC ACCGACGACT CTTATAATTA ACTTTTTCAT CAATCAACCA 240

CCTAAAAAGT ATTAATACTA TTGTAAAAAA CAACACATTA ATTAGCAAAT TTTCAACACT 300

GACATAACTG TGTCGTTTCG ATAAAACAAA ATCATCTTCA GGCATAATTT TAACGTCATA 360

AAGATTTTCC CTACACTCTA TATCATAACC TATCTTTATG TTTTCAGGTT GAATTTCATT 420

ATTAAGATTA AAATATGTAT AAAAAAATGG ACAGTTAAGG TATCAAATGA ATACCATCAA 480

CTGTCCGACT ATTCTTCATC AAAAAACCTG ATAAAACAAA TTGCCTTATC AGATTAGTAT 540

CATTTGTATA AGCATATTAA TGACCAAATG TTGCTTTAAT CAGTGATGTC GTTTCTCCAC 600

CTGGATATAA TACATATAAT AATAAGTAAA CTGCTACACC TGTAATTGCA GTACAGAACC 660

ATATAACTGA AGCGAATGGC CCGAATTTGC GGTGTACATT ATATTTATCT TTAAATGCAG 720

TAATAATTTG AACTAGGCCT AGAATACCAC CAATTGTTGC TAAATTAATG TGGAAAAATA 780

AGAAAATCGT ATAATATTTC TTAATTGATG CTGGTCCGCC AAATGCTGTA TTACCGATAA 840

TAACATTTTT GTGTTTATTT ATTTCCCTTT TCCAAATAAG TCTCCAACCA ATGGCAATTA 960

AAATTGCACT AATGACAATA CATGTCGTAC TAATCGTTGG TAAAATTGGA ACGCCCATAT 1020

TTTTCATCCT AACTTAATTA ATCTAGATCA AAGTAAGTAA TGAAACAATC ACAGCTAACA 1080

CGAAAAAGAT CACTAAATAA TTTAGTGAAT ATATAAACAT TTGTGTTGCC CATTTTGTTT 1140

GATCTGAATT TTTCTTAAAT GTTGTTAAAC CTAATGCAAT CCATCCTAAA TTTAATAAGG 1200

TrGCTAACAC TaCGAATACG ACACCTAAAT TTATTAGTAA TAAAGGTACT GGCAATAAAA 1260

TAATCAACCA GATAAACATA CTGACACGTG TACGTTTAAA GCCCTTAACT GATGGTAACA 1320

TTGGAATATT TGCAAGTGCA TATTCATCTT TACGTTTAAT AGCTAAGGcA TAAAAATGAA 1380

TTGGtTGCCA ACmAAATACA ACTAAAAACA GCGCAATCGC TGTTAAACTA ATTTGTCCTT 1440

CAATTGCAAC CCATCCAATT AGTGGTGGTA CTGCTCCAGG AAAACTCCCA ATCACTGTGT 1500

TCCATGTTGT ATGTCTTTTA GACCATATTG AGTAATAAGA CACATAACCT ACAATCCCCA 1560

TAAGACCAAG TACGCCTGAT GGTATATTCA ATAAAAACAA ACAAATTTCT CCAACTAACA 1620

TCATACCAAA ACTTAATAGT AATAAATTTT GATCTGTAAT TCTATTATTT ACAGTTGGTC 1680

TATTTTGTTT ACTAGGCATA ATACGATCAA TATCTTGGTC GTAATAATTA TTTAACGCAC 1740

ATGCGCCACC CATAATTAAA GTAGATCCAA ATAGCATTAA TAAAATTTGA GGTATTGATG 1800

ATAAGAAGGA ATGATTTGTC ATTACAACTG CTAGCCATGC GCcCGCAAAA GCCGGAATTA 1860

AGTTACCTTG AACAAGTCCC ATTTTAATTA TCTGTTGCAA TTCTTTGAAG TTAACTCTGC 1920

TAATATTTTG TGACmAAGTA TGCTCTTTGC TCATAATCCC CCTCCTTAAA TTTGTTCATA 1980

TAAGATTATG ATATCTTAGA TTGCATAAAA AGACTAGGTT TAATAAAATT AAATTGTGAC 2040

AAATTAACGA CAAGAGAAAA TGTCAATTTT GTGACACAAA TAACATTTAA TTTATTGCTA 2100

TAATGTATAT GTTAGAAAAT TTTAATAAGT AGAATCATGC ATCTAAAAGA GATTAATATT 2160

TAAGCTTCAA ATTTGAGTAA ACGTGGATTA CATAATTATC CCAATAAAAA AATCATTACG 2220

ATTAAGTTCT TTTTATGTCG TCCACATACA ATACTTGTAA AATTAAATCA TATTTCCTGC 2280

GTTGGATCCC ATCTTTTCAT ATCCTACAAT CAGGTCTATT TATAGTATCA TCTCAAATCC 2340

GGCTATTAAT TCTAATTCTC AGTGATGCGT TTTTTTATGA TGGGGTGTAT AAATTGTTTG 2400

GCAAAAAGAA TTTAAAATGG TTAGGTGTCG TAGCAACGTT AATGATGACA TTTGTACAAC 2460

TTGGTGGAGC CTTAGTTACC AAAACCGGAT CAGCTGATGG TTGTGGTTCT TCTTGGCCAC 2520

TATGTCATGG TGCGTTGATT CCAGAATTCT TTCCTATTGA TACGATTATT GAGTTAAGTC 2580

ATAGAGCCGT TTCAGCTTTG TCTTTATTAA TGGTCTTATG GTTAGTTATC ACTGCATGGA 2640

TATTGCAAGC ATTAATCGGA GCTGCTGCTG TTATTTGGCA ACAAAACGAT TACGTTTTAG 2760

cATTGCACTT TGGTATATCA TTAATCAGTT TCTCATCTGT ATTTTTAATA ACATTGATTA 2820

TTTTCTCTAT AGATCAAAAA TATGAAGCTG ACGAATTATA TATCAAAAAG CCATTAAGAC 2880

GTTTAACATG GTTAATGGCA ATCATCATTT ATTGTGGTGT TTATACTGGT GCACTAGTGa 2940

GACATGCGGA TGCAAGTTTA GCATATGGTG GTTGGCCATT GCCATTACCA CGATCTTGTA 3000

CCACATTCAG GAACAAGATT GGGTTCAACT CACGCATCGT ATCAnGGTCn nTTAA 3055

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 748 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

TTCTTATTTA AAGAAGTCAT TTTTAGAAAT TGTTGAGACT TTAAAAAATG ATCCGTATAA 60

AATAACACAA TCTTTTGAAA AATTAGAGCC TAAATATTTA GAGCGATATT CAAGAAGAAT 120

TAACCATCAG CACAGGGTCG TCTATACCGT AGATGATCGA AATAAAGAAG TATTAATACT 180

ATCGGCATGG TCACATTATG ATTAATGAAT ATTCAATATC TGAATAACTT TAATGATAAG 240

TTAATTAAAG AAACTAGTAT TTAAGTGTAG GGAAAATAGC GACGTTAATG CGTTGTTATC 300

TCTACACTTT TTAATTTTAT AATAGCGCAA GACTAAACAG ATTGAAATTA GTAACAATAA 360

AAGAATAACG TATTATAATA AGGAATTTTA AATTGTGACT TTTTCGGAAT ATTAAATTTT 420

AGAAATATGA GGTTTTTAAG CGGATTCCTC ACAAAATTTT AAAAATATTT AAGCCTGAAA 480

ATGATAAAGC GGTAGGGAAC GTTTTTCTGA AaGTTAGTGA TACAATAGTT TTAAGTTGAA 540

ATACAGGAGG ATGAATAACA TGAATCAGTC AGTCAAATTA CTTAAACATT TAACAGATGT 600

AAACGGCATT GCTGGTTATG AAATGCAAGT TAAAGAAGCA ATGCGTaACT ATATAGAGCC 660

TGTCAGTGAT CaAATTATTG AAGATAACTT GGGTGGCATT TTTGGAAAGA AAAATGCTGA 720

GAATGGTCAA TACTCAATTA TGGAnTTC 748

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4718 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

ACCTCCGAAT AATTGATTCC ATTAACTTTT TTTGTGaAAA AtTTAAACAG GCGAAGTCTT 60

CAATAAGTGA AGATGTCCAA ATTATAAAAA ATACATTCCA AAAAGAAAAG TTAGGTACAG 120

TAATTACtAC ycTGGCGCAA GTGGTGGTGT TACGTATAAA CCAATGATGA GTAAAGAAGA 180

GGCGACTGAA GTTGTTAATG AGGTCATTAC TCTATTAGAA GAGAAAGAAC GTTTGTTAcC 240

TGGCGGATAT TTATTTTTAT CAGATTTGGT AGGTAATCCA TCGCTACTAA ACAAAGTTGG 300

TAAGTTAATT GCCAGTATTT ACATGGAAGA AAAATTAGAT GCTGTTGTTA CCATTGCGAC 360

AAAAGGTATT TCATTGGCAA ATGCGGTTGC TAATATTTTA AATTTACCAG TAGTAGTGAT 420

TAGAAAAGAC AACAAGGTGA CTGAAGGTTC TACAGTTTCA ATTAATTACG TTTCAGGATC 480

TTCAAGAAAA ATAGAAACAA TGGTACTTTC GAAGAGAACT TTAGCAGAAA ATTCAAATGT 540

TTTAGTTGTC GATGATTTTA TGAGGGCTGG TGGCTCTATT AATGGTGTTA TGAATTTAAT 600

GAATGAGTTT AAAGCCCATG TAAAAGGGGT ATCAGTACTT GTAGAATCAA AAGAAGTTAA 660

ACAAAGATTG ATTGAAGATT ATACTTCCTT AGTGAAATTA TCTGATGTAG ATGAATATAA 720

TCaAGAGTTT AACGTAGAAC CTGGCAACAG TTTATCTAAG TTTTCATAAA AGGAGTTTTA 780

GTATTATGAA AATCATTAAC ACAACAAGAT TACCGGAAGC ACTTGGACCA TATTCGCATG 840

CAACAGTTGT GAATGGTATG GTTTATACTT CTGGTCAGAT TCCATTGAAT ATTGATGGAC 900

ATATCGTAAG CGCTGATGTT CAAGCACAGA CAAAACAAGT TTTAGAAAAT TTAAAGGTTG 960

TTTTGGAAGA AGCAGGATCT GATTTGAATT CTGTTGCGAA AGCGACCATT TTCATTAAAG 1020

ATATGAATGA TTTCCAAAAA ATAAATGAAG TGTATGGTCA ATATTTTAAT GAACACAAGC 1080

CAGCGCGTAG TTGTGTAGAG GTTGCGCGTT TGCCAAAAGA TGTGAAAGTA GAAATTGAAT 1140

TAGTAAGTAA AATTAAGGAA TTATAATTTT CGATTAATAT GTTTAATCAA GCTTCTAAAT 1200

AAAACAGAGA GATATATACT ATAGGGGGGC TCACTACATG AAAGTGACAG ATGTAAGACT 1260

TAGAAAAATA CAAACAGATG GACGAATGAA AGCACTCGTT TCCATTACAT TAGATGAAGC 1320

TTTCGTAATT CATGATTTAC GTGTAATTGA AGGAAACTCT GGCTTGTTCG TTGCAATGCC 1380

AAGTAAACGT ACACCAGATG GTGAATTCCG CGACATCGcg CATCCTATTA ATTCAGATAT 1440

GAGACAAGAA ATTCAAGATG CAGTGATGAA AGTATATGAT GAAACAGATG AAGTAGTACC 1500

AGATAAAAAC GCTACATCAG AAGATTCAGA AGAAGCTTAA TCAATTTTAT ATTTAGCGAT 1560

GTAATACATT TGCAATAAGT TGATTTGATA CTGTCGATAA AGCATAAAGC TTTGTCGGCA 1620

GTTTTTTTAG TTTGTATTAA TGTTTTTTTA TTTTTAATGA AAGGCTAATA AATATATACG 1680

TGaTGCTCGT ATTTTTGAAG TAAGAAAAAA GTTGTTTTTA AAATTACAAC GAATTAAAAA 1800

CAATGCCTTT TATATGTTGA AAGAGTATTG CaGATTAAAT TaTAATAATG ACGAaGgTAA 1860

AATTTAATGG GGGTTAATGT TCATGCGAAG ACACGCGATA ATTTTGGCAG CAGGTAAAGG 1920

CACAAGAATG AAATCTAAAA AGTATAAAGT GCTACACGAG GTTGCTGGGA AACCTATGGT 1980

CGAACATGTA TTGGAAAGTG TGAAAGGCTC TGGTGTCGAT CAAGTTGTAA CCATCGTAGG 2040

ACATGGTGCT GAAAGTGTAA AAGGACATTT AGGCGAGCGT TCTTTATACA GTTTTCAAGA 2100

GGAACAACTC GGTACTGCGC ATGCatGCAA ATGGCGAAAT CACACTTAGA AGACAAGGAA 2160

GGTACGACAA TCGTTGTATG TGGTGACACA CCGCTCATCA CAAAGGAAAC ATTAGTAACA 2220

TTGATTGCGC ATCACGAGGA TGCTAATGCT CAAGCAACTG TATTATCTGC ATCGATTCAA 2280

CAACCATATG GATACGGAAG AATCGTTCGA AATGCGTCAG GTCGTTTAGA ACGCATAGTT 2340

GAAGAGAAAG ATGCAACGCA AGCTGAAAAG GATATTAATG AAATTAGTTC AGGTATTTTT 2400

GCGTTTAATA ATAAAACGTT GTTTGAAAAA TTAACACAAG TGAAAAATGA TAATGCGCAA 2460

GGTGAATATT ACCTCCCTGa TGTATTGTCG TTAATTTTAA ATGATGGCGG CATCGTAGAA 2520

GTCTATCGTA CCAATGATGT TGAAGAAATC ATGGGTGTAA ATGATCGTGT AATGCTTAGT 2580

CAGGCTGAGA AGGCGATGCA ACGTCGTACG AATCATTATC ACATGCTAAA TGGTGTGACA 2640

ATCATCGATC CTGACAGCAC TTATATTGGT CCAGACGTTA CAATTGGTAG TGATACAGTC 2700

ATTGAACCAG GCGTACGAAT TAATGGTCGT ACAGAAATTG GCGAAGATGT TGTTATTGGT 2760

CAGTACTCTG AAATTAACAA TAGTACGATT GAAAATGGTG CATGTATTCA ACAGTCTGTT 2820

GTTAATGATG CTAGCGTAGG AGCGAATACT AAGGTCGGAC CGTTTGCGCA ATTGAGACCA 2880

GGCGCGCAAT TAGGTGCAGA TGTTAAGGTT GGAAATTTTG TAGAAATTAA AAAAGCAGAT 2940

CTTAAAGATG GTGCCAAGGT TTCACATTTA AGTTATATTG GCGATGCTGT AATTGGCGAA 3000

CGTACTAATA TTGGTTGCGG AACGATTACA GTTAACTATG ATGGTGAAAA TAAATTTAAA 3060

AcTATCGTCG GCAAAGATTC ATTTGTAGGT TGCAATGTTA ATTTAGTAGC ACCTGTAACA 3120

ATTGGTGATG ATGTATTGGT GGCAGCTGGT TCCACAATCA CAGATGACGT ACCAAATGAC 3180

AGTTTAGCTG TGGCAAGAGC AAGACAAACA ACAAAAGAAG GATATAGGAA ATAATCATTT 3240

ACGTATTTAA AATGGCTAGG ATAAAAGGAT AATCCTATGT AATATTAATG TAATCTTTAT 3300

GATTTAATGA TTCGCATAGT AATGGAGTTA CATyTTATAT ATAATAGTAA TTGCGTAAGT 3360

AAATAATTGG AGGACTATAA ATGTTAAATA ATGAATATAA GAATTCGTCA TTAAAGATTT 3420

TTTCATTGAA AGGAAACGAA GCATTAGCGC AAGAAGTTGC TGACCAAGTA GGAATTGAAC 3480

GTATTCGTGG TTGTGACGTA TTTATTATTC AACCAACATC ATATCCTGTG AATCTACATT 3600

TAATGGAATT ATTAATTATG ATTGATGCTT GTAAACGTGC TTCTGCAGCA ACAATCAATA 3660

TTGTAGTGCC ATATTATGGA TATGCAAGAC AAGATAGAAA AGCCCGTAGC CGTGAGCCAA 3720

TCACTGCTAA ATTAGTTGCA AACTTAATCG AAAcAGctGG CGCAACTCGT ATGATTGCGT 3780

TAGACTTACA TGCACCACAA ATTCAAGGAT TCTTTGATAT TCCAATTGAC CACTTAATGG 3840

GTGTGCCAAT TCTTGCTAAA CATTTCAAAG ATGATCCGAA TATTAACCCA GAAGAATGTG 3900

TCGTTGTTcA CCAGACCATG GCGGsnTTAC ACGTGCACGT AAATTAGCTG ACATTTTAAA 3960

AACTCCAATT GCAATTATAG ATAAACGTCG TCCTAGACCA AATGTTGCTG AAGTGATGAA 4020

CATTGTTGGT GAGATTGAAG GACGTACGGC AATTATTATT GACGATATTA TTGATACAGC 4080

AGGTACAATC ACTTTAGCTG CACAAGCATT AAAAGATAAA GGTGCTAAAG AAGTATATGC 4140

TTGTTGTACA CACCCTGTTT TATCAGGACC GGCTAAAGAA CGTATCGAAA ATTCTGCTAT 4200

AAAAGAATTA ATCGTAACAA ACTCAATTCA TTTAGATGAA GATCGCAAAC CATCTAACAC 4260

TAAAGAATTA TCTGTTGCTG GTTTAATCGC ACAAGCTATC ATTCGTGTAT ACGAAAGAGA 4320

ATCAGTTAGC GTATTATTTG ACTAATATTT AAAAGGCGTT TGACGAACAT ATTCCAAACG 4380

TGTATAATAG TTTCGTTCGT GATTATACGA ATAAATAAAC ACTTGCAAGC AACGATGATG 4440

TTGATGGGTA AGTGAGGTGC TCGTTTTGAG CAAAAATGAA AGGTGGAAAT GAGAATGGCT 4500

TCATTAAAGT CAATCATCCG TCAAGGTAAA CAAACACGTT CAGATCTTAA ACAATTAAGA 4560

AAATCTGGTA AAGTACCAGC AGTAGTATAC GGTTACGGTA CTAAAAACGT GTCAGTTAAA 4620

GTTGATGAAG TAGAATTCAT CAAAGTTATC CGTGAAGTAG GTCGTAACGG TGTTATCGAA 4680

TTAGGCGTTG GTTCTAAAAC TATCAAAGTT ATGGTTGC 4718

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

AAAATGCATA TAAATACATA TTAAGGAGGA TTTTATGAAT TTTCTTAAAC CTGCAAAGCA 60

TATTAAGCCT TTGCCAGAAA ATCAGATAGA TGATACCTAT AAACGATTAC GTCTCCAAGT 120

ATTTCTTGGT ATTTTCATCG GTTACGCTGG GTACTATTTA TTACGTAAAA ACTTTTCGTT 180

TGCTGTTTCC ATCGCATATG GATTTAGTAA GTTCTTTATG GGTACTGTAA gTGATCGGAG 300

CAATGCTCGG ATATTCTTAG TTCTTGGATT AGCACTCACT GCTATCGTCA ATTTGTTAAT 360

GGGATTTGTA CCGTTCTTTA CATCAGGTAT CGGTATTATG TTTGTCCTAT TATTCTTAAA 420

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AGAAAAACAT TTCGACTTAA AAGCATCAGG TTGGGCATAC TTCTTATACG AATGGGCTGG 960

AATTCCTGGT ACATTATTAT GTGGTTACAT TTCTGATAAA TTATTCAAAG GTCGTCGTGG 1020

ACCTGCAGGT TTCTTCTTTA TGTTAGGTGT CACAGTATTT GTATTAATTT ATTGGTTAAA 1080

TCCTCCAGGC AATGCTTGGT TAGACAATGT CTCATTAATT GCCATTGGTT TCTTAATATA 1140

TGGACCAGTT ATGTTAATTG GTTTACAAGC ATTAGATTAT GTACCTAAAA AAGCAGCTGG 1200

CACAgcAGCT GGATTAACAG GATTATTTGG TTATCTGTTT GGTGCTGTAA TGGCCAACAT 1260

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TTCATCTCTT ATAAGTTCAA CCATATGACT TTTTATTAGT ATTCAAAAAA ATATTTACAT 1500

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TGATGCCATT GTTACTTTCA AAATAAATGt CGCCATCTCA ACAATGGCTT GATCAGTAGT 2340

AAATAGTCCG ACCATATGAT GTCCAATTGT AAATACAGCA CTCATACATA CAACAAAGAT 2400

AACGCCGATA GACATGATAA CTGCTTTGAT AACGTCTTTC ATACGGCCTT TATTTGCCAT 2460

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AACTGACACA ACGTCACTAT TTTTCATAAA ATAAATGATA AAGAACAGAG CAGCAGCAAC 2760

ATTACTGATT GCAGTACCCA AAGCTGcACC AACAACGTTT aAATCAAAAC CAAAAATTAA 2820

AATTGGATCT AAAATAATAT TTAAGCCTAC ACTAGCTAAC ATACCAATCA TAGAAACCAT 2880

TGGTGCCCCA ATTGCACGTG CAAATTGTTC TAATATGAAG AACAAAATTA CAAAAGGTGC 2940

ACTTAAAAAC ATTACTTTCA AATAATTACT TGTTAAAGCT AACGTTTCAC CTCTCGCCCC 3000

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TGCAATACCA CCATAAATAG AGAAACTACT TACAAATTTA CTCTTAmTAT AGTCTTTCGC 3120

ACCTAATAAA CGTGAAATAT AAGTTCCTGC ACCAACGCCA AATAAATTAC CTAACCCCAT 3180

T 3181

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4029 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

TCATCACCTT CAAATAAATA GGCATGCGAT AATTTATTTG AATGATATGC ATTCGTCAAT 60

TGTTGCTGTT CATCCATTCA TTACAAACTC CCTTTTGCTT TTATATAAAA AGGTTGCCAA 120

AGAGCAACTA ATTACTGCAA CAATAGCGAC CATGATTTGT GATTATTTTT AGAACCACAA 180

TTATTAATAC ACTATTTTAA GTATCTCTAA TTGATGATTG TATTATAGAA TTAAAATTGA 300

TGGAATGCAT CAACTGGCAT AACAAATACA GTAGCACCGC CAACTTCAAC TTCAACTGGA 360

TATGGAATGT ACGAATCCGC ACTGCCTCCC ATAGGTGTAA TAGGTGAAAC CAACTGTTCT 420

CTATTACCAC ACGTTTGATT AATCACAGAC AATATTTCAT CTACACGGTC ATCATTGACA 480

CCACATAAGA ATGTTGTATT ACCCGCTCTT AAAAACCCAC CTGTTGTTGC CAATTTTGTT 540

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CTTGATAAGC TAATGAACTA TCGATATAGC GATCACACAA CACAACCTTA CCTTCTTTTA 1020

AAGCTGGTAT GACCTTTAAT ACAAGATGTT CTCTTCTAGA TGCAGCAAAT AACATTGcTT 1080

CaGTtCTAAT GTCCATATCA TTGCCcTTCT AATACAATTT TACGTATTTC TTCACCAGTA 1140

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GAATATCATG ACCTGTAAAA CCTTCATATT TTATCAGCAA CTTCAACGGA TCATCAACTT 1740

GAAGCATTTC AAAACCCTTC TTCTCCAAAC ATTCGATTAA TTGCGCTCTC TTATCAAAAA 1800

ACACGGTACT ATCATATGTT TTATAGAACT CGGCAGCTGA CTCTAAACTA GCCATAATCA 1860

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AATCCAGGTA TTTCAGTTTT ATCCATTGTC ATTGATAATT GAGATAAATG ACCGATAGTC 2520

ATATTTTTAT GACCCGGAAC ATGCAAAGAA ATCGCTTCTT CTTGATTTAA ACTTTCTAAT 2580

TTATTTAAAA TAGGTTGCTT CATGATATAC GCTTCCTTTA TTTACACTGT TTTGGAATTA 2640

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TCCTTCGGCT CTCGCTTACT CATTTAGCTC TACTAAACTC GTTGCGCTCT TTTCTCGTTT 3360

CGTCAGATTC AAACGTTTTC ACTTCGCCAA GCCATTTTTC TTTGTGTTTA CTTTTTATTT 3420

TGACGTTTTA GrCATAAAAA AAAGAGACcT TGCGGTCTCA ATGCGGCTCA TCGCATCCAT 3480

TTTTTGCCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT GGCTACCATC GwCGCTAAgA 3540

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AAGTCTTCGA TCGATTAGTG ATTCGTGCAG CTCCACATGT GCACCATGCT TGCCACCTCG 4020

GAACCTATT 4029

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

GATGCAATAG TTGAGTAGTT ATAAGTAGCT ACATACAACC GCTCAAATAT AGGTTCAAGA 60

ACATTTTTAA TGAAGAAAGC GATTTTCCCm CAGAGTGCAA ACGCTTGACT CAATAACGAA 120

ATGTCACCTA TGTATGGCGT GACTTATTAT ACAGGaGGTG CAAAGTATGT TTGCTATTAT 180

TGAAACAGGT GGAAAACAAA TCAAAGTAGA AGAAGGTCAA GAAATCTTCG TTGAAAAATT 240

AGACGTAAAC GAAGGAGATA CTTTTACATT TGATAAAGTA TTATTTGTAG GTGGAGATTC 300

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AGGTCGCGGT AAAAAAATCA CTGTATTCAC ATACAAACGT CGTAAAAATT CAAAACGTAA 420

AAAAGGCCAT CGTCAACCAT ACACTAAATT AACAATCGAT AAAATCAACG CGTAATTATT 480

ATGATTACTG TTGATATTAC AGTTAATGAT GAAGGCAAAG TAACAGACGT TATTATGGAT 540

GGCCATGCTG aCCATGGTGa ATATGGTCAT GATATCGTTT GTGCTGGAGC TTCAgCTGTA 600

TTGTTTGGTA GTGTTAATGC GATTATAGGA TTGACATCTG AGAGACCAGA TATCAATTAT 660

GACGACAATG GTGGTCATTT TCATATAAGA AGCGTTGATA CAAACAACGA TGAAGCGCAA 720

CTAATTCTTC AAACAATGCT TGTGTCTTTA CAAACTATTG AAGAAGAATA TAATGAGAAT 780

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CATCTAAAAA AGGGGTAAGT TCTACAAAAA ACGGACGTGA CTCTGAATCA AAACGCTTAG 900

GTGCTAAACG TGCTGACGGT CAATTCGTAA CAGGTGGTTC AATTTTATAT CGCCAACGTG 960

GTACTAAAAT TTACCCTGGT GAAAATGTAG GTCGTGGTGG CGATGATACA TTATTCGCTA 1020

AAATCGACGG CGTTGTTAAA TTCGAACGTA AAGGTCGCGA CAAAAAACAA GTTTCTGTAT 1080

ATGCAGTAGC TGAATAATTT TGTCTAGTTA ACACCAGAAG TGAATCTTCT GGTGTTtTTT 1140

AGACGTTATA CTAAATGTGC AcTGTATAAG AGCCCCTAAT CACTAAACTA TAAGGGGGAC 1260

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CGGTGGTAAA GGTGCTTCAG TCGTATTTGA AGTGGATGAA GGTTTAAGAA CGTTATTAGA 1620

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TGTTGGTATG TTGGCACGTG TACTAGATGT TATATCAAAG TTAGAACTAT CTGTATTAAC 3060

GATTCATCAA AGTATTCCAA TGGAAGAAAA AGCAACAATA ACATTATCAC TGAATGCTAA 3120

ATCTAAAGAA ACTTCAGTAG AAGATGTTAT TGGCGCTTTG AGAAATTTAG ATTATGTATC 3180

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TTCATACATC TTTAATTGTT CGTGAAGATG CACAATTATT GTATGGATTT AGTAGTGAAG 3420

AAGAGAAAGA TATGTTCTTG AGTTTAATTA AAGTTACTGG TATTGGTCCG AAATCAGCTT 3480

TAGCTATTTT AGCGACAAGT ACGCCTAATG AAGTAAAACG TGCCATTGAA AATGAAAATG 3540

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ACAAAAACTG TGCGAAACA 7159

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

TCCATTTATA GAAATTTCTA AAGCAGAnAA TAAGATAGAA GATATCGGCC AAGGTGCAGA 60

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ATTTGATTTT GTAAAAGATA AAAAATATAA CAAAGATGCC CTAGTTGTTA AGATGCAAGG 180

CTTCATTAGC TCTAGAaCAA CATATTCAGA CTTAAAAAAA TATCCATATA TTAAAAGAAT 240

GATATGGCCA TTTCAATATA ATATCAGTTT GArAACGAAA GACTCTAATG TTGATTTAAT 300

TAATTATCTT CCTAAAAATA rAATTGATTC AGCAGATGTT AGTCAGAAAT TAGGCTATAA 360

TATCGGCGGA AACTTCCAAT CAGCGCCATC AATCGGAGGC AGTGGCTCAT TCAACTACTC 420

TAAAACAATT AGTTATAATC AAAAAAACTA TGTTACTGAA GTAGAAAGTC AGAACTCTAA 480

AGGTGTTAAA TGGGGAGTGA AAGCAAATTC ATTCGTTACA CCGAATGGTC AAGTATCTGC 540

ATATGATCAA TACTTATTTG CACAAGACCC AACTGGTCCA GCAGCACGAG ACTATTTCGT 600

CCCAGATAAT CAACTACCTC CTTTAATTCA AAGTGGCTTT AATCCATCAT TTATTACAAC 660

ATTGTCACAC GAAAGAGGTA AAGGTGATAA AAGCGAGTTT GAAATcACTT ACGGCAGAAA 720

CATGGATGCT ACATATGCTT ACGTGACAAG ACATCGTTTA GCCGTTGATA GAAAACATGA 780

AAAAATTAAA AGCATCACAC CTAAGTAAAC AGTTCaATCA TCTTAAAAAA TCCTGGGACA 900

CTTCATACTT GTCTCAGGAT TTTTTmACAA ATTGAATCAG CCTCATAACA TTAAATTATT 960

TTATCGTACA TTAAATTTAA TAATAACAAC TGATTTTTAT AAGAATAAAG TATCGAmCCA 1020

TAGTAGATAC ACAAATAATA CAAATGAAAC AATTTAACTT GAAAGCTTAa ATAAATATTA 1080

TCAAGTTAAT AAACAATTAA TTTTTAGATG GATTCATCAA AAATCGTAAA AAAGCACAAT 1140

TTGTATTTTA CAAACATTAA TTAAAAAAGA AAGCAAGACA TTCGTGCAAT CGGTTACCTT 1200

AAATTGTTTA CAACTGTCAA CAATACCAAG GTTTTATTAA CTATATTTCT CACAAAATTA 1260

GCTTTTAGCA TTCCAAACAA AAAAGGTTAA ATCGAACGGA ATTATGGCAT TTTTAACTTA 1320

ATTGTAAAAA AAGTTGATAA TGGTCAATTG TTAATGAACA GTTAATTATA ATAACGCCCA 1380

AAATATATTA TTATTTAATT AAGTTAAATA AAATTATAGA AAGAAAGTGA AACTTATGCT 1440

TAAAAATAAA ATATTAACTA CAACTTTATC TGTGAGCTTA CTTGCCCCTC TTGCCAATCC 1500

GTTATTAGAA AATGctAAAG CTGCTAACGA TACTGAAGAC ATCGGTAAAG GAAGCGATAT 1560

AGAAATTATC AAAAGGACAG AAGATAAAAC AAGTAATAAA TGGGGCGTGA CTCAAAATAT 1620

TCAATTTGAT TTTGTAAAGG ATAAAAAATA TAACAAAGAT GCTTTGATAT TAAAGATGCA 1680

AGGATTCATT AGCTCTAGAA CAACATATTA CAACTATAAA AAAACTAATC ATGTTAAAGC 1740

TATGCGATGG CCATTCCAAT aTaATATTGG TTTAAAAACA AATGATAAAT ATGTTTCTTT 1800

AATTAATTAT TTACCTAAAA ATAAAATTGA ATCTACAAAC GTGAGTCAGA CATTAGGATA 1860

CAATATCGGT GGTAATTTCC AATCAGCCCC ATCACTCGGT GGTAATGGAT CATTTAACTA 1920

TTCTAAATCG ATTAGCTATA CACAACAAAA TTATGTAAGT GAAGTAGAAC AACAAAACTC 1980

AAAAAGTGTT TTATGGGGCG TCAAAGCGAA TTCATTCGCC ACTGAATCAG GTCAAAAATC 2040

AGCCTTTGAT AGCGATTTAT TTGTAGGCTA CAAACCTCAT AGTAAAGATC CTAGAGATTA 2100

TTTCGTTCCA GACAGTGAGT TACCACCTCT TGTACAAAGT GGATTTAACC CTTCATTTAT 2160

CGCCACAGTA TCTCATGAAA AAGGTTCAAG CGATACAAGC GAATTTGAAA TTACTTACGG 2220

AAGAAACATG GATGTCACTC ATGCCATTAA AAGATCAACG CATTATGGCA ACAGTTATTT 2280

AGACGGACAT AGAGTCCATA ATGCATTTGT AAATAGAAAC TATACTGTGA AATACGAGGT 2340

CAATTGGAAG ACTCATGAAA TCAAGGTGAA AGGACAGAAT TGATATGAAA ATGAATAAAT 2400

TAGTCAAATC ATCCGTTGCT ACATCTATGG CATTATTATT ACTTTCTGGT ACTGCTAATG 2460

CTGAAGGTAA AATAACACCA GTCAGCGTAA AAAAAGTCGA TGACAAAGTT ACTTTATACA 2520

AAACAACAGC CACAGCAGAT TCTGATAAAT TTAAAATTTC ACAGATTTTA ACATTTAATT 2580

ACTCAGGCTT TGTGnAACCT AATCCTAATG ACTATGACTT TTCAAAATTA TATTGGGGAG 2700

CTAAATACAA TGTATCTATA AGCTCACAAT CTAATGATTC AGTAAACGTC GTTGATTATG 2760

CACCAAAAAA TCAAAATGAA GAGTTTCAAG TTCAAAATAC TTTAGGCTAT ACATTTGGTG 2820

GTGACATTAG TATCTCTAAT GGTTTATCTG GTGGACTTAA TGGAAATACA GCTTTTTCTG 2880

AAACAATTAA TTATAAACAA GAAAGTTACA GAACAACATT AAGTCGCAAC ACAAATTATA 2940

AAAATGTTGG CTGGGGAGTT GAAGCACATA AAATTATGAA TAATGGTTGG GGACCTTATG 3000

GAAGAGATAG CTTCCACCCA ACATATGGTA ATGAACTCTT CTTAGCTGGC AGACAAAGCA 3060

GTGCATACGC TGGCCAAAAC TTCATAGCGC AACACCAAAT GCCATTATTA TCTAGAAGTA 3120

ACTTCAATCC AGAATTTTTA AGCGTACTAT CACACAGAC 3159

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3821 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

GCAAAAACTT TTCTCCAACT ATGTCAGACT ATAATGGCAT GAACAAAATT GATATGATGA 60

ATCAAATTAA AGTTGATACG ATGTTGCATG GTTATCACGC TGGATTTTTA TTTGCATTAT 120

TGATTACAGT TGTTAGTTTC TTTTGTTCAT TTATGTTACA AGGTAAGAAA AAAGAAGTTG 180

ATTCTCGTCA ATAAATATAA GTTGCTAGCT ATATAAAGCT TTTTAGCAAA AGTTCAACAT 240

ATTGACTTAT CCGGCATTTC AGATTAAAAT ATTTTTATTC CGATTAGAAT AATAAGAATA 300

AGGAGATATA TTCTATGAAA AGACTTTTAT TTGTGATGAT AGCTTTCGTT TTCATATTGG 360

CTGCATGCGG AAACAATTCG TCGAAAGACA AGGAAGCTAG TAAAGATAGC AAGACAATTA 420

ATGTTGGGAC TGAGGGGACT TATGCACCAT TTAGTTTCCA CGATAAAGAT GGTAAATTAA 480

CTGGTTACGA TATTGATGTT ATTAAAGCAG TGGCTAAAGA AGAAGGTTTA AAACTTAAAT 540

TTAATGAAAC TTCTTGGGAT TCTATGTTTG CAGGTTTAGA CGCAGGGCGT TTTGATGTAA 600

TCGCGAACCA AGTAGGTATT AATCCTGATA GAGAAAAGAA ATATAAATTT TCTAAGCCTT 660

ACACATTCTC AAGTGCTGTT TTAGTTATTC GTGAAAATGA AAAAGATATT AAAGATTTTG 720

ATGATGTTAA AGGTAAGAAG TTAGCACAAA CATTCACATC TAATTATGGT AAATTAGCTA 780

AGGATAAAGG TGCTGATATT ACAAAAGTTG ATGGCTTTAA CCAATCAATG GATTTATTAT 840

AAAAACCTAA TGcTAAGATC AAAGCAATCA AAGGTAATGC TGAACAAAGT AGATCTGCAT 960

TTGCATTTTC TAAAAAAGCA GATGATGAAA CAGTTCAAAA ATTCAATGAT GGCTTGAAAA 1020

AAATCGAGGA AAACGGTGAA TTAGCTAAAA TAGGTAAGAA ATGGTTTGGT CAAGATGTTT 1080

CTAAATCTAA ATAGCGAACA ACAACATGCG CTAGATGCTG CAAAACAAGC TTTCGGACCT 1140

ATGCTAGAAG GTTTGGTCAA ATATTCAATT CCTATTACAT TAGTTACATT TGTTTTAGGA 1200

TTGATTATTG CATTATTTAC AGCATTAATG CGAATTTCAA CGAGTAAAAT TTTAAGAAGT 1260

ATTTCACGTG TCTATGTATC TATTATTCGA GGAACACCAA TGATAGTACA ACTATTTATC 1320

ATATTTTATG GTATTCCAGA ATTAGGTAGA TTATTAACAA ATGACGCTGA CAACCAATGG 1380

ACATTGGCAC CTGTAGTGGC TGCTATTATT GGTTTATCAT TAAATGTAGG TGCGTATGCT 1440

TCGGAAATTA TTCGTGGCGG TATTATTTCT ATACCGAAAG GACAAACAGA AGCTGCaTAT 1500

TcCaTCGGTA TGACGTATGG TCAAACGATA CAACGTATCA TTTTACCGCA GGCAATTCGA 1560

GTGTCGATTC CTGCACTAGG TAATACATTT TTAAGTTTAA TCAAAGATAC ATCATTATTA 1620

GGATTTATTT TAGTGGCTGA AATGTTTAGA AAAGCTCAAG AAGTTGCGTC TACAACATAT 1680

GAATATTTAA CAATTTATGT GTTAGTTGCG CTAATGTACT GGGTGGTATG CTTTATTATT 1740

TCAATTATCC AAGGTATCTA TGAATCTTAT ATTGAAAGAG GGTATCGCTC ATGATTCAAT 1800

TGAACAATAT CCATAAATCA TTTAATGATG TTGAAGTCAT CAAAGGTATT GATTTATCTG 1860

TTGAACAAGG TGAGGTTGTA ACCTTAATCG GTCGATCTGG TTCAGGTAAA ACAACATTGT 1920

TACGTATGAT TAATGCATTA GAAATTCCAA CTGAAGGTAC AGTTTATGTT AACGGCAAAA 1980

CATATACATC TAAAGATAAA AAATCACAAA TAGAAGTTCG TAAACAGTCT GGTATGGTAT 2040

TTCAAAGTTA TAACCTTTTT CCGCATAAGA CGGCATTAGA AAATGTAATG GAAGGTCTTA 2100

TCACAGTTAA AAAGTTGAAA AAGGATGAGG CACGTGGGAA ATCACTTGAG TTACTTGAGA 2160

AAGTTGGTTT AACACATGTC AAAGATCAAC GTCCACATGC ATTATCAGGT GGTCAACAAC 2220

AACGTGTTGC TATTGTCAAG AGCACTAGCA ATGAACCCTA AAGTGATGTT GTTTGATGAA 2280

CCAACATCTG CACTTGATCC TGAACTTGTG AATGATGTTT TAAAGGTTAT TAAAGATTTG 2340

GCTAATGAAG GCATGACAAT GGTCATTGTG ACACATGAAA TGCGTTTTGC TAAAGAAGTA 2400

TCTAATAACA TTGTATTTAT TCmTGAAGGC ATGATCGGAG AACAAGGGGC TCCAGAAGAG 2460

ATGTTCAATC GTCCGAAAAC AGAAGAATTA AGACGTTTCT TAAATGTTAT AAATGAAGAA 2520

TAATCAAATA GAACCACGTA TCATGTTTTA GTATGGCGAT GAAGCCATAT ACATGATGCG 2580

TGGTTCTTTG TTATGTTGTC ATAATCTTGG AGCGATATTT TAACGACGTT TATGATTTAA 2640

TTCTACATGT GCGTTAAAAC CTTTTTTGAA TTGTTGGACG CCATAGTCTT CTGATGACTC 2760

TGAAAAGTCA CCGGTAATAC CATAAAAATT ATAGCGATCA ATATGATGCG CTTTAGCAAA 2820

CTTAATCATT TCCCaCTGCA AATGGTAGGC ACCCATATAA GCATTATATT TAGGGTTTGA 2880

ACCACTAGAT AAGTAATAAA CTTCATGCTC ATTGTAGATA AATAAAGCAG AAGCTAAGTT 2940

TAAGACTGCA CCATCTTGTT CAATTTGTTC TATTGTATTG TCGATTTTAC GCTTATTGCT 3000

ATTTAGCTGT TGTTCTAGCT GTGTGCGTTT CGTTTTATTT TTCTTTGAAT TAGGACTTTC 3060

TTCCAATGCT TCTTCAACAC CTGAGAGTTC AGCTGTTAAT TGTTGTTGCT TTAATTGTAA 3120

CGTTTTTAAA TACTCGTTTA AATCAATATA CGCCAACTTT AACATGGCGT GGTCATCGTA 3180

TAACTTTTGC ATTTCTTCAA AGTATGGTAA CTCACGGAAT TTGAAACCGT GCTTTTCCTC 3240

AGCCATATGG AATAAGTCGA AAAAAGTTTG CGTTTCATCA ATCGTTAAcG TTTTaGTTTT 3300

GACACCAAtA TCaTATGTtT tTtTAATATT ACGTCTCGtT TGATAATCCA TTTCTTTTAA 3360

AAGTTGGTCT TCAGTCTTAT CTTTTAAATC TAACACTGAC AGCCAACGGA TTTGGCTCAT 3420

TGAATCATAA CCTACAGGGA AACCTTGGTG TTTATAACCT AATTTATCCA TTGTTCTaAC 3480

AAATGCTCGG TTATCATAAG ATTTAACAAT TTCACCGTCT GCATTGCGTA AATTTTCAAT 3540

TAAATATGGA TCTACAAGGA CATATAAACA ATTGTGTTTC TTTAAATATG ACGTTAATGC 3600

TTTAAAGAAA AATGCTACTA ATGATTGATT TGTATAATCC ATCACTGGCC CGCGATGTGT 3660

ATAAAAATAT TTGAAAAATT TAAGTGTGCG TGCTTCTGTC AATAAGCATC CTGCAATCAC 3720

TTGACCATTG TCATCTTTAA CCCCTACrAG ATGCACATCG CCTTTTAAAT CAACTCTATG 3780

ATTGTAATGA ATAGCTGATT GTGTGTAATG TGAAAAATGC T 3821

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1422 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GCGACACCAT TGTTTGCAGC AACTGTTAAT TTACCAGTTG ATGGTTTCGA CGGTGTTGTT 60

GGTTTTGATG GTGTAGTAGG GGTAGTTGTA GATTGCGTAC CCCATGGCGC CACTTTACCC 120

ATTTTTATTA AATATTTTTC ATTAATTAAG TCATATAATT GATCATAACT ATAATTATGA 180

CTTCTTAAAT ATCCATGTGG ATcGGCATGG TCAGTACCAC CTAAATATTT ACTTACAGCG 240

TATTGTAATT GTGTAGCTGC ATAGTCAGCA TAGTTATTCA TTGAACGTGC AAATGAAGCA 360

TAGTCGTGTG TGTGTACGAT TTCAACATTG ATGAATCTAG GGTTACCGAC TGCACCGACA 420

CCCCAAGATA AGTAATCCGT TGGTGCTGTT TCGATTATAC GATCCCCATC AACAAATGCA 480

TGTACGAATG CGTTTTGATA GTTATTTTTC ATATAACTAA TTTCACCATT TATCGTCGAA 540

CGATCATTAG CTGTATCATG AACTACGATA CCTTCAGGAC GACCTACGCC GTTACGGTAT 600

GCGTATTTAG GGAAGTAAGA TGTATAATCT TCTTCAATTT TAGGTGCTTT TAAGTTATTT 660

TTACAAATGT AATCGTTAAT TGAAGAGTTT ACTTGTGGTT TATATTTTGG CAAACTCGTT 720

TTTGGTGTTG CAGCAACTGA TCTTGGTTGT GCTGAAGCGC TAAAAGTAGT TACTTTAGGT 780

GTCGCTTCAG TTTTAGCTTT AGGTGCTGAT GTAGTTGCAG CTTTAGGTGC TGCGGTTTTA 840

TATTGCGTyT CAAGAGCTGC AGGTTTAGCA GCTGATTTAA TTAATTCTGG ATTAATTTGA 900

TTTTCTGAAT TATCATCTTC ATCATCAACT AAACTATAAC CAGCATTTGT AACATTAGTG 960

TTAGTTTTAG GTGCTGTAGT GCTTGTTGAC TTTGCAACAG GCTGCGTATT ATTTGTAGTC 1020

GCTGATTGAT TAGCACGAGT GTCACCATTT ACTTGTGCAG TATCAACTTT TTGACTTACT 1080

TGAGCATTGC CTGTTTTGTT ATTTGCTGTT TTTGGTTGGA CAATAGCAGG GTCTTGATAT 1140

ACTTGAGTGC CAGAAATGTT TTGCGTTGGA TTTTTTACCT CAGCTTTTGC TTGTTCAGTA 1200

GTTGCTTTAA CTTTATTACT ATCTAAAACG TTTTTATTAG TAGTTTGATC TTGTGTCGTC 1260

TCAGCTGCTT GAACTTGATG TGCAGTGACT GCTGAACCTA CAAGCGTTAA TGCAACCATT 1320

GAgGTAGTTT GTAATTGAAT TTTTTCGCCA TTCTATTTAT TACTCCyAAC ATTTATTAAT 1380

TATtACTAAC ATTATAGTAC CTGTnTTATA TACCTGTGCG TA 1422

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6076 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

ACGCGTTGGT TATTTCAATC ATAATATTAC TCTGCAAATA CACAGCCCTG TAACCGAGTA 60

AATGGATAGA GATTTGAACA AATGAAAACA ATCAACTAAT GGAAAGGATA AAATATTATG 120

CACAACAATA ATGAATTCAA CAAAAAACTG AAAGATTTTA TAGGTAGCGA TAAACGGATG 180

GCTTTAGTAA AGGGTTATGT TAACGAGTAT AAATTAACAA CTGTTTTAAG AGCTTTAAAT 240

GTAGATAATC GAATTATTCC TAAAAATATA ACTCAAAACA CAATCTTCAA ATTGAGTAAT 360

TTAACCTTAG AGGTTAACCT CTATGAAAGA AACACAATTT ATCACGGAGA CTTTGCTATT 420

TACTATCCTG TAGAATCTGC TCTAATAATA GAAACAGATA CTCCTAGGCT AATTAATCAT 480

ATAAATAACA ACCCAGTCCA AAAAATATTT ATAATAACAA CAAATGACTG GAGCTTTAAT 540

ACACTTGaAT TAGAAAAAAT AGTAGACGAA ACTATAATTT ATGATTTAAA ACAAGAAGAT 600

CCTAAACAAT ATGAAATTTT ATATAAAAAT AAACACGGAA AATTGCCTTA TTGATGAATT 660

AAAACGCAAA CTTAGAACAC CTTACCCCTT TTCCGTCCTT ATTGTAATTT TCCAACTACT 720

CAAATTAAAA ACCACCCGTG CAAACAGGTG GTTTTATTAT ATATAATTAT TCCCACTCAA 780

TTGTGCTTGG TGGTTTTGAT GTAATGTCAT AGACTACGCG GTTGACGTGA TCTACTTCGT 840

TTACGATACG ACTAGAAATC TTTTGTAAGA CTTCCCAATC GATGCGTGCG AAGTCACTTG 900

TCATACCGTC GATAGATGTT ACTGCACGAA TACCTACTGT GTGATCATAC GTACGGTAGT 960

CTCCCATAAC ACCTACTGAT TGAATGTTTG GTAACACTGT GAAGTATTGC CAAATTTCTC 1020

TTTCAAGACC TTCTTCTCTA ATCACTTGGC GTAAAATCGC GTCTGATTCT CTAACGATTT 1080

CTAGTTTATC TTCAGTAATT TCTCCAAGTA CACGAATACC AAGACCAGGT CCTGGGAATG 1140

GTTGTCTCCA TACTAAATGT TCTGGAATAC CTAACTCAAT ACCTAATTTA CGTACTTCAT 1200

CTTTAAACAA TGTATTGATT GGTTCGATTA ATTCGAATTC CATGTCTTCT GGTAATCCAC 1260

CAACATTGTG GTGTGATTTG ATTGTTTGTG CTGTTTTAGT ACCTGATTCG ATGACGTCTG 1320

TATATAGTGT TCCTTGCGCA AGGAAGTCTA CACCTTTCAG TTTTGATGCT TCATCATCAA 1380

ATACGTATAC AAATTCATTA CCAATGATTT TACGTTTTTG TTCAGGATCT GAAACACCTT 1440

TTAATTTATT CATAAAGCGA TCTTTCGCAT TAACACGAAT AATATTCATG TTGAAACCTT 1500

CACCGAATTG CTCCATAACC ATGTCGCCTT CACCTTTACG AAGtAAGCCA TGGTCTACAA 1560

AGATACATGT TAGTTGATCA CCTATTGCTT TATGCAATAG TACAGCTACA ACAGATGAAT 1620

CTACGCCGCC ACTCATCGCA CATAATACAC GACGGTCTCC TACGCGTTGA CGAATCTTTT 1680

CAATTTCGAT TTCGATAAAG TTTTCCATTG TCCATTGACC TCTACAATCA CAAACACGAC 1740

GGACAAAATT ATTTAATAAA TCATTACCAT ATTCTGTATG ACGTACTTCT GGATGGAATT 1800

GAACACCATA AATGCGACGT TTCTTATCTT CGATTGCTGC ATAGTCTGTG CTTGGGCTAT 1860

CAGCGATAAC TTCAAAGCCT TCTGGAATTT CAATAACTTT ATCAGAATGA CTCATCCAAA 1920

CAGTTTGTTC TGCTGGTAAG CCAGCGAATA ACTCATCTGA CTTCGCATTA ATGATTGCTT 1980

TACCGTATTC ACGTTCATTG GCACGTTCAA CTTTACCACC TAATAATTTA GTAGTTAATT 2040

TAAATGAACC TTCTTCATAA ACTGAATTTG GACCACCTGA TAAGATAATA CCTTTTGGAT 2160

TCATTTTCTT AATTTCTTCA ATTGAAATTT CATGATCGTG TAATTCACTA TAAACGCCCA 2220

TTTCACGAAT TCGGCGTGTA ATTAATTGGT TGTATTGGCT ACCAAAGTCT AAGACAAGGA 2280

TTAACTCTTG TTCTTTTGCC ATTTCCATAT TTGTCGTTCT CCTTTATCTT AATTAGAATG 2340

AGTAGTTCGG TGATTCTTTC GTAATTTGAA TATTATGTGG ATGGCTTTCT GCTAAACCAG 2400

CAGGACCCAT ACGTGTAAAT TGTGCTTCTT CGCGTAATTC TCTTAAATCG TGTGAACCAG 2460

TATAACCCAT ACCAGCACGC ACACCGCCCA TTAATTGGTA AATTGTATCT TGTAACGCAC 2520

CTTTATAAGC CGTACGTCCT TCGATACCTT CAGGAACAAA TTTCTTAGGC GCTTTGTCCT 2580

CTTGGAAGTA ACGGTCGTTT GAACCTTTTT CCATCGCACC TAAAGAGCCC ATACCACGGT 2640

ATACTTTATA TTGTCTACCT TGGAAAATTT CTGTTGCGCC TGGGCTTTCT TCAGTACCTG 2700

CTAATAAGCT ACCTAACATA ACCGCATGTC CACCAGCAGC TAATGCTTTA ATGATATCTC 2760

CTGAGAATTT AATACCACCA TCAGCAATGA TAGCTTTACC ATGTTTGCGT GCTTCAGTtG 2820

CACAATCATA AATTGCTGTA ATTTGTGGTA CACCAACACC TGCTACAACA CGCGTCGTAC 2880

AAATTGAACC TGGGCCAATA CCAACTTTAA CAATATCTGC ACCCGCTTCA AATAAATCTT 2940

TTGTTGCTTC TGCAGTTGCT ACGTTACCTG CTACTAATGT GATTTCTGGG TAAGTCTTCT 3000

TAATATGTTT CACTTGATCG ATAACACCTT TAGAGTGACC ATGTGCTGTA TCGATAACTA 3060

AGACATCCAC ACCTGCTTCG ACTAATTTTT GAGCACGAAT ATCAGTATCT TTTGAAATAC 3120

CAATTGCTGC GGCTACAAGT AGACGACCAT GTTCATCTTT TGCTGCATTA GGGAATTCGA 3180

TAACTTTTTC AATATCTTTA ATAGTAATAA GACCTTCTAG ACGTCCGTCT TTAACTAATG 3240

GTAACTTTTC AATCTTATGT TTTTGGAGAA TTTTTTCTGC TTCTTCAAGT GTTGTATTCA 3300

CTGGAGCTGT AATTAAATTt TCTTGCGTCA TTACATCTAC AATTTTAATC GAGAAGTCTT 3360

CAATAAAACG TAAGTCACGG TTTGTTAAAA TACCTACTAA GTTGCGATCT TCTTTATTAT 3420

CAACAATTGG TACACCTGAA ATACGGTATT TACCCATTAA TGCTTCTGCT TCATAAACGC 3480

TTTCTTCTGG CGTTAAGAAA AATGGGTTTG AAATGACACC ATTTTCTGAG CGTTTTACTT 3540

TTTGAACTTC GTCCGCTTGT TCTTCAACGC CCATATTTTT ATGAATAACA CCTAAACCAC 3600

CTTGACGAGC CATAGCAATC GCCATTTTAG ATTCAGTTAC AGTATCCATA CCAGCAGAAA 3660

TAACTGGAAT ATTTAATTTA ACTTTGTCTG ATAATTGTAC GCTTAAATCA ACGTCTTTCG 3720

GTAAAATATC AGATTGTGCT GGAATTAATA ACACATCATC AAACGTTAAT GATTCTTTTG 3780

CAAATTTACT TTCCCACATT AAAAACAGCC TCCATTTTTC AAATTAATTA GTTATATTAT 3840

GCAGAGATTG CGCCTAAAAC AATTCCGTTT TGAGTCAACC ATGCAAATTG TTCACCTAAA 3960

CCTTTAAATG CTTGTGGTAC AGCGCTTATA CCAGTACCTA AtCCTACTGA TACAGCGATA 4020

ATTAATAAAT TGTTTTGATT TTTAAAATCG ATATGTCCTA ATATACTAAC ACCATATGCC 4080

ATTACCATGC CAAACATAGC TATCATCGCA CCGCCTAACA CAGGTAGCGG TATGATATTT 4140

GCTAATGCGC CAAGCTTAGG TATACAACCA CATATAAGTA ATAACACGAC CATGCCGTAT 4200

ATAACATTGT TTTTCTTAGC GCCGGATAAA GAAACAAGTC CTACATTTTG CGAATAGGCT 4260

GTATACGGAA ATGAATTGAA TATAGAACCT AAcACTATCG CTAGACCTTC CGCAGTATAA 4320

CCTTTACGAA AATCTTTTCT TTCTAACTTC TTACCGGTAA TTTCACTTAA CGCATGATAG 4380

ACACCTGTCG ACTCAATTAA ACTAACGATA GCTACAATAA AGAACACTAA CGTCGATGTC 4440

ACATCAAAGC TAAATCCAGA GAATCTAAAC GGCACTGGGA TGCCTAACCA ACCGGCATGA 4500

TTGACTTGAT TAATATCGAC CATCCCAAGT AAGCCAGCAC CTATCGTTCC TAAAACGAGT 4560

CCAATTAATA TGGCAATACT CTTAATAAAT CCAGTTGTGA ATCTTTGTAA AAGAAGAATA 4620

ATGATTAATG TCATTAAACC TAACAAAATG TTCTTAACAT CTCCATAGTC CTTTGCACCT 4680

TGACCTCCAG CTAAGTAATT CATTGCTACT GGCATTAAAT TGATACCAAT GATAGTAACA 4740

ACACTACCCG TTACTACTGG TGGGAAGAAT TTTACAAGAT GTGAAAAGAA AGGCGCGATG 4800

ATAATAACTA ATATCCCTGA TAAAAATAGC GAACCATAAA GTACATCTAT TCCTTTCGTT 4860

TGACCAATTA AAATCATGGG CGCAACAGCC GTGAATGTAC ATCCAAGAAC GATTGGTAAT 4920

CCTGTTCCTG TTACTTTATT GGCTTGTAAA AATGTGGCAA CCCCACACAT AAATATATCT 4980

ACTGTAACTA AGTAAGCGAT TTGTTCAGGT GTAAACTTCA AACTTGTACC AACAATGATT 5040

GGAACTAAGA TAGCACCTGC GTACATAGCT AAAAGATGTT GAACACTTAG GATTAAATTT 5100

TTCATTATTC TTCTCCCACC AATGTCACTT TGTTTCCTTC TAGTGAAGCA ACCTTGCAGA 5160

GAGAAGAAAC TGTTAAACCT GCTTCTTCTA AACGTTGATG CCCATTTTGG AAACTCTTTT 5220

CAACAACAAT ACCAATACCA GCTGTCTTAG CATTCGCTTG CTGTGCGATA TCGTATAATC 5280

CTAATGAAGC ATCACCATTT GCTAAAAAGT CATCGATGAT AAGTACAGTA TCTTCTTCTG 5340

ATAAAAACTC TTTTGAAACA ATGACCGTAC TTGTTTTATT TTTAGTAAAT GAATGAATAG 5400

ATGTTTCATA ATAACCATCC GTCAAAGTGC TAGGTTTTGC TTTTTTCGCA AATAAACATG 5460

GCACATCAAA ATGCAGTGCA GCCATGATTG CAGGTGCGAT ACCGGAAGCT TCAATGGTTA 5520

AGATTTTAGT AATCCCTTTA TCTTTAAATT GCTCGTAAAA AGTGCGACCA ACTTCATTCA 5580

TTAACTTTGC ATCAATTTGA TGATTTAAAA ATCCATCGAC TTTTAAAATC TTCTCATCAA 5640

ATTTGTGTGA AACATTTTGC TCTTAAATTG GTGCTAGATA CAAAAAAATC CCCAAACTAA 5760

ATAATAGTTT CAGGGTTTAT GAGTGAACGa ACATGCATAA CGAATTTGTC ATGCAATCAA 5820

TGTAAAAGAA GTTTCATCAA ATAAACTGTG ACCATCATAT AAAATGATAT AAATCACCCA 5880

CCATGGTTAC AATTTAATGG CTGAAGCTAC TCCTAGTATT GTGTTGTTAC TCATAGTCAT 5940

GTCGTTCAAG GCAACATGGT AGAAACTTCT AAAGCCATAT TCTTTAGATT ATATGAGTTT 6000

ATGTAAATTA TTTAACGATA ATAGCAAATT TTCGGCATTT TTTCAATAAC TGCTTAGGTA 6060

ATCTTTTAAT AGTTTT 6076

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

ACCGCCGATT GATAGCTTTA CTGCTGCGAT AAAACTGCCT TCAACAATTG GTGCATCAAC 60

TTTTAACACA CGATGATTAC CATCATACAT TTCAATTGCC ATATCTACAT TCATTTCTGA 120

AGATCCAATA TCGTAAAAAC ACAATGCATC ATCCTCTAAT TTAGTCAAAA CTTCTTGGAT 180

GATATCAAAT GAAGTTCCAA TTGAACCATC TGGTAATCCC CCGATTGGTA TAATATCAAC 240

GTCACCTGCC ATTTGCTTTA ACAAAGATTT TGTACCACTT GcAATTTCTT TACTGTGGCT 300

AACAAGTATA ATTTTAGGCA TTATCTTCAT CTCCAATCAA AGCGTTTAAA ATATAAACCA 360

TACTTTGAGC ACCTGGATCA ATATAACCTT TTGATTCTTC TCCAAAATAT GCAGCTCTAC 420

CTTTCGTTGC TACCATATCT TTTGTATTAT CTGCTAATTG CTGTAAATCA TTGAATGTTA 480

AAGTTTCACC ATTTTTAAGC TTCTCTGCTG CTCGCGCTAC TACATCATAC ATTGTCTTTT 540

CATTTAAAGT AACTTTACCA CGTGATTCAA CCGCTTCGGC AAATGCCTGA ATTAGTGTAA 600

TGAAATCTTG ATTATCCATA TCATCTTTGG TGACTGCAGA CATTTTAACA AAGCTAAAGC 660

CATACAGTGG TCCTGATGCA CCCCCAACAT TTGACATCAA TGCCATACCA GTTGATTTGA 720

ACAATGATTG CATTGAGCTA TCATCAAGTT TGTCTTTAAG ACTACTAAAC CCACGAACCA 780

TGTTAACCCC GTGGTCACCA TCACCAATTG CTCGATCTAA TTCAGTTAAT TCAGATTCAT 840

GTTTTTTAAA CGTTTCTTCT AAATTTAATA AACGTGCTTT CATATCATTC ACTTTCATTT 900

GTGCCACCTC ATAAATGTAT ATTTATTCAT ATTCACTTCT TATTTAAAGT ATTGACTTGT 960

ACCTTGCATG TCTAAAGATG TCATATAATC ACCAACAAAC CATTTAGCAA CATTAACCGT 1080

TCTTGCAGCT AAATTTTGTT GAATATATTT AGTTACGATA TTTAATTCAG ATAACGGCGT 1140

ACCACCCATA CCATTTACCA TTAATATGAC ATCATTGGCA GTAACTTCTT TATACAATTC 1200

GTCTAACAAT GTTCCAACAA TATGATCAAT ATCCTTTACT TCTTCCCTAT GAATACCTTT 1260

TTCACCATGT ATACCAATAC CGATTTCCAT TTTGTCGTCT TCAATATCAA AGCCATATTT 1320

TCCAGTAGTT GGAACAAGCG GTGGCTCAAT TGCCATACCA ATACTTTTAA TTTCAGGTAA 1380

CAACGCTTCT ACACGCGATT TTATCTCTGT TAATGAATAA CCTTTTTCAG CAAGATAACC 1440

GGCAAGCTTA TGAACAAACA CTGTTCCTGC AACACCACGA CGTTGTACTT CGTTTGTCAC 1500

AGCAATGTCG TCACGAACAA TAACAGTTTG AACATTTATA CCTTCCATTT CTGCAAGCTC 1560

TTGTGCCATT TCGAAATTCA TCACGTCACC TGCATAGTTT TTTACAACTA GTAATACACC 1620

ATCACCAGTA TCTACTGCTT TAATAGCTTC TAATATTTTA TCAGGTGTAG GTGATGTAAA 1680

TACTTCGCCA CAAACCGCTG CATCTAGCAT ACCTTCTGCA ACAAAACCGG CATGCGCAGG 1740

TTCATGTCCG CTTCCACCTC CAGAGACTAT TGCTACACCA TGTTCTTTCT TAGCTTTTTT 1800

TACAATAACT GTATTAGCAA TCAGATCTAA CTCTGGGTGC GCAATTAACA ATCCTTCAAG 1860

CATATCAGTT AAAAATGTTT CTTTTTTATT GATTAACTTT TTCATCATGT TGTACCTCCT 1920

TGGTATTATC AGTCATAGTA TAAAACAGAA TAAATGAATG CGCTATCATA AAGAATTAAC 1980

CTGATACCGT TATCAAATAT ATTTTTGATA AGATCCTCTT GATAACTTAA TGGTTCATTA 2040

TTGAAAAAAT AAATAGTCTT GAGTGGCTCA TTAAATAAAA AATGCTATGA AAAGCCTTAT 2100

AATAAAGTGC CTTTCATAGC aATAAGTTGT GTCCATTGAC ACTATACATT TTTCGTTTTG 2160

TACATTAAAT ATAAGAAATA CGGTGCACCA ATAATTGCTA CGACAATACC TGCTGGAACC 2220

CCACCTGGTT GTAATACAAT TTTGCCAATT GTATCAGCTA TAACAAGTAA ACATGCCCCT 2280

ACTAAAATGG CAATTGGTAA AAACAACTGG TGACGTGGTC CAACGATACG TTTGGCAATA 2340

TGCGGACCCA TTAATCCGAT AAACGAAATT GAACCTGCTA cTGCTACAGC AGCAGATGAT 2400

AACATCACTG CGATAAAGAA TAATATTAAA CGTTCTCTGC TTAACCTTAC ACCTAGACCT 2460

CGTGCAATAT TATCACCCGT ATGAATAATA TTTAGTGTAT TCGATTTAAA TAGTAAGTAA 2520

GGAATAATAA TCAACACCCA CGGTAAAAAT GCAATGACAA ATGGCCATTC GTCACCCCAA 2580

ATATTACCTG CAAACCAAGC AGCGATGAAA TCAGATTGCT TATCATCAAA TTTTGACATA 2640

ATTGTAATTG AGCCACCATA TAATGCTGTT TGTAAACCTA CACCTATTAA TACCATACTC 2700

GCAGGTGTAA CACCTTCATT TTTATTAAAA CTGaAAATAA AAATAATCaA TGCAGTGgTG 2760

CCAATTGCAA TAAATAATGC GATTGCAAAT CCGCCACtGC GTTAATACCT AATATACCTG 2880

GTTCAGCTAT TGGATTTTTT GTGACACTTT GCACTATTGC ACCACTAATA CTAAgCtGCG 2940

CCAGCCAAAA TAGTAATCAT CATCCGAGGT AACCTGAAAT CTAATAAGAT TAACTCATCA 3000

ATGGCATCAC CTTGTCCAAT TAAAGTTTTG AAAAATCTTT CAACAGGTAT GTTGTATTCA 3060

CCTGAGGTAA TACTCCAAGT ACAACCTAGA AATAGTAGAA TGCTAAAAAC AGCCAGTGCT 3120

ATCAATTGTC TGCGTTTATT ATTTGAACTA ATCATATTGA GCGTCCTCCT TTTTTAACTA 3180

AATATAAAAA GTAAGGAACA CCGATAAATG AAATGATTGC ACCAACAGGC GCTTCTCCTA 3240

AATATCGTGC TATCACATCG GCAACAAGCA CGAGTATCCC ACCTAACAAG GCTGTTAATG 3300

GTAGAATTTT AGCATAATCA GTTCCAATTA AAAATCTTGC TATATGAGGT ACCATCAAAC 3360

CTACAAATGC AACTTGTCCA GCGATAGCAA CTGCAATACC TGCTAGAATC ATAGCAATAA 3420

TTAAACATAT GCCTCTGATC ATTGTTACAT TTTGACCTAA ACCTTTAGCT AATGATTCAC 3480

CAAGATTTAA AATGGTAAGT TGTTTACTAA TTGTTAATAT AATGAATAAC GCAATACCAA 3540

TTAATGGAAT TGCCCACTTA AGGTGTGACC ATGTTGTGCC TGAAACGCCT CCAGCAGTCC 3600

AAAATGTTAC TGTTTGATTT AGTCTAAAAG CTAATGCAAT ACCTTGACTT AGCGCTGTTA 3660

ACATAGCACT TACTGCTGCA CCCGCTAAAA TAATACGCAT CGGATTAAAT CCATCACGTC 3720

TAGATCGGCC TATCATTAAT ACAATAGCAC CTCCTAGAAT AGCACCTAAA AATCCAGCAA 3780

ACATCAATAT TAAAAATGAA GTGTTTGGTA AAACTGCATA TGTTAATGCT AAAGCAAATG 3840

AAGCACCTGA ATTTAAACCT ATGAGCGCCG GATCAGCAAG ACCATTACGA GTAACACCTT 3900

GTATAATCGC ACCAGAAACT GCAAGCGCCA TACCTACAAT TACTGCTGCT ATATTTCTGG 3960

GAATCCTAAT CTCATTGATG ATGTTTTGCT GTTGATTGCT AGGATTATAA TTAAAAATAG 4020

CCTCTATAAT TGTAGAGGCT TGAATTTTGG CGTCACCTAT TAATGTAGAA ATAAATAGTG 4080

TGATTAGTAG TATCATACTT AAACCTATAA TATAGGATAA AAACTTCAAT GGCGTTGGGT 4140

TCTCTCTATT TGTCATGTTA ATTGTCCTTT TTATCATATT AACTTACTTA ATTAAGAATA 4200

AGCTCTGCGA CATAAGTCAT AAGTTACCAG TAAAGGTTTT CCAGTTTTAG GATCTTTACT 4260

TAAAACAACA TCAATATTAA AAACTTTTTC TAATATTTCC TGTGTTAATA CGTCTTCTGT 4320

TGAACCTGTA GCGATGATAT CCCCTTCTTT CATCGCAATA AGATGATCTG AGAAACGAAT 4380

CGCTTGGTTG ATATCATGAA GAACCATGAC AATTGTACAA CCTTGTTCCT GATTTAGCTT 4440

CTGAACTAAT TCTAGTATTT CTAATTGATG ACAGATATCT AAATATGTTG TTGGTTCGTC 4500

TAAAAAGATA ATATCAGTTC TTTGTGCTAA TGCCATTGCA ATCCAAACAC GTTGTCTTTG 4560

TGCCCAATCA ATtTCTTTCT TAtCCTCAGC AgTTAATCTA CCAAATCCTT TTTGATGTGG 4680

AAAACGACCA TATGAAACTA ATTCCCCAAC AGTTAAGCCA TCTGCTACTT CaGGTGaTTG 4740

aGGTAAAaTG GCtATTTTTt TGcAATCyCy TTCGTAGATt GTGtATGAAT ATTTTCACcA 4800

TCTAAAAATA CTTCGCCTTC TTTAACTGCC AATAAACGTG ACAATGCCTT TAGCAAAGTA 4860

GATTTCCCGC AGCCGTTAGG ACCAATGATT GACGTCACTT TGCCATCTGG TATTTCAACA 4920

TCTAATTTAT TTATAATCGT GTTATCCCCG TAACCAATTT TAACTTGTTG TCCATGCAAA 4980

CGATTCATAA TTTCCCTACT TTCAATAAAA TTCTTTCTGT TTATAAAAAA TAATTTCTAT 5040

TTTTAAATTA TCAATTTTCA AAGACATCCC AATTGATAAT GATTATCATG AACATCATTA 5100

TAACATTTTT CAATCTTATT GACTAACATT ACTTTTTAAA TTGGATAGCT CGATTTGTCA 5160

TGTCTTGTAT ATTACTTTTA TAAAATAAAA AACGCCCACA GATAAGTCTT CATAGTTCAA 5220

AAACTTGTCC GTGGACTTCT ATTTAAGTAT GTGTGCTCAT ACCATTTATT TATTCATCTG 5280

CAAGAAAGCC ATTACCATAG ACATCTCTTA CATCATGAAT TACGAGGAAT GCATCTTTAT 5340

CGATTTGTTT AATTAATCGC TTTGCTTTTG AAACTTGTGT TTTAGAAATA ACAACGTATA 5400

AGACATCTTT TTCTTCACGC GTATAATAGC CATGTCCGTT TAAAATGGTT AAACCTCTTC 5460

CAATTTGCTC GTCTATTGCT TTGGCAAGTT TGTCGGGATT AGTTGAAATA ATCGTCATAG 5520

CTTTTTTAGT GTTTAAACCT TCTATGACAT ATTCCATCAC TTTTGTTCCT ATATAAAGTG 5580

ATATTACTGT TACTAATACT TTATCAAGTG GAATAACTGT AAGTGAAATT GCAACAACGA 5640

TCATATCGAA GAAAAGCAAA GCATATGGCG TGCTTACATC GAGGTATTTC GTTGCAATTC 5700

TCGCCAAAAT TGTTGTACCT GCTGTTGTAC CGCCTGCAAG GATAATTACT CCGATTCCTA 5760

GTCCAACGCT TACACCACCA AAAATGGCAT TCACAATGCT GTTTCCAGTT TCTACTTGCC 5820

ATGATTCTGT TAAACTCAAA AATATTGAAA TAAGAATTGT TACAAGAATA GTTAAGTACA 5880

TACTTCTCTT ACTCAAAAAt TTATAAcCTA TGGCAATCAA TACTGCGTTG ACCAAGAAGT 5940

TAGTGATGGC TGGTGAAATA TGAAACGCAT AATATAAAAT AATTGCTAAA CCTGTAACCC 6000

CGCCTTCACC TAAGTTACCA GAAATAATAA ATGCATTTAC ACCTGCAGCA AAGATAAATG 6060

AACCTAAGAC AACTAGTATT AAATCTTTAA CCGTTTTATT CACGAAACCA TCCCCTTTAT 6120

ATATTTATTA GACTAT 6136

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

GATATCGTAs CTACTGAAAA GTCATCACCA CCATGGAATG ATTTCTTTAA ACGTTTTAGC 60

TTCTATGCAA TTGCAATTCA ATACTTTGTT GTACAATTTA TCATTACATT ATTCTTAATT 120

TGGTTACCGA CGTATTTAAC AGAAGTATTC CACGTTAACT TTAAAGAAAT GAGCATTAGT 180

TCATTACCTT GGTTATTAAT GTTCTTCTTA ATCTTATCAG CAGGTGCAAT TTCTGACCGT 240

GTATTAGGAT TAGGTCGTTC AAAATTCGTA GCTAGAGGTG TAATTGCAAT TGCAGGATTT 300

ATTGTGTTTG CAGTTTCAAT TATCTTTGCT GTACGCACAG GAAATTTATA TGTAAGTATT 360

TTCTGGTTAT CACTAGGTCT TGGTGGTATC GGTATTTCAA TGGGTATGAG TTGGGCTGCA 420

GCAACTGACT TAGGACGTAA CTTCTCTGGT ACAGTATCAG GGTGGATGAA CTTATGGGGT 480

AATATAGGTG CATTAATCAG TCCGCTATTA GCAGGTCTAT TCGTAGAACA TTTGGGTTGG 540

ACAATGACAT TCCAATTGTT AATCGTTCCA GCAGTAATCG CTGTGATTAT GTGGTTCTAT 600

GTGAAACCAG ATCAACCTTT AATTGTTAGT GATGATAAAG CAATAGAAAA ATAATTTAAA 660

CAAGCAGTAA GCTTTCACAT AGTTGGGGCT TATTGCTTTT TTTGCGTTGA AATTGAAACT 720

TTTTAAAACA GATATGGTTT AAGATGAAAA TGAAGTTATT GAAATGATAT ATGTAAAGAA 780

ATAAGGTTTT AAAACATTAG TCAGGTAACG CTTGTaAAAG TACATATAAA TTTTAACTAG 840

CGCAAAGGTG GGCGACCAAA GtTcAACGAT GTTAAATAAC aTTAGrAATT AATTTTAATT 900

GGACTTTAAA AGTTTTTAAA TTTAGATAAT TGAGCATAAG GTGTTATAAT GACATATGTT 960

GCGTAATTAA AATTTATAGC AACAAATTCA TTTTAACTAT GCTAATAAAA AGATTATGGA 1020

AATATTTTGA CAAGGAAAGG AGAAGTCGAA ATGACATCTT TTTGACATCA CTCATAAAAA 1080

TCAATCGACT TAACTTAGAC TTTTATAAAG GTGTAAGACA GGGACTGTTA ATGATTATTC 1140

CTGCAATAAT CGGTTACTTA TGTGGTAATT TCCAATTTGG ATTATTAGTT GCAACCGGAA 1200

CACTAGCCCA TATTTATGTT TTTAAAGGTC CGTCGCGATC TAAGCTGCGA ACTGTAATAA 1260

TTTGTAATTT AGCGTTTGCA ATATGTATGA TGCTTGGTAC GCTAACAGCC AAAACGCCAC 1320

TCGTTTTTGG AATGACATTA TTAATTGTTA CGGTTATACC ATTTTATATA TTTACTGCCT 1380

TAAAAATAGC TGGACCGTCA TCGACATTCT TCATTGTGAC ATTCAGTCTA CCCATTAACT 1440

TACCTATAGC TCCCGAAGAA GCATTATATA GAGGCTTTGC GATTTTAGTA GGCGGTATAC 1500

TTGCCACTAT GATGGTGTTA ATCACGATCG TATTTTCTAA AAACAAAGCT GAAGAACAAG 1560

CAATTCAAAA TGATTTTAAA CTCATATCTA AGTTGTTACA CACTTATAAT GATAAATCTG 1620

TCACTTCTAC TTCAAGTAAC GATAAATTAA GTAGACGTTT CCAAAAATTA TTATTATTAC 1740

ACACATCTGC CCAAGGGATT TATTCTGAAC TGTTAGAGTT GAACGCTAAA CAAATTCGAC 1800

CATTGCCAGA TGAGTTAATT GAAATGATGG ATCATATCAT TGCACAACTA GATAATAGTG 1860

AGGAAAATGT AAGATATTGG CGAAAAGAAG TGACAGTAAC AGAGGAATTT CAAAATTTAT 1920

TCAACCATAT ATTGAAAATT GATGAAATGG TGCATGCAAA TGAAGCGCGT ATTGCGTATG 1980

AAGCAGACAT GCGAAAACCT TTATATAGTA AACGCATTTA TCaAAATTTA ACaTTAGACT 2040

CtATkGTTTT TAGAAATACA TTGAGATATA CAGCGATTAT GATGATAGCG ATATTTATTG 2100

CGTTAATGTT TGATTTTGAA AAAGCATACT GGATACCGTT ATCTGCACAT ACAATATTAC 2160

TAGGAACATC AACTATACAT GCAATCGAGA GAGGTATGGC ACGAGGTTTA GGTACTATTT 2220

TAGGTGTGTT AGTACTTTCA GTCATATTGT TGTTTTCAAT ACCAACACCT GTTGCAGTAA 2280

TTTTAATGGG CATTGCAGCA TTGTTTACTG AAGCATTGGT GGGAGCAAAT TATGCGATTG 2340

CAGTAGTTTT TATTACAATA CAAGTTATTT TAATGAACGG ATTAGCATCA CAGAATTTAA 2400

CAATTAACAT TGCGTTTCCA AGAGTTATTG ACGTTGCAAT GGGTATTGTG ATTGCAATCA 2460

TAGGTTTATT TGTCCTTGGA CAACGTACCG CATCCGCATT GCTTCCTAAT GTAATGGCTG 2520

AAGTTGTTCG TAAAGAAGCA ACGCTCTTTC ATTATTTATT TTCTGAAAAT CAATAT 2576

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 668 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

CAAGCACATT ACGATGGTCT AATACTTTGC TAATAATTTC TTCTTGTCCT GGTCGAAACG 60

TTTCATACCC AAAGTAATGC GATAATGTTT GTTGCATCAT AAATTGACCC CTTATTGTTG 120

TTCTTTAATT TCTTCTAACT CACTCCATCT TGTGATGTCT AAATCATATT GAATTTCAAG 180

TTGTTCTTTT TCTTCGTTTA ATTCTTTAAT TTTCCCATAA TCTGCACTTG CCTCAATCAT 240

GAGCACATCA ATTTCTTCCA TTCTTACTTC CGCTTGTTCT ATGCGTTTCA TCAATTGTTC 300

ATATTCTAAT TTTTCTTTAT ATGATAAACC ATTTTTCTTA CGTACAGTTG TAGAAGATTT 360

AGATTGTTGC TTCAATGTGG ATTTATTTTT ATCTAATGAT TTTTTATAAC TTTCATAATC 420

TTCAAAAGTT CCGATAATCT TTTCCATCTG ACCATCATGA ATAAACCAAT ATGACTGTGC 480

AATATAATCT TCAAGTATTG TTAAAGTCTC AGTATCTAAA TCATTTGTCG GTTCATCTAA 600

CAACAGAACA TTTGGCTGGT GTACGAGTAG ACGTAATAAA TACAAACGCT TTTGCTCTCC 660

ACCAGATA 668

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

CATCAGTTTA TTTTGAAAGG CAATGCGATC ATTTCATGTA TTTATGTTGT TTGAAACATC 60

GTTAGATAAC AATAGTGATA TTGCACATTT TAAGCTGAAG ATGGAAAAAT ATTCGATAAT 120

CAAATAAACA ATGAATTTTA GAAGGTACAA TGACGTTCAC TAATTTAAAT ATAGCTGAAT 180

GTGTTGGTGA GTGATGTTCA CTATAGATTT ATATTAATAT ACAAAGACAA AGGTTGTTAA 240

TTTTTATTAA GCGTTAGGTT GAATGTATGA GAATTTTAGA TTTATAATAG AAGATAGAAA 300

CGAAAATTTT TCTTAAAAGC AGTAATGTTG ACTCAAAATA AGCTATAATA ATGACACTTA 360

TTTAATTGAT TAACATTTGC TAATAAATAT CAATATAGAA TATAACTTTC CAATAATGAC 420

TGAGAAAATC GAAATGTCAG TCTCGAATCA TATAATTAGA AAATTGATTA TTTTCTGTCA 480

ATTTAGGGTT GAACTATACA TATGATATTG TTAGAATATT TTTTAACATT ATATTTTATT 540

GCTTTAAAGT GGAATATACT TGAAATAATT AGTAGAGGTG AGTAAGGATG AGTAATAAAT 600

TAGAATCATA CAGAAGTGAG ATTGTATCAC TGAATCATCA AATTTTAGAC TTATTATCTA 660

AACGTGGTGA ACTAGCACAA AAAATTGGGG AAGAAAAATT AAAACAAGGT ACACGTATTT 720

ATGATCCACA ACGTGAAAAA GAAATGCTTA ACGACTTAAT CGATAGTAAC AAAGGACCAT 780

TCAACGATAA TACTATTAAG CAATTATTTA AAGAAATTTT CAAAGCCTCT ACAGATTTAC 840

AAAAATCTGA AAATGAAAAA CATTTATATG TATCACGTAA GTTGAAACCT GAAGATACGA 900

TTGTAACATT TGATAATGGG GGCATTATAG GAGACGGCAA TAAATCATTT GTATTTGGGC 960

CATGTTCAGT TGAATCATTT GAACAAGTTG AAGCTGTTGC TAAAAACTTA CATGCTAAAG 1020

GTGAAAAATT TATTCGTGGC GGTGCATTTA AACCACGTAC ATCACCATAT GATTTCCAAG 1080

GCCTAGGTGT TGAAGGACTT AAAATACTTA AACAGATTAA AGATAAATAT GATTTAAATG 1140

TTGTCAGCGA AATCGTAAAT CCAAATGATT TTGAAGTGGC TGATGAGTAT TTAGACGTAT 1200

AAAAGCCTAT TCTATTAAAA CGTGGTTTAT CTGCTACAAT CGAAGAGTTT GTTTATGCAG 1320

CTGAATACAT TGCTTCACAA GGTAATCAAA ACATTATTTT ATGTGAACGT GGAATCCGAA 1380

CTTATGAAAA GGCGACACGT AACACTTTAG ATATTTCAGC AGTACCAATT TTAAAACAAG 1440

GTACACACTT ACCAGTCATG GTAGATGTTA CGCATAGTAC AGGTCGTAAA GATATCATGT 1500

TACCAACTGC GAArsAgCAT TAGCAGTTGG TGCTGATGGA GTTATGGCTG AGGTGCATCC 1560

AGATCCATCT GTTGCACTTA GTGATGCGGG TCAACAAATG GATTTAGATG AATTCCAAGC 1620

ATTTTATGAT GAATTAAAGC CTTTAGCTGA TTTATATAAC GCTAAAAAGT TAAAATAATA 1680

TTCCAAGGAA ACTATAGACT ACTTAACTAA TATGTCATGT TGAAGTAGAA TATTATCTTT 1740

GAATCGACAA TTTTAAACTT ACAGCCATTC TAAGAGTATA TTACTTTTAG AGTGGCTATT 1800

ATTTTTTGTA TAGAAATAAA GGTATACTGC ACTTAACGAT TGTTATAATA CTTCGACACT 1860

TGTTCAATTT CACAATTATT AAAGATTATG ACTGATAGCA GTAATTAAAA TTATAACTAT 1920

GAATTATCTG TAAAATATAA TAGATTCACA CATTTGTTGC TGAAATGTGA ACATTTTTCA 1980

ACAAATGCAA TTGATATTTG AAAAGGCTTT CTCAAAACAT TACAATTAAA AATGAAAAAA 2040

GTTTATATAA AATTAAAATA TATCGTTCGT TATCATTTAG CGTTTGTTTT TATTTCAAGC 2100

TTTTCGCTAA ATTTTTCCAA ACAAAAATAT GTTACTGTAA ATTAAAATAT GGTAAACTAT 2160

GAAAATGAAA TGAAAACATG TTATTATAAT GAATAAAACG TTTACAAGGA GGAAATTATG 2220

ACAGTTACTA TATATGATGT AGCAAGAGAA GCGCGTGTCT CTATGGCCAC AGTGTCGCGT 2280

GTTGTTAATG GGAACCAAAA TGTTAAAGCA GAAACTAAAA ATAAAGTTAA CGAAGTCATT 2340

AAGCGTTTGA ATTATCGTCC AAATGCTGTT GCTAGAGGTT TAGCTAGTAA AAAGACAACA 2400

ACAGTAGGTG TGATCATTCC AGATATATCT AATATCTATT ATTCACAACT TGCTCGTGGA 2460

CTTGAAGATA TTGCAACAAT GTATAAATAT CACTCAATTA TTTCAAATTC AGATAACGAT 2520

CCTGAAAAGG AAAAAGAAAT TTTTAATAAC TTATTAAGTA AACAGGTTGA TGGTATTATT 2580

TTCCTTGGTG GTACAATTAC TGAAGAAATG AAAGAATTGA TAAATCAATC ATCTGTACCT 2640

GTAGTAGTAT CAGGAACAAA TGGTAAGGAT GCACATATAG CATCAGTTAA TATTGATTTT 2700

ACTGAAGCTG CGAAAGAAAT TACGGGAGAA TTAATTGAAA AAGGCGCTAA ATCATTTGCT 2760

TTAGTAGGTG GAGAACATTC TAAAAAAGCT CAAGAAGATG TTTTAGAAGG TTTAACTGAA 2820

GTGTTAAATA AAAATGGCCT TCAATTAGGT GATACATTGA ATTGTTCTGG TGCTGAAAGT 2880

TATAAAGAAG GCGTAAAAGC TTTTGCCAAA ATGAAAGGCA ATTTGCCAGA TGCCATTTTA 2940

TGTATCAGCG ACGAAGAAGC AATTGGTATT ATGCATAGTG CAATGGATGC TGGTATTAAA 3000

CCACAACTTT CTAGTGTTAT TCAACCATTA TATGATATCG GTGCAGTAGG GATGCGCTTA 3120

TTAACAAAAT ATATGAACGA TGAAAAGATA GAAGAACCAA ATGTAGTTTT ACCTCACAGA 3180

ATTGAATACC GAGGAACTAC AAAATAAATT CACAAAATTA GGCATTCATC TAACGACCCA 3240

AATTATATGG GTGTTGGAAG AATGCCTTTT ATTTATCTTT TAAAATCGTT GCAGATTAGG 3300

TTACTTATTG ACGAGTAGAT TCGTACCAAC TCGCTATATG TAAAGCTAAT TTTTTATTTT 3360

TTTCACTAAT TTCTTTTGTG CGGGGGACAT AGGTATAATC ATTTAAACGA TCTTCCCATC 3420

TTTTAGGTAA TAATTCAGAT GAATAATGTT TCCATTTATT AATCCATTCT AACGGTAAAT 3480

AACCACTTTG AATTGGTTGA TCAATTAAAC TTAAGAATAC ATGACTCCAT GCACGTGGTA 3540

CGACTCTCCA AATATTGTAG CCTCCGCCAC CAAACATAAT TACCTTTCCA TTCGTATAAG 3600

AATCAGCTAA ATATTTTACA AAATATGGAA TTTCATATAA TGAATGTAAC GTACAATTTA 3660

GATGAGTTAG TGGATCACGA TAATGTATAT CGACACCATT TACGCTTAGA ATAATATCAG 3720

GTTTAAAACT CTTTACGACA GGCTCAACTG TTAATTTAAA ACACTCCAAA AATGATGCAT 3780

CTTCTGTATA CGGTTCAAGT GGGACATTTA CAGTGTGTCC ATAGCCGATA TCTTCACCGC 3840

GCTCAGTATA GTGACCAGAG CCTGGGAAAA GAAATTTTCC GGTTTCATGG ATAGAATAAG 3900

TAGTAACATG GTTATCGGCA TAGAAACTCC ATTGTGTACC ATCTCCATGA TGTGCATCGG 3960

TATCTATGAT TAAAACGCGT TGATTGTATT CTTTAGCTAA GTATTGTGCG GTAATTGCAA 4020

TATCATTGTA TATACAAAAA CCACTTGCTC GACCAGGTTG AGCGTGATGC AAACCACCAC 4080

CTAAGTGACA ACCATTTAAT ACTTTGCCTG ACATAATAAG ATCTGCTAAA GTTAAAGCGC 4140

CTCCAACAAT TGTGGCACTA TGGCGGTGCA TATGCTTAAA TTGACCATTC TCTTCATCAT 4200

TTAATCCATA TTTCTTAGCC TCATCTTCAC TGATAATGCC ATGTGAAGCA TGCTTAATAG 4260

CTTCGACGTA ATCATATTTA TGAATTAACA TTAATTCGTC ATCTGTTGCA ATTCTAGGTT 4320

GTACTATTTG TTCTGGAGAC AATAAATTTG CATTCAAAAG TAGCTCTGTT GTTAATTTTA 4380

AACGCATTTG ATTGAAGGGA TGTTGGTCAT GAAATCGATA TTGTAATAAC TTATCTGAAT 4440

AAACATATGC AGTTTTTGAT GAATGTTGTT GCATATAATC CCTCCGATAT TCCAAAAATT 4500

AAAAGAAAAA CCGATTCATA TAACGAATAT CATCAAACGC TTGTTGCTGT TCTAATGTAA 4560

TGTTTTTGCC AATTCTTGCC ATTAAACAAT TAGCTGGATG ACTTGTTATT TCTGGATCAT 4620

CTGTAGCGAA TATTTCAAGT CCACCAGTTG CCATTAACCG CTGCATTAAT TTTTTATAGT 4680

CAAATACATC TAACTTTGAA TTTTTTAAAT CCCAATGCCA GTAATATTCT GTAGTTATAA 4740

CGATATAATT CTCGAATTCT GGTGTAGAAA GGCTAAGTTG TATCAGCTTT TCTGCAAGTT 4800

TACCTGTAGA CCAGCGCTCA ATTTCATCAG GATAGTGGAA AGTGACATAA CCCACAATGA 4920

GTTGATCTTG GCGAGCAACA TAAATTCTAC CTTCTGGTAA TGTTGTAATT TCTAACAAAG 4980

CTTTATACTG ATCTTCAGCA TCTCTAAATG CGGTTAAATG CGCATCGAAA GTAAGCGCTT 5040

TCAAATCTtC GTGTGTTAAA GGACCTTCAA TAACAAATTG CTTGTCATGA ATGTAATAAT 5100

CTTCGGATTG ATACGTCTTT AAATGATTCA TATTTTCAAC TCCTCAATCG ACGTCGTGAT 5160

TGTATTAAAT TCATTATATA GAAaATTTAC AATAATTAAT ACTAGAAAAA GGATAAAAGT 5220

AAAAATTTTG AATAATTAGA AATGTTATGT ATAATATTGA GAAAGAAAGC GTTTTCACAT 5280

AACAAAGGGG GAGTTTCAAA TGAAAGTCGA AGTTTATAAA GGAGCGCAAG GTAAACATAA 5340

CCTTAAAGAT TATGAAGAAA CATATAATAC TTTTGATTGG AAAGACGTAG AACAAGCATT 5400

TTCTTGGAGT GAAACTGGAA AAATGAACAT GGCATATGAA TGCATAGATC GCCATGTAGA 5460

TCAAGGATTA GGGGATAAAA TAGCGTTAAA TTACAAAGAT GAGCACAGAA AAGAATCGTA 5520

TACTTATAAA GATATGCAAC GGTTATCTAA TAAAGCAGCG AATGTTTTGT CTGAACATGC 5580

AGAAGTTGAC AAAGGTGACA GAGTATTTAT ATTTATGTCG CGTACACCTG AACTATATTT 5640

TGCGTTGTTA GGTGTTTTAA AAATTGGTGC AATTGTTGGG CCGTTATTTG AAGCATTTAT 5700

GGAAAAGGCA GTTGCGGATA GATTAGAGAA CAGTGAAGCT AAAGTGTTAA TTACTAATAA 5760

GGCATTGTTA CCTCGAGTAC CTGTAGATAA ATTACCAAAC TTGAAAAAAA TTGTTGTCGT 5820

AGATGAGGAT GTAGAAGACA ATTACATAGA CTTCATTAGT TTGATGGAAA CTGCTAGCGA 5880

TGAATTTGAC ATTGAATGGT TAAAGTCGGA TGATGGTTTG ATTTTACATT ATACATCAGG 5940

TTCTACTGGG cAACCTAAAG GtGTATTGCA TGTTCAACAA GCAATGTTAG TGCACTATAT 6000

TTCTGGAAAA TATGTATTAG ATTTACAAGA AGATGATGTT TATTGGTGTA CAGCAGATCC 6060

AGGTTGGGTT aCAGGAACAT CTTATGGTAT TTTTGCACCA TGGTTAAATG GCGCTACAAA 6120

TTGTATAGCT GGTGGTCGCT TTTCGCCAGA ACAGTGGTAT AGTATGATTG AAGATTTTAA 6180

AGTGACGATT TGGTATACGG CACCAACAGC TTTAAGAATG TTAATGAGTG CTGGTGACGA 6240

TATTGTTGAG AAATATGACT TGTCATCGTT ACGTTCGATT CTATCAGTAG GTGAGCCTTT 6300

AAATCCTGAA GTTATAAAAT GGGCGAAAAA AGTATACGGT TTAACGGTGT TAGATACTTG 6360

GTGGATGACA GAAACAGGTG GACATATGAT TGTTAACTAT CCAACGATGG ACGTcAAGCT 6420

TGGCTCAATG GGCAAACCAT TACCTGGTAT TCAAGCTGCA ATTATCGATG ATGCAGGGAA 6480

TGAATTACCA CCAAATCGAA TGGGCAACCT TGCTATAAAA AAAGGCTGGC CATCAATGAT 6540

GTATCGTATC TGGAAGAATC CAGAAAAATA TAAATCATAT TTTATTGGAG ACTGGTATGT 6600

TGATGTAATT ATGACAGCTG GTGAACGAGT TGGACCATTT GAGGTTGAGT CTAAATTGGT 6720

TGAACACGAA GCAGTTGCCG AAGCAGGAAT TATTGGTAAA CCTGATCCGG TTCGCGGTGA 6780

AATAATTAAG GCGTTTGTTG CACTGAGAAA AGGATATGAA CCAACAGACG AATTAAAAGA 6840

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CTGATGCATT CCATGAGTTA AATAAAAACG TTATGGTTGC ATTAAGAGAG CCTGCTTTAG 7740

GACCAACATT TGGTATCAAA GGTGGTGCGA CTGGTGGTGG TTATGCGCAA GTCTTACCTA 7800

TGGAAGATAT CAACTTACAT TTCAACGGAG ATTTCCATGC GATTACAACT GCAAATAATG 7860

CATTGTCTGC GTTTATCGAT AATCATATTC ACCAAGGTAA CGAATTAGGA ATCGATCAAA 7920

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CGTCTGAAAT TATGGCGATT TTATGTTTAA GTAGAAGTAT TAAAGACTTA AAAGATAAAA 8100

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AAGTGGAAGG TGCACTTGCA ATGATTTTAA AAGATGCAAT AAAACCAAAC TTAGTACAAT 8220

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GTAACTCAAT TTTAGCAACT GAAACAGCAC GTGATTTAGC TGATATCGTT GTAACGGAAG 8340

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AAAATCAAAA TAATAATGCA ACTACAACTC AGCCACCTAA GGATACAAAT CAAACACAAC 9660

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TCAATTTCCA GTTATTAGAT AAAAACAATG AAACGCAGTA CTATCACTTT TTCAGCATCA 9840

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GCACACAAGA ATTGAAAATT GTTTCTTCGA CTCAAATTGA TGATGGAGAA GAAACAAATT 10080

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TTGAACCAGC AACTGTCATT TTTACAAAAA CAGGACCAAT AATTGAATTA GGTTTAAAGA 10620

CAGCTTCAAC ATGGAAGAAA TTTGAAGTTT ATGAAGGTGA CAAAAAGTTA CCAGTCGAAT 10680

TAGTATCATA TGATTCTGAT AAAGATTATG CCTATATTCG TTTCCCAGTA TCTAATGGTA 10740

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CATTCTATAC AGCAACTTTA AATGGTCAAA AATATGTAGT GATGAAAACA AAGGATGACA 11220

GTTACTGGAA AGATTTAATT GTAGAAGGTA AACGTGTCAC TACTGTTTCT AAAGATCCTA 11280

AAAATAATTC TAGAACGCTG ATTTTCCCAT ATATACCTGA CAAAGCAGTT TACAATGCGA 11340

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CCGATATGTC GGATAATAAT CACTTCGATA AATATGATTT AAAAGAAATG GATACTCAAA 11700

TTGCCAAAGA TACTGATAGA AATGTGGATA AAGATGCCGA TAATAGCGTT GGTATGTCAT 11760

CTAATGTCGA TACTGATAAA GACTCTAATA AAAATAAAGA CAAAGTCATA CAGCTGAATC 11820

ATATTGCCGA TAAAAATAAT CATACTGGAA AAGCAGCAAA GCTTGACGTA GTGAAACAAA 11880

ATTATAATAA TACAGACAAA GTTACTGACA AAAAAACAAC TGAACATCTG CCGAGTGATA 11940

TTCATAAAAC TGTAGATAAA ACAGTGAAAA CAAAAGAAAA AGCCGGCACA CCATCGAAAG 12000

CATGGTGGGG CTTATATGCG TTATTAGGTA TGTTAGCTTT ATTCATTCCT AAATTCAGAA 12120

AAGAATCTAA ATAATTAnCT AAATATAGCA TATGTATGAT TAACTTTGTA GAC 12173

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

CAACATTAAT ATTGATATTA AATCTTCCTG GATAACGTGC TTGTTCGAGT GATAAGTATG 60

CACGCACTTG ACTTAACTCT TTATCTAAAG TAATCGTATG TTGCTTAGAG CCTTGTAAAT 120

TCGCTCTGAA AAAATAACTC AATTCTAATA GTAACTCTCG TGCCTTTTCG CTATTTATTC 180

TAACTAAAGC TGAGATCGTG TTAATTGAAT TGAAGAAAAA ATGTGGACTC ACTTGTGCCT 240

GTAATGACTT AATCTCAGCA TCTTTCAATA ACTTACTTTG CGTTTCGGCT TCACCAAGTT 300

CAATTTGGCT ACTAAAAATA TTTGCCAATC CTTCTGCAAG TTGACGTTCC ACAAAAGTTA 360

AATCATTAGG GTTTGTAAAA TACATCTTCA ATGTACCGAC GATAGAACCA TGCATCTCAA 420

GTGGTATCAC GATAGCTGCT CTAAGCGGGC AATTCGGATG ACTACAACCA ATCTCTTCTT 480

TAGTATGAAC TTCTTTCAAC TTTCCTGATT TCAATACATC TTTAGACAGA CTTGTTAATA 540

TTTCATTTGT TGGTATGTGA TGATCACTAC CTGCACCTAC ATGCGATAAG ATTTCATTTT 600

TGCTTGTAAT TGCTACGGCA GATACTTTCA TTAAATTTTT AATAATCATC GCAATTTGCT 660

GTGCCGATTC TCTATTCAAT CCTTCTTTAA AATACGGCAA TGTCTGGTTC ATCAATTGCA 720

GTACATCATG TGTTTGAACA GCCTTCATTT GCTCCTCTTG CTTTAATGTT GAAATGATAA 780

TAGACATAAA AATCGCCGTA CCAACGCTAT TAACAATAAT CATTGGTAGT GCAATTAATG 840

ATATGAGGTC AACCGCATAT GCTTTGTCGT GGGAAAATGT TAAAATGCTC AACATTTGAA 900

TCATTTCCAT AACAATTCCA ATCATGGCAC TTTTCGCAAT ACTCGGGTAA CGCTTGCGTC 960

TTTGAGCTTG TAAGCCAAAA TAACCAGCAA TTATACCAAT AAATATAGAT GAGATAAGAT 1020

AAACTTGTGC ATCCGCCCCA CCCATATACA CTCTGAAAAT ACCTGAAATA ACGCCAACAA 1080

ATAGACCTAC AAAAGGGCCA CCAACTAATC CTGCGACACC TATCGTTAAT ACACGTGTGT 1140

TAGCTAAAGA TACATCATCA TCTAAACGGA AGTACACACT TCCTGACAAA CTATGTTGAT 1200

GATCGATGAC GATACCAGTT AAATTAGACA TTAAGGCAAA CAAACTGAAA ATAATACATA 1260

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7972 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

TATAAATATT ATTTTATTAT CGTTTATCGC TATTTGTGTT ACATAATCAA AACCATAAAT 60

TCTTACTCAT TCAGATTTAC CCAATATTTT TACTTTTATA ATGTAATGCG TTTTATCCAA 120

GTTATTTTTT AAAAATAAAT ATTGAATTnG GGGCTGnTTT CATGTCATTA AGAGATGAAG 180

CATTGGAAAT GCACAAACGT AATCAAGGTA AATTAGAAGT TAAACCAAAT GTAAAAGTTA 240

CTAATAAAGA GGAATTAAGT TTAGCATACT CACCTGGCGT TGCTGAACCG TGTAAAGATA 300

TTTATGAAGA TAAAAGAAAA GTATATGATT ACACAATTAA AGGAAATACA GTTGCAGTTA 360

TTACTGATGG AACAGCGGTA TTAGGTTTAG GTAACATTGG ACCTGAAGCA AGTATTCCTG 420

TAATGGAAGG TAAAGCAGTA TTATTCAAAA GCTTCGCTGG TATCAATGGG GTGCCTATTG 480

CGTTAAATAC AACTGATACC GAAGAAaTCA TTAAAACAGT TAAGTTGTTA GAACCTAATT 540

ATGGTGGTAT TAATTTAGAG GATATTTCGG CACCACGTtG TTTTGAAATT GAAGAACGAT 600

TGAAAAAAGA AACTAATATT CCGGTATTCC ATGACGATCA ACATGGTACA GCAATTGTAA 660

CATTGGCAGG TTTGGTAAAT GCATTGAGAG TTGTTAACAA AGATATTGCT AAAATAAAAG 720

TTGTACTAAA TGGTGCTGGT GCAGCAGGAA TAGCCATTGT TAAATTACTA TACGCGTATG 780

GTGTAAGAAA TATGGTTATG TGTGACTCAA GAGGCGCAAT TTTTGAAGGA CGTTCATATG 840

GTATGAATCC TACGAAAGAT GTTGTAGCAA AATGGACAAA TAAAGATAAG ATTGAAGGGT 900

CTTTAGAAGA AGTCGTAAAA GACGCAGATG TATTTATCGG GGTTTCTGTA GCTAATGCGC 960

TGTCACAAGA TATGGTTAAG AGTATGGCAG ATAATCCAAT TATATTTGCA ATGGCTAATC 1020

CAAATCCTGA AATAATACCT GATGATGCCA AAGCGGCAGG TGCACGAGTT GTTGGTACAG 1080

GACGTTCAGA CTATCCTAAC CAAATTAATA ATGTATTAGC TTTCCCTGGT ATTTTTAGAG 1140

GTGCATTAGA GGTTGAAGCT ACACATATAA ATGAAGAAAT GAAAAAGGCA GCTGTAGAAG 1200

CGATTGCTGA TTTAATCGAT AGTTCTGAAT TAAATGAAGA CTACTGTATC CCAGGACCGT 1260

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AAATAAATTT AAACCCGTTT TTAACTGGTC AAGTTCAGTT TAAGGCTCTA AATGGTTAGA 1560

ACAGAGGTTA TTTGGAGGTT TTCCTATGTT TAAAGATTTT TTTAATCGAA CAAAGAAAAA 1620

GAAATATCTT ACAGTACAAG ACTCTAAAAA TAATGATGTG CCTGCAGGTA TTATGACTAA 1680

GTGTCCAAAG TGTAAGAAAA TTATGTACAC AAAAGAATTA GCTGAAAATT TAAATGTGTG 1740

CTTTAATTGT GATCATCATA TTGCTTTAAC TGCGTATAAA CGTATAGAAG CAATTTCTGA 1800

TGAAGGATCA TTTACAGAAT TCGATAAGGG AATGACCTCT GCGAATCCAT TAGATTTTCC 1860

aAGTTATTTA GAAAAAATTG AAAAGGACCA ACAAAAGACA GGTCTTAAAG AAGCAGTTGT 1920

GACTGGTACA GCACAACTAG ATGGTATGAA ATTTGGCGTT GCTGTCATGG ATTCACGTTT 1980

TAGAATGGGA AGTATGGGAT CGGTTATCGG TGAAAAGATA TGTCGCATCA TTGATTACTG 2040

CACTGAGAAC CGTTTACCAT TTATTCTTTT CTCTGCAAGT GGTGGTGCAC GTATGCAAGA 2100

AGGTATTATT TCCTTGATGC AAATGGGTAA AACCAGTGTA TCTTTAAAAC GTCATTCTGA 2160

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TCGTCGAGTT ATTGAACAGA CAATAAACGA AAAATTGCCA GATGATTTCC AAACTGCAGA 2340

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ATTGTCTGAA ATTCTAAAAA TCCATCAAGA GGTGACTAAA TAATGTTAGA TTTTGAAAAA 2460

CCACTTTTTG AAATTCGAAA TAAAATTGAA TCTTTAAAAG AATCTCAAGA TAAAAATGAT 2520

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ATATATACAA ATCTAAAACC ATGGGATCGT GTGCAAATTG CGCGTTTGCA AGAAAGACCT 2640

ACGACCCTAG ATTaTATTCC ATATATCTTT GATTCGTTTA TGGAACTACA TGGTGATCGT 2700

AATTTTAGAG ATGATCCAGC AATGATTGGT GGTATTGGCT TTTTAAATGG TCGTGCTGTT 2760

ACAGTTaTTG GACAACAACG TGGAAAAGAT ACAAAAGATA ATATTTATCG AAATTTTGGT 2820

ATGGCGCATC CAGAAGGTTA TCGAAAAGCA TTACGTTTAA TGAAACAAGC TGAAAAATTC 2880

AATCGTCCTA TCTTTACATT TATAGATACA AAAGGTGCAT ATCCTGGTAA AGCTGCTGAA 2940

GAACGTGGAC AAAGTGAATC TATCGCAACA AATTTGATTG AGATGGCTTC ATTAAAAGTA 3000

CCAGTTATTG CGATTGTCAT TGGTGAAGGT GGCAGTGGAG GTGCTCTAGG TATTGGTATT 3060

GCCAATAAAG TATTGATGTT AGAGAATAGT ACTTACTCTG TTATATCTCC TGAAGGTGCA 3120

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AATTCAATAT TTAAAACGTT TACATCAATT CAATACATTA GTTTTGATGG AATGACATAT 3600

CAATTTGTGG TAATTTAGAG TTAAAGATAA ATCAGTTATA GAAAGGTATG TCGTCATGAA 3660

GAAAATTGCA GTTTTAACTA GTGGTGGAGA TTCACCTGGA ATGAATGCTG CCGTAAGAGC 3720

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TGATAATAGA GTGTCTGTGT TAGGTCACGT TCAACGTGGT GGTAGCCCAA CAGGTGCGGA 4440

TAGAGTTTTA GCATCACGTT TAGGTGGATA TGCGGTAGAC TTATTAATGC aAGGTGAAAC 4500

AGCTAAGGGT GTTGGAATTA AGAACAATAA AATTGTAGCA ACATCTTTTG ATGAAATTTT 4560

TGATGGTAAA GATCATAAAT TTGATTATAG TCTATATGAA CTTGCTAACA AGTTATCTAT 4620

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TCGTACGCAT AATATGAAAG ACGGTATCAT TGAACTTGAA CGTGGCAACG AAGTTATTGT 4920

TAGCATGAAT GAAGTTGAAG GAACACCTGA AAAGTTCTCA GTAACATATG aAAACTTAAT 4980

TAAAGATATT GACCATGCTA AAAAAGAAGT TAAATGTGAT ATTTTAAACT CTGGTGAGCT 5100

TAAAAACAAA AAAGGTGTTA ACTTACCTGG CGTAAGAGTA AGTTTACCTG GTATTACAGA 5160

AAAAGATGCT GAAGATATCC GTTTCGGTAT TAAAGAAAAT GTTGACTTCA TTGCAGCAAG 5220

TTTCGTACGT CGTCCTAGTG ATGTTTTAGA AATTCGTGAA ATTTTAGAAG AACAAAAAGC 5280

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AATTCAATAA AATGAATTTT CTGTGTTGGG TCCCTTCGTA TAATTTAATA AATACCACTA 7020

AACTAAATTA ACGAGGTGCC TTATGTATAA AATTTATAAC ATGACCCAAC TTACACTACC 7080

AATAGAAACC TCTGTTAGAA TTCCTCAAAA TGATATTTCG CGATATGTTA ATGAAATTGT 7140

TGAAACGATA CCTGATAGCG AATTCGATGA ATTCAGACAT CATCGTGGCG CAACATCCTA 7200

TCATCCAAAA ATGATGTTAA AAATCATCTT ATATGCATAT ACTCAATCTG TATTTTCTGG 7260

TCGTAGAATA GArAAATTAC TTCATGACAG TATTCGAATG ATGTGGTTAG CTCAAGATCA 7320

AACACCTTCT TATAAAACTA TTAATCGTTT TAGAGTGAAT CCTAATACTG ATGCGTTAAT 7380

TGAATCTTTA TTTATTCAGT TCCATAGTCA ATGTTTAAAG CAAAATCTTA TTGATAATAA 7440

TTCAATTTTT ATTGATGGTA CAAAAGTAGA AGCTAATGCC AATAGATATA CATTTGTGTG 7500

GAAGAAAAGT ATTCAAAATC ACGAATCGAA ATTGAACGAA AATTCAAAAA CATTATATCG 7560

TGACTTAGTT GAAGAAAAAA TAATACCAGA GATAAAAGAA GATGGAGATA GCGATTTAAC 7620

AATAGAAGAA ATAGATTTAA TTGGTAGTCA TTTAGATAAA GAAATCGAAG ATTTAAATCA 7680

TTCTATTGAG AACGAAGATT GTGCTCAAAT TAGAAAACAG ACCCGTAAAA AAATAACTGA 7740

GATTAAGAAG TTCAAAAAGA AATTTGATGA TTATTCCGAA AGAAAAAATA AATATGAAGA 7800

ACAAAAATCG ATTCTTAAAG ATAGAAATAG TTTTTCTAAA ACTGATCTGA TCATGATGCA 7860

ACTTTTATGA GAATGAAGGA AGACCATATG AAAAATGGCC AACTTAAGCC AGGATACAAT 7920

TTACAAATAG CGACAAATTC TCAAAAATGT TTTATCCTAT GACCTATTTC AA 7972

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

ATTTTTTAGT TAATTGTCTT TCTTAAAATA ATTTTAGCTT TCATTAAATT AAACAATTTT 60

ACAAGCTTGG AACACCAATC AAAATCCTAA GTTCTAAAAT GCAATATTAG TAGTCGTTGA 120

CTGAATGAAC ATATGCTTAT AATATTTTTT TGCAATGCTA GTCAAGTTGA TTTATGCTCA 180

CAAGGATATG CGATTTATAT TTTCTTACAA CAATGAAAAT GCCTGATACA ATGCGATCCT 240

AATTAAATTA TTGTTGTTTT AACCATTGTA CTATCGTCGG AATCATAAAT CCTGTTGGCC 360

CTTTTGGACC ATTATATGAA GCTTTATTAG TCGTTGCTGG ACCTGCAATA TCGAAATGAA 420

TGTGAGGTGT TTGACCACTA AAATGTGTTA CAAAACTTGC CGCAAATAGC GCTTTACCTT 480

GTCCATTCGT ATGGTTAACT AAATCAGCGA TATCACTGTG TTTAATACTT GCACGTTCGG 540

TTGCAGTAAT CGGTAATTCA AATACCATTT CATCGACTTC AGAACTTATT TGTAATATAT 600

CGTTTAATAT CACTTTACTA TTCGATTCAA ATGCAGCAGC TTTATCATCG CCTAGTGCAa 660

CAATTGCTGC ACCCGTTAAT GTAGCAAAGT CCATAATCAC ACTAGGCTGA TATTGATTTG 720

CATAAAACAC AGCATCTGCA AGGACTAATC TACCTTCAGC GTCTGTATTC ATTACTTCTA 780

CAGTTTCACC ACTTAATGCT GTAAATACAT CATCTGGcTT CATTGATGCT TCATTTATCA 840

TATTTTCAGC ACACGCAAGC ACTCCGACAA TATTTACAGG CAGTTGTAAA CGAcTAGCCG 900

CTTCAATGAT ACCAACGACA TTCGCAGCGC CACACATGTC AAACTTCATT GTAGCCATGC 960

CATTCTTCGT TTTAATACTA TAACCACCAG AATCATACGT TATACCTTTA CCAACTAAGG 1020

CAATTGGTGC TTCATCTTTG TCTTTGCCAT TATATGTGAT GGTTACTAAt CTCGGTTTAT 1080

GCTTACTACC TTTACCTACT GCTTGTAAAA GTCCGAATCC TTCAGAAACT AAAGTGTCAT 1140

AATCTTTAAC ATCTACTTTG ACCTTTGTAT TTTTAAAATG ATTAACAATA TCTTCTGcAA 1200

ATGTTTGTGG TGtTAATACA TTCGGTGGcA TATTACTAAA GTCTCyTGcC AAATTAATGG 1260

aTTGGcCAAT ACTGATACCC TCATGAATAA AATCTAATTC AATTAATGAT TCACTAATAA 1320

GGkTTAAATT CGTCTTAAAC GGtGCCTTCT kACTTgrTTT ATAATGATCG aATyCATATG 1380

kTGcACGCTC ACTTTGGAAT ACCGCATGCC ATTAATACAT CTGgATAACT GgATCcATAT 1440

TTTGgAnATA AATGaATCCa TAAGTAAATA CGTATCTTCa ATGTGTTCTG ACTTTATGTA 1500

TTGGAAAAGA TGTCCCCaTA TTTTCAACAT ATCTTGATAA tACGTGTCTT TAAGTTTCCT 1560

AAACCAACTG TAATTAAACG ATATGTTTGA TCTTGTACAT CAAATGCAGT TGTATAAATC 1620

TTCCCAACTT TACTACCAAT AATATGTTGA TGTTTTAGTC TTTCAAGTGA TTCTGTAATA 1680

TCGATATGAT TAAAACTAAT GCGCTCTAAC TGATTTAAAT GTTCTGGTAT ACCAATAATC 1740

AATGTATTTA TTTCGTTGCT TAGTGTGTTA TTTAATTTAA AATTCATAAT GTACCTCCTT 1800

AGATTTGATA TGTTACTCAC TTCAAATTGT ACAACAATAA AGCCCTcAGT GACACTGAAG 1860

GACTTTATAA ATGAATAATT TAATTTTATG TGTTTAGCTG AAACTTTATT TAAAGCCTAG 1920

AATTTACCTT TTTTGAATGC TAAACCGATA CCACCGATTT TGAATACCGC ACGTGTATCA 1980

ATCACTTTTT TCATGAATGC TGCTTTTTTA CCAGCGATAG GTTTACCAAA TACCATACCT 2040

GTTGATTCAC CGTTTAAGAT GCGTTTAATG TTTTTAGCAA CACTTTCACC TTGTTGCATT 2160

GCAATTTGTG CTGTAGTTGG TAATGGACGT TCTTCTCCAG CTGGGATAAA CGCTGAACAG 2220

TCACCAATAA CAAAAATGTT GTCGTAACCA TTGATTGTTA AATCTTGCTT TGTAACGATA 2280

CGTCCACGTT TAACGCCTTC AAATGATTCT TCCATTAATT TACTACCACG TACACCAGCT 2340

GCCCATACTG AAGTACCTGC ATTTAATTGT TGTTTTTCAC CATCTACTTC AACTACAAAA 2400

CCTTTTTCGT TACAAGCAAC GATTGGTGTA GCAATTTTAA ATTCAACACC GCGGTCTTCT 2460

AAGTAGCTAA cTGCGTGGTT AACTAATTCT TCTGAGAACA TTGGTAACAT TTTAGGTGCT 2520

GCTTCAACAC AAGTGATTTT AACTTTATTT TGATCCACAC CATATTTGCT ACATAATTCA 2580

GGAATTCTGT CTGTTAATTC ACCTAAGAAT TCAACACCAG TGAATCCAGC ACCACCAACT 2640

AAGATAGATA AATCGTTATC ATCTTTTTCT TTTGATGCTG CATAGTTAGC AAATTTGTCT 2700

TCGATATGAC GTGATAATTC ACGTGCTGTG ATAACATTTT CAATTTGGAA AGCATGATCT 2760

TTCATACCTT CGATGCCGAA TGTTTCACTA ACGAAACCTA ATGCTACTAC TAAAATATCA 2820

AAGTCATAAA TACCTTGATT TGTTTCTACC TTTTTAGCAT CACGGTCAAT TTTTGTTACT 2880

TCTGCtTGAA CAAAGTTCAC TTTGTCTTTC TTCAAGACAC TTTCCACAGG ATATAATACA 2940

TCTTCATAGT TTAGTGTACC TGCTGATGCT TCATGTAACC ATGTTGCTTC ATAGTGATAT 3000

TCATTTTTAT TAATAAGCGT AATTTCTGCT TCTTCTGTTG ATATCGCTTT TTGCAATTTA 3060

GTTACAGTTT GTAAACCTGC ATAACCAGCA CCAAGTACAA GTACTTTTTT ACGATCTTGA 3120

GCCATTTAAT TnCACCTAAG CnTTCATATT TTTTTAACCA AATGCTGATA ATTAC 3175

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 702 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

CATCATTATT AAAGATTTTC AATCAATACA gAATCACAAT ACGTACGCAT TGTGCACGAT 60

AAAAATACAG ATGTGTATAT TAACTATGAA CTACAAGAGC AACTAACGAA CAAAGCTTAC 120

ATTGGTGATC ATATTTATGT TGAAGGGATA TGGCTCGAAG TACAAGCTGA TGGTTTAAAT 180

GTATTGAGTC AGAATACAGT GGCATCGTCA TTAATTCGCT TAACACAAGA GATGCCACAT 240

GCACAGGCAG ATGATTACAA TACGTACCAT CGTTCGCCAA GGATTATTCA CCGTGAACCG 300

TGGCGTTCCA TTATACCGCC ATTAGTAATG ATTGCTTTAA CTGTTGTCAT CTTTTTAGTG 420

AGACCAATTG GTATTTATAT TTTAATGATG ATTGGTATGA GTACAGTAAC GATAGTATTT 480

GGTATTACAA CGTATTTCTC TGAAAAGAAA AAGTATAACA AAGATGTTGA AAAACGAGAG 540

AAAGATTACA AAGCTTATTT GGATAATAAA TCTAAAGAAA TTAATAAAGC GATTAAAGCA 600

CAACGTTTTA GTTTGAATTA CCATTATCCA ACGGtTGCTG AAATTAAAGA TATCGTTGAA 660

ACGAAAGCAC CAAGAATATA TGAnAAAACC ATCGGCATCA TC 702

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

TATGTTCCGA CAACGAAACA AAGTGTAATT ACAAGAGCAA AGATAACTTT GAATGTTTGT 60

AAACGTCCAT CTTTACCTTC AGTTAAATGC ATGAACATTA ATAATTGArG TCCTGCTTGG 120

ACGAATGCAA AGCCAAAGAT AATTGTCAAC TTCGCGTGGA ATGTTAATGA CGTGTATAGT 180

GTTACGTAAA CTGCTAAAAG CGTTAATACG ATAGATGCGA TAAATCCTAC AGTATGTTTC 240

ATTATTGTAC TCATCCGCTA TACACCATCC CTATCATATA TACGGCAGTA AAGATGAAAA 300

CCCAAACAAC ATCTAAGAAG TGCCAGTATA AACTTACTAT AAATAATTTT GGCGCATTAT 360

ATTTGTCTAA TCCGCGTCGT TGGATTTGGA TTAATAAACA AATGGCCCAA ACGATACCTA 420

GCGATACGTG ACAACCATGC GTTCCTAATA GGATAAAGAA ACTAGACCAG TAAGAACCAA 480

TTGTTGGGTT AACGCCTTCT GATGCATAGT GTGCGAATTC ATAAATTTCG AATCCAACAA 540

AGACTAAACC TAAAAGTAAC GTAATGATCA TCCAAAACAT CATTAACTTT TGTTTTTCTT 600

GGCGCATGTA GTAAATAGCA ATACCACATG TGTAAGAACT GAATAATAAT GCAAACGTCA 660

TTATTAAAAC AAGAGGCAAT TCAAATAACT CAGTAGTCAT TTTACCTGCA TAATCGCCAC 720

CATGTTGCAA AGTTAATAGT GTCGCAAATA GGGTACCGAA TAACGCAAAT TCGGCTGTAA 780

TGAAAATCCA AAAGCCAAGC TTATTTAATT CGCCTTCATG TGTGCGTGAA TCAATAGTGT 840

TTGTATCATG ACTCATGACT TACAGCCTCC CTTTCTTTAA TACGCGCTTC TCTTAATCTA 900

GCTTCAGTTT CTGCAACTTC AGCAGCAGGG ATATGATATC CGTGATCGAT TTGGAAACTG 960

CGATAAATCA TAGTACCAAA AATACCGAAT AAACAAATTA ATGCTGGAAT TACAGTTTCG 1020

TTGTTTGGCA TATGAATGTC TTTGTAATTA TGGTTGTCTA AGTAATGACG ACCATGTTCT 1140

TTCATATCAA CAAATGTGTC GTAGTCATTC CAATCTGGTG TAATGGCAAA GTTGTATTTA 1200

GGTGGAATTG CTGATGCAGT AGTCCACTCT AGAGTACGAC CAAGGCCATC CCAGTTATCT 1260

CCAGTTGCTT CACGTGGAGA TTTGAAGTGA CTGTATACGA TACTAACAAC AAGGAATAAG 1320

AATCCGATTG CCATTAATAA TGCACCGATA GTTGAAATTA AGTTTAATAA GAACCAACCA 1380

TCTGATGGCA TATAAGTGTA TAAACGACGT GGCATACCAT CTAATCCAAG AATGAATTGT 1440

GGTAAGAAAC AAACGTTAAA TCCGATCATG AAGAACCAGA AGCACCATTT GTTTAATGTT 1500

TCGTTTAATT TGTAACCCAT CATCTTTGGA TACCAGAAGA TTAAACCAGC TAAGCAGGCA 1560

AATACAACAC CAGTAACCAA TGTATAGTGG AAGTGAGCTA CTAAGAAGTA CGTATTGTGA 1620

TATTGATAGT CAGCTGATGC CATTGCTAAC ATTACACCCG TAACACCACC TAAAAGGAAG 1680

TTAGGGATAA ATGCTAATGA GAATAGCATT GGTGACTCAA ATGTAATACG TCCTTTATAT 1740

AATGTTAATA ACCAGTTAAA CAATTTCACA CCAGTTGGAA TACCAATCAG CATTGTTGAA 1800

ATTGAGAAGA ATGAGTTGAT TAACGCACCA TTACCCATTG TGAAGAAATG GTGAACCCAA 1860

ACTAAGAAAC TAAGGAACGC GATACCGGCA GTTGCCCATA CCATACTTTG ATGTCCGAAT 1920

AAACGCTTAC GAGCGAATGT CGGGATAATT TCTGAGTAAA TACCAAATGC TGGAAGGATA 1980

ACGATATAAA CTTCAGGGTG CCCCCATACC CAGAAGAAGT TAGCCCAAAG CATTGGCATA 2040

CCGCCATGTG CAACTGTGAA GAATGCTGTG TCAAATATTC TATCAGTTGT CATTAATGCT 2100

AACGCTACTG TTAAAGGAGG GAAAGCAAGA ATAACAATTA ATGTAGTAAT AAATGTTGTT 2160

ACTGTAAACA TTGGCATTTG CATAAACTTC ATAGTTGGTG TTTTACATCT TAAAATTGTT 2220

ACAAAGAAGT TGATACCTGT AGCTAAGGTA CCAAGCCCTG AAATTTGTAT AGCTATTAAG 2280

TAATAGTTAA CACCCGGACC AGGACTGAAT TCACCTGCTA GTGGCGCATA GTTTGTCCAA 2340

CCAGCTGCTG GTGAACCACC AATAATAAAT GACAGGTTGA ATAAAATCAT ACCTGCAAAG 2400

AATAGCCAGA AACTTACGTT GTTTAATACT GGGAATGCAA CATCACGTGC TCCAATTTGT 2460

AATGGAACAA CGATATTCCA TAAACCAAAG ATAAATGGCA TTGCCATGAA GATAATCATG 2520

ATTACACCAT GTGTACTAAA AATTTCGTTA TAGTGGTTAG ATTCTAAAAA TTTGTTATCA 2580

GGTACTGTTA ATTGCGCACG AATAAGTAAC GCATCAATAC CACCACGGAC GAACATTAAT 2640

ACGGCACAGA TTAAATACAT AATACCGATT TTCTTATGGT CTACAGATGT GAACCATTCT 2700

TTGTAAAGAT ATTTCCATAA TTTAAAGTAA GTAATTACTG CGATTAAACC AATAACTAAG 2760

AATGGGGCAC CAATTTGTGC CATTGTAATC ATcCAGTTAC CTTTAACTAG TAATTGATCC 2820

TTGAAATTTT CTTCATTTCT TTCGCATTTT TCGATTCATC TTTCTTGAAC TCATTGTTAT 2940

ATGGTTCGTC ATTTCCAAGA ATCATCAACT TCATACCATG TCGTTTATAG TTCGCATTTG 3000

TAATTTGAGC TTTACGAGCA GGTATTAATG GTTTGTCTGA TACATCTTTA AACATATTTT 3060

CTTCACTAGT GAAGTTTGGA TCTTTCAATT CGAAATTGAA ACGTTTATAT GCATAGAAGA 3120

TGTATTCTGG ATCGGCTGCT GGATCAACAA ACGCCATATG TGTACCATTA AATTCTAAAG 3180

CTTTATTAGG TGTGCTTGGT AATAATTGTT TATCAAATGT ATCTTGATCT AACGTTTTCT 3240

TACCTTTAAC TTCTTTCACC CATTTGTCGT AGTCTTTTTG ACTAACGGCA TTTACTTTAA 3300

ATGTTTGACG TGAGAATCCT TCACCATTGA AGTTAGAGTT ACGACCTCTG AACGTACCAG 3360

TTTGAGATGC TTCTAACGTC CAATTCATTG TCATGCCAGT CATGGCATAT TTTTGACCAC 3420

CTAATTGTGG AATCCAGAAA CTTGTCATTG TATCCATAGC TTGAAGCTTA AATACAACAG 3480

GACGATCTTT AGGGATTGTT AATGTATTAA CAGTCTCTAT ATGTTCATCT GGATAAGCAA 3540

AGAACCATTT GTATCCTGCA CTTACTGCAT ATACAACCAT TGGATCTTTC TCACTCTTCG 3600

GTGGTTTTTC GTAATCGTAT AAAGTTTTAA CTGTAGGAAT AGctAAAGCA GCAACGATTA 3660

TGATAGGTAT TACAAACCAT ATTGTTTCAA TGATGGCATT ATGGTGCATC TTACCAGATT 3720

CGGCATTCTT ATTATAACTA TACTTGTAAA TAAAAATGGC GAACATGCCA AGTACAACGA 3780

AACAAATAAC AAGCATGAAG ACGATTGAAT AAAGAATCAA GAACTTCTGA CTACTTGCTA 3840

CTGGCCCTTT TGCGTTGAAA ATTTCTATAT TTGAACAACC ACTAAGTAAA ATTAGTGTGC 3900

CAAATAATAG AAGCAAAGAC TTAAATTTTG ACACTTTTTT GACCTCCTAA TACTACAAAT 3960

GTAGGGCTTA ACATTAATTT TAAGTTATTA CACAATATTT ACAAGGGCTT ATGGGAAAAA 4020

AATTAATAAA ATTGTATCAA AAATGTTGAT AAATCAAGGT GTGACGTGGG TTCACACATT 4080

TGTTAAAATT ATGTGTACAT TTTGTGACTA ATAGCGTTTT T 4121

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

CGAGTGAGTA CAmACATATT TTTATTTGCA AGGGGTAAAT GGCATATAAC TATCTTTTTT 60

ATGTAAGCTG GTATAAAATT TATACTAATA GGAGGGATAG TATGAATATA GTAGGGCATC 120

TTGGATTACG ATTAGTTGAA AAGTCGGTTA ATCAAGACAA TCCTTCAATG TATCATTTGT 240

TTTATGGGGA CGAAgTAGGT ACAGCCGGAA CAATTTTAAG CTTTTTTGAA ATTCCCAATG 300

CGGGTCATAA GCAGCCAGGT ACTGAAACGA TTTATCGATT TTCATTATTA GTACCAAATC 360

AAGCGGCACT TCATTATTTT GAAAAACGTC TTGAGAATAA TGGTATTAAG TCTGAACGTT 420

TGTACTATCT TGGACAAGAA GGTGTTGTCT TTAAAGATGA AGACGACTTA GAAATCATAT 480

TGCTTGTTAA TGATAGTTTT GAAGTACCAC ATCAATGGCA ACATAACGCT TATAGTGAAA 540

TACCTCAAGC ATATCAAATT TTAGGAATAG GGCCAGTCGA ATTAAGAGTT AGAAATGCAG 600

CGCGTACGGT AGAATTTTTG GAAAATGTCT TAGGTTATCG CAAAAGAGAT AATAAATCAT 660

TCGATGTGCT GACATTAGCA CCACAAGGTT TATATTCGGA TTTTGTAGTT ATTGAGCAAC 720

AGGGACAACG TGAAAGACCT GGACGAGGTT ATATCCATCA TATTGCAGTT AATACACCAC 780

AAATGAGTGA CTTAGATGCA ATTTACAAGA AATTACAACA ACAACCACAA AGTAATTCAG 840

GTATAATTGA TCGCTATTTC TTTAAATCAT TATACTATCG CCATAATTCA ATTATGTATG 900

AATTTGCGAC TGAAGCGCCT GGATTTACTA TTGATACACC TGTTGAACAA TTAGGAAGTC 960

AATTGAACTT GCCTGACTTT TTAGAAGCAG AACGTGAACA AATTGAAAGT AAGTTACACG 1020

AAATATAAAG GAGAATGTTT AATGGCCAAA TTAGAAATGA ATAAAAATAC GCCTCTTGAG 1080

TTTGGTTTGT ATTCCTTAGG TGATCATTTA TTGAATCCAT TGAAAGGTGA AAAAGTTAGT 1140

TATGAGCAAC GTATTAATGA AATTATTGAA GCAAGTAAAT TAGCAGATGA AGCAGGTATT 1200

GATGTTTTTG CAGTTGGTGA AAGTCATCAG GAGCATTTTA CAACACAGGC ACATACGGTT 1260

GTGTTAGGTG CAATTGCCCA AGCGACAAAG CATATTAAAG TTTCAAGTTC TTCAACGATT 1320

ATTAGTGCAc AGATCCTGTA AGAGTATTTG AAGACTTCGC GACATTAGAT TTGATTTCTC 1380

ATGGTAGAGC CGAAATTGTA GCTGGCAGAG CATCAAGAAC AGGTATTTTT GACTTGTTTG 1440

GCTATGATTT AAAAGACTAT GATGAATTGT TTGAAGAAAA ATTAGGTTTA CTTTTAGAGT 1500

TAAATAAAAC TGAGCGTATT ACTTGGTCTG GAAAATATCG TCCAGAACTT AGAAATATGA 1560

AAATATTCCC AAGACCAATC GATAATATAT TGCCAATATG GCGTGCTGTT GGTGGTCCAC 1620

CTGCAAGTGC TATTAAAGCG GGAAAACAAG GTGTGCCAAT GATGATTACA ACCCTTGGTG 1680

GCCCAGCAAT GAACTTTAAA GGTTCTATAG ATGCTTATCG TCAAGCGGCA ACTGAAGCAG 1740

GTTTCGATgc TTCGCCTAAG TCTTTACCAG TAAGTACAGC GAGTCTGTTT TATACAGCTG 1800

AAACAACTCA GGATGCTATG AGAGAATTTT ATCCACATTT GAATACAGGG ATGTCATTTA 1860

TTCGTGGTGT TGGTTATCCG AAACAGCAAT TTGCTAATTC GTCAGATTAT CGAGAAGCGC 1920

GTCATCAACG TTTTATGGCA CAGCTTGATT TTGGCGGTGT GCCATTTGAA AATGTTATGA 2040

AGAATATTGA GTTAATTGGC AACGACATTA TACCGGCGAT TAAAAAGCAT TTATCAAAAT 2100

AGGAGGGGCG TCATCATGAA TATTGTATTA TTGTCAGGTT CCACAGTAGG TTCTAAAACG 2160

AGAATTGCTA TGGATGATTT AAAAAATGAA CTAGAAGTCA TCAATGAGGG ACATCAAATA 2220

GAGTTGATGG ATTTACGAGA ACTTGAATTA GAATTTAGCG TTGGAAAGAA TTATCTAGAT 2280

ACTACAGGAG ATGTATATAA ATTAACGACG TCGTTAATGC AGGCTGATGT GATTTTTATT 2340

GGTTTTCCAA TTTTTCAAGC TTCCATCCCT GGTGCTTTGA AAAATGTGTT TGATCTACTT 2400

CCAGTCAATG CGTTTCGTGA CAAGGTAATA GGACTTGTAG CGACAGCAGG TTCTAGTAAA 2460

CATTATTTAA TTCCTGAAAT GCATTTAAAA CCAATATTGA GTTACATGAA AGCACATACG 2520

ATGCAAACGT ATGTATTTAT TGAAGAGAAA GATTTTTCAA ATCAACAAAT TGTCAATGAT 2580

GATGTTGTAT TTCGGTTAAA AGCGTTGGCA CAATCCACAA TGCGAACTGC CAAAGTACAA 2640

CAACAAGTGT TTGAAGAAGA AAACAACCAA TACGACTTTT AAAGTATAAA AATAAGACGC 2700

TCGGCACACT AAATTTGTAA GTGTTTGAGC GTCTTTTCAT ATTAACTATA TAGCCAATGA 2760

ACGACGATAA AGGCAAGTGA TGACAAGCAT ATTGAGGTAA TAATGATTGT CATAAGCGGT 2820

TTAAGTGCGC GATTTTTAAG ATCTTTAAAT GCAACATTTA ACCCTAAAGC AACCATGGCC 2880

ATTAATAAGC AAATTGTTGA TACAGTATTT AAAATATTTA GCAATGCTGA CGGAATAGTT 2940

ACATATGTAT TCACTAAGGC CATAATGACA AATCCAATTA AAAAGTATGG AATGCTTATT 3000

CGACCCTTGC TAGATGATTC TGATGAACGG AAACGCATAA TTAAAATAAG TACGATGGTT 3060

AATGGAATCA GTAAGAATAC TCTACCAAGT TTACCAAGAA GTGCAATTTT AAGTGCATCA 3120

CTACCACCAA AGCCACCAGC TAAGACAACG TGTGCAATTT CATGAAGACT AACACCAGAC 3180

CAAGCGCCAT AAACATTTGT CGTCATTGAA AAGATAGCGT AGATAGCTGT ATATATAAGT 3240

GAAAATATCG TACCAATCAA TGCGATGATA CCGATACTAA TAGCTGTATC CTTTTCACGT 3300

GATTTGAATA TTGGAGCGAC TGCGGCAATA GCAGCAGCAC CACAAACGCC TGTGCCGACA 3360

CCTAGTAATA ATGCGATGTT TTTGTCACCA TGCAACAGTT TGTTGACAAA GAGCATCATT 3420

ACAATACTGA AAATAACGAC ACCTACATCG ATGGCTAATA GTTTACTACC TTGACCGATA 3480

ATATCGAATA TATTGAGTTT AAGTCCATAT AGGATGATTG CAAATCTTAA TAAATATTTA 3540

GATGAAAACG TAATACCTGA GCTATATTGT TCAGGATATC CTCTAAAGTG ACGATATAGA 3600

ATAGCGATTA ATATCGCGAT AGTTAATGCG CCAACCTTAT CTAGGATTGG CAATTTAGCT 3660

GCTAAAAAGC TAAATAATGC GACTATAAAT GTTAGTGATA GCCCAATCAT AAAATGCTTA 3720

ATTTTTAAAT ATAAATTTGG AATGAATAAT AAAGTAGTGA TTAAATTAAG TTGTGTGATA 3840

GGAAACTTGG ACATCAATCA AAGTAATAGG CACTACAACG CTTATTGGCG GGGCCCCAAC 3900

AAAGAAGCTG ACGAAAAGTC agCTTGcAAT AATGTGCAAG TTGGGGATGG GCCCCAACAT 3960

AGAGAAATTG GGTCCGTAAT TTCTACAGAC AATGCAAGTT GGCGGGGCCC CAACATAGAG 4020

AATTTCGAAA AGAAATTCTA CAAGCAATGC AAGTTGGGGA AGGACAACAA ATTTAAGATA 4080

CAATGCGTAA CATTAATATG TTATTATAAT GATAATTTAC AGAATTATAT GAAAAATGAA 4140

TGAGGATGTG ATGGTATGTT TGGAATGAAA GTGAATGAAC AAATAACATT AAAAATTTTA 4200

GAAGCTCATG ACACAGAAGC GCTTTTCAAT TTAGTCAATC GTTCAAGAAA TTCACTTAGG 4260

GAATGGTTAC CTTGGGTAGA TGCAACTGAG CAACCATCAG ATACGCGTGC ATTTATTAAA 4320

AGAGGACTTT TGCAATTTGC TGATGGTAAT GGATTTCAGT GTGGCATTTG GTATGAAGGA 4380

ACGCTAGTTG GTGTCATCGG TTTACATGAA ATTAATCACA TGCACAGAAA AACTTCATTA 4440

GGGTACTATT TAGATAAAGA ATTTGAGGGT CATGGGATTA TGACACAAGC AGTTGAGGCA 4500

TTGATAAAGT ATTGTTTCGA AGAGCTTGAC TTAAACCGAA TTGAGATTAG TGCCGCAGTT 4560

AATAATGAAA AAAGCCGGGC TATTCCTGAA AGGCTGGGAT TTACTAGAGA AGGTATGTTA 4620

CGTGACAATG AATTACTAAA TGGTATTTAT TCATCGAGTT ACATCTATAG TTTATTAAAA 4680

TCAGAATACG ACCAAAAATG ACAAATTAGA CTTACAAAAG AGTGATGACA TTTAAAATGG 4740

CAGCGCTCTT TTATTTAATT TTTGAAAATA AAAGGTTGTT GACAGTATTA TTTTATAACA 4800

ATATAATGAT TTTGATAATT ATTATCAACT AGATGATGTT TATGGGAGGA TGCTTTAAAA 4860

CAGCCGTTTT AAGTGTAATG TATTATTTTA GCGTGTAGGG AATGCGAAAA TAATATTTAT 4920

AAGAACACAT CTATGGGGAT AATAGAATTT CTATAATGAG GTGTCAAAAT GAAAAAGTTA 4980

ACAACGCTAT TATTAGCATC AACGTTATTA ATTGCTGCAT GTGGGAACGA CGATAGTAAG 5040

AAGGATGATT CAAAGACATC GAAAAAAGAT GATGGTGTTA AAGCAGAATT AAAACAAGCA 5100

ACAAAAGCAT ATGATAAATA TACTGATGAA CAGTTAAATG AATTTTTAAA AGGTACAGAA 5160

AAATTTGTTA AAGCGATTGA AAATAATGAT ATGGCCCAAG CAAAAGCGTT ATATCCAAAA 5220

GTTCGTATGT ATTATGAACG CTCTGAACCA GTTGCAGAAG CATTTGGAGA TTTAGATCCT 5280

AAAATTGATG CACGTCTTGC AGATATGAAA GAAGAGAAAA AGGAAAAAGA ATGGTCAGGA 5340

TATCATAAGA TTGAAAAAGC ATTATACGAA GATAAGAAAA TTGATGATGT GACTAAAAAA 5400

GATGCACAAC AATTATTGAA AGATGCAAAA GAATTGCATG CCAAAGCTGA TACATTAGAT 5460

ATCACACCAA AATTAATGTT ACAAGGTTCT GTTGACCTAT TAAATGAAGT TGCAACTTCT 5520

GTTGAAGGCG CACAAAAAAT TTATGACTTA TTTAAACCTA TTTTAGAGAA AAAAGATAAA 5640

AAATTAAGTG ATGATATCCA AATGAACTTC GATAAAGTGA ATCAATTATT GGATAAATAT 5700

AAAGATAACA ACGGCGGTTA TGAGTCATTT GAAAAAGTAT CGAAGAAAGA CCGTAAAGCA 5760

TTTGCGGATG CTGTTAATGC ATTAGGAGAG CCACTAAGTA AAATGGCTGT GATTACTGAA 5820

TGACAAATTA TGAACAAGTT AACGATAGTA CGCAATTTTC AAGACGTACA TTTTTGAAAA 5880

TGTTAGGTAT TGGCGGTGCC GGTGTTGCAA TTGGCGCAAG TGGTGTTGGT AGCATGTGGT 5940

CTTTCAAATC AATGTTCAAT ACACCAGAAG ATCCGGAAAA AGATGCGTAT GAATTTTATG 6000

GTAAAGTGCA ACCAGGCATT ACCACACCCA CGCAAAAAAC ATGCAATTTC GTTGCGTTAG 6060

ATTTGAAGTC AAAAGATAGA GATGCAATTA AGGCAATGTT TAAAAAGTGG ACGGTTATGG 6120

CTGATCGTAT GATGGATGGT GATACAGTTG GCAAGCCGAG TAACAATCCT TTAATGCCAC 6180

CAGTAGATAC CGGTGAATCG ATAGGATTAG GTGCAAGCAA GTTAACGATT ACCTTTGGGA 6240

TTAGTAAGTC TTTGATGAAG AAAATTGGGT TATCTAGTAA AATTCCCGAT GCCTTTAAAG 6300

ATTTACCGCA TTTTCCGAAT GATCAGTTAA TAGACGATTA CAGCGATGGT GATATTATGA 6360

TTCAAGCATG CTCAAATGAT TCGCAAGTAT CCTTTCATGC GGTTCATAAT TTAGTTCGTC 6420

CATTTCGAGA TATTGTTAAG GTACGTTGGG CGCAATCTGG TTTTATCTCT GCTAAAGGTA 6480

AGGAAACACC TAGAAATTTA ATGGCATTTA AAGATGGAAC AATTAATCCT AGGAAGAATA 6540

ATCAACTTAA AGATTATGTG TTTATTGATG ACGGATGGGC GAAACATGGA ACTTATTGCG 6600

TTGTCAGACG TATTCAAATA CACATTGAAA CGTGGGATCG TACTGCGCTG GAAGAACAAG 6660

AGGCTACATT TGGTCGGAAA CGACATAGTG GTGCACCGTT AACAGGTGGG AAAGAGTTTG 6720

ATGAAATTGA CTTAAAAGCG AAAGATAGTC ATGGCGAGTA TATTATTGAT AAAGATGCCC 6780

ATACGAGGCT AGCGAAAGAA GCAAATACGT CAATTTTACG TAGAGCCTTT AATTATGTGG 6840

ATGGTACGGA TGACCGCACA GGTAACTTCG AAACAGGCTT ACTTTTTATT GCTTTTCAAA 6900

AAGCGACAAA ACAATTTATC GATATACAAA ATAATTTAGG TAGTAATGAT AAATTAAATG 6960

AATATATTAC ACATAGAGGT TCTGCTTCAT TTTTAGTATT ACCAGGTGTT AGTAAGGGAG 7020

GATACCTTGG TGAAACATTA TTTGACTAAA TTTGTAGCAA TGCTAATAAC TGCTGCTATG 7080

GTGTGTAGCT TTGGGTTACT GAAAAGTCAG GCAGCAGAAC AACAAAGTAT TAGTGATGTA 7140

TATAGTGTGA TAACGGATGC GAAATCTGCA CTTTCTAATA ATTCGATATC GAATGACAAT 7200

AAGCAGAAAG CAATTGAGCA AGTGGTAAGT GCAGTTAAGA AATTATCGCT TGAAGATAAT 7260

AGTGAAAGTA ATGCTGTCAA ATCAGATGTG AGAAAGCTTG AAGATGCAAA AGCGAATGAT 7320

GCTAGTAAAG ATGCGGGTTC TAAAATTAAA CTATTGCAAC AGCAAGTCGA TGCTAAAGAT 7440

GCTGCGATGA CAAAAGCGAT TAAAGATAAA AATAAAGCGG AATTAGAATC TTTGAACAAT 7500

AGTTTGAATC AGATTTGGAC AAGTAATGAA ACAGTGATTC GCAATTATGA CGCAAATCAA 7560

TATGGACAAA TTGAAGTCGC ATTATTACAA CTTAGAATTG CAATTCATAA GTCACCATTA 7620

GATACGGCAA AAGTGTCACA TGCTTGGACA ACTTTTAAAT CAAATATTGA TCATGTCGAT 7680

AAAAAAAGTA ATACGTCTGC AAATGATCAA TACCATGTAT CACAATTAAA TGATGCGTTA 7740

GAGAAGGCGA TTAAAGCTAT CGACGACAAT CAATTGTCGG ATGCTGcaTg TGCGCTTACA 7800

CATTTTATAG AAACTTGGCC GTATGTTGAA GGTCAAATTC AAACTAAAGA CGGTGCTTTG 7860

TATACGAAAA TTGAAGATAA AATACCATAT TATCAAAGTG TATTAGACGA ACATAATAAA 7920

GCACATGTGA AAGATGGTTT AGTAGATTTA AATAACCAAA TTAAAGAGGT TGTTGGCCAT 7980

AGTTATAGCT TCGTCGATGT GATGATTATC TTTTTACGTG AAGGGCTAGA AGTGTTGTTA 8040

ATTGTAATGA CATTGACTAC CATGACGCGT AATGTAAAAG ATAAGAAAGG GACTGCAAGT 8100

GTGATTGGTG GTGCAATTGC CGGACTTGTA CTGAGTATTA TCTTAGCAAT TACGTTTGTA 8160

GAAACTTTAG GGAATAGTGG CATTCTTCGT GAAAGTATGG AAGCGGGATT AGGTATCGTT 8220

GCGGTCATAT TAATGTTTAT CGTTGGTGTT TGGATGCACA AACGTTCAAA TGCAAAACGT 8280

TGGAATGACA TGATTAAAAA TATGTATGCT AATGCGATTA GTAATGGTAA TTTGGTATTG 8340

TTAGCGACGA TTGGTTTAAT ATCTGTGTTG CGTGAAGGTG TCGAGGTTAT CATTTTCTAT 8400

ATGGGGATGA TAGGTGAGCT AGCGACCAAA GATTTTATTA TTGGTATTGC TTTAGCTATC 8460

GTTATTTTAA TCATCTTTGC ATTATTATTT AGATTTATAG TTAAATTAAT ACCTATTTTC 8520

TATATATTTA GAGTGTTGTC GATCTTTATT TTTATTATGG GATTCAAAAT GCTTGGCGTA 8580

AGTATTCAAA AGTTACAATT ATTAGGTGCG ATGCCAAGAC ATGTTATTGA AGGATTCCCA 8640

ACGATTAACT GGTTGGGCTT TTATCCAAGT TATGAACCAT TGATAGCACA AGGTGCTTAT 8700

ATTATGGTAG TTGCTATCTT AATCTTTAAA TTTAAAAAAT AAAAAACAGG CCGAGTGCCT 8760

GTTTTTTTTG TTGCTATATT GGAAATATTC GGTATTGCAG TATAACGATA ATCACAGCAT 8820

TGATTCGTAT AAGGTTAATG TGTTGGCGGT TTGCCTCGGC ATGTGAACTT AACGATGAAC 8880

ATACTGAACT CAAAGAGCAA TATGAGTGGC AATGTGAGTA ATATATTTAA TGTTAAATCG 8940

GGTGGTGCAA TGATACTTGC TAATACAAAG CAAGCGAAAT AAATATATTT ACGrTAATGT 9000

TTCAATGATG TGGTATCTAT AAGACCGAAT TTTGCAAGAC CCATAAATAA TATTGGTAAT 9060

TGAAATAGAA GACCAAATGT GAATAACCAA CGTATGAGTT CAATCAAATA TGCTTTAAAG 9120

GGAAAGCCAA CATAAAATGC AAAAGCGACG CCAGCACAGA ATAATAACAC GCTGAAAAAA 9240

CTATATTTAT AAATAAATTG ACGTTCATTA TTATGTAATC CAGGTGCAAT GAATGCCCAC 9300

AATTGATAAA 9310

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3458 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

ATTAGTATTA CACACTAATG TAAATAGATT GGTTGGAGAA GAGATATTTG CTAATAAGTG 60

CCTTGCTAAT AATGATGTTC AAATTATGAA TTCAATAAAA AAATTAATTG AAGCTGAGTT 120

ATTAACAACG ACTAATGATT TTGAAGTTAG TATATATAAA AAGACAAGAC CTGAATTACA 180

AAGTATTTTA AAAAGTTTTG GTATAAAAAC AACAGGTAAT AAACCTGACT TAATTAAACG 240

TATTGACGAC AATTTTCATA TTATTAATAA CTTAGATTTA CCATATGTAT ATATACCAAT 300

TAAGAAAGGA GAAGAAATTT TAAAGAAAAC AGAGTACTTA ACCTCTTTTA TACAAAGTTA 360

TGGTGAAATT TCTCTTGAGC GTGCTTATTA TTTGGTTGAA AACTATATAG ATGAAAATTG 420

CGATGATAAA GTTGCAGAAA TATACAAGTT TGAATTTCAA AGAAAATATG ACAATGGCGA 480

GTTTGATTTT AATCATGGAT ATAATTTCGA ATTGAATATG TTGATAGATC ACTATAAAAG 540

AGATGTAAAA GACTACGATA ATGCCAGAAA GTATTCAAAT ATTTATCTTT ACTTTGGTTT 600

GAGAGATTTC TTAAAAAAAT TAATGAGTAA TTATTCATAT TACGATAgTA AAGGGAATAT 660

AGATTTGAAC GAAATACAAA ACGATCTGAA TAGATTTATC AACTCTAGCG CTTCTGGTAT 720

GTACGAGCGA TTAATATATA ATGAAAATTT ATCCAATAAT ATTATGTTTG AATTATTTAA 780

AAAGGACACA CAAGATTATA GTGATTTGGA AGAACAATTG ATTGAAAAGT TCATAAACTA 840

TGTAGTGTCT AATGTAAAAA AAGAAAGTAG GAGTAATACT CTTATAGAGT TATCAAAAAT 900

TTTAGAGAAC GGATATACAA TTGATAAAGA AGAATTTAAA AAAGAAGATG ATTATCTTTC 960

TAAGTACATA TTTACTGACA TAGATTATTT GAAAAAGTTA GAATCAAAAA TAAACGTTGC 1020

TATTGATATT CGAAGTGGAG AAATTCATTT GGTATTAGAT GATGATAGCC TTGATATATT 1080

AATACAAAAT CAAAAATACG GCAATGAGTT TTGAGTCATA ACTAAATATA ATATGTTGAA 1140

GAGAGGTTTT ATTTAAATGG CTAAAATTGG TTATGATCGT GTATCAACGA AAGATTAATA 1200

AACGTACAGA GCTTGTTAAG TGTTTAGATT ATTTACGAGA GAGCGACACA TTAGTTGTCT 1320

ATCAACTTGA TCGGTTAGGT AGAACGACAA AACTATTaAT TGAATTaTCA CAATGATTCG 1380

ATGATAACGG AATTGACTTA CAAATTAGTA ACATGAACAT TTCAACGAAA GACACAATGG 1440

GCAAAATGTT TTTTACGATG ATGAGTGCAT TTTTCaGGAT TAGAAGTTAA TTTACTATGT 1500

GAGTGTATAA AATAGACTTA GCAGCAACAA GAGCGAGAGG CCGAAAAAGC GGGCGCCCCT 1560

CTTTACCAGA GAATAAAAAA TGAGAAATTA AATTTTTATA TGATGAACAA ACGATAACAG 1620

GGGAAGAAAT AGCTAGTTAG ACAAGGGTAT GTCACTCAAC TGTTTATCGA GTTGATTAAG 1680

AAATGAAAAA ACTTATACTA TGAATTACTG TTTAAAAGTG TGCATGTTAT AATATTTATT 1740

GAGCAAGTTG GATAGATGGT GGCTAATCTC TTAATAAAGG GGTGATGCCT ATGGTTATAG 1800

TTGTTACTCC TAGnAAAGGA CTAGCATGTC TGATTTTGAA ATGCTTATGG TTGTATTAAC 1860

AATCATTGGT TTAGTATTGA TTAGTACTCA AGACCATAAA AAATAaCCTT CTATTCGCTT 1920

TGACCGGCAT TTTTGAAGGC TATTTTTAAA TAAAATATAA GGTCACCGTC TTTTTAACGG 1980

GCTCATTAGG GTAACATGTT TCCGAGTGTT GCCCTTTTTG TGTTTCAAGA GTTAATGATT 2040

TTCATCTTTT GCTTCTACTT GCTACAAATA TATTTTAACA CATTTTTCTT ATGAATTGTA 2100

GTTCTGAACA TAATCAGAAT TAATAAAACC AACTTTCCAT ACAGCAGAAA ATACAATTAA 2160

AAGTATAGAA TGTAATCACG AATTATATAA AAAGTATTGG AGACCTCTTC ATATATAGAT 2220

AATTCACTTA GTTATTTTAG AAAGAAGCCC CTAaCAACTA AAGTTGAAAA ATAGAGGAAC 2280

ACAGTTgGAT TACGCATCAA CTGCATaAGg CCCCTAAmAA CTAAAGTTGT AAGGGGCyCT 2340

AAAATTTATT TTGGTTGATT GTCTTCTGGT TTATCTGAAG TCATTGTTTT TGTTGTATTA 2400

TCATTTAATG AATCTTGTGC TTTTTCTGTT TTTGTTTCAA CAGATGTTGT CACTTTATCA 2460

TTTTCTACTT TTGTATTTTT TGGTTCAGTG ACAACTTTTT TATTCTTGTC AGCTGTTTTT 2520

ACTTTATCTT TAGTAATTTT TTGACCACGT TTTAAGTAAT ATTGAACGAT ACCCATTAAA 2580

ATGATTGCAT GAATAACAAC GAATAAAATA ATTGTCATTA CTGTATAAAC TCTTATGATA 2640

TTTTCTGCAA CACTTTGAGA GAGTGATTGC GTATTAAATG AAATCAAGTA ACCAACAGGT 2700

GTTTTAAATA AAATAATAAT TAAGTTTAAT AATAGTATTC CAATGAAAAA TTTGAAAAAT 2760

GTTTTTTGAC CATTTTTCAT TGCTTTAAAT CCATTAGCTA AGTGTGTTTT TACTTTATCG 2820

TTAGTTGATT CaACGAAACT AGTCaTAAAG TTGAAAATAG GTATTAACAA TAACCAAGTA 2880

ATAATTGCTT TAATCAATAA AACAACAATG ATTATGATGC TTTGAGTTGT AATAGCAATA 2940

CCAATCAGGT GTGTACTATC TGCATATGAT GATTGTACTG AATTCATAAT CATTTCTGAT 3000

ATAGATACAA GACCGATCAG AACGCTCTTT AAATAATTAC CTTTTTTAAA TGCAATAAAT 3120

AAATCGGTAA ATTTTACTTT TTCATGACTC ATTGCTCGTT TCATAACATT TGTAATTCCG 3180

ATAAAAATTT GAACTAAAAC AAACAGTGAA ACTACAGCTG CTATAAGTAA TACAGCGATA 3240

ACTTTTAAAT ATGCATCTAC TGGTGGTTTT TGCCCAAATT GTGAATAAAT TGCAATAGTT 3300

TGTGCATACT TAGCAAGCTG GAAATTAGCA AGTAAATATA CAACTGCAAT TACAGCAAAT 3360

GCTATAAGTG CATATATCAA TGTTATTAAT AATTGTGGTT TAGCATTTTT AAATGCTGAT 3420

TTAAAGTAAG TAAACAAAGT GGTGCCTCCT TTTCTTCA 3458

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 695 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

GCTTGCAAGA TGCTTTCATT AAAGACAAAG TCATCGATAT TATGAATATG TTCCAAAATC 60

ACACTGATAT CACTTATACG TTGAATAAGT CTCATGCACA TATTATATGT ACGCCAGAaA 120

TATTTGCTAA ATTGTTACAT ACGATTGCAA CTAGAAATAT CGACATTCTA TCTGCCAATT 180

ATAGATCGTC ATCTATGAGC AAAGCTCGTA TATCATAATA AAAGACACAT CTATACGATG 240

ATCATTTACA ATGATTGCGT ATAGTGATGT GTCTTTTTTT GTATTATTTA TCTTCGGAcG 300

ATTGATCCTC AACCATTTGT TCAAATGCTT CACGAACTTG TGGTACTGTC ATACCTACTA 360

CAACTTGGAT ACTCTTACCA CTCTTTACTA ATCCGTGTGC CATTTGTTGA TGCGTGAAAT 420

ATTCCGTATC TGCAACTTTA CTTTCATCAT AAACAGTTAA GCGTAATCTT GTTGTACAGT 480

TAGTAACATC TTTGATATTT TCTTTGCCGC CTAAACCGTC GAGGTAATAT GCAGCTTTGT 540

CTTCGTATTC ATTACCAGAT GAAGCACGTT TAGAATCTAC GCTATCACCT TTTTTATTTT 600

TGTAATCTTG CTTAGAAAAT AATTTAACTT CCTCTTCTGT TTyCTTACGT CCAGGTAATG 660

GAATATCAAA TTyCAAAATT AAGAATCTGA ATAAG 695

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 875 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

AATATTGaTa TTATATATAG TCGAATCaAT GATGACCCaC ATCGACCtAA TGCAAATAAT 60

AAGACAATCA AGCAGTTAAA TGACTTGTAT TGCTCGCGGA ATTTAAGATA TAATGAAATC 120

GCATTCAAGA AATTTGATAG TCATTTGCTA TCAATTTCAG AAATATATTA TGAATTGCTA 180

AATTTAATAA AAGCGAGTGA TCAGTATTAG AGAGAATAGA GCGTTAAGAC TCTATCGCCG 240

AAGtGCAAGT AATTTATTAC GAAACTCTCA GGcAAAAGGr TAATACTGTA ACGCGTTCCT 300

GAATTGGTGA TTTATAAACA GGGTAGCGAT TGCTATCCTG TTTTTATAAT TTTAAGGGGG 360

TATTTCAATG TCAAGTGATT TAAAACAAAC ACCTTTATAT CAAAATTATG TTGATAGAGG 420

TGCAAAAATT GTGGAATTCG GAGGATGGGC GATGCCTGTT CAATTTTCAA GTATTAAAGA 480

GGAGCATAAT GCTGTTCGAT ACGAAATTGG CCTGTTTGAT GTTAGTCATA TGGGTGAAAT 540

TGAAGTAACA GGTAAAGATG CTAGTCAGTT TGTGCAATAT TTATTATCAA ATGATACTGA 600

TAATTTAACT ACTTCAAAAG CATTATATAC TGCTTTATGT AATGAAGAAG GCGGTATTAT 660

TGATGATTTA GTAATATATA AATTAGCTGA CGACAATTAT TTATTAGTTG TTAATGCTGC 720

TAATACTGAA AAAGATTTTA ATTGGATTTT AAAACACAAA GAGAAATTTG ATGTTGAAGT 780

ACAAAATGTA TCAAACCAAT ATGGTCAATT AGCAATACAA GGACCAAAAG CtAGAGATTT 840

AATTAATCAA TTAGTTGATG AAGAkGTAAC TGAAA 875

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5897 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

TCTTTTTACG AAGGCTACCG TTTAGGATCT GATAACTTAA CTGTAGGAGA AATTGTATTT 60

AATACAGCGA TGACAGGTTA TCAAGAAACT ATTTCAGATC CATCATATAC AGGTCAGATC 120

ATTACTTTTA CGTATCCATT AATCGGTAAT TATGGTATCA ATAGAGACGA TTTTGAATCA 180

TTAGTACCTA CATTAAACGG TATTGTAGTG AAAGAAGCGA GTGCGCATCC AAGTAATTTT 240

AGACAGCAAA AGACACTTCA TGACGTTTTA GAATTGCATC AAATTCCAGG GATTGCAGGT 300

GTTGATACAA GAAGTATTAC GCGTAAAATT CGACAACACG GTGTGTTAAA AGCTGGTTTT 360

ACTGATCGAA AAGAAGATAT TGATCAACTT GTCAAACATT TACAACAAGT AGAATTACCT 420

AGTGTCGTAC TTGTAGACTT TGGTAAGAAG CAAAATATTG TTCGAGAATT AAACGTCAGA 540

GGTTGTAACG TCACAGTTGT ACCATATACA ACTACTGCCG AAGAAATTTT AGCAATGGCT 600

CCAGATGGCG TTATGCTATC AAACGGACCA GGTAATCCTG AAGTTGTAGA ATGTGCGATT 660

CCAATGATTC AAGGAATTTT AGGGAAAATT CCGTTCTTTG GTATCTGTCT AGGACATCAA 720

CTTTTTGCAT TATCTCAAGG AGCAAGCTCA TTTAAAATGA AGTTTGGTCA TCGTGGTGCG 780

AACCATCCAG TTAAAAATTT AGAGACTGGA AAAGTTGATA TTACGAGTCA AAACCATGGA 840

TATGCAATAG ATATAGATTC GTTAAAAAGT ACTGATTTAG AAGTTACTCA TCTTGCATTA 900

AATGATGGTA CTGTAGAAGG TTTAAAACAT AAAACATTAC CAGCATTTTC TGTTCAATAC 960

CATCCTGAAG CAAATCCAGG ACCGTCAGAT TCAAACTATC TATTTGATGA TTTTGTAGCA 1020

ATGATGACTA ATTTTAAGGA AAAGGAGCGT CATATCAATG CCTAAACGTA ATGATATCAA 1080

AACAATTTTA GTAATAGGGT CTGGGCCAAT TATCATAGGT CAAGCAGCTG AATTTGATTA 1140

TGCTGGAACA CAAGCATGTC TAGCTTTAAA AGAAGAGGGA TATCGAGTTA TTCTTGTAAA 1200

TTCAAATCCA GCGACAATCA TGACTGATAA GGAAATTGCG GATAAAGTAT ATATCGAACC 1260

GTTAACTCAT GATTTTATAG CGCGAATTAT ACGTAAAGAG CAACCTGACG CTTTACTTCC 1320

AACTTTAGGT GGTCAAACAG GTTTAAACAT GGCGATTCAA CTACACGAAA GTGGTGTGCT 1380

TCAAGATAAT AACGTCCAAT TATTAGGAAC TGAGCTAACA TCAATTCAAC AAGCAGAAGA 1440

CCGTGAAATG TTTAGAACAT TAATGAATGA TTTAAACGTT CCTGTACCAG AGAGTGACAT 1500

TGTAAATACA GTAGAGCAAG CCTTTAAATT CAAAGAGCAA GTGGGATACC CGCTAATTGT 1560

TAGACCGGCA TTTACGATGG GTGGTACCGG AGgCGGTATT TGTCATAATG ATGAAGAATT 1620

ACATGAAATC GTCTCAAATG GTCTTCATTA TAGTCCAGCA ACGCAATGTT TATTAGAAAA 1680

ATCTATCGCA GGTTTTAAAG AAATCGAATA CGAgTAATgC GTGaTAAAAA CGATAATGCC 1740

ATCGTTGTAT GTAACATGGA AAATATTGAT CCAGTTGGTA TTCATACAGG CGATTCAATT 1800

GTTGTGGCTC CTAGTCAAAC ATTATCAGAT GTTGAGTATC AAATGTTACG TGATGTTTCA 1860

TTAAAAGTTA TTCGAGCTTT AGGTATCGAA GGTGGTTGTA ATGTTCAATT AGCATTAGAT 1920

CCCCATTCAT TCGATTATTA TATTATAGAA GTAAATCCGC GTGTATCACG TTCATCAGCG 1980

TTAgCTTCAA AAGCAACAGG ATATCCTATT GCAAAATTAG CTGCTAAAAT CGCGGTTGGT 2040

CTAACATTAG ATGAAATGTT AAATCCAATT ACAGGAACAT CTTATGCAGC GTTTGAACCA 2100

ACTTTAGACT ATGTGATTTC AAAAATACCA AGATTTCCTT TTGATAAATT TGAAAAAGGA 2160

GAACGAGAGC TTGGCACACA AATGAAAGCA ACAGGTGAAG TTATGGCCAT TGGTCGAACT 2220

TTACCAAATG GTGAAAGCTT CGATCTTGAT TATATTAAAG AACGTATTTC ACACCAAGAT 2340

GATGAACGAT TATTTTTCAT CGGCGAACAA TTAGAAGAGG CACAACATTA GAAGAAATTC 2400

ATAATATGAC TCAGATTGAT TACTTCTTCT TACACAAGTT CCAAAACATT ATTGATATTG 2460

AGCATCAATT AAAAGAGCAT CAAGGTGATT TAGAATATCT TAAATATGCA AAAGATTATG 2520

GATTTAGTGA TAAAACAATA GCGCATCGCT TTAATATGAC GGAAGAAGAA GTATATCAAT 2580

TGCGTATGGA AAATGATATT AAACCTGTTT ACAAGATGGT TGATACTTGC GCAgCTGAAT 2640

TTGAATCTTC AACACCATAT TATTATGGTA CATACGAAAC TGAAAATGAA TCCATAGTTA 2700

CTGACAAAGA AAAAATCTTA GTATTAGGCT CTGGACCAAT TCGAATCGGC CAAGGTGTAG 2760

AATTTGACTA TGCGACAGTT CACGCCGTTT GGGCAATTCA AAAAGCAGGG TACGAAGCGA 2820

TAATTGTGAA TAACAATCCA GAAACAGTTT CAACAGACTT CTCAATTTCT GACAAATTAT 2880

ACTTTGAACC TTTAACTGAA GAAGATGTGA TGAATATCAT TAATTTAGAA AAACCTAAAG 2940

GTGTCGTTGT ACAATTTGGA GGACAAACAG CGATTAATTT AGCAGACAAA TTGGCTAAAC 3000

ATGGTGTTAA AATACTTGGT ACTTCACTAG AAAATCTAAA TCGTGCTGAA GATAGAAAAG 3060

AATTTGAAGC ACTATTAAGA AAAATTAACG TGCCACAGCC ACAAGGGAAA ACAGCTACAT 3120

CACCTGAGGA AGCATTAGCG AATGCTGCAG AAATCGGATA TCCGGTTGTA GTAAGACCTT 3180

CTTATGTATT AGGTGGTCGC GCAATGGAAA TTGTAGACAA TGACAAAGAG TTAGAAAACT 3240

ATATGACCCA GGCTGTAAAA GCGAGTCCGG AACATCCGGT ACTAGTCGAT AGATATTTAA 3300

CTGGTAAAGA AATTGAAGTT GATGCGATTT GTGATGGAGA AACGGTCATT ATTCCAGGAA 3360

TCATGGAACA TATTGAACGT GCTGGTGTGC ATAGTGGTGA CTCAATCGCT GTATATCCAC 3420

CACAAACTTT GACAGAAGAC GAGTTAGCAA CACTTGAGGA CTATACTATA AAATTAGCTA 3480

AAGGTTTAAA CATCATTGGC TTAATCAACA TTCAATTCGT TATAGCTCAC GATGGTGTGT 3540

ATGTTTTAGA AGTAAATCCA CGTTCTAGTA GAACGGTACC ATTCTTAAGT AAAATTACTG 3600

ATATTCCAAT GGCACAATTA GCTATGCGAG CAATCATTGG GGAAAAACTA ACAGATATGG 3660

GTTATCAAGA AGGGGTTCAA CCATATGCTG AGGGTGTCTT TGTGAAAGCA CCAGTATTTA 3720

GTTTTAATAA ATTGAAAAAT GTTGATATTA CTTTAGGACC TGAAATGAAG TCAACAGGTG 3780

AAGTGATGGG GAAAGATACT ACATTAGAAA AGGCGTTATT CAAAGGGTTA ACAGGTAGTG 3840

GCGTTGAAGT TAAAGATCAC GGTACAGTAT TAATGACCGT CAGTGACAAA GATAAAGAGG 3900

AAGTTGTTAA ATTGGCACAA CGCTTAAATG AAGTTGGCTA TAAAATTTTA GCAACGTCTG 3960

GAAcAGCTAA TAAATTAGCT GAGTATGACA TACCTGCAGA AGTAGTAGGC AAAATTGGTG 4020

TGACTAAAGG TAAAGAAGTA GAAAGGGATG GCTTCCAAAT TAGACGTACT ACAGTTGAAA 4140

ATGGTATTCC ATGTTTGACA TCTTTAGATA CAGCTAATGC CTTAACGAAT GTAATTGAAA 4200

GTATGACATT TACAATGCGT CAAATGTAAA TCAATCAAAC TGTATCGGTG GGGCTGTAAT 4260

TAACCATTTA CTTAAAGAAG TTTATATTAC AGCCTCATTA TTTTAATGAA TTTCTTAATA 4320

TAAAGGGAGA CaTATATGAT GAAAGATTTA CCAATTATTG CATTAGATTT TGAATCAAAA 4380

GAAAAAGTAA ATCAATTTTT AGATTTATTT GATGAATCAT TATTCGTAAA AGTAGGTATG 4440

GAACTTTTTT ATCAAGAAGG TCCTCAATTA ATTAATGAGA TAAAAGAAAG AGGCCATGAT 4500

GTATTTTTAG ATTTAAAACT GCATGATATT CCTAATACAG TTGGTAAGGC GATGGAAGGA 4560

CTAGCTAAAT TGAATGTTGA TCTGGTAAAT GTTCATGCTG CTGGTGGCGT AAAAATGATG 4620

TCTGAGGCCA TTAAAGGATT AAGAAAACAT AATCAAGATA CAAAAATTAT TGCAGTAACA 4680

CAGCTTACGT CAACAACAGA AGACATGTTA CGACACGAAC AAAATATACA AACATCGATT 4740

GAAGAGGCCG TTTTAAATTA TGCCAAGTTA GCAAATGCAG CTGGTTTAGA TGGCGTTGTT 4800

TGTTCACCTC TTGAAAGTCG TATGTTGACT GAAAAGTTAG GTACATCATT TTTAAAAGTA 4860

ACACCAGGTA TTAGACCTAA AGGTGCATCT CAAAATGACC AACACCGTAT TACGACACCG 4920

GAAGAAGCAA GACAGCTTGG TTCGACGCAT ATTGTAGTCG GTAGACCGAT TACACAAAGT 4980

GACAATCCAG TCGAAAGTTA TCATAAAATT AAAGAAAGTT GGTTAGTATA ATGGCTAAAG 5040

AAATTGCAAA ATCATTATTA GATATTGAAG CTGTAACATT ATCACCAAAT GATTTATATA 5100

CATGGAGTTC AGGTATTAAA TCACCGATTT ACTGTGATAA CCGTGTTACG TTAGGTTATC 5160

CTTTAGTTCG AGGCGCAATC CGCGATGGTT TAATTAACTT AATTAAAGAA CACTTTCCTG 5220

AAGTAGAAGT TATTTCTGGT ACTGCAACAG CTGnTATTCC ACATGCAGCT TTTATTGCTG 5280

AAAAATTAAA ATTACCAATG AATTATGTTC GTTCATCAAA TAAGAGTCAT GGTAAGCAAA 5340

ATCAAATCGA AGGTGCTAAA AGTGAAGGTA AAAAAGTAGT TGTGATAGAA GATTTAATTT 5400

CGACAGGGGG ATCTTCAGTC ACAGCAGTTG AAGCCTTAAA ACTAGCAGGT GCAGAAGTAT 5460

TAGGTGTTGT AGCTATCTTT ACTTACGGTT TGAAAAAAGC AGATGATACA TTTAGCAATA 5520

TTCAACTACC TTTTTACACT TTAAGTGATT ACAATGAATT AATTGAAGTA GCTGAmAmTG 5580

AAGGTAAAAT TTCTAGTGAA GATATCCAAA CATTAGTTGA ATGGAGAGAC AACTTAGCAT 5640

AATATAGACA CTAGAAGGAG GAATTCAACA AATGAATGAC AAAACATCTA ATGATTTATA 5700

TGGGAAGATA AAACATTGTA ACGAATTTAT CAATCATTCA AATGATTCCA ATCTATCTAG 5760

TAGTCACGAT GTCGACGAAA GTTCAACGAA GCAAAAACAT ATAAAAAATA AAACAACTAT 5820

TTAAAAACAA AAAAGCT 5897

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7965 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

TCATTCTAAA TCAACTTATT TTCCATTGCA TAAATTGCTG CTTGTGTACG ATCGCTAACT 60

TGTAATTTAC TAAATATATG ACTGACATGT GTTTTAATTG TTTTTTCAGA TACAAATAAA 120

GTTTCTGCAA TCTCTTTATT TGTTTTACCT TTAACCATTT CACGTAACAC TTCAATTTCT 180

CTCTTTGACA ACTTATTCGT GTAGTGTGGT TTTTGGCTAA CTGTTTCGAA TACATCTTGT 240

GCCTTAGGAT GTATCATTTT TTCACCGTTC ATAACTCGTC TAATAGTTTC AATTAATTGC 300

TGAGGCTCAA CGTCTTTCAT TTCATAACCA TCAGCACCTT TATTGATTGC TGAAATTACA 360

TGTTCATCAT CAACATAACT TGTTAATACC AAAACTTTAA TATCCGGATA ATGTGCCTTA 420

ATATATTCCG TAATTTCAAT ACCATTCATG CCAGGCATCA CTAAATCTAA TAGCACAATA 480

TCAGGGTGCT CATGCTCTTT TAAATATTCT AAAAATGTTT CTCCATCTGC AAAGTCTTGT 540

AAAACTTCTA TGTTTTCAaT CGTGGaTAAT AAAAATCGCA ATCCTTGtCG CACAATATAA 600

kGGwCATCTA CTAATATnAC TTTGTTCATG GGTTATCTCC TTAAAtCAAG CTATTTTATA 660

GGAATTGTGA ATTGTATTTG TGTACCCTTT GTTGGCTGAG AATGAAAGGT CACTTTACCT 720

CTTAATAATT TAACTCTTTG TTTTATGTTA TTAATACCGT GTGATGAAGC TATCTGAACA 780

TTATCGATCT CAAATCCTTG ACCATAATCA ATCACGTCAA TATATAGTAT ATCGTTCATT 840

TGTTTTAATG TAAGATCCAT TTTATTCGTA TCAGCATGTT TCTTAACATT ATTAATACAC 900

TCTTGTAATG CTCTGTATAT GTTTTCTTCG ATTTCATTAG ATAAATCGAT TAAACCTTCT 960

ACATTTACAT TTAATTGTAT ATGCATTAAT TTACTATATG CTGTCAAAGC ATGAATTAAA 1020

CCTTGCTCAA GTCCAACTGG CTTAAGTnGC CAAATCAATG CACGCATTTC ATTAACGGCA 1080

TTTTGACTCG TTtCCTCAAT CGTCTTGAAT GCTTGTTTAG CGATGGATTC GTTTGACATG 1140

CCATACGCAG CATGTGCtGT TAGTTTTACA GAAAATAACA TTTGATTTAC TGAATCATGT 1200

AAATCTCTAG CTAAACGATT ACGTTCATTA ATTTTTGCCG CTTCTTTTTC ACGGTCTGTT 1260

AAATAAATAC GTTTGATGGC TGACCCTAAT TGAAATGCGA CAGACTCTAG CAACTCTAAA 1320

TGACCCGATT TAAGTGGTAC CGTTGCATGA TGTGTAATAT TGTCATTTTG GCTAGGAAAT 1440

GCTTTAGAGG CTAAGTTAAT ACGAGAACAA TTGACGATAT TCGACGCTTT CATTAGCCTA 1500

CGTTGATTAA ATGCTTTCAC ACACCAACAA GACCCATCTT TAATATAGTG ACAGTGGTCT 1560

GCTGTCAAAG ATTGTGGTAG AGCCACATGT GATACAAGTT CATGTTCACC TACGCTATTG 1620

ATGAAAAATA TCCAGCCTGT CGTGAAATTA CTGCCCTCAA TTAAATATTT TAACGCACCT 1680

TGGGTCATGC TATACATTTC rGTTTCTTCG TTTAAAAATT CGGCAATCTC TTTTAATAAA 1740

GCTAGTCGCG TCCTTTGTTC CATCAAATCG CTCCAATTCA TTTTTACGTG TATTAACTAT 1800

TATACATTGA GTTATTATAT TTTTAAATCT TAGACGTAAA CATGATAAAA TGGCCTTGAT 1860

TACTCAATAG TTATATTTCG GAGAACTGAT TTGTGATATG ATATTAAAGA CTATAGGAGG 1920

ATTTTATGAA ATTTAAAATA CCAGAAAACT TTAATGACTT AAGTTTACGA GATATTTTCC 1980

AACAACTTAA GGTACCTAAA AAAGATTTAC ATCATTTAAA TATGTCTAAA GATATTACTA 2040

TTAATGATAA ACCTGCGCGA TTAATGGATA AAGTGCATAC TGGCGACGAT GTATTTGTTC 2100

CAACCATCGA TGAAAAAAGT AATTATGTTC CAAGTTATCG TTATGCACAA ATTAAATACG 2160

AAGACGATGA TATGGCAATC GTAATGAAAC CTAAAGGTGT TAAGACTCAC CCTAATGATT 2220

TAAAAGAAAG CAATACTTTA ATGAATCATG TGATTTACAC TATTGATAGT GACTATGTCG 2280

AACCAATTCA TCGACTGGAC CAGGAAACAG TAGGATTATT AATTGTTGCT AAAAATCCTT 2340

TAATGAAAAA AATTCTTGAT CGCATGTTAG AAGACAATGA TATTACGCGG ATATACAAAG 2400

CAAATGTTAA GGCACTTTTA CCTTTAAAAC CACAAACGAT TGATATGCCA ATTGGTAAAG 2460

ATAAATTCCA TTCGAATAAA CGACGTGTGT CTCCTACTGG ACAGCGTGCA ATTACACACA 2520

TTTTAACTTC AAAAATGATA AAAGAAGCTG TGTGCCmACT TGAAATCAAG TTGGATACTG 2580

GACGTACTCA TCAAATwCGT GTGCATTTAG CTGAAATTGG TCACCCTGTT ATTGGTGATC 2640

CTTTATATGG TGATTCAACG TTAAGACAAT TAGAACTTGA AAGTTACAAA ATAGAGTTTG 2700

TGcATCCCTT GACTAAGGAA GTCATTTCCG TTTCTTTGGA TGACTAATTT GATTAGTTTT 2760

GCATGATATT tAAACATGCA ATACCGCATT GTAACTAAAT CAAGTATCAA CtTAAAcGGA 2820

TAGATGGAAA ATTATTAATT TTTTCAGATG TTCGGTTTTT TTGTTTTTTA CGATGCTTAG 2880

GATTTTATAT TTTGATATTT TAGTAATTAT TCATTTTATA ACATCCTTGG ATAATGACTT 2940

GTAGTCTTTT TCAACTGCGT TACGTGTATC TATGGACAAT ACATGACATC ATAAGATTTT 3000

TATCACAGGT TGTTTGGCCA ATACATGTAC AACAATTCAT CATATAAAAA ATAGGTTCTA 3060

TAATAAAACG GACTCCATGA AAAGTTTTTC CTTTTCATGG CTCTATATCA AATCAGACTT 3120

CCAAACTTTA TTTTATATTA ATATTTAATT AATGAGGATC TACCATATCT TCTGGTTTAA 3240

TCCATGCTTC AAATTGTTCT TCTGTAACAT ATCCAGTTTG AATTGCAGAT TCTTTTAAAG 3300

TTAAACCTTC TTTATGGGCT TTCTTAGCAA TTTGAGCTGC TTTTTCATAA CCAATATGTG 3360

GATTTAATGC AGTAACTAAC ATTAATGATT GATTTAAATA ATTATCAATA TTCTCTTCGA 3420

TTGGTTCAAT GCCCACTGCA CAATTGTTAT TAAATGTTTC CATACCATCA GCTAAAAGAT 3480

AAATTGATTG TAGTGTATTA TGCATAATAA CTGGTTTATA AACATTCAAT TCAAAGTTAC 3540

CTTGTGAACT TGCGAACCAA CAACTGTATC ATTACCCATT ACTTGGACTG CnACCATTGT 3600

TAACATTTCA CATTGTGTAG GATTAACTTT ACCAGGCATA ATTGATGAAC CTGGTTCATT 3660

TTCAGGGATA GAAATTTCTG CCAAACCAGC TCGTGGCCCT GAAGCCAACC ATCTCACATC 3720

ATTAGCAATT TTCATTAAGT CTCCTGCTAA TGCCTTCAAT GTTCCATGCA ATTGAACAAC 3780

TTCATCATGC GCTGTAAGTG CGTGGAATTT ATTTTCAGAA GATACAAATG GATAACCCGT 3840

ATTTTCTGAA ATATAATGTG CCACTTTATC ACCAAATTCA GGATGCGCAT TAATACCAGT 3900

ACCAACAGCC GTACCACCGA TGGCAAGATT TAAAATGTGC TTCTTAGATT CAGATAACAT 3960

TGTTTCACAA CGGTCAAGCA TATAACGCCA GCCACTAATC TCTTGTCCTA GTTTGATCGG 4020

CGTTGCATCT TGTAAATGTG TACGACCAAT TTTAATAATT GAATCAAATT TATCTTCTkT 4080

TTCTTTCAAA GTATTTCTTA AAAGTTTTAA TGCAGGTTCT AATTTTGTTT CAACCTCTTG 4140

ATATAATGCA ACGTGCATAG CAGTTGGGaA TGTATCaTTC GaACTTTGAG ATTyATTTAC 4200

ATCATCATTk GGGTGGATAC TTTCATCACT TTGATGATCT TTTAAATACA TATTAGCAAC 4260

ATAACTTACT ACTTCGTTCA CATTCATATT ACTTTGTGTA CCGCTTCCTG TTTGCCATAC 4320

AACTAGTGGG AAGTGTTCAT CTAATTCACC TGATAAAATT TGATCACATG CGTATACAAT 4380

GGCATCTTTC TTTGCCTCGC TTAATTTTCC TAAATCAAAA TTAGCTATTG CTGCTGCACG 4440

CTTTAGTTGT GCAAAACCAT AAACTACTTC GATTGGCATA CGCTCTTTAC CAACTGGGAA 4500

ATTACGTTTA CTTCTTTCTG TTTGAGCACC CCAATATTTA TCTGCAGGTA CTTCTATTTC 4560

TCCAAAAGTA TCATGTTCAA TTCTTACTGA CATTCAATTT CTCCCCTTAT CACTGTTTAT 4620

TTAACTGTAG TATATCATTA AATAATTTAA TTGAGCAATT TATGATTAAA ACGTTTTCAT 4680

AATTTGAAAT AAAAATACAC TAATCGCACG TGTTCACCCT TTATTACAGT GATACGGTCA 4740

TACGATTAGT GTGTTATCTA TCATTATTTA GTTATTATTG AACTAAGTTT AATTACGATA 4800

CTTTGTTTTA GTAGCTTCAA CCGtAGCAAT AGCTGTAAGT ATATATAATA CAGCACTAAC 4860

AATTGTCGTA TATGGATTTA GAGCAACAAG CGTaCCTAAA ACTCCTGTTA AACTCGCATA 4920

TACAATACCT GATTGATTAC TTTTAATGAA TGTTTGCGCA TTAACATCAT CAATTAATCC 5040

TTTTGATAAA TTGAGTTGTA ATTTTATTAC TTTGAAAATA ACAGGTAAAT ATAATGCCCC 5100

AATTGCCAAT GGAAAAGCTT TAATTGATAT TAAACTTATA ATAACTGTTG CTATCAATAA 5160

TTGAATCCAG TATTTTCCTA ACATAAATAT ATAAATCTCC TCTAATTTCA TTCTTCAATA 5220

GCATATCATA ATCTTGGCAT ATTAAGAAAC GCGGTTTAAT GATTTCATTA AAAATATTAC 5280

TGATAGATGA CTTCTTTCAA TTATGTCTGG AGTAATTAAT TATCAATTCC GTTTAAATGG 5340

TGTTTTAATA TTTAAAATTG AACTTTTGAT ATATTACTAT GTCTGGTACA CAAATCAATG 5400

TTTTATGCTT TACAAAGTTA TATTGGCAGT AGTTGACTGC AGTCCACAAC ATAGAGGCTT 5460

CGGAATGTCA GCTTCTATTT CATGCAAGTT GGTGGAGCTC CAACATAGTG GAATTGGATT 5520

CCCAATTTCT ACAGACATTG CAAATTGGGG AAACGGGCCA CAAACTCAGA AACTGGTGGA 5580

AAGTCAGCTT AAAATAACAT GCAAGTTGGC GAGGCCCCAA AATAGTGAGA TCGGATTTCT 5640

AATTTCTACA GACATTGCAA ATTAGGGAAA CGGGCCACAA ACTCAGAAGT TGGTGGAAAG 5700

TCAGCTTAAA ATAACATGCA AGTTGGCGGG GCCACAACAT AGAAAAATTG GATCCTCAAT 5760

TTCTACAAAC AATGTAAGTT GGGGAAACAG CCCCAACACT GAAACTAGCA GAAAGTCAGC 5820

TTCTATGAAT ATAATAAAAA AGCTAGGTAA CAAAATGCTA CCTAACTTCA TATTCAAGAT 5880

AATCAATCCT ATTTGATATA TGTTCTATAC TATACATTAT TTACATGATA AATAACTGAA 5940

TATTACACAA TTATAATACT TTACTGACTG TCTTCTTCAG AATTCTTTTC TTGATCATTT 6000

TGATCAGAGA TTTGTTCCaT TTCTTTACCT AATTCTTTTA AATCTTCAAA ATCCGTTACC 6060

ATACTGTTTT CTTCTTCATG ATAATTTAAT TTTGGATCTT TGTCTTTAGA CATAATCAAT 6120

ACCTCACAGA TTTTTAATTA AGCAAAGCGT GACGTAAAGT AAGCTTTAAC ATCTTCAGGT 6180

AAACCTGCAG CCGCTTCTTT ATCAAGAATA ACATTTACCA TTCTATGTGC TTTTAAATCG 6240

GCTGGTTCGA AGCTTGTTTT ACCATTTTCT TGATATAATT TTTCAACTAC ATCTCGTTTA 6300

TTAGCACCTG TCACTACTAA GAAAATTTCT CTTGCTTCCA TTAGTCCTTG ACGAATACTA 6360

ACATTTAACT TACCTTGCTC ATCGATAGAA ACAACTTGTA ATGTTAATTT CCCTTTATTT 6420

TCTTTAGTTT TAATCTTATC AGCGATTAAT TCGATTGCAT CTTTTTCATA AGCAATTGGA 6480

TAAACTTGAC CTGCTGGTAC ACCTAACGCT TCGAAATATG ATTTTTTATC GTCATAATCT 6540

AAAATATTTA TTTGGCTAAA ATCAACAGCA TGTTTTTCAA CATTTTTCTT TAATTCATCT 6600

AGAACTGGCG CTTGATCTGT ATCTAAATGA AAACCTGCAA TTGTAGTAGG ATTATTGTTA 6660

AATTGCTTTC TAATAATATC AGCAGCATAT TCTGCTACAA GTTGACTATT GTCAAAGACT 6720

GATATTAATA ATTATTATAC CCTAACTTTC AATATATCAA ACCATTTAAC TTTAACATGC 6840

TTATACTCTA AATATAGCAC TTAAGCATCA TTTTTATAAT GAAAATGAGT AAATTTTAAT 6900

TCAATCCCGG rAAATCTTGT TGACGTAACG CTTCATAAAT TAACAACGCA GCAGTATTTG 6960

ATAAATTTAA TGAACGAATA TGTTCACTCA TAGGAATTCT TAACGCTGTG TCTTGATATT 7020

TCTCTTTCAC CCAGTCTGGT AATCCTGTCG TTTCTTTTCC AAAAATGAAG TAAAAATCTT 7080

TGTCATGATT TGAAAAATCA AAATCACTAT AAGTCTTTTT ACCAAATTTT GTTAATAAGT 7140

AATACTCGCC ATTTGTGACT TCAAAAAATG CTTCAATACT ATCATGATAC GTAATATTCA 7200

CAAATTCCCA ATAATCTAAA CCGGCTCTTT TTAACATTTT ATCATCAGTT CTAAATCCAA 7260

GAGGTTTAAT TAAATGTAAA TGTGTGTTTG TACCTGCACA CGTACGgCAA TGTTACCAGT 7320

ATTAGCTGGG ATTTCTGGTT GATATAAAAC GATATGATTT GTCATATTAC TATTCTCTCC 7380

TTGTGTCTAA TCCTTTTATC ATTTCATTCT GAACTTCTGC ATCCTCTTGA TCATAATTAG 7440

CATTGATAAA ATCTCTTGCT TCTTCCCCAA GAATTTGACC AATGGCCCAA TAAGCAGTTG 7500

CTCGAATCAA CGGTCTTTCA TCTGTTGTTG CAACTTTTTT CAATTCTGGA ATTGCATCCA 7560

CTTCATTAAA ATGCGCCAAT GCTAAAATAG CATTTCGTTG TATCGGCTTT TTACCACGCC 7620

AAGCACCTGC AAGgTGACCA TATGTTTGTT TGAATTCTTT ATTAGACATA CGTAGtAAAG 7680

GTACTAATCT TGGCTTTAAA ATTTCTGGTT CCAAAATGAT GTCATCTTGT TCGGTATTAA 7740

TACCTCTATT TTTCGGACAA ACTTGTTGAC ACGTATCGCA ACCATATAAT CTATTCCCAA 7800

TTTTATAACG ATATTGGTCA GGCATATAGC CTTTTGTTTG CGTTAAAAAA CTAATGCATT 7860

TCTGACTATT TAATTGGCCA TTTCCAACTA ATGCACTTGT TGGACAACGA TCAACACAAA 7920

TTGTACAATG CACCACAGCT ATCTAATAAT GGATCATCAG GTTCC 7965

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

GCCCTGTTGG AGAAATCACC TTTATACGAT GGTTGAAAAA GCATCATTAG GTACAATCGT 60

GGCAATTATA GTTATTTTGC TGTTTTTAAG AAACATTCGT ACGACGGCAA TTTCTATTAT 120

ATCGATTCCG TTATCACTTC TTATGGCGCT TATTGCTCTG AAATTGAGTG ATGTTTCATT 180

TGTAGTTGTT GAAAATATTT ATCGACGCTT AACAGATTCA GAAGAACAAC TAAAAGGTGA 300

AAATTTAATT ATCAGTGCGA CAACTGAAGT ATTTAAACCA ATAATGTCAT CGACACTAGT 360

TACTATTATC GTCTTCTTAC CACTTGTGTT TGTATCAGGT TCAGTAGGCG AAATGTTTAG 420

ACCTTTTGCA TTGGCTATTG CATTTAGTTT ATTAGCATCG TTATTAGTGT CAATTACACT 480

CGTTCCAGCG TTGGCAGCTA CACTATTTAA AAAAGGCGTT AAACGTCGTA ATAAACAACA 540

TCAAGAAGGA TTAGGTGTTG TTAGTACAAC TTATAAAAAA GTATTACATT GGTCATTAAA 600

TCATAAGTGG ATTGTAATTA TATTAAGTAC ATTAATTTTG GTTGCAACTA TTGTATTTGG 660

AGGACCGAGA CTAGGCACTA GCTTTATTTC AGCAGGTGAC GATAAATTTT TAGCTATTAC 720

TTATACACCG AAGCCTGGTG AAACGGAGCA AGCAGTGTTG AATCATGCGA AAGATGTTGA 780

AAAATATTTA AAACAGAAAA AGCATGTAAA AACAATTCAA TACTCAGTTG GCGGTAGTAG 840

TCCAGTAGAT CCAACGGGTA GTACAAATAG TATGGCAATC ATGGTTGAAT ATGATAATGA 900

CACGCCTAAT TTTGATGTAG AAGCGGATAA GGTTATTAAA CATGCAGATG GCTTTAAACA 960

TCCTGGAGAG TGGAAAAATC AAGATTTAGG AACAGGTGCA GGTAATAAAT CTGTAGAGGT 1020

TACTGTAAAA GGTCCATCAA TGGATGCCAT AAAATCAACT GTAAAAGATA TTGAACAGAA 1080

AATGAAACAG GTTAAAGGAC TAGCCAATGT CAAATCTGAT TTATCGCAAA CATATGATCA 1140

GTATGAAATT AAAGTCGATC AAAATAAAGC GGCAGAAAAT GGTATTTCTG CAAGTCAACT 1200

TGCAATGCAC TTGAATGAAA ACTTACCAGA AAAAACAGTT ACGACTGTTA AAGAAAATGG 1260

TAAAACTGTT GATGTTAAAG TCAAACAAAA TAAGCAAACA GC 1302

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

ATATATATTA ATTTAAACGT GTTTCACATG TACCAGTGTT AATGACAGAT AATGCTGCGT 60

TTAAACCACC TTCAACAAGG TTTTGTACTG CTTCATCAGA GAAGAAAGCA ATATGTGGTG 120

TTACTAAAAT TCTTTCATGT TCGATTAACT CTAATAATGT TTTATCGTCA ATGTCTTTAT 180

TAGTCCAGTC ATTTGTGAAG TATGCTGCTT CATTTTCATA AGTATCAATC GCAGCACCTA 240

ACAAAGTACC ATCGTTCACT GCAGCGATTA AATCAGGTGT ATTGATGACT GCACCACGTG 300

GATAGCTTTC TTTGTTCGCT GGAACATGTA AAGAAATAAT ATCGGCATCT TTAATAGCTT 420

CTTTAACACT ATCTTTATAA GTTAAAAAGT CTAAATCTTT ATTAGGATAG GCGTCATAAG 480

CTGTAATTGT AGCACCAAAT CCTGCATATA TtTTAGCTGT AGCAGCACCG ATACGACCCG 540

TACCAATAAT TGCAACAGTC ATATTTTTAA CTGGTTTAGA CATGATTTCT GCTTGCCAAG 600

TAAAATCATG TGCTTGTACA CGGCGTTCAA TATCTGGGAA GCGACGCACT AATTGTAGGG 660

CGATAGArAC AGAATACTCT GCAATtGTTT CAGGTGAATA ACTAGGAACG TTAGATATCA 720

CAATATTGTG TTTTTTAGCT AAATCTAAAT CATACATATC AAATCCAGCA GTACGTTGTG 780

CAATTTGTTT AATACCGTAA GATTCTAATT TAGGATAAAC GTCATTTTCT AACTTACCAA 840

ATTGCATTGT AGTTACGCCA TCGTAATCTT TTAATTGAtC GACTGTAGCA CTTGATAATA 900

GCTCTTTAGA AGTAGTTACT TCGACATTAT TCTtTtTCCC CCAATTTAAT GCCATCTCTT 960

TCTCATAATC ACGCGTaCCA AAGAACATAA TTCTCGTCAT TAT 1003

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5030 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

GGCTTTTATA GTGTTTACGA TTATTATGAT TACTTATATT CACGCTGTTA AAAATTATCC 60

AAATAACCGT ACTGTTCATT ATGGTTATAC AGCTGCATTT ATACTTGTTA TATTACAAGT 120

TATCACAGGT GCATTATCTA TTATGACAAA TGTTAACCTG ATAATCGCAC TTTTCCATGC 180

ATTATTTATC ACTTATTTAT TTGGTATGAC AACATACTTT ATCATGCTAA TGTTACGATC 240

AGTAAGAAGT GACArGCAAT AACaAAAAAG cmAACCGTAA TTTTAATGGC ACGCCCATTA 300

AAATTACGGT nTTTTATATC AATATTTAAA AtTAAACCtA AGCCATGTAA AAACGAGATT 360

ACACGTCAAT TGTTGTGTAA TCTCGTTTTA TnTTAATCAT TTTAGTCAGT TGCTTTTTCA 420

ATTTCGATTA ATAAATCGCC TGTCGCTATT GTGTCACCAT TATTTACAGT TACTTGTTTA 480

ATCACACCGT CAAATGGTGC TTGAATTGTT GTTTCCATTT TCATAGCTTC AGTAATTAGC 540

AACGGCTGAT TAGCTTTCAC AGTTTCACCT ACACTAACCT TGACTTCAGT TACTGAACCT 600

GGCATTTGAG CACCGATATG ACTTGGATTA CTCTTATCTG CTTTTGGCTT AACGTTCGCA 660

TTTGTATGCA CATTTTCATC TTTAATGTAA ATACGTCTCG CTTGACCATT CATCGCATAG 720

CGTTTACCTT TATCGATTTC GATTTCTACT GTTTCACCAT TACGCATTCC AAAGAAGAAT 840

GTAGGCGTAT CAAGTAACGA TAAGTTTCCG TATTGATTTC TAGTTTGAAT ATATTGTTCA 900

TATACTTTTG GATATAGTAC ATAACTAATA ATATCTTGCT CCGTAACAGG ACCTTGTTGC 960

TCTTCTTCAA GCAACTCACG GACTTTTTCA AAATCAACTG GCTCTAGATA TTCACCTGGA 1020

CGAGCTGTTA GTGCTTCTTG GCCTTTTAAA ATAACCGCTT GTAAATCTTT ATTAAAACCA 1080

TTTACAGGTT GTCCTATTTC ACCTTTGAAG AACGACACTA CTGATTCTGG GAAATCTAAT 1140

TTATAGCCAT CTGTAATCAC GGATTGTTCA TCAAGATCAT TTTGTACCAT ATAAAGTGCC 1200

ATATCACCAA CTACTTTAGA CGATGGTGTT ACTTTTACGA TATCACCAAA TAAGAAATTC 1260

ACTCTGCGAT ACATATCTTT GACTTCATCA AATCTTTCGC CTAAACCTAA ACTTTTAGCT 1320

TGTTGACTTA AATTCGAATA CTGTCCACCA GGCATTTCAT GTTGATAAAT TTCAGTATTC 1380

GGTGATTTGA TATCACTTTc AAAGTCTGAA TAATAAGTAC GTACAGTTGA CCAATAATGA 1440

CTAAGTGACT CCATACCTTC AATATCAGTT CTAAGGTGGC GTGGGAAGCC ATTTAATGCA 1500

TAATATAACG AATTGGCGCT TGGCTGACTT GTTAAACCAC TCATTGAAGC AACAGCAGTA 1560

TCAATGATAT CGACACCAGC ATCTATTGCT TGTTTGTATG TTAATAAACC ATTACCACTT 1620

GTATCATGAG TGTGAAGATG AATTGGTAAA TCTACAGCTG ATTTTAACTC ACCAATCAAT 1680

TCGTAAGCGG CTTTAGGTTT TAATAAGCCT GCCATATCTT TAATCGCTAA AATATGGAAA 1740

CCTTCACGTT CTAACTCTTT AGCTAGTTTG ACATAATACT CTAAAGTATA AATGTTTGAT 1800

CGCTCAGGAT TTAAAATGTC ACCTGTATAA CAAATAGTAC CTTCTGAGAT TTTGCCCGCT 1860

TCTTGTACTG CTTCATTGGC AACTTTCATT TGATCTACCC AGTTTAATGA ATCGAAAATT 1920

CTAAAGACAT CTATGCCTGC TTTAGCACTT TCTTGTACGA ATTTATGAAT AACATTATCA 1980

GGATAGTTTT TATAACCAAC TGCGTTTGAA GCACGTAACA ACATTTGGAA TAATACATTT 2040

GGAATAGCTT TACGTAGACG TTCAAGTCGT TCCCATGGGT TTTCCTTCAA GAAATTATAT 2100

GCCACATCAA ATGTAGCACC GCCCCACATT TCTAGTGAGA AACCATCTTT AAATACGTCC 2160

GCTGTTTTGG ATGCGATATT AATCATATCC TTAGTTCTAA CTCGTGTAGC TAATAATGAT 2220

TGGTGTGCAT CTCTAAAGGT TGTATCTGTT AGTAAGACAT CATCCTGCTT TTTAACCCAT 2280

TCAGCTACAC CTTTTGGACC TACTTCATCA AGCAATTGTT TCGTACCACT AAATGAAGCG 2340

ATTTTACTTG AAGATACAGT TGGAATTGAT GCTAATTCAT AGTCTGGTTT CGGACGTTTC 2400

TCAACATTTG GGAAACCATT AATTGTTACA TTACCTATAT ATTCTAATGT TTTAGTACCT 2460

CTATCTAGAG ACGGCTGAAT GTCGAAAAGT TCTGGTGTTT CTTCAATAAA TTTAGTTGTG 2520

TTAACACCAC GAATACGCAT TTCTCGTAAT GAGCGTACCA TTTTTTCTTC TGCTTGTTTA 2640

AATGATATCG CGTGTGTAGA TAATTTTACG AGTAATGAAT CATAATAAGG TGATATCTCA 2700

GCACCTTGGA AACCATCTCC AGCATCAAGA CGTACACCAA AGCCCCCGCT TGAACGATAA 2760

GCAATGATTG TTCCAGTATC CGGCATGAAA TCATTTAACG GATCTTCTGT TGTAATACGA 2820

CATTGGATGG CATAGCCTAA TGTTGTAATA TCTTTTTGTT GCGGCATATT AATCTCTTCA 2880

CCAAATAAAT CGGCACCTGC TGCAACTAAA ATTTGTGTCT TAACAATATC AATTCCTGTT 2940

ACCATCTCTG TAATTGTATG CTCTACTTGT ACACGAGGGT TAACTTCTAT AAAGAAGAAT 3000

TCGTCACCAG ATACTAGAAA TTCAACAGTA CCTGCATTGA CATATTTAAT ATTTTCCATC 3060

AATTGAATTG CAGCATCACA AATACGTTGA CGTAATGTTG ATGATAATCC AACTGATGGT 3120

GCAACTTCTA CAACTTTTTG ATGACGACGT TGTACTGAAC AATCACGTTC AAATAAGTGT 3180

ACGATATTTC CATGTTCGTC ACCTATGACT TGTACTTCAA TATGCTTTGG ATTATCAATG 3240

TATCTTTCTA TGTAAACTTC ACTATTACCA AATGATTTTT CAGCTTCTGA TTTTGCTCTA 3300

TGGAAAGCAT CTTCTAATTC ACTTTCTTCA CGAACGATTC TCATACCTTT ACCGCCGCCA 3360

CCACTTGTGG CTTTAATCAT TAGCGGGAAA CCAGCTTCTT CTGCAAATTC TTTTGCTAAT 3420

TCATATGATT TAATTGGACC GTCTGTACCA GGAATAACTG GTAAATCTGC CTTGATAGCC 3480

GTTGTACGAG CTTTAACTTT ATCTCCAAAC ATATCTAAAT GTTCTAAATG AGGACCAATA 3540

AATTTAATTC CTTCTTCTGC ACAACGACGC GCAAATTGTT CATTTTCACT TAAAAATCCA 3600

TAGCCAGGAT GAATCGCATC CACATTCGCT TGTTTTGCTA CATCAATGAT ACGCTCAATA 3660

TTTAAATAAC TTTCAGCAGG ACCTAAATCA CTTCCAACTA AATAGGATTC ATCTGCTTTA 3720

TATCTATGTA ATGAACTTTT GTCTTCATTC GAATAAATTG CAACTGTGCT GATGTCTAAT 3780

TCTGCCGCCG CTCTGAATAT ACGAATTGCA ATTTCTCCAC GGTTAGCAAC AAGTAACTTT 3840

TTTATTTGTT TCAATAGCGA TACACTCCTC AAACTATTAG AATTTTCTAA CTAATTAGAT 3900

AATAAAATTT TATCTTAAAG CGCTCTGTTT TGCTATAGTt mTGTTTCmAA TTTTCAAAaT 3960

TTaACATyCT tGAGACAATT AAAaCCyCCG CTTCmGaAAT AATAATTTCA AAAATGACTA 4020

TGCAACAACA GGTAGTTCCA CGTTTTTGTT GTGAAACATT TTCGATTTCT ACAACTCTAA 4080

AAAATTAAAA ATAAAATTGC AAAACATCAA CATTTATTAT CAATAGCGAT AACTTTATCT 4140

TATCATCATG ATTCTAATTT CGCCACCACA TTTAGTAATT TTTAGTCATA AAATTTAGTT 4200

ATAATTATAC GTTGTTTTGT TTATAAAATT TGATAATCak GAGTAATCtC GTAATATCAA 4260

AACaAAAAGG AAGTTAAGCG TTGTTTGGTT GcCTAACTTC CGTTATTGAA CTCATCcAGT 4320

TCTCGTACTA AATATTGGCT AGTATTTTTT TAATTAAATT GTCTTCTTAT ATCAACTTTT 4440

TGTTGTTGTT TCTTTCGTTG CTGGTCTACT TTGATTTGTT TACCTACAAT CAGAAGTAAA 4500

CCCATAGCAA TACTTAAACT AATCATTGAT GATCCACCAA AGCTGATAAA TGGCAATGGC 4560

ACACCAGTTA ATGGAATTGT TGCCGAAATA CCGCCAATGT TTACAAACGT TTGACTTCCA 4620

AAGTATGTGG CAATCCCAAC ACACACAAGT TTATAAAAAT ATGATGATGT TTTATTTGCA 4680

AACTGGAAGG CACGATATAC AATAAAGAAC TCTAAAGTAA TAACTAGCAA TCCTCCGATT 4740

AAACCTAATT CTTCGCAAAT AATTGCAAAA ATAAAATCTG TATGTGGTTC TGGTAAATAG 4800

CCCAATTTCA TTGCACTATT TCCTAATCCT TTTCCAAATA CGCCACCGTT ACCTATCGCA 4860

AGCAATGAAT TGGAAATATG GTATCCAGTT CCTGATTCGA ATTGGAATGG ATCTGTTAGC 4920

GTACTAAATC TGGCAGTTAA ATAACTTGGT AACCAACCAG CCATTAATGC AATGACAAAT 4980

ACTACTAAGA ATCCTAGCAC TGCTGGTATA CCAAATCTTA GGACTTTGTT 5030

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

CTTGTTAATC CGAAAATTAT TAGTCAATCA AATGAAACAA TAACAGACTT nGAAGGTTCA 60

ATTACATTGC CAGATGTTTA CGGCGAAGTG ACAAGAAGTA AAATGATAGT TGTCGAAAGT 120

TATGACGTCA ATGGGAACAA AGTTGaACTA ACTGCACATG aAGATGTAGC AAGAATGATT 180

TTGCATATTA TAGATCAAAT GAACGGTaTC CCTTTTACAG AACGTGCGGA CCGTATTTTA 240

ACAGATAAAG AAGTGGAGGC ATATTTTATA AATGACTAAA ATAATATTTA TGGGTACACC 300

AGACTTTTCA ACAACTGTTT TAGAAATGCT TATTGCAGAA CATGATGTCA TTGCAGTCGT 360

AACGCAACCA GATCGACCTG TTGGACGTAA ACGTGTTATG ACACCACCAC CAGTTAAAAA 420

AGTTGCAATG AAATATGATT TACCTGTATA TCAACCTGAA AAATTAAGTG GATCAGAAGA 480

ATTAGAACAA TTGCTTCAAT TAGATGTAGA TTTAATTGTA ACTGCTGCTT TTGGACAATT 540

ATTACCTGAA TCATTGTTGG CATTACCAAA TCTTGGGGCA ATTAATGTAC ATGCATCATT 600

GTTACCGAAG TATAGAGGTG GTGCACCAAT TCATCAGGCA ATTATCGATG GTGAACAAGA 660

AACCGGCATA ACAATTATGT ATATGGTTAA AAAATTAGAT GCGGGTAATA TTATTTCGCA 720

ATTAGGGGCA GATTTATTAA AAGAAACTTT ACCATCTATT ATAGAGGGCA CAAATGAAAG 840

CGTACCTCAA GATGATACGC AAGCAACATT TGCTTCCAAT ATTCGACGCG AAGATGAGCG 900

AATTAGCTGG AATAAACCAG GAAGACAAGT GTTTAATCAA ATTCGTGGAT TATCACCATG 960

GCCAGTTGCT TATACAACTA TGGATGACAC TAACTTGAAA ATATACGATG CTGAACTCGT 1020

TGAGACTAAT AAGATAAACG AGCCTGGAAC CATTATAGAA ACGACTAAAA AAGCCATTAT 1080

TGTTGCTACA AATGATAATG AAGCTGTTGC AATTAAAGAT ATGCAATTAG CTGGGAAAAA 1140

GAGAATGTTA GCTGCCAATT ATTTAAGTGG TGCGCAAAAC ACACTAGTAG GGAAGAAACT 1200

TATATGATAG AAAACGTGAG AAGTCTTGCT TTTGACACGA TTCAAGATAT ATTAAATGAA 1260

GGTGCGTATA GTAACTTGCG TATCAATGAA GTGTTGTCAG AAAATGAATT AAATGCAATG 1320

GATAAGGCTT TATTTACAGA AATTGTCTAC GGAACCGTTA AAAGAAAATA TACGTTAGAT 1380

TTTTATTTA 1389

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2746 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TTTGCTAATA ACAATAAAGC CAAAGCCGAT TCACACTCTA AACAGCTAGA AATTAATGTT 60

AAGAGTGACA AAGTACCTCA AAAAGTAAAA GATCTAGCAC AACAACAATT TGCTGGTTAT 120

GCTAAAGCAT TAGATAAACA AAGTAATGCA AAAACTGGTA AATATGAACT TGGCGAaCTT 180

TTaAAATTTA TAAATTTAAT GGTGAAGAAG ATAATAGTTA CTATTATCCA GTTATAAAAG 240

ACGGTAAAAT TGTTTATACT TTAACACTTA GTCCTAAAAA TAAAGATGAT TTAAACAAAT 300

CAAAAGAAGA CATGAATTAC AGTGTTAAAA TTTCAAACTT CATCGCTAAA GATTTAGACC 360

AAATTAAAGA TAAAnATTCA AATATCACTG TTCTTACTGA TGrAAAAGGG kTTTATTTTG 420

aAGAAGATGG cmAAGTTAGA TTAGTAAAAG CTACGCCTCT ACCTGGTAAT GTAAAAGAnA 480

AAGAAAGTGC TAAAACAGTT TCAGCAAAAT TGAaACAAGA GTTaAAAAAT ACAGTAACAC 540

CTACTAAAGT TGAAGAAAAC GAaGCGATrC AAGAAGATCA AGTTCAATAT GAAAATACAT 600

TAAAAAACTT CAAAATTwGA GaACAACAAT TCGATAACTC ATGGTGTGCA GGATTCAGTA 660

TGGCAGCATT ATTAAATGCa ACTAAAAATa CAGACACTTA TAATGCACAT GATATTATGC 720

AAATGATTGA ATACGGTAAA TCACAAGGCA GAGATATTCA TTATCAAGAA GGCGTACCAT 840

CATATGAACA AGTTGATCAA CTTACAAAAG ATAATGTAGG AATTATGATC CTTGCACmAA 900

GTGTATCTCA AAACCCTAAT GACCCACATT TAGGACATGC GCTAGCAGTT GTTGGTAATG 960

CTAAAATTAA TGACCAAGAA AAACTTATTT ACTGGAATCC TTGGGATACA GAaTTATCAA 1020

TCCAAGATGC AGATTCAAGC CTATTACATT TATCATTCAA TCGTGATTAT AACTGGTATG 1080

GTTCAATGAT AGGTTACkAA AAAGTAATAT AGATATTGAT TAAAGGCAGG TAAAACTATG 1140

TATCAACTAC AATTTATAAA TTTAGTTTAC GACACAACCA AACTCACACA TCTAGAACAA 1200

ACCAATATCA ATTTATTCAT TGGTAATTGG AGTAATCATC AATTACAAAA ATCAATTTGT 1260

ATACGTCATG GCGATGATAC AAGTCACAAT CAATATCATA TTCTTTTTAT AGATACGGCA 1320

CATCAACGCA TTAAATTTTC ATCTATTGAT AATGAAGAAA TCATTTATAT TCTTGATTAT 1380

GATGATACAC AGCATATCCT CATGCAAACG TCATCCAAAC AAGGTATTGG CACTTCGCGA 1440

CCAATCGTTT ATGAGCGCTT AGTATAACTA ATTTAAATGA TTTCACTTCA TAAAGCGGGT 1500

TGGCGAGAAT TCAATTTCTC ACCAGCTCGT TTTTTCATTG TAATAATAAT CTTTAACATT 1560

TATTCTTTCT CTATTAATTT TTCTCAAACT ATCTTATCTT TATGATAATT AATTAAAATG 1620

CCCTTTTAAA TTCTTATAAA ATAAAAAAGC CACCTATCGT CGCTAATAAA CGACGCAAGT 1680

GACTTAATAT CATATTCAAA ATAACTTATG GGAATTTAGG GAATTGATCG AAGTCAGGAT 1740

CACGTTTTTC TTTAAACGCA TCACGGCCTT CTTTCGCTTC ATCAGTTGTG TAATAAAGCA 1800

ATGTTGCATC CCCAGCCATT TGTTGTAAAC CAGCTAAACC ATCTGTGTCA GCATTCATAG 1860

CTGCTTTAAG GAATCGTAAC GCTGTTGGTG AGTGTTTCAT AATCTCTTTA CACCATTGCA 1920

CAGTTTCATC TTCAACTTTC TCTAAAGGTA CCACTGTATT TACTAGACCC ATATCTAAAG 1980

CTTCTTGTGC ATTGTATTGA CGACATAAGT ACCAAATTTC ACGTGCTTTC TTATGTCCAA 2040

CGATACGTGC TAAATATCCT GAACCATAAC CCGCATCAAA TGAACCTACT TTAGGACCAG 2100

TTTGTCCAAA AATAGCATTA TCAGCAGCAA TCGTTAAGTC ACAAACAACA TTTAGTACAT 2160

TACCGCCACC TACAGCATAA CCTTTTACCA TCGCGATAAC CGGTTTTGGA ATAATACGAA 2220

TTAAACGCTG TAAATCTAAT ACATTTAAGC GAGGGATTTG GTCTTCACCT ACATAACCAC 2280

CATGTCCACG TTTCTTCTGG TCACCACCAG AACAGAATGC TAAATCACCT TCACCAGTTA 2340

ATACGATAAC TGAAACGTTT TGATCATCAC GTGCACGTGA AAATGCGTCA ATCATTTCAG 2400

CAACTGTTTT AGGTGTAAAC GCATTGCGTA CTTCAGGGCG ATTTATTGTT ACCTTAGCAA 2460

TCCCTTCGTA AAATTCATAT TTGATTTCAT CATATTCTCT AAGTGTTTCC CATTGTCTGT 2520

TCCACATGAA TTGTATGACC TGTAGCAGAA ATTAATTTAC ATTTACTATT AGGAATTAAA 2640

TTTGCCATTT TTTTCGCAAT CTGTACAAAT TTTTCATCAT ATTCTCCAGC TAATATTAAT 2700

GTTGGTACTT TAATTTCTnT CAGCGCGGCC ATAAGTTTGG CATTTG 2746

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 900 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

TAATGTTTAG TTTATTAACA GTAAGTTCGT ATATCAATGT TTAGTGCTCC CCAAAATTGA 60

AGTTTGAATT TTAAAAGCAT CTTGTAGAAT TTAGTTGTAT TTTTTTCAAA GAAATTCATT 120

TTGATTATTT TTGATAATGA GCATTTTAAT AGTAATACAT GTTTATAGTG TGTAGTATAT 180

GTCTATACTA GTAGTAACTA TATAGAGAAA GTAGGAATAA ACTATGTCAC AAGATGTAAA 240

TGAATTAAGT AAGCAACCAA CGCCAGATAA AGCAGAAGAT AACGCATTTT TCCCATCACC 300

ATATTCCCTT AGTCAATATA CAGCACCTAA AACAGATTTT GATGGTGTTG AACACAAAGG 360

TGCCTATAAA GATGGTAAAT GGAAAGTATT GATGATTGCT GCTGAAGAGC GATATGTATT 420

ATTGGAAAAT GGAAAAATGT TCTCTACGGG TAATCATCCT GTTGAAATGT TATTACCTTT 480

ACATCATTTA ATGGAAGCAG GTTTTGACGT TGATGTTGCG ACATTATCTG GTTATCCAGT 540

TAAATTAGAA TTATGGGCTA TGCCAACTGA AGACGAGGCA GTTATAAGTA CTTATAATAA 600

ATTGAAAGAA AAATTAAAAC AGCCAAAAAA ATTAGCAGAT GTGATTAAAA ATGAATTAGG 660

ACCTGATTCA GACTATTTAT CTGTCTTTAT CCCAGGCGGA CATGCTGCAG TTGTTGGTAT 720

TTCTGAAAGT GAGGACGTTC AACAAACATT AGATTGGGCA TTAGACAATG ACCGCTTTAT 780

AGTTACATTA TGTCATGGAC CAGCAGCACT ACTTTCAGCA GGGCTTAACA GAGAAAAATC 840

TCCATTAGAA GGATACTCTG TTTGTGTCTt CCCTGaCTCA TTAGATGAAG GTGCAAATAT 900

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATCTGAnTnG AGATAGTGAT AATGTGTCAC CcAATTTTaA AcCtTTATTT TTaAGcGtTT 60

CaTCaGCTAA CaCtTCaTTa TCtTTAGtCG cTTTATGcCC tTCtATTAAA CtCGGaACtA 120

AAAATGaTGa CtTTTCAACa CCGAACaCTA AAACaTTGtC tTTTTGATGG CCaTTAGACA 180

CAATTTCCCC TGTTTGCTTC AAAGTAGCTT GCTTCTTGTA TTTATTTTCA ATATCTTTCT 240

TGTTAAAAAC AGATTGTTGC ACAGTTTGAT TGGCATCTTT ATTTAGAACA ATGGCATCTG 300

CTTGCCACTT ATCAATGCCT TCTTTATTCA TATTGATAAG ACCATTCGCC AATCCAGATA 360

ATAAAAATAG CAAGTAACTA ATCATCGTTA ACACACCAAT AATTAGTCCA AACTTCAATT 420

TGTTGCGCCG TATTTCATTC CAAGCTAAAA ACATGCATTT CTCTCCCTAC TACTATGATT 480

TAAACATTGT TTATATTCTT AGATGCACGT ACGTCGTGTT GCGCTCTGTA ATGTTATACA 540

TACACTTATC CTTCATTATA CCCGAACTTT TTATATTAAA AGCAAATTTA TGGAAAATGC 600

AATTAATTGT CTATTATTTT TGTACGGTAC ATTTAAAATT AAGGATCAAT TTAAAAACGC 660

CTACATATAC CTTTAAGTAC ATGTAGACGT CCAATTCATA TATTATTTAA CTTCGCCTGT 720

TTTAGGATCG AATTGCTTAA TAGCATTTTT ACGTAATTTA TCTTTTGCTT TrTCACTTGC 780

TTTATAGTTA TTGTTGTAAA TCGTAGCTTC CCAACTACCA TACATTGGGT TAGGGAAAAT 840

GATATATTTC TTACCGAAAT CGTCTTTATG TTTTTCAATT AATGCTTCAC GAGATTCAGC 900

TGTAGCTTCT TTTGGATCTG TAAAGTCTAA TAAATTATCT CCAAATAGCA TGACAAGTTT 960

ATGATCCTTT TGAACCATTT GTCTGCGTGA TTCTTTACTC TTATCATCTT TACCTTTTAG 1020

TAAAATATGA CTCTTCTTAG CTTGAGGGAT ACCTTGTTGT TTTAAGTTCT TTTGTGTTGC 1080

CTTTAAATCT TTTTCTTTAT CTCTATCAGA AATATAGTAG ATATCGACAC CTTTTTTGTC 1140

AGCATATTTC AAGAATTCTT TTGCGCCATA GACAGGTTTA GCTTTAGCAG cTTGTACCCA 1200

TTCATGCCAA CCTTCTGGGA AAGGTTTATT ATGTATTGAT GCATAGCCTT GATATGGAGA 1260

ATTATCTAAA ACTGTTTCAT CTAAATCCAA AGCAATAGCT AACTTATGTT TACCTTTATT 1320

CTTTTTAATC TCTTTATCTA ACTGTGTCTT TGCACTGTTA TAACCTTGTA AATATAATGC 1380

TTTTGCTTCA GCTGAATTTT GATACCAAGC CACTGCCATA ATATTTTGAT TACCAAGATT 1440

CGCCTTTTGT GATGCTGGTA TAGAAGCTTG TTGCGTTTGT TGAACTTCAG CAGAACTTTT 1500

GGCAAACGCT GTAGAATTTG TCGTTTGTGG TGCTGAAACT GTAACCGCTA CCGATAATGA 1560

TGCTATTGCA ATATACTTTG AAATTTTATT CATCTTATCA CCTCATGATT AATATTTAAA 1620

ATACAGTTAA AATTATAAAT GCATTTATTT AATATTGCTA TACTATGAAA AGATATTTAA 1680

TATTATTTCT TGgAAAAGCT AACAAATATG TGAACATTTC ATATAAGCAT GATTTAATGG 1740

GTGACTAGGC CTTCCTATCA GACATATTCA CTCATCCACG TATCATTATG TGTACAGTGT 1860

GCTATCTCTT ATTTACCTAT TGGAACAACC ATAAACTCAT CCATAGTTTA CCTTTTATAA 1920

ATAGCAGTCC TCACTCATAC AATTTCTCAT AAAAATCACA ACGCTCCAAC GTATTTCCAA 1980

CTTACTTTCA CCTATTTTAA TTCATAAAAA CGACACTTTA ATTGTCATTA TCCAATAATA 2040

GCAAGACGTT ATTATTGCAA TCTTTTTTAT AAAATAATAG AATCATAGTA TTGTCATTTA 2100

AAGATAAAGT AAGAACGTTT TTATTTTTCA GATTTTTTAA ATTATTATGA ATATCTAGTT 2160

TTAGGAAGGA AATTACATTG AAAAAACAAG TTATTATTTC GGGCCTCATG TTATTTTCAC 2220

TATTTTTTGG AGCCGGAAAT TTAATATTCC CGCCCATGCT TGGCCATACA GCGGGTCAAA 2280

ATATGTGGAT TGGTATGCTA GGCTTTGCCC TTACAGGCAT ATnACTCCCC TTTATTACTG 2340

TTATTGTTGT TGCATTTTAT GATGAAGGTG TTGAAAGTGT AGGCAATCGT ATACATCCAT 2400

GGTTCGGGTT TATTTTTGCT GTCGTGATTT ACATGTCTAT CGGAGCATTT TACGGTATTC 2460

CACGTGCTGC AAATGTCGCG TACGAAATTG GTACAAGACA CATTTTACCT GTGCATAACC 2520

AATGGACTTT AATTATATTC GCAGCAATCT TTTTTGCCAT CGTTTACTGG ATTAGTTTAA 2580

ATCCATCGAA AATCGTTGAT AATTTAGGTA AATTATTAAC ACCGTTATTA CTATTAATGG 2640

TCGCTCTATT AAGTATTGCT GTCATTTTCA ACCCTGAATC TGCACTAAGT GCACCTAAGG 2700

ATAAATATAT AACACATCCT TTCATTTCAG GAAGTTTGGA AGGCTATTTT ACAATGGATC 2760

TTGTTGCTGC GTTAGCTTTT TCCGTAGTCA TTGTCAATGG CTATAAGTTT AAAGGCCTCA 2820

CAGATCGCAT GAAAATTTTA AAATATGTCT GCTTTTCAGG TCTTATTGCA GCCATATTAC 2880

TTGGAATGAT TTACTTTGCA CTTGCATACG TTGGGGCATC AACAGCTCCA GGAAACTTTA 2940

AAGATGGTAC AGATATATTG ACGTACAACT CATTACGATT ATTTGGTTCG TTCGGTAACC 3000

TCGTATTTGG AATGACGGTT ATCCTTGCAT GCCTAACAAC ATGTATAGGA CTCGTcAATG 3060

tTGCGCCACA TTTACTAAGA AACACGTACC TAAGTTTTCT TATAAAATAT TCGCACTTAT 3120

TTTCtCTATC ATAGGGTTCT TATTTACAAC ACTTGGTTTA GAAATGATTT TAAAAATTGC 3180

TGTCCCATTA TTGACTTTAA TATATCCCGT GTCGATTGCA CTTGTACTCA TATCATTTGC 3240

TAACATGTTT AGCACATTCA GATTCAGTTG GGCCTATCGA CTCGCAACTG TTATTACATT 3300

GATTATTTCA ATTTTACAAA TACTAAATAG TTTCAACTTA TTACACGGTG TTATTTTGAA 3360

ATCGTTTATG ATGTTACCTT TAGCAGATAT CGATTTAGCT TGGCTTGTAC CATTCATGCT 3420

CTTTGCTATT ATCGGTTTCA TAATCGATGT ATTTATACGC CGTCCGAAAC AAGCGACAAC 3480

TTAATAAATG CTCACTGCCT AGTAATGATT GACCCATCGT TACTAgGCTT TTttATATGA 3540

TAAAAAATCC TAGCTGTTAT TCAAAAATAT TAGTTTTTAA AA 3642

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

TTATTGATAT TGAAAATTCA AAAACTGCAA CACATCTTAT CACTAAAAAC CAACACTATC 60

ATCAAACTGA CACTCATTTT GAACAGTATA AGAAATTTAT TTTAGATTCA GGTATATCAT 120

CAACACAATT TGTATATAAT AACCTGTCTG TAAGCGGATT TAAATATACT AATGATGGTA 180

AGAATCCAAT TCAATTATCT GACATAGTGT ATCACTTAAT CGCATTATTA CGATATGGCG 240

GTGGCATTAG CTATCAATTA TTAGATGACC ATTCAAATTA TATTTCCTTG TACAACAAAT 300

ATGGTAGCCC CCTACCATTA ATGCATTTAT ATAAAATGTT TAGACCTTTT GTTAATGAAG 360

ATATTGAAAT TACAAATAAT TATGTATTGA GTCGTAAAGA TAATAACTAC CATTTCTTAT 420

TATTCAATAA AATTAATGAT CGATATATGT CAGACGTAAA ACAAGATTTC ATTTTCCATA 480

ATGAATTACC TCAAGACTCT TTGATGATTA TTAAAACATT GAATCATGAA CATGGTTCAA 540

TTCAACATTT GCTTCCAATA AGCGATCAAC TTGTTTATAT AGAAAAAGAA ATTTTAGATG 600

AATTAGACAA AACGAATTAC CCTAAAACGG AGCTTGCAGT TCAAGAAGAA ACTGGTCGTA 660

CATTTGAACT CAAGTTAAAT CACGACGAGG TTAAATATAT TTGCTTTAAA CCAAGCTAAA 720

TACTAACAGT CCTCTTGTGT TTAGTTTCTT ACGTTAAAGG CTATTTATAT CATAAGGAGA 780

TGATTTGTAA TGAGTAACTC ACAAGCAATT CAAGCAATTG AAAACGTGTT AGTAACGTCA 840

AAAGTTGGTG TATTATCAAC TGCATATAAT AATAAnCCTA ATAGTAGATA TATGGTCTTT 900

TATAATGATG GTCTTACTTT ATATACTAAA ACGAATATCC ATTCTGCTAA GGTCAAAGAA 960

ATTAAAGATA ATCCAGCAGC ATATGTTTTG TTAGGCTATA ACGACACAAC TAATCGTAGT 1020

TTCGTTGAGA TGGAAGCGAC AATCGAAATC GTTACAGAAC AAGAAGTGAT TGATTGGCTA 1080

TGGGAAACAC AAGACAAAAG CTTTTTCAGT TCAAAAGAAG ACCCAGAGTT ATGTGTTTTA 1140

AGAGTAGTTC CGCAATCCAT TAAGCTAATG AATGATAAAT CATTAGATAC ACCTATCAAA 1200

ATCGATTTAT AACACAAAGT GTATATAGGA AATAACTTTT ATGAATTCTA GATATAACAA 1260

TGTTAAATAC TTAAAATAAC TCGCTATAAT TAAAGTGTTT AATATGTTTA CAATTCAATT 1320

TTTAAATTAA TTTTATGTAA TATAAATACT GCATTTGCAA ACTGTTGCAC TTTTAGGTAT 1440

AACAGAATTA ACTACATTTA AGGAGATTGA TGAACCATGA AAAAGAAAAA AGGTTTTGGT 1500

CTTGGTATTA GTTTAATCGC CATCATGTTA ATTGTATGTA TTGTATTAGT AATCATGATG 1560

ATGACTGGCG GAAAGAAAGA TACATACTAT GGAATTATGA AAGATAATAC TACTATTGAA 1620

AAAATGATTA GTGAAAAAGA TGAAAGTATT GAAAAAAATG TTAAATTACC TTCAGATTCA 1680

GATGTTAAAG TTAAAAAAGG TGATTTTGTA ATTGTTTATA AATTAGCAGA TTCAGATAAA 1740

ATTGTTAAAG TTAAAAAAGT TGACCATGAC GATGTACCAC ATGGTTTAAT GATGAAAATT 1800

CATGACATGG GCAAAATGCA CATGAAACAC TAATTGTAAT TTAAATTACA AATTTTAGTT 1860

GCCATCAAGG TATATACGAG TAAAAGCAGC GGTAAGTTGA TTTCCAATTT GGAATCATTT 1920

TACTGCTGCT TTTTATATTT GAAATACTTT CATATTGAAT AGCTCCACTT GCCGTTCGCC 1980

TgcgCTTTGC GCATGCATAA AAGCCCCTAA CAACCTGAGG TCACTGCGCT CCGGTTCGCC 2040

TGcgCTTTAG CGCATGCATA AAAGCCCCTA ACAACCTGAG GTCACTACGC TTCGGTTCGC 2100

CTGCGCTTTA GCGCATGCAT AAAAGTCCCT AACAACCTGA GGTCACTACG CTTCCGTTCG 2160

CCTGCGCTTT AnCATGGCCA TAAAAGC 2187

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1788 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

CCnCCTTTTT AAACCTGGnG AAATGtmCAG tTTTGATGGt ATTGGGtTCT TTAGTATTAT 60

GCTTAAGATA GAGTGTAATA CGCTCCTGTT GTTCTTTATA GTATATTGCT TTTTGTTTTT 120

CTTTTTCGTC ATATTTCACT TTTAAATAAA TGACTGATGC AACTATACAT ATACATAAAA 180

TGACACCAAT AATTATAAAA ACATGTTTTT TGTTCATTAA AGTAACTCCT AAAATGTGGT 240

GGAAAATGAA AAAATTTTTA TAATCTATAA TTATGAACAT TACAGATTAT AAACCATAAC 300

ACTAACATCG TCGCCTTCAT TAACTTGATT GTTAAAATCA GCAATTACTG AGAATTGTAC 360

AAGGAATAAT TGCCTATTAT GCCCTCATGT AATTATTGCC TTACTAACAT TAACAAAATC 420

GATAGCTATT ACATTAAATG CCTATACCCC AGACCTCAAA CACCTTTTTA TACAGGACGC 480

ACTGTAATTT CATyyACGTT AACGTGCTTT GGTTGTGTTA ATGCATATAA TACTGCTTCT 540

GTATCTACCA TTCCTGGAGA AATGCTTGTT ACTTTAACGC CTGTCTTTGC CAACTCTTTT 660

TCTAATCCTT GAGTAATAGT GTGAACTGCT GCTTTCGTCG CACTATAAAT CGTACTACTT 720

TTCGTTACTT CAAAGCCAGA AATAGATGcA ATGTTAATAA GATGGCCACT TGATTGTTCT 780

AACATAGTTG GTAATGCAGC CTGTGCCGTA TATAAAGTGC CTTTGATATT CACATCAATC 840

ATACTATCCC ACTCATCTAC TTGATAATCA GTAATCTTAG ACGACAACAT TTGCCCCGCA 900

CTATTGATAA CAATATCCAA ACCACCGAAT GTTTGTTGTG CAATTTTTAT CAATTCATCG 960

ACTTCTTCTT TATTCGTTAC ATCTGTTGGC ACTACCTTCA CACTATCTTG TGACAATTGA 1020

TTCGCTACGT TTTGTAATTT TTCTTTATTT CTACCTGCTA AGACAACTTT TGCCCCTTCT 1080

TCATGTAGTA ATGTTGCAAT TGCTTCTCCA ATACCACTAC CTGCACCTGT AACTACTGCT 1140

ACTTTATCTG TTAATACTGT CATAATGATC GACTCCTTTG ATTCTTTTTA TTTTTTCAGG 1200

GTAAATCATA AATACATATT ACTTTTAAAA AGCGTATCAC AATTCATATA ACGGTCATAA 1260

TAACTCGCTT CATTTTCATA GATAAATTAC ATTACAAGCC ATTCGAAACA TACAATTAAT 1320

CGTTGCTTAT ATTTTTTATT TTTAAAAATG TTGAAAAATC GTCACTTCTT TATTGTAAAA 1380

ACATTATATT AGTAATAAAG TTAATACTGT GnATTTaTCA TTCGATTGAA TGATTAGAGG 1440

GAGGAATAAA ACgTGACATA TCATGAGCGT GTTTTAGCAT TAAGAGCAGA AAGTAAAAGA 1500

ACCGCATTTG ATTTTCGATT CGAAGATTTA TTTAGCAAAG AAGAATGGcT AAGTATGTCT 1560

CTTGCAGAAA GACAAAAAGC TGAAAAAGCA TTTCGACACG AgTTAAAAAT ATGGACGATG 1620

TAAGAATGCC CTTCTCAAGT GTCCATGACG CCCAAGTAAA ATTATATAAT GTTGTATATT 1680

CTTATAACGG CaTTAAACGT AATTTTAAAC AAGTTGAAAA TGGAAGGATT CTAATATCAT 1740

TTCGTTTATA TATnGCAGAC CATGGATAGA ATTTTnTATG GTnAATCC 1788

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

TAAGCCAAAT CCATTGTTAC CAGAAGAAGT TCGCTTCATC TTAAAACAAA TGGGTCTTAA 60

AGAAAAGACT ATCGATGTTG AACTCGAAGT TGGCGAGCAA GTTCGTATTA AATCAGGTCC 120

ATTTGCGAAT CAAGTTGGTG AAGTTCAAGA AATTGAAACA GaTAAGTTTA AGCTAACAGT 180

GCTTTAATTA ACAATTAAAG TTATTAAACT AACCAAAAGA TAAAAAAGAG TATTGATTTT 300

TTAATTAGAA AAGTGTTAAA ATTATGTGGT cGcGCTTTTA GAGCGCCCAT TTCGTcACGA 360

AATGTTAAGA GTGGGAGGGC AAAACTGAGC CCTGTGACCA CATCACGATA TCAAGGAGGT 420

GCACATCGTG GCTAAAAAAG TAGATAAAGT TGTTAAATTA CAAATTCCTG CAGGTAAAGC 480

GAATCCAGCA CCACCAGTTG GTCCAGCATT AGGTCAAGCA GGTGTGAACA TCATGGGATT 540

CTGTAAAGAG TTCAATGCAC GTACTCAAGA TCAAGCAGGT TTAATTATTC CGGTAGAAAT 600

CAGTGTTTAT GAAGATCGTT CATTTACATT TATTACaAAA ACTCCACCGG CTCCaGTATT 660

ACTTAAAAAA GCAGCTGGTA TTGAAAAAGG TTCAGGCGAA CCAAACAAAA CTAAAGTTGC 720

TACAGTAACT AAAGATCAAG TACGCGAAAT TGCTAACAGC AAAATGCAAG ACTTAAACGC 780

TGCTGACGAA GAAGCAGCTA TGCGTATTAT CGAAGGTACT GCACGTAGTA TGGGTATCGT 840

TGTAGAATAA TTTTACGAAT ATTAAATTTG ATTACATGAT TTAAACGATG AAGCAGATAA 900

CAGAGATAAT AATGATGAAT TATAAATATA ATCTGAATGA CTAGATTAAT GATTGATTTA 960

TTCATAAGAT TAATTCTTCT GTTGTCTGCy CTTAACTTGC ATATAGCAAG TAATGTGGGA 1020

GGAAATTCCG CTAAAACCAC TAAAGGAGGA ACTATAAATG GCTAAAAAAG GTAAAAAGTA 1080

TCAAGAAGCA GCTAGTAAAG TTGACCGTAC TCAGCACTAC AGTGTTGAAG AAGCAATTAA 1140

ATTAGCTAAA GAAACAAGCA TTGCTAACTT TGACGCTTCT GTTGAAGTTG CATTCCGTTT 1200

AGGAATTGAT ACACGTAAAA ATGACCAACA AATCCGTGGT GCAGTTGTAT TACCAAACGG 1260

AACTGGTAAA TCACAAAGTG TATTAGTATT CGCTAAAGGT GACAAAATTG CTGAAGCTGA 1320

AGCAGCAGGT GCTGACTATG T 1341

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

CTCTAAATCT TCAATAGGTA ACTTCATTTT AATAATTCCC ATTTGAACAA TTGCTTCTTC 60

ATCATTGACA ATTTCTAAAA CTTCACCCTT TTGACCGTAA GAkAATACTT TkACTTCATC 120

ACCAGCAACA ATTTTATCGT ATTTTTGCTT TTGTACATTT TGCTTTATAG ATTTCGCTTC 180

ATAATGATCA TCTAATCGTT TCTTCTTATC AATCAATTCA TGTTCTTTAA CATCTGCACC 240

CTTAATCTTC TGATTTGCTT TkTCTTTCGC TTCCTCTATT AGAGACTTTT CATAATTTTG 360

GAATTGTTGA TACTGCTTAG ATAAATCATC ATGCACTTGt CCGCkTskTT TACAAGACGG 420

TCCAGkTCTA ACCTCTGTGT CTCTACACGT TTGTAATTAC GCTCTAATGA TTCAATCATT 480

TCATTTATTT CTTTTTCATC AGTACCAATC ATCGTCTTAG CCTTATTAAT AATATTCAAA 540

CTAAGACCTA ACTTTTTAGA AATGTCAAAA GCATTTGAAC GACCCGGCAC ACCCATTAAT 600

AACTTATACG TTGGACTCAA AGTATCTACA TCAAATTCTA CACTCGCATT CATAACGCCT 660

TCTCGATTAT AACTATATGC TTTAAGTTCA GGATAGTGCG TCGTTGCCAT TACTAGAGAA 720

CCAATTTTTC TAACATGATC TAAAATGCTC ATTGCTAATG CAGCACCTTC ACTCGGATCT 780

GTACCTGCAC CTAATTCATC AAATAAAACT AAACTATGTT TGTCTGCATG CTTTAAAATT 840

TCAACTATAT TCGTCATATG AGATGAAAAA GTTGATAATG ATTGTTCTAT TGATTGTTCA 900

TCTCCGATAT CGCAATATAC ATTTTTAAAT ACACTTAACT GACTACCATC AAGTGTGGGA 960

ATCAACAATC CTGATTGAGC CATAACAATA ATTAAACCTA ATGTTTTTAA TGTTACAGTT 1020

TTACCACCTG TATTCGGTCC TGTAATAATT ACCGTTTCAA TATCTTCCAT AAATTCGATG 1080

GTATTAGCTA CAACAGTCTC ACGATTTAAT AATGGATGGT ATGCTTTAGG TAAATATACA 1140

GTACGGTCCT CTTTAAATAT CGGCTTTGTT CCTTTAATAC TTCTACTATA TCTCGCTTTT 1200

GCGATTAAAA AATCTAACTG ACCCATGACT TGTTCTGCCA CAAGTAGTGC ATCTTTGTCC 1260

GCAGCCACAT AACCAGTTAG TTGCGTTAAA ATGCGTTCTT TTTCAATTGC TTCGTCATGA 1320

CGTAATCGAC TAATTTGATT ATTCATTTCA ACAACTGATG ATGGCTCAAT ATACAATGTT 1380

TGTCCTGAAG CAGATTGATC ATGTACAATC CCATTAAAAT CTTGTCGATA TTCAGCTTTG 1440

ACAGGTATAA CGTTTCTTTC ATTCCTAACT GTTACAATAG CATCTGATAA TTTTTTCTGA 1500

TTTGCTTGGC TTTTAACAAT ACGGTCCAAA TTTTGTCTAA TACGTTGATT CGTGCTAGAA 1560

ATTTTACTTC TAATCCCTTG CAATTCATAA CTCGCATTAT CATATAAATC ATACGTATCG 1620

CATGTTTCAT TTATTTGTTG AAAAAGATCA GTTAACACAG GTAATTGATT CATCTTGTCA 1680

TCTAATATTG GGTATTTAAC ACCTTCATCT TCTTCAACCA ATTGATTATA AAATGTCTTG 1740

AATTGATTTT GTACTTGAAT TAATCTTTTT ATCAAGTTAA GCTCTGATAC ATTTAAAACG 1800

CCGCCAATAT CAGCGCGATG AATGAATGCT GATACTTTAG ATAAGCCACT CAAGCTTGGT 1860

AAACGATGCT TATTATAGAT TTGAGCAATC TCATCCGTTT CTTCCATTTG AAAAACAACC 1920

GTTTCAAAAT TAGTAGCTGG CATCATTTGA TTGACCTTTT CCAAGCCTAA GTCACTAATA 1980

GTTTCATTGG CAACGAGTGA TTTTATTTTT TCAAATTCTA AGACGTCTAA TGTTTTTTGT 2040

TCACGCGATA ATGCGTTAAT CACTCTATCT TTTGTtACAA ATCCTTTTTG CGCAGTTGtA 2160

CGCCATAATT CATAAAATCT AAATGATTTG TATGATGCGC ATCAGTGTTA ATAGTTAATT 2220

TCACATTTGG ATATTTACGA ACGATATCAG CGCTCAGATC CAGTCGATGT GGATTGGCAT 2280

TAATTTCTAA TACTGTATTC GTTTCTTCAG CTAATGCCAT TAATTGTTCA ATATTCGGTT 2340

TATAACCATC TCTTCTACCT ATAATACGCC CTGTTGGATG CGCTATATGT CGCACGTATG 2400

GATTGCGACA TGCATTAGCT AATCGTTCCA TAATTTGTTC TTCTGATTGG TTAAAGCTTT 2460

GATGAATAGC TCCAATTACA TAATCAAGTT GTGCTAAAAT TTCATCATCA TAATCCAGCG 2520

AGCCATCAGG TAATATATCC ATTTCTGTAC CTGAATAAAT ATCAATTTCA CTATATTCTT 2580

TATCTAAAGC CTTAATTTCT TCGTTTTGTC TTAAAAGTCT TTCTACTTGT AAGCCATTAG 2640

CAACACGTAA ACTTTGTGAA TGATCAGTAA TTACCATGAA TTTATAACCT TTTGCGATAT 2700

TTGCTTCTAC CATGTCTCGA ATAGAAAACG CACCATCACT ATACGTTGTA TGCATATGAA 2760

TATCACCATT AATATCATCT ATTGTAATGA TATTACTTAG ATCTTTATCA AATTCGCTAC 2820

CATCTTCTCG CATAGCAGGT GGTATAAAAT TCACATTAAA ATGTTCATAT ATCTTGGCTT 2880

CACTATCATA TTGAATTAAT GTACCATCAG CTTGTTCAAT TCCATATTCA CTTACTTTTT 2940

CATCACGTGC TTTAGCAAGT TGTCGAATTC TTATATTATG TTCTTTTGAC CCAGTAAAAT 3000

GCTGCAATGT ATGATAAAAA GCACTTGGTT CAATTAATCG AAAATCGACA CCAATCGTTT 3060

CATCATCATA CGCTAATTCT AATGAAACTT TTGTGTTCCC CACTGCAACT TCTTTTACTT 3120

TATTGGGAAT ATTTAATAAT TGCTGCTGCA CTGCTTTTGG GTTATCGGTA CTTATTATGA 3180

AATCTAAATC TTTGCTCATT TCTTTAAAAC GACGGAAGCT TCCTGCAGAT GAATATTGAT 3240

CGATATAATT TAATGTATCT ATATAATCAA TGATTTCTTG ATTAAGTCTT CTCATTTGAT 3300

CAATTGGATA TCTATCTTTC TTAGCACCAA GTTGTTTCAC AGCTTCTAAT ATGTTTTGTT 3360

CCGTTTTCTT AGCAAATCCG CTTAATTCAC TAACTTTTCC ATTTTCACAA GCAACTTGAA 3420

GTGACGCTTT ATCAACAATA TTCAACTCTT TATATAGCTT AGCAATTTTC TTGCTTCCAA 3480

GTCCTTGAAT TTTCAAAAGT GGAATAAGAC CTTCCGGAAC TTCTTCCTGT AATTGCTGTA 3540

AATACTGAGA TTCACCGGTC TCACGGTAAT CATTGATTAC TTCTGCAACA CCTTTACCAA 3600

TGCCTTTtAA CTCCGTtACA TCAGATATTT CATCTAATGG TCGTTCATCT AATTCAAGAC 3660

TTTGAGCTGC TTTTCGaTAC GCTGaTATTT TAAAAGTATT TTCCCCTTTT AATTCCATAT 3720

AAGTAGCAAT TTGTTCTAAT AGTTTGATAA CATCTTTTTT TGTCATAATA ACACTCCATA 3780

AAAAGAAGAC CAGGACGTAT CATTAATATA TACCTTTGTC CTGACCTCTT ATGATAATTT 3840

TAGATATTTT AAGCTGATGT TGTAATGCTT CGTTAGGATA TAATGCCAAT AGATATAACG 3960

TAAAGTGTAA GACAATTATC GTCATAAACA CACCAACTAT CATTCCCATT GCACGACTGA 4020

AAATATGAAT GTTTTGATAC GCTATTATTT TATCAAAAGT TACGATAATT AGATATAAAA 4080

TGAACTTACA AAACAATGTA ATCATTAAAA AAGCTACAAT CGCTTCAAAT CGATTTTGTA 4140

GATGATTAAA ATGAAACGCA AAAGTTGTAT TAAATGCTGT TGTTTTAGGA TATGGAATAA 4200

ATACAATTAA TCTTTCTACA ATAGATTTGT AAAATTGACT GGCAATCCAC AATGATACAA 4260

nCGTTGCACT CAAATGTATC ATAGATAACC AAAAACCTCG TCTGAATCCA ACGATGACAA 4320

AATACACAAA GAAAATGATT ATGATAAAAT CAATGACCAT TTATTGCTCA CGCTGCTGCA 4380

ATTTGTGAAT TTGTTGTTTC AAACGTCGAT TTTTTTTCTT CTAGTAGTAC TTTTTCATGC 4440

ATAATATTCA CAGCAGTTAG TATTGCTTTT CTTGAAGTAT CTAAACCTGC TGCTTTATAC 4500

CCTAATTCTT TTATTTTATC ATCAACTAAA TGTGCTACAT ATCGTATGTG CTCTGGGTTA 4560

TCTTCCCCAA CAATTGTAAA AAGCTGATCA TTAATTGATA CATTTACCTT GTTTTTAAAC 4620

TGTGTCATTT ATAATTTCTC CTGATCCTTT TTTTAAAATC TAAATTCACG TTATAAAATA 4680

TGACTGGATA GTTTGTCTGA ATTTGATACT AATATTGTTA TATTGCAATT ATGATAAAAC 4740

AACAACACAA TCTCTATAGA TGACTTAATG TTCTTTTTAT AATGAAATAA TGTAAAGAAT 4800

TTTCTATTCA ATACTTTATC ATGTTTAAAT TGTGTCACTA TAACATTTTC ATAAACATTA 4860

TACATGACCA CTATGTATTT TGTAAGTATC CGCAATTAAT TCTTTACAAC ATACATAAAT 4920

GTTTCTGACG TTATTATCAT TTATGATATG ATTATTTTTG CTAAAGACAA TGAAATTTTA 4980

TGAAAGGATT TACACAAATG GCGAATATCG TTTTTAAATT GTCGGATAAA GACATAACGA 5040

CATTAATGTC ACGCATTTCT TTTGATACTG AGAATTTACC TCAAGGnATG AnAGCACGTG 5100

CAAAGTATCC AAAATACAAC TGTAAATATT TACCAT 5136

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

GGCCAAAATT GCACCTCCAC TTTCCTTTGA ACAAATCTAT TTTAAACGCA CATTCCCATT 60

ATGACAAATT AAATGTGAGT nACATTTGTT TGTATTTTAA CATGACTACT AACGCAAACT 120

GGTATCTTTC AAAGATAAAA TCTTAATAAT TTCTTAGTAA ACTCTTTTCT CTAGATTTAT 240

CACAATATTA TATAGACCTA TTTTATTTTG ACGTAAGTTG CTAGTATCTT CAAACAAAAA 300

ACCTTTATAA AAATTCATAC CTTTATGCTA TCGCTGTAGG CTCATTAACT TGTTACATAT 360

AATTCTTAAC TATCCTTTGA TGATTGTTTT ATTAGATTGT TTCGTTGATG GATACTTTCA 420

CGAATTTCTA TAGTTCAATG CTACTAAAAA AACAGCCCAA AACTTTAATT TGTTTTGGAC 480

TGTTTTATAA TTATGCTTGC GATGGTGTTT TAGTTTCTGA AGTTTGTTCA GCAATGTCAT 540

ATTTAAACTC TTTACCATCA TGATCTACTG TAACTTTCTT ACCTTCAATT TGATTACCAT 600

CTAATATTAA TTCACTTAAA TTATCTTCGA TAGTTTTTTG TATCGCTCTA ATTAATGGTC 660

TTGCACCATA TTCTGGATCA TATCCTTCTT CTGCGATTTT GTCTTTCGCT TTATCAGTTA 720

CAATAATATT TATGTTTTGT TCAGATAATC GATTTGTTAA TTTATTAACC ATCATTGTTA 780

CAATTTCTTT TAATTCTTCT TTTGTTAGTT TATGGAATAC AATGATATCA TCTACACGGT 840

TTAAAAATTC TGGACGGAAT GAATTTTTTA ATTCTTTTAA CATCGTTTTT CGAATTGTTT 900

CATAATCTTG TCCATCACTT GAACCACCGA ATCCAGCAAA TCGTTGATCT TGTAATTCTT 960

GTGCCCCAAC GTTTGATGTC ATTATGATAA TTGTATTTCT GAAATCAACT GTACGTCCTT 1020

TTGTATCTGT CAAATGTCCA TCATCTAAAA CTTGTAATAG AATATTAAAT ACATCTGGAT 1080

GAGCTTTTTC AATTTCATCA AATAAAATTA CAGAATATGG TTTACGTCTA ACTTTTTCAG 1140

TTAATTGTCC ACCATCATCA TGACCAACAT ATCCTGGAGG AGCACCAACT AATCGGCTCA 1200

CTGCGTGTTT TTCCATAAAT TCACTCATGT CTACACGGAT CATCGCATCA TCATCGCCAA 1260

ACATTGATTC AGCTAAAGCT CTAGCTAATT CAGTTTTACC AACACCAGTT GGTCCAAGGA 1320

AGATAAAGCT ACCAATTGGT CGTTTAGGAT CTTTTAACCC TGCACGGGCA CGTCTAACCG 1380

CTTTACTGAT TGAATTAACA GCATCTTTTT GCCCAATAAC TCTCTCATGT AATGTATCTT 1440

CTAGACTAAG AAGTTTTTCA GATTCTGTTT CATTGATTTT AGTTAATGGG ATACCTGTCC 1500

ATCCTGCAAT AACTTCAGCA ATATCTTCTT CTGACAATGA AGTTGaCATG CCATTTTGTG 1560

CATTCTTCCA TTCATTTTTA GCTTCTTCAT ATTGCTTTTC AAGTTTTGTT TGTTTATCAC 1620

GCAGgTTAGC AGCATTTTCA AACTCTTGAG CATGTACTGC GGCATCTTTT TCATTTTTAA 1680

CTTTTTCAAT TTCTTGTTCA ATTTCTTTTA AATTATTAGG TGTCGTATGA CTCTTAAGTC 1740

TTACTTTAGA ACTTGCTTCA TCAATTAAAT CAATTGCTTT ATCTGGTAAG AAACGATCTG 1800

AAACGTATCT GTTACTTAAT TTAACAGCTG CTTCAATAGC TTCGTCTGAA ATATTAATAC 1860

GATGGTGTGC TTCGTAACGA TCTCTTAATC CTTTTAAAAT AGCAACTGTA TCTACTACTG 1920

TTTTGCGATA TTCATCTAAT GTAGTAGCAC CAATACATTG TAATTCACCA CGTGCTAATG 2040

CCGGCTTCAA AATATTCGAA GCATCGATAG CACCTTCAGC ACCACCAGCA CCAACTAAAG 2100

TATGCAACTC ATCAATAAAT AGGATGACAT TACCTGCTTG TTGGATTTCT TCCATAACCT 2160

TTTTCAGACG CTCTTCAAAT TCACCACGAT ATTTAGTACC TGCAACTACT GTTCCCATAT 2220

CTAAAGACAT AACACGCTTA TCTTTTAATG TCTCTGGTAC CTCATTATTC ACTAtGGCtT 2280

GCGCTAAACC TTCAGCAATA GCAGTTTTAC CAACACCTGG CTCTCCAATA AGCACAGGAT 2340

TGTTTTTCGT ACGTCTACTT AATACTTCAA TTACACGTGT AATTTCTTTA TCACGTCCTA 2400

TAACAGGATC TAATGTACCG TCTTTGGCAA TGACTGTTAA GTCACGAGCT AAACTATCTA 2460

AAGTTGGAGT ATTATTTGAC TTACTAGCTT GTGCATTTTT ATTACTCATT TCAGGGTTTC 2520

CTAAAGCTTT CACAACTTGT GCACGTGCTT TAGTAATATT TAAATCTAGA TTTGCAAAAA 2580

CTCTTGCTGC AACACCTTCA TTTTCACGAA TCAAGCCTAA TAAAATATGT TCCGTTCCAA 2640

CAAAATTGTG ATGTAATTTT CTAGCTTCAT CCATCGATAA TTCAATGACT TTTTTAGCTC 2700

TAGGTGTATA ATGCAATGTA CCAACATGAT CTTGACCATG TCCGATTAAT TTTTCAACTT 2760

CTTCAATTAC TTTATCTTCA GTGATATTAA AACTTTCTAA TACTTTTGCA GCAATTCCTT 2820

CAGGTTCTTT CATTAACCCC AATAATAGGT GTTCTGTTCC TATATTTGAA TGATTTAAAC 2880

GAATTGCTTC TTCTTGGGCA TGTGCTAATA cGCGCTGTGC ACGCTCAGTT AATCTACCAA 2940

ATAACATAAA TAATGACCTC CTACTTTATA TGTTCTCTTA GTATATCTGC TCGTTTTTCT 3000

TTTACAGATT TGTCATCTTC TTCATCTAAT AAAAATGGTG ACTGTATAGC TACCATCAAT 3060

TCATTAAATT TAAAGTTTTG TAATTCAATG TAATTTAAAT CTATACCAAG TTTAACTcGC 3120

TTAATCTATA AGAAGCCTCT TCCATAGTTA TCATTCTACA GTTTTGTAAA ATACCTAGCG 3180

AGCGAAAAAC ACGGTCTTGT GTTTCTAATT GATTATAAGT GTCTAACTTT TGTCGTATTT 3240

GTTTTTCTTC ATGAATGATT TGATTAACAA CTTCTGTTAA TGTTTCTATG ATTTCTAACT 3300

CAGATTTACC AAGTGTAAGT TGGTTGGATA CTTGATAAGT ATGTCCATAA ACTTGCGAAC 3360

CTTCACCGTA AATACCTCTG ATTGTATATC CAAAACGATT AATGGTTTGA GCAATCCGTG 3420

TCATTCTTTT CATAATAGAT AGACCTGGCA AATGTAGCAT CACGCTTGCT CTCATACCAG 3480

TACCTATATT GGTAGGACAT GTAGTTAAAT AACCAAGTTG TTCATCATAA CTTATATCAA 3540

GGCTTCGATC TAATTCATCA TCAATTGATG AAGCTTGATT ATATAAAGCC TGTAATGTCG 3600

TGTCAGTTCC CATAGCTTGA ATACGAATAT GGTCCTCTTC ATTTATCATG ACACTTAAAG 3660

ATTCATCGTC ATTCACTAAT ACTGCGGCTG CTGGTTGTTT TATTAGTTCA GGACTAATCA 3720

CAAAGTTTGG CAAGGCATCT TGTACCTCAT TTATAACTCT AAATCCcATC ATTTTCAGTA 3840

GCATACATTA GTGGATGCAC ATGATTTTCT AAAtTACGCG CTAACCGAAT TCTAGAAGAC 3900

ATAACAATTG GTGTTTCTTC ATTACTTTTC ATCCATTGGC TGATATTATC ATGAATATTA 3960

TGCGTCATCA TGTTGCACCT CACTCTCAGC TTTTAGTGCT TTAATTTCAT CTCTAACAAT 4020

GGCTGCTTCC TCAAAATCTT GGATTTCAAT AAGTTTTTTC AAATATTCAT TCTTTTCTTC 4080

GATTTTTCGC TTTAAAGCTA TCTTTTTATG TGAAGAATGT GGTGTCTTTC CAACGTGCTC 4140

AAATTGTCCA CCTTGAACTC TGCGGACGAT ATCAATGATG TCATCTTTAA ATGTTGcATA 4200

ACAATTAGCA CACCCAAATT TACCAACATG TGCAATATC 4239

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

CAAAACTTTG ATTATGTCGT GTCAGTTATT AATGCATACA GTAATGCATC GTTGTTATTT 60

TTTATTTATT TACTATTTAT TATGTACCAA ATCAGCCTTt CAGTAAAATA GGTCAAATTA 120

CTGATTTTCT AAATATAAAA TGCCTCCTAA TAACATACTA TTAGTACATC ATTAAGAGGC 180

TCTTGTGTTA TTTGCATACT AAGCGCTCAA ATTTAAATTT AAGATGAAGA TTCTTGCAAT 240

AATATTTCTA TATTTGTCGA TATATCCAAT GGATCTTCCA TTGGCAAGAA TCGATTTACA 300

ACATTTCCTT GTCGATCGAT TATAAATTTT GTGAAATTCC ATTTTATTGG GGaCCCAAAG 360

ATTCCTGGTT GTTCaTTCTT TAAATGCGtA AATAACGGAT GTTCATCGTT CCCGTTCACA 420

GATATTTTAG CTAACACTGG AAATGTTACA CCAAATTTCT CACGACTAAT TTTCAAGATT 480

TCTTCATTAG AACCTGGTTG TCGATTGTCA AAATTATTAT TCGGAAAACT CAACACTACA 540

AACCCACGAT CCTTATATTT TTGAAATAAA GTCTCTAGTT TTTTCAATTG TTCGCTATAT 600

ATACATTCTG TTGCAGTATT AACAACTAAA ATCACTTTAC CTCTAAATGC TTCTAATTTA 660

TAAGTTAAGC CTTTATAATC ACTTACTTCG ATATCATACA CATTTCTATT ATTCATAAGA 720

CACCCCTACA CAGCCTTTTT TATATTGAAT ATGTTCTTTT TAGAATGTTC TGATAAAATA 780

AGTGCGCGTT TACACCGTGA ACACACATTA TATAGCGTGA TACATTTTTC GAGCACACGA 840

TAAATAATGT TCGAGTTTAT GTTGTTGCTC AACCTATCCG ATTTACCGTC TTTTTTCACC 900

CCGTTATAAC CCCTCATTAT AATCATCCTT ATTTTCTATT TTTAAAAAGA CAATTAGACC 1020

GCTCTTTAAA CTATAGaTTA ATACTTAAGk TAAACTCATA CATACTGATA CCATACGTTA 1080

GATCTAACAA TTTAAAATTC GTTATAACTA TGGATTAAAG AGCTGCCCAA CTCATATAAT 1140

CCTTAAAAAC TTCACATGTG ATTGTkTATT AAGCCCTCCT TTATCnTATT AAATATCCTT 1200

ATAACCCTTT TAAAATTAAA CTGACACACT CATACATTGT TACAC 1245

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

CTTGTAAAGG TAGTTGTTCA TTTAAATTAA AACAGTATGC TAAGTTnGTG CTTATATTTT 60

GCAACTTCAA TTCGACAGGC TCATCTTGAT ACATGAATGC CTCAATTTCA TCATGTGATA 120

ACTTTTTCAA AATATCAATT AAATGrATAC TAAAAACGAT AAATAACATA TCCCAATTTG 180

AATTCAGCCC TAGCGATTTT AATTTGTTTA AAATCTTATC TTTTTGAAAA ATTCGATTCC 240

TAATGTCTTG TATATCGTTA TCAGTCAAAG TTTCCCAATC TATATGTGAA TGAAGACCTA 300

AATAACACTT ATCCATTAAT AATTCATATA CCGTTAATGC AGAGACATCG AAACAACGTT 360

CTTCACTTAr AAAAACGCCA TCAACATCAA ATAAAATTTT CTTCACAATC CCCACTCCAT 420

TTCTGaAAAT TCAGaTATAA ATCATTCTAC TATTTGACTA AAAAAAGCGC AAACCCTATT 480

GAAGTaGATT TGCGCTTTAG CTGTTnAAAT TTTATAAATG TnTTTCAATT TCATCAGCAA 540

CCTGCTGTAC GTGTGTACCG ACAATAACTT GAGTTGAATG TTTGCCATTA ACAGTAACAC 600

CAACTGCACC GGCGTTTTTA ATCTTCTGTT TATCAATAAT AGATGTGTCT TTTAACTCTA 660

GACGCAACCT TGTTGCACAA TTGGTTAAAT TAACAATATT CTCTTGACCG CCTAAACCTT 720

CTAATATTTG TATAGCATGT TGATGATATT TACTTTGTTT AATATCATTT TCACCAGGAG 780

CAATATTATC TTTTACAACT GTTGGGTCAA CTAATTCATT TTCACCTCTA CCAATCGTAT 840

TCAAGTTAAA TACTTGGATT ACTACACGGA AAATCACATA GTATAAGATG AAAAATACAA 900

CACCTTGAAC AAGCAACATC AATGGATGAT TTGATACTGG ATTAATTAGT GATAACACAT 960

AATCTATCAA ACCTGCACTA AATGAAAATC CAGCTGTCCA ATGGAATGTA GCTGCGATAA 1020

ATAAAGATAA TCCTGTTAAT AACGCATGAA CAACATATAA GATTGGCACA ACAAACATAA 1080

ACCAACCGTA AACTTGTTTT TTCTGAGTAG TTTTAGCTGT ATGATACATT GcTAACGCAG 1200

CCGCTGGAAT ACCGAACATC ATGATTGGGA AGAATCCCGC TTGATAGCGT CCTGTAATAC 1260

CTTTTATAGC ATCTTTGCCA CTTTGGAATT TACCAATATC ATTAATACCA ATCGTATCAA 1320

ACCAGAACAC ACTATTCAGT GCATGATGTA ATCCTGTAGG AATTAATAAT CTATTGGCAA 1380

CACCATATAT GAAAGCTCC 1399

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

TATAGTTnTA TTATTTAGCG AAGCATTAAT ACTACCACCG GTTATAACAA ATGTATTTTG 60

CGTATTAAAT TGAATGGTAG GACCAATCAA AGTATATTCA ATCGCTGGAC CATCATTGTT 120

AATTAATGAC TGCGCAACCT TAAAACTAAA TTGATCCATG GCACCTGCGC CTGAAAATCC 180

AATATGTTCA TAACCTATTC TTCCTAGATC TTGTACCGTT GAAAAGAGAC CTGGTTGTAA 240

AATCTTAATT GACATTTTCA ATCACCACCC AGTCATCAAC ATTAAAGTTG CCATCTGATA 300

TATCTCTTTC GATTTGTATA AATTTCTGTT CATCTATTGC ATAAAATTGT ATCCATTCTC 360

CTGCTTCGTA CATTGACATT GGTTCACGCT CGCTGCTAAA TACTTTTAAc GGTGTGCGTC 420

CAATAATTTG CCATCCGCCA GGAGAATCTG ATGGATATAG TCCTGTTTGA TTATTCGCAA 480

TACCTACAGA ACCTGCATGA ATTTTTAACC TTGGCTGATT ACGTCTAGGT GTATGTAGTT 540

GTTCATCAAG TcCGCCTAAG TATGGAAATC CTGGCATAAA TCCTAGCATA TATATTAAAT 600

AAGGTTTACT TGTATGTTTT TCAATAACTT GCTCAACAGT TATTCGATTA TGCTTTGCTA 660

CTTCTTCAAT ATCTGGTCCA TATGTACCAC CATATTGAAC AGGTATTTTA ATAATACGAT 720

TGGTTTGATT CACAGCATGA ACATTTTTTT CATTAAATTT GTTAAGTTCT AAATTTTCAA 780

TTAATTTAGA AGATGTTATA GCTTGTTCAT CAAAATATAT TAGAACTGCT CGATACGAAG 840

GGACAATATC TTGAATTTCT AATATTTCTT TTTCTCGTAT CCACCGTACC ATTGCTGTGA 900

CATTACGATA TGTCTCTTCG GATATTTTAT TTTCAAAATA AATCATAATT GTCTGCTCGT 960

TAATAAATCT TACATCCACT TTAAATCCCC CTTTGTATTG CAATAAACCA GTATTGAATA 1020

CCTTTTCATT GTATCATTGA GAAGCACAAG TTGTTTAATA AGTAATTCAA ATCGCATATA 1080

TTAATATTGT AACTCTTACA CTAATTTAGG TTCTGCTATC ATTCGGTCTG ATGGAAAATT 1200

TTTACTTTTC ATCTGTCCGA TTTTTTGATT TTGAATATAA AAAAGCACGA CCGAAGTATC 1260

ATTAACACAC TTCAATCGCG CAATTAAATA ATCTATTTGA TCATTTATTG GATATTAACA 1320

ATTTTTACG 1329

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

GAATAGTGCC ATTTGGAAAG ACATAAAGAA TCCAGAAGCA CCTTTAGCGA ATATGCCGTG 60

TTCATATAGA TTTGTGAAAC TGGCATGCCC GAATTGAGTT TTAAATGCAA ATAGAATCAT 120

GACGAAACCA ACTACTATTA AACCAATAAT TGTCGCTATT TTAATGATAG AGAACCAAAA 180

TTCTAATTCT CCGAAAAGTC TTGCGCTAAG TAGGTTGAAT GACATTAATA ACAGTACACA 240

AAATAGTGCA CTTATCCAGT TTGGAATTTC TGGGAACCAA AAGCTAACAT ATTTTGCCAC 300

AGCCGTTACT TCAGCCATAC CTGTAATAAT CCAACAGAAC CAGTATGTCC ATCCGGTAAC 360

AAATCCTGCA AAAGGCCCAA TATATGTATT GGTTACATCT GCGAAAGATT TAAATTCAGT 420

ATTCTGTATA ATGATTTCTC CTAAACCTCG CATAAACATA AATAACATAA ATCCTATAAT 480

GATGTATGTT AATAGAATTG AAGGGCCGGT TAATGCAATC GTTTGACCAG CACCTAAGAA 540

TAAGCCTGTA CCAATTGCAC CGCCAATTGC AATTAATTGT ATGTGGCGAT TGCTCAGTTC 600

CCTTTGTAAT TTTTCAGCCA TAATACATCT CCCTTAAATA TAGATATGTT TATTATGCAC 660

TTATATTGAG ATATATACAA TTATTTTCGG TAAAAATGTG TAAAATTCCA TGTTAATATA 720

CTTTGGTTTT TATAATCATA TATAATAACC AATTGAAAAT TTAATTCTAT TGTAAAATTC 780

ATGGATTATT CACATCTTGA AAAAGCTTTA ATGGTGCTAT TTGTGGCTAT TCTGTGACAT 840

TTACATAGAT TTACAAAAAA ATTGTTGCAC ATATAATGCC AGTtTTTATA TTTCACAAAC 900

GAAATGCGTT TAcTATAATA TTAGTTGAAA GCCATTTCAT AAAGAAACAG TAAAGGGGAA 960

ATTtATCaTA GCmGaATTAC AAAGAGGTTT AGAAGGGGTT ATCGCmGCGG AGACTAAAAT 1020

AAGTTCAATT ATTGAAAGTC AATTGACTTA TGCCGGCTAT GATATTGATG ATCTAGCTGA 1080

AAATGCGCAA TTTGAAGAAG TTATTTTCCT ATTATGGAAC TATAGATTGC CAAACGAAGA 1140

TACACATTTT GAGGAGTATG TTACAGATCA CGTGCATCCA ATGACAGCAT TACGTACGTC 1260

ATTATCATAT ATTGCACATT TCGATCCTGA TGCTGAAAAT GAATCAGATG AAAATCGTTA 1320

TGAAAGAGCA ATGCGTATAC AGGCTAAAGT AGCATCATTA GTTACAGCGT TTGCTCGAGT 1380

AAGACAAGAT AAAGAACCAC TTAAGCCTAA TCCTGACTTA AGTTATGCGG CAAACTTCCT 1440

ATATATGTTA CGTGGGGAAT TACCAACAGA TATAGAAGTA GAAGCCTTCA ATAAAGCACT 1500

TATTTTACAC GCTGATCATG AGTTGAACGC ATCTGCATTT ACGGCACGTT GTGCGGTATC 1560

ATCATTGTCA GATATGTACT CAGGTATTGT AGCAGCCGTA GtTCTCTGAA AGGGCCATTA 1620

CATGGTGGTG CAAACGAACA AGTTATGACG ATGTTATCTG aGATTGGGTC AaTTGAAAAT 1680

GTTGATGCTT ACTTAGATGA AAAATTTGCT AATAAAGrTA AAGTAATGGG cTTCGGTCAT 1740

CGTGTATATA AAGATGGTGm tCCTAGaGCG AAaTATTTaA GaGAAaTGAG CCGTCAAaTT 1800

mCGAAAGACG CTGGTCGTGA AGAATTATTT GAAaTGTCAG TGAAAaTGGA AAAmCGTATG 1860

GCAGAAGAAA AAGGATTAAT TCCTAATGTT GATTTTTATA GTGCGAGTGT TTATCACTGT 1920

ATGGAAATAC CTCATGACTT ATTCACGCCA ATCTTTGCTG TAAGTCGTTC TGCAGGATGG 1980

ATTGCTCATA TTTTAGAACA ATATAAAGAT AATAGAATTA TGCGTCCTAG AGCGAAATAT 2040

ATTGGCGAAA CGAATCGTAA GTATATCCCG CTTGrAGaAA GAAAmTAATC AATACAAATT 2100

AAAAATGAAG ATGTAAAATT TGGAGGTAAA ATAACTATGA CTGCAGAAAA AATTACTCAA 2160

GGAACTGAAG GATTAAACGT ACCTAATGAA CCAATTATCC CATTTATTAT CGGTGATGGA 2220

ATTGGACCGG ATATTTGGAA GGCAGCAAGC CGAGTTATAG ATGCTGCtGT TGAGAAAsCC 2280

TATAATGGCG AAAAACGCaT TGAATGGAAA GAAGTGCTAG CTGGCCAAAA AGCATTTGAT 2340

ACAACTGGTG AATGGTTACC TCAAGAAACA CTTGATACAA TTAAAGAATA TTTAATTGCT 2400

GTTAAAGGAC CTTTAACAAC ACCAATTGGT GGTGGTATTA GATCATTAAA TGTGGCTTTA 2460

CGCCAAGAAT TAGATTTATT TACTTGCTTA AGACCGGTAC GTTGGTTTAA AGGAGTACCA 2520

TCACCTGTTA AACGTCCACA AGATGTTGAT ATGGTTATTT TCCGTGAAAA TACTGAAGAC 2580

ATTTATGCTG GTATTGAATT TAAAGAAGGT ACAACAGAAG TTAAAAAGGT AATTGACTTC 2640

TTACAAAACG AAATGGGTGC GACAAACATT CGATTCCCAG AAACTTCAGG TATTGGTATT 2700

AAACCAGTTT CTAAAGAAGG AACTGAGCGA TTAGTTAGAG CAGCTATACA ATATGCTATC 2760

GATAATAACC GTAAATCAGT TACTTTAGTT CATAAAGGTA ATATTATGAA ATTTACAGAA 2820

GGCTCATTTA AGCAGTGGGG TTACGATTTA GCATTATCTG AATTTGGTGA TCAAGTATTC 2880

ACTTGGCAAC AATATGACGA AATTGTTGAA AATGAAGGCA GAGATGCTGC TAATGCTGCT 2940

TTACAACAAA TTTTAACTCG TCCAGCTGAG CATGATGTTG TAGCAACTAT GAACTTGAAT 3060

GGTGACTATA TTTCAGATGC TTTAGCTGCA CAAGTTGGTG GTATTGGTAT TGCGCCAGGT 3120

GCAAACATTA ATTATGAAAC AGGTCATGCT ATTTTTGAAG CAACACATGG TACAGCTCCA 3180

AAATATGCAG GTTTAAATAA AGTGAATCCA TCTTCAGTAA TTTTAAGTTC TGTATTAATG 3240

TTAGAACATT TAGGATGGCA AGAAGCGGCA GATAAGATTA CAGATTCAAT TGAAGATACA 3300

ATTGCTTCAA AAGTTGTTAC TTATGACTTT GCCCGTTTAA TGGaTGGtGC TGAAGAAGTT 3360

TCTACATCAG CATTTGCAGA TGAATTGATT GnAAATTTAA AATAAGCAGA ATAGAATTAG 3420

G 3421

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

CCCTnGATAC CCAAACTGCC CTAATACCAC TGGCTAAACC TAATGGATAG TACCATTTAT 60

TTTCCAATAA ATAAnCCAAC TGCAATnGCT ATaACTCTAA ATATAATAGA GATAATCmcA 120

TTAATTGGAT TAAtACGCCA AATACTAGTA ATAATAGGCT AGATAATAAT CCACCTAAAA 180

AGTACTTTTT AATTCCAAAG AAAGCTAATA TCAATAATGC TGCCGGTGCA GATAATTGAA 240

AATCTAATCC TGGTATAATG GACGGTATTT TCAAAACTGC CAAAATGGTT AAAATCGCAG 300

CAATGACACT AATTTGAGTA ATATCTTTTG ATGTCATACT AAAACCCCTA TACCGTTTCA 360

TAAACAACTT GCTTCGGTGT GCTTTCTAAA AATGATATGT AATGATTTAA ATCAATACAA 420

TCGTCCACAA ATATTATTCT GCCTCCATAT CTCGTATTAA CTGGTTTAAT ATCAAATAAT 480

CGATGGTAAC CAATTTTAGC AGCGGCAAAA TAACCTGTCG TATACGTTAA GTCATCGGAC 540

ACGCAAAGTT CTCCTTTGAC ATACGGATGC GCATTGATAC AACTAGCAAT TGCTAAGGCA 600

TCAGTCACTC TTTCATTAAG ATCACCTTTA TTATTTATAT CTTCAAACGA AAAATGTGTT 660

GCCCTAATCC CCCTTTGTCC AAATGAATCT AAACGTTTAC CAGATATAGC AGATAGAATA 720

ATAGCTCCTG TATAAACCGT TTCATTTTTA ATATATGTCA TCCCTTGATT TAGCGCTTGT 780

TCAGTGACAC CACATTCTTG TGTTAAATGT TGGAGATTTG CTTTATCATC CTCAATAATT 840

TGTAATGCTT TTATTTGTTG AATCGGTTCC ATGATTTTTT GTATTTTTAT ATTGAGAAAA 900

ATTTTGTCAA ACTCACAAAT CGTTTCAGCA CCACTAATAT GAACATCTTG ATTGCTAGAA 1020

CGCATTTTTA TACTATACAT GACGATCACC TcAATCTTCT TGaTGCAAAA TTTCAAACAA 1080

CCTATCTATA TCTTGTTCAG TATGAAAATA CGACAATGAT ATTCTTAACA TTGGCTTAGT 1140

CACAGTtGGA TACCTTAAAT AACTTGTAAA CACATGATGC TTTAATAATG TTTGATGAAT 1200

GTTCTCAGCC GCTTCTATGT CATCAAACTC AATAAACTTA ATCGGCGAGT TTGaACTATT 1260

ATAATkAACA TTGAGTGCTT TTAACTTTTG GTTAAAATAT TTACTCAAAC TATTTAATTT 1320

AGTGCGTCTA TCATCAGCAT TTATTAACTT TTCAATGTTT CTTTTTATAA AATACAAATT 1380

ATAAATTGGC AAACTACTTG AGTAGATGAG TGGTCTACCG TGATTAATTA aCATATCCtT 1440

CaCATCaTTT GaACTkaAAA TcACACCCCC GTATGCACCA CATGCTTTAG ATAAACTAGA 1500

AGTGAGTATA TCTACACCTT GATAATTCGA GTAAtTCTCT ATtCCAAAAC TATGTGAAAC 1560

ATCGAGTATC AGTGTTGCGT TAnATTTATG CTTTAATGAG ACTAATTGAC CAATATCCAC 1620

AACGTCGCCA TTCGTTGAAA ATACACTATC AGATATGATT ATTTTTGGTA TATTTTGATT 1680

AGGGTATTTC TCTAACCTTT TTTCTAAATC AGCAATATCT AAATGCTTAT ATATCACTTT 1740

TTCTAAACCA CTTAACTTAA TACCGTCAAT AATACTCGCA TGATTTTCTT GATCTGAAAA 1800

CACGACACAA TTTGTATTTT TGAAAATATT AAATAACGCC AAATTAGCAT CATAACCACT 1860

ATTTAAGATA GTACATGcAC TATATCCGAG CCAACCTGCT AACATTGTTT CAATTTCTTC 1920

ATAAGCTGTC GAACTTCCAC TAATTAATCT TGAACTTGAT AAGTGATAAC TATACTTCCG 1980

CATAAATCTT TCGAAATCAT CCTTATCAAA CGCTATTTGA CCTAATCCTA AATAATCATT 2040

AGATGTATAG TTCGTACATC TCTTATTTTC TACTTCAATA TACTGTCTAT CTATATACCC 2100

TACCGATTTA AGCGACCGAT ATAACCCTTT CTGTTGTAAT AAATCAATTT GCTCTTGAAA 2160

CTTCATTCTT GTTTTCCTTA TTTTCACAAG TGTCATAATC AATTTCAAAG CCTAAATCAT 2220

TAATCATATC GTAGTCTAAT TGGTTCGGTT GCCCACCAGT AATTAGATAA TnCACCGACA 2280

AATATTGAAT TCGCCGCTTT TAATGCTAAT GGCTGTAACG AACGTAAGTT GACCTCTCTT 2340

CCTCCAGCAA TACGAATTTC TTTCGTAGGA TTGATTAATC GGAATAATGC TACGATTCTT 2400

AAACATTTCA TTGGTGTTAA ATCATCCATG CTTCCAAACT TTGTGCCTTT GATTGGATGC 2460

AAAAAATTAA TCGGAATACT GTCGGCATCC ATTTCTTTTA AAGCAAATGC CATATCAACA 2520

ATATCTTGAT TAGATTCTCC CATACCACAA ATCACGCCAG AACATGGTGA TATATTATTC 2580

GCTTTCATTA GTTCTATCGT ATCTGTTCTA TCTTTATAAC TATGCGTTGT CACGACGTTA 2640

TCATGGTAAT TTTCACTTGT ATTAATATTG TGGTTATATC TGTCTACACC AGCTGACTTA 2700

TGTTGAGATT TAATCGTTCT TACAGTATTA CTAATATGAT CAACTTCTTT ATCGCTCGGT 2820

CCTCTACCAC TCATAACAAT ACAATATGTT CCAATATGAT TATCATGTGC CACCTTTGCT 2880

CCATCGATAA TTTGTTCCTC TGGAATTAAA GCATATCGCT GTTTTTGTTT AATATCTCGT 2940

GATTGTCCAC AGTACCCACA ATTTTCAGGA CATATACCAC TTTTAGCATT TAAAATCATG 3000

TTTAATTTTA CTTTTTTACC AAAATAATGT TTTCTTAAAA TGTACGCCTC ATTTAATAAA 3060

TCTAAGGTAT CAATATTAGT ATCCTCATAA ATtTTCAATA CAGTCTCTTT TGTtAATTGT 3120

tCCCCTTGTA ATATGCGTTT AGCCAAATTC ATATTAACAC TTCCTATCTA AAA 3173

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1694 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

CGATTATCCA TTAATACAAC CCTAAGTAAA TGTATAAAAA TTATCTTCCA CAAACTTCAA 60

CAAAAGCCTA AATAAATTAC AGCAATTTAT CAAATATTGC TTACTTTGAT TTTATGAAAT 120

nACTTAATTC TAACACATAC TAAATCATCA TATACTAATT CGAAATCAAA TGCATTTAGA 180

GATAATCaAA ATGCGGAAAC ATCTCCaATA ATCAATAATC TATTCCCAAT AAATATGAAT 240

GTTCTCAACA ATACATTATT TATATCTCTT TACACTGTCA TCGACAAAAA CTAAATCTTT 300

CACTTTCAAT TTCGAACGTG GTTCTACGAC ATTTGCTGCT ATATCATTTA ATGGGATTAA 360

AACAAATGCA CGTTCATTCA TTCTCGGATG TGGCACCGAC AGTTTTGGTA AATCTATCAT 420

TTCTTCTCCA TACAACAAAA TATCCACATC TAAAGTTCTA GGACCCCATC GTTCCTTTCT 480

AATACGGTGT AAACATTCTT CTGTCkTCAA ACAACATTCC AACAGTTGTA ATACTGTGAG 540

TGTTGTTTsA ATTTCAACAC ACAAATTTAA AAAGTTAGGT TGCTCAGTAT ACCCAACTGG 600

TGCTGTTTCA TAAATCGGAG AAATAtTAGA TACGTTAATA CCATCATATT CATTCaAAAT 660

CTTyATAGCA TCGTTTAACt GGCTTTCTCT ATCACCAaTa TTACTACCTA AyCCTAAGTA 720

TGCTTGAATC ATyTATTCTC CCTCACTATT TCGATACCTA CTCCATCATA ATGACCCGGA 780

ATCGGTGGGT TTTCTTTAGT GATTCTCACT TTCGTTTCCA TTACACGATT ATATTGTGAA 840

TTTATACGAT TTGCAATACG TTCAGCTAGA TGCTCAAGTA AATTAACGGC CTTACCTTCC 900

ATAATTGATT TAACCTCTTc GAACACTTCA CCATAATGAA CTGTATCAAT AACATTATCA 960

ATTTCATTTT CAGCTGATAA AGCACCATGA TATCCATAAA AGCGCATACC TTTAAGAAAG 1080

ATTGTGTCTT GCATTTTCAT TCTCCTTTAA AAAATCTATA CCTTTAGCTA ATTTAGCATT 1140

CAACTCGACA TTATGAACGC GTACTGCTCT AACGCCTTTC ATAATACCAT ATGCAGTCGT 1200

AGCTGCAGTT ACTTCATCTC TTTCAACCGG TGTTGTATCA TAACCCATCA TCTCTTTAGT 1260

GAAACGTTTC CGGCTTGTCG CTAATAAAAC TGGATATTCT GTTGCAACAA GTTCATCCAG 1320

TCTTGCCATA ACTTCGGCTT CTTCATTTCT AGTTTTAGCG AAACCTATAC CTGGATCTAG 1380

CCAAATTTTA TTTGAAGGTA TACCAGCTAT TTTAGCTTGA TGTGCTTGTG CTAACAAAGA 1440

TGTTAACATT TCTTCGACAA CCGGTTCATC ACGATTACCA TTTCCATTAT GCATTAAAAT 1500

AATTTCCGCG TCATAtTTAG CTACAATTTG GAACATACGA TGATCATACA GACCgCCcAT 1560

tGATCATTAA TCATATCAAC GGCTAATTTT AAACATGCTT CAGCAACCTC ACTTCGAAAT 1620

GTATCGACTG AAATTTTTTA CATCAnAACC GACAATAGCT TCAnCAACAG TAATACTCTG 1680

TTCCATCTCT TCTG 1694

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

AGCATTTCTT TTCTATAAAC ATTTAATTGA ACATTATTAA GTACACTATT ACTATAGTCA 60

CTATATTGAA CaCATACCTC ATTTAATTCT AATAGCGGTT CAGATTTGTA CTTATTATCA 120

TTATTTGCAG ATGTTTCATC TATCCATTTT TTCACTTTAA ATTTAACATG TTCACTCATA 180

CAAACGTCAC GTAAATTCGC TAAGTTATCA ATGGATTCGA CATCTACTTC TGCATATTTA 240

AGCGCTGTAC AGTATAATGG TTCACGTATG CCTGCTTCTT TAAGCTTAGA TGATTTTAGC 300

AAATCACTAG GCGTTGTATT AGCGATGATT TTTCCATCTT TAAAAAGAAG AACTCTATCA 360

AACGTATCAT CTAATGATTC TTCTAATCGA TGTTCGACAA TAATCATCGT TGACTTTGTT 420

TCTTCATGAA TATTGTTTAA CAATCTCAGC GTTTCATGTC CTGTCGCAGG ATCTAAATTG 480

GCCAGTGGCT CATCCAATAT TAAAATAGGC GTACGATGGA TTAATATACC ACCTAATGAA 540

ACGCGTTGTT TTTGACCTCC AGATAAATCT TGCGGTCGGT GATTTAAATG TTCTATCATG 600

CCAACTTTTT CAGCCCAATA ACTTACATTT TTCTTCATAT CATCTTGTTC AACACAATTA 660

TCTTGTAAAA CTGTACCAAC AACATTAGAT CTATCATGTA AACAACTAAC GGTTGCATCT 780

TGATTATTTA TATATAGTTC CCCAGTTATG TTACCTTTAG TTTTAAATGG AATTAATCCG 840

TTTATGCAAT TTGCAAAAGT CGATTTACCA CTACCCGAAG CACCAACTAC TAATACTTTT 900

TCTCCTGGAT AAATATCAAC ATTTATATTC TGTAATGTAG GTGTTGCTTG ACTATGATAT 960

TGAAAACTAA AGTCTTTGAA CGAGATAATT GGTTCAGTCA TGATATATCA TTACCTTTCT 1020

ATATTCATTT ACATATCTGA TTCAACAAAA TAACTATTCC TTACGTAAAC TACCTTTTTT 1080

AATTTGAGAT GAaGCATATG CTTTTAATAA TATTGTCCCA ATAATGCCAA CTGAAATAAT 1140

ATTTAATACT GCAGAGATAA CACCTTGTGT ATAAACCTTG TTAGCTGGTT CGTTATAAAT 1200

CAAAATATCT AATGTTGGTG CAATAAGTGC CCAGCAAATA ATATTCGCAA TAATTTGACC 1260

GATATTAAAA TAAACCATCG ATTTCCTAGA AAATCGGCCT GAAGAAAGAT TTAATTTTAG 1320

TCCAATCCAG CCATATAAAC AGCCTATAAT TCCCGAGC 1358

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

TAGAAGAATT GGAGAAAATG CTAATTCAAT TGTCAACATT CCATAGTTAT CATGATTTAG 60

AGTTTCTATT TGTGACACGT GAAGATGAAG TTGAAACATT GAAATGGGCA CGTTGGTTGC 120

CACATATGAC ATTGAGAnGG CAAAACATTA GAGGATTTGT TTACAATCAA CGAACGCGTG 180

ACCAAATTTT AACGTCAATT TATAGCATGA TTAAAGAACG TATCCAAGCT GTGCtGaACG 240

CAGCAGAAGT AATGAGCAAA TTATTTTCAC ACCGCAATTA GTGTTTGTCA TTACAGATAT 300

GTCATTAATT ATTGATCATG TCATTTTAGA ATATGTAAAC CAAGATTTAT CAGAATATGG 360

TATTTCATTA ATCTTTGTTG AAGATGtGAT TGaAAGTTTG CCAGAGCATG TAGATACCAT 420

TATTGATATC AAGTCTCGTA CTGAAGGCGA ACTGATTACG AAAGAAAAAG AATTAGTTCA 480

ATTGAAATTT ACACCTGAAA ATATTGrTAA CGTCGATAAA GAATATATCG CGCGACGTTT 540

GGCGAATTTG ATACACGTCG AACATTTGAA AAATGCAATT CCTGATAGTA TTACATTTTT 600

AGAGATGTAT AACGTGAAAG AAGTAGATCA GCTTGATGTG GTTAATCGAT GGAGACAAAA 660

CGAAACATAC AAAACGATGG CAGTACCTTT AGGTGTAAGA GGTAAAGATG ATATTTTATC 720

AGGGAAATCT GAGATTATCC AATCATACAT TTTATCTTTA GCTATTAATT TTCACCCTCA 840

TGAAGTTGCA TTCCTATTGA TTGACTATAA AGGTGGGGGT ATGGCGAACT TATTTAAAGA 900

TTTAGTCCAT TTAGTTGGTA CGATTACAAA CTTAGATGGC GATGAAGCGA TGCGTGCCTT 960

AACATCAATC AAAGCCGAAT TGAGAAAACG TCAACGTTTA TTCGGAGAGC ATGATGTTAA 1020

CCATATTAAT CAATACCATA AGTTATTTAA AGAAGGTATT GCGACAGAAC CAATGCCACA 1080

TTTATTCATT ATTTCCGATG AGTTTGCCGA ATTAAAATCA GAACAACCTG ATTTTATGAA 1140

AGAACTTGTA TCAACGGCAC GTATTGGACG TTCGTTAGGT ATTCATTTAA TACTTGCGAC 1200

ACAAAAACCA TCGGGTGTTG TTGaTGACCA AATTTGGTCT AACTCTAAAT TTAAGTTGGC 1260

ATTAAAAGTA CAAGATAGAC AAGACAGTAA TGAAATTTTA AAAACACCAG ATGCAGCAGA 1320

CATTACmTTA CCaGgTCGTG CGTATTTACA AGTTGGTAaT AATGAmATTT ATGAATTATt 1380

CCAATCTGCA TGGAGTGGTG CAACATATGA CATCGAAGGC GATAAATTAG AAGTTGAAGA 1440

TAAGACGATT TACATGATTA ATGACTATGG TCAACTTCAA GCAATCAACA AAGACTTGAG 1500

TGGACTTGAA GATGAAGAAA CGAAAGAAAA TCAAACTGAG TTAGAAGCGG TCATAGATCA 1560

TATCGAATCT ATTACAACAC GATTAGAAAT CGAAGAAGTT AAGCGTCCAT GGCTACCACC 1620

ATTGCCAGAA AATGTATATC ArGAAGATTT AGTAGAAACa GATTTCAGAA AATTATGGTC 1680

AGATGATGCA AAAGAAGTGG AATTAACATT AGGACTTAAA GACGTACCAG AAGAACAATA 1740

TCAAGGACCG ATGGTATTGC AATTGAAAAA AGCTGGGCAC ATCGCGTTAA TCGGAAGTCC 1800

AGGATATGGT AGAACAACGT TCTTACACAA CATTATTTTC GATGTTGCAA GACACCATCG 1860

TCCTGATCAA GCACACATGT ACTTGTTCGA TTTCGGTACC AATGGTTTGA TGCCAGTTAC 1920

AGACATACCA CATGTCGCTG ATTACTTTAC AGTAGATCAA GAAGACAAGA TTGCTAAGGC 1980

GATACGTATA TTTAATGATG AAATTGATCG TCGTAAGAAG ATTTTAAGTC AGTATCGTGT 2040

CACTAGTATT TCTGAATATC GAAAATTAAC TGGTGAAACA ATTCCGCATG TCTTTATTCT 2100

TATTGATAAC TTTGACGCAG TAAAAGATTC ACCTTTCCAA GAAGTTTTTG AAAATATGAT 2160

GATTAAAATG ACGCGTGAAG GGCTAGCATT AGACATGCAA GTAACCTTAA CTGCTTCAAG 2220

AGCTAACGCT ATGAAAACAC CAATGTACAT TAATATGAAA ACGCGTATCG CAATGTTTTT 2280

ATATGATAAA TCAGAGGTGT CGAACGTAGT AGGACAGCAA AAATTTGCGG TTAAAGATGT 2340

TGTGGGTCGA GCATTGTTAA GTAGTGATGA CAACGTATCA TTCCATATTG GCCAACCATT 2400

TAAACATGAT GAGACCAAAT CATATAATGA TCAAATTAAT GATGAAGTAT CGGCGATGAC 2460

AGAATTTTAT AAAGGTGAAc ACCAAATGAT ATtCCTATGA TGCCAGATGA AATTAAATAT 2520

GGATTAGATT ATGAAGGTGT TACACTACAA AAAATTAAAT TAACTGAACC AGCAATGATT 2640

TCATCAGAAA ATCCGAGAGA AATTGCGCAT ATTGCTGAAA TTATGATGAA AGAAATTGAC 2700

ATATTAAATG AAAAATATGC GATTTGTATC GCAGACTCAA GTGGAGAGTT TAAAGCTTAT 2760

AGGCATCAAG TGGCTAACTT TGCCGAAGAA AGAGAAGACA TTAAAGCGAT TCATCAACTA 2820

ATGATTGAAG ACTTAAAGCA AAGAGAAATG GACGGCCCAT TTGAAAAAGA TTCACTTTAT 2880

ATTATCAATG ATTTTAAAAC ATTTATTGAT TGCACGTATA TTCCGGAAGA TGATGTTAAA 2940

AAGCTTATTA CAAAAGGACC AGAACTTGGC TTGAACATTT TATTTGTCGG CATTCATAAA 3000

GAATTAATAG ATGCTTATGA TAAACAGATT GATGTTGCAC GTAAAATGAT TAACCAATTT 3060

AGTATAGGTA TTCGTATTTC AGACCAACAA TTCTTTAAAT TTAGATTTAT TCAACGAGAA 3120

CCTGTTATTA AAGAAAATGA AGCATATATG GTCGCAAACC AAGCTTATCA AAAGATTAGA 3180

TGGTTTAAAT AGCAATGAAT TAAATAGGAG GGAGGTATGT TATGAATTTT AATGATATTG 3240

AAACAATGGT TAAGTCGAAA TTTAAAGATA TTAAAAAGCA TGCTGAAGAG ATTGCGCATG 3300

AAATTGAAGT TCGTTCTGGA TATTTAAGAA AAGCTGAACA ATATAAGCGA TTAGAATTTA 3360

ATTTGAGTTT TGCACTAGAT GATATTGAAA GCACAGCAAA GGACGTACAA ACTGCAAAAT 3420

CTAGTGCTAA TAAGGACAGT GTAACTGTTA AGGGAAAGGC GCCCAATACG TTATATATTG 3480

AAAAAAGAAA TTTGATGAAA CAAAAGCTTG AAATGTTGGG TGAAGATATC GATAAAAATA 3540

AAGAATCCCT CCAAAAAGCT AAGGAAATTG CTGGCGAAAA GGCAAGTGAA TATTTTAATA 3600

AAGCAATGAA TTAATATTGA GGTGAAGATA TGGGTGGATA TAAAGGTATT AAAGCAGATG 3660

GTGGCAAGGT TGATCAAGCG AAACAATTAG CGGCAAAAAC AGCTAAAGAT ATTGAAGCAT 3720

GTCAAAAGCA AACGCAACAG CTCGCTGAGT ATATCGAAGG TAGTGATTGG GAAGGACAGT 3780

TCGCCAATAA GGTGAAAGAT GTGTTACTCA TTATGGCAAA GTTTCAAGAA GAATTAGTAC 3840

AACCGATGGC TGACCATCAA AAAGCAATTG ATAACTTAAG TCAAAATCTA GCGAAATACG 3900

ATACATTATC AATTAAGCAA GGGCTTGATA GGGTGAACCC ATGATGAAAG ATGTTAAGCG 3960

AATAGATTAT TTTTCTTACG AAGAATTAAC AATTTTAGGT GGTAGTAAAT TGCCTCTCGT 4020

AAATTTTGAA TTGTTTGATC CATCAAATTT TGAAGAAGCT AAAGCTGCTT TAATTGAAAA 4080

GGAATTAGTA ACAGAGAATG ACAAGTTAAC TGATGCAGGT TTTAAAGTGG CTACATTAGT 4140

CAGAGAGTAT ATTAGCGCCA TTGTAAATAT TCGAATTAAT GATATGTATT TTGCACCATT 4200

TAGCTATGAA AAAGATGAAT ATATTTTGTT AAGCCGGTTT AAAAATAATG GGTTTCAAAT 4260

ACGAATTATC AATAAAGACA TTGCATGGTG GTCGATTGTA CAATCATATC CTTTATTGAT 4320

CTTAAATAAT GAAAGTATCG ATACGATTGG GCGTGTTTTA GAAATTGAAA TATACAATCA 4440

TCAAGGTGAC CCTCAACAAA GTTTATATAA CATTTATGAA CAAAATGATT TGTTATTCAT 4500

TCGATACCCA TTAAAAGATA AAGTGCTGAA TGTTCATATT GGTGTCATTA ATACATT 4557

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3931 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

TTGAGTGACT TTATTGAAGC GCGTGTAGAA GAAATATTCT TCGAAGTATT TGATGTTTTA 60

CAAGATTTAG GATTAACAAA AGTAAATGGT GGGTTTATTG TAACTGGTGG ATCTGCAAAC 120

TTACTTGGCG TAAAAGAATT ATTATCAGAT ATGGTAAGTG AAAAAGTTAG AATTCACACG 180

CCATCACAAA TGGGAATTAG AAAACCTGAA TTTTCTTCAG CAATTTCTAC AATTTCTAGT 240

AGTATCGCTT TTGATGAGTT ATTAGATTAT GTTACAATTA ATTATCATGa TAATGAAGAA 300

ACTGAAGAAG ATGTTATTGA TGTGAAAGAC AAAGATAACG AATCTAAATT AGGCGGaTTT 360

GaTTGGTTTA AACGTAAAAC AAACAAAAAA GATACTCATG aAAATGAAGT AGAGTCAACA 420

GATGAAGAAA TTTATCAATC AGAAGATAAT CATCAGGAAC ATAAACAGAA TCATGaACAT 480

GTTCAAGACA AAGATAAAGA TAAAGAAGAA AGTAAATTCA AAAAACTAAT GAAATCTCTA 540

TTTGAATGAT TATTGGCCAA TAAAACTAGG AGGAAATTTA AATGTTAGAA TTTGAACAAG 600

GATTTAATCA TTTAGCGACT TTAAAGGTCA TTGGTGTAGG TGGTGGCGGT AACAACGCCG 660

TAAACCGAAT GATTGACCAC GGAATGAATA ATGTTGAATT TATCGCTATC AACACAGACG 720

GTCAAGCTTT AAACTTATCT AAAGCTGAAT CTAAAATCCA AATCGGTGAA AAATTAACAC 780

GTGGTTTAGG AGCAGGAGCT AATCCTGAAA TCGGTAAAAA AGCTGCAGAG GAATCTCGTG 840

AACAAATTGA AGATGCAATC CAAGGTGCAG ACATGGTATT TGTTACTTCT GGTATGGGTG 900

GCGGAACTGG TACTGGTGCA GCACCAGTCG TTGCTAAAAT TGCAAAAGAA ATGGGCGCAT 960

TAACTGTTGG TGTTGTAACT CGTCCATTTA GTTTTGAAGG ACGTAAACGT CAAACTCAAG 1020

CTGCTGCTGG AGTAGAAGCT ATGAAAGCTG CAGTAGATAC ATTAATCGTT ATACCAAATG 1080

ACCGTTTATT AGATATCGTT GACAAATCTA CGCCAATGAT GGAAGCATTT AAAGAAGCTG 1140

ACAACGTGTT ACGCCAAGGT GTACAAGGTA TCTCAGACTT AATCGCTGTT TCTGGTGAAG 1200

GTATTGGTGT TTCTTCTGGT GAAAATAGAG CGGTAGAAGC TGCTAAAAAA GCAATCTCTT 1320

CTCCATTACT TGAAACATCT ATCGTTGGTG CACAAGGTGT GCTTATGAAT ATTACTGGTG 1380

GCGAGTCATT GTCATTATTT GAAGCACAAG AGGCTGCTGA TATTGTCCAA GATGCTGCAG 1440

ATGAAGACGT TAATATGATT TTCGGTACAG TTATTAATCC TGAATTACAA GATGAGATTG 1500

TTGTAACAGT TATTGCAACT GGTTTTGATG ACAAACCAAC ATCACATGGT CGTAAATCTG 1560

GTAGCACTGG ATTCGGAACA AGCGTAAATA CTTCTAGCAA TGCAACTTCT AAAGATGAAT 1620

CATTCACTTC AAATTCATCA AATGCACAAG CAACTGATAG TGTAAGTGAA AGAACACATA 1680

CAACTAAAGA AGATGATATT CCTAGCTTCA TTAGAAATAG AGAAGAAAGA CGTTCAAGAA 1740

GAACAAGACG TTAATCGGTT AATATATATA CACAAATAAT TCAACACAAA TCATCAGATA 1800

ACATATCTGA TGATTTTTTT ACTAATTTTT AGaACATGTA GAAGGACATT TAAGTTTTTC 1860

aAAGTTATTA AAAGTGTTTA AGTATCGTGT GAAAATTAAG TCaAAAATTA TTTGCGCAAC 1920

ATTTTAACTT TAAACATAAA TGTTATATTA TATAATTATT AACTTTGTAC AGTTAGACGA 1980

AGATAATTTA AATGAAATGA TGGTGACGAT CGAGTGAATG ATAATTTTAA AAAGCAACCG 2040

CATCATTTAA TATATGAAGA GTTATTACAA CAAGGTATTA CTCTAGGTAT TACAACTAGA 2100

GGAGATGGTT TAAGTGACTA TCCTAAAAAT GCTTTTAATA TGGCGAGATA TATTGATGAT 2160

CGCCCATATA ATATTACTCA ACATCAATTG CAATTAGCTG AAGAAATTGC GTTTGATAGA 2220

AAAAATTGGG TGTTTCCCAT TCAAACACAT GAAAATAAAG TCGCTTGTAT TACAAAGGAT 2280

GATATAGGCA CAAATATAGA CACTTTAACT GATGCGCTTC ATGGTATTGA TGCGATGTAC 2340

ACATATGATA GTAATGTCTT ATTAACGATG TGTTATGCAG ACTGTGTACC AGTATATTTT 2400

TATAGTACAA AACATCATTT TATTGCATTG GCGCATGCAG GTTGGCGTGG TACCTATACT 2460

GAAATTGTAA AAGAAGTGCT AAAACATGTG AACTTTGATT TGAAAGACTT ACATGTCGTT 2520

ATTGGACCAT CTACATCATC AAGTTATGAA ATTAATGATG ATATTAAAAA TAAATTTGAA 2580

ACATTGCCAA TTGATAGTGC CAACTATATT GAAACTAGAG GACGAGATCG TCATGGTATT 2640

GATTTGAAAA AAGCCAATGC TGCATTATTA ATTTATTATG GTGTTCCTAA AGAAAATATT 2700

TATACGACAG CGTATGCTAC ATCTGAACAT TTAGAATTAT TTTTCTCTTA TCGATTAGAA 2760

AAAGGTCAAA CAGGACGCAT GTTAGCATTC ATTGGTCAAC AGTAAACAAG GAGGAGATAT 2820

GTTTGCGTGT GAAAGATAAT TTACAACAAA TCTCAACACA AATTAATGAC AAAAGTGAAA 2880

AAAATAATTT TTCAACAAAA CCAAACGTGA TTGCAGTTAC AAAATATGTT ACAATAGAGC 2940

GAGCTAAAGA AGCGTATGAG GCTGGAATAA GACATTTTGG TGAGAATAGA TTGGAAGGCT 3000

AATCTCGAAA AGTTAAGGAC GTTATAAACG ACGTAGATTA TTTCCATGCT TTAGATCGAT 3120

TGAGCTTAGC CAAAGAAATT AACAAACGTG CAGAACATAA AATTAAATGT TTCTTGCAAG 3180

TGAACGTTTC GGGAGAAGCT TCTAAACATG GTATTGCTTT AGAAGATGTT GATCAGTTTA 3240

TAGATGATCT TAAAAAATAT GACAAAATCG AAATTGTAGG TTTAATGACG ATGGCACCAT 3300

TGACAGATGA TGAAGCATAT ATTAGATCGT TATTTAAACA GTTACGTTTG AAAAAAGAAG 3360

AAATACAACG ACTCAATTTA GAATATGCGC CTTGTGATGA ATTATCAATG GGAATGAGTA 3420

ATGACTATCT TATTGCAGTT GAAGAAGGTG CGACGTTTGT TAGAATTGGG ACTAAACTTG 3480

TAGGAGAAGA GGAGTGAGCC ACTTGGCTTT AAAAGATTTA TTTAGTGGAT TTTTTGTAAT 3540

AGATGATGAA GAGGAAGTAG AAGTACCTGA CAAACAACAA CAGGTAAATG AAGCGCCAGC 3600

AAAAGAGCAG TCACAACAAA CAACAAAACA AAACGCAATC AAATCAGTCC CTCAAAAATC 3660

TGCATCAAGA TATACAACAA CGTCAGAAGA AAGGAATAAC CGTATGTCTA ATTATTCAAA 3720

AAATAATTCA CGTAATGTTG TAACTATGAA CAATGCTACA CCAAACAATG CATCACAAGA 3780

AAGTTCAAAA ATGTGTTTAT TCGAACCACG TGTTTTTTCA GATACACAAG ATATTGCTGA 3840

TGAGCTTAAA AACCGCCGTG CGACACTTGT CAATTTACAA CGTaTTGATA AAGTATCAGC 3900

GAAAAGAATT ATTGATTTTT TAAGCGGTAC T 3931

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

AATTGTCGGG GGACTCTTAG GTTTTGTCAT GCAAAGAACA AGATTTTGTT TAACAGGTGG 60

CTTTCGAGAT ATGTATGTGC AAAAGAATAA TAAGATGTTC TATGCATTAT TAATCGCTAT 120

TACTATTCAA AGTATAGGAT TATTGATTTT GACGGCAACA GATATTTTAC AAATTCCTGC 180

ACATAGTTTT CCAATATTGG GAACAATTAT AGGTTCTTTT ATTTTTGGAA TTGGAATAGT 240

ATTGGCTGGA GGATGTGCAA CAGGtACTTG GTATCGCGCT GGTGAAGGGC TAATTGGTAG 300

TTGGATTGCA TTAGTATTAT ATGCTGTTAC TGCAGCAATC ACTAAAACAG GGATTTTAAA 360

GCCAGTAATG GATAAAATTA ATCAACCAAC GAATGTAAAT AGTGATATGT CTCAAACAAC 420

TGGCATTCCG TTTTGGGGAT TAGTCGTTAT ATTAACTATA ATCACCATTT TTCTAGTTGT 480

AGGTATTAGA TATTACCTTT TCGAAAAACG ATACCATCCA TTTATTGCAG CAATTGTAAT 600

TGGACTTATC GCACTCTTAG CTTGGCCAAT GAGTGCATCA ACTGGAAGAA ATGACGGTTT 660

AGGTATAACA ACGCCTTCAG CAAATTTAGT ACACTTTTTG ATTACAGGTG AAACTAAATT 720

TATTGATTGG GGTGTCTTTT TAGTTCTAGG AATTTTCATT GGTTCATATA TTGCAGCTAG 780

AGGATCAAGA GAATTTAAAT GGCGATTGCC AGACAAGATT ACAATACGAA ACAGTGCCAT 840

TGGTGGCATA TGTATGGGAT TTGGTGCGTC AGTTGCTGGT GGTTGTTCTA TCGGTAACGG 900

TTTGGTTGAA ACGGCAACGA TGACTTGGCA AGGATGGATT GCGCTAgCAT gCGATGATAG 960

TTGGTGTATG GACAATGAGT CATTTTATCT TTGTTCGTCC AATGAAAAAA GTACACCAAC 1020

AATCTGCAAA GGTTAAACAG CAAACGCAAA TAGTATAGAA GATTATTATG CAAATGATGT 1080

TGATCAAATA AAAGTGATTG GAAAAGGAGA AATAATTATG ATACACGAAT TAGGTACAGT 1140

AGGAATGGTA TGTCCATTTC CGTTAATTGA AGCGCAAAAG AAAATGGCAA CATTGCAATC 1200

TGGAGATGAA TTAAAAATTG ATTTTGATTG CACGCAAGCG ACGGAAGCCA TTCCAAATTG 1260

GGCTGCAGAA AATGGTTATC CTGTAACAAA CTATGAACAA ATTGATAATG CTTCATGGAC 1320

AATTACAATT CAAAAAGTTT AACGTTATCA TTTTAACAAT AAAATAGATA TTAGATTCTA 1380

TGGCTACTTC CGCTAATTTA AAAGTGAGTA AGTAGTCTTT TTTTTTTTAG TTCATGAAAT 1440

CATTTTTATA TAGTGTGGCA CATTTTATTC CAAAAGATGT AATAAAACTT AACGCATTTT 1500

TGCTTTTTAT AAATTGTCAG ATTATTATGA AAAAAAGGGA GTGGTAAGTA TGAATCTTAA 1560

CGATACGATA TTTATGTTTT TGTGTACATT ATTAGTTTGG TTAATGACAC CAGGATTAAG 1620

TTTATTTTAT GGTGGGTTAG TTCAATCTAA AAATGCGCTT AATACTGTCA TGCAAAGTAT 1680

GGCAGCAATT GTGCTTGTTA CATTTGTATG GATAACAGTT GGTTTTACAA TTAGTTTTGG 1740

GAATGGGAAT TTATGGTTCG GAAATTGGGA ATATACTTTT CTTAATCATG TAGGTTTTGC 1800

GACTCAAGAA GATATTAGCC CACATATTCC TTTCGCTTTG TTTATGTTAT TTCAAATGAT 1860

GTTTTGTACG ATTGCAATTT CTATTTTATC TGGTTCAATC GCTGAGAAAA TGAAGTTTAT 1920

TCCTTATTTA TTATTCGTAG TAATATGGAC TGCTCTTGTA TACAGTCCAG TAGCACATTG 1980

GGTTTGGGGC GGCGGTTGGA TTAACAAACT CGGTGTATTA GATTTCGCTG GAGGTACGGT 2040

TGTTCATATT ACATCAGGTG TTTCTGGTTT AGTATTAGCT ATTATGATTG GAAAAGGAAA 2100

CAAACATTCT GAATCAACAC CACATAATCT TATCATTACG TTGATTGGCG GTATATTCGT 2160

GTGGATTGGT TGGTATGGAT TTAATGTAGG TAGTGCTTTT ACATTTGATA ATATTGCGAT 2220

GCTTGCATTT ACAAATACTG TCATTTCAGC CAGTGCAGGT GCTATAGGTT GGTTAATTTT 2280

ATTAGTTGTC ATTACTCCTG CAGCAGGATA TGTAACATAT CTTAGTGCAA CAATAATGGC 2400

TTTAATAGGA GGTATCTGTT GTTATATTGT CATTAATTAC ATCAAGGTAA AACTAAAATA 2460

TCATGATGCA TTAGATGCAT TTGGTATTCA TGGTGTTGGT GGTATTATTG GTGCTGTTTT 2520

AACAGCAGTT TTCCAAAGTA AAAAAGCCAA TCCTGACATT GAGAATGGCT TTATTTATAC 2580

TGGTGACATA CATATTATAC TTGTACAAAT ATTATGTGTA ACAGCAGTTG TAATTTTTAG 2640

TATAGTCATG ACGTTTATTA TTGCGAAAGT AATTAAATTa ATTACACCAT TATCTGTTAC 2700

GGAACAAGAA ACGAATATAG GATTAGACAA GATTGTTCaC GGTGAACATG CTTACTTTGA 2760

AGGTGAGCTA AATAGATTCA ATAAACATAT TCGATATTAG AATATATTTA CATAGAATAT 2820

TCATTGTCCT GACATTTAAC TAAAGGTTGA TGTTGGGACA TTTTGTTATA CAAAAGTTTT 2880

ATTTTGAAAT CTTTTTATGA AAGAAGCAGA AATATTATTT AAAGCGGTTA CACATATGCT 2940

AAAATAAGGC TAAGTGTCAC AAATAATGAT AGGTGAATAA GTATGAAAAA TATATCTGAT 3000

ATTGCCAAAT TGGCAGGCGT TTCAAAAAGT ACAGTATCTA GATTTTTAAA TAATGGATCT 3060

GTCAGTAAAA AAACAAGTGA AAAATTAACA AGAATTATAG CAGAACATGA CTATCAACCG 3120

AATCAATTTG CTCAAAGTTT AAGAGCGAGA 3150

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3719 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

GTTATAGTGA AATTGACTCA TCACATTTCA CAGACCGTGA CAAACGCGTT ATTAGACGTG 60

ATCATGTTAA AGAAGCACAA AGCTTAGTAG AGAACTATAA AGATACACAA AGTGCTGATG 120

CTAGGATGAA AGCCAAACAA AAAGTTAACA CATTAAGCAA ACCGCATCAA AACTATTTCA 180

ATAAACAAAT TGATAAGGTT TATAATGGAT TACAACGCTA ATCCAAAGTA AATTATAAGT 240

TATACATCTC GTTTTTAAAT GACAATTTAT CCCCGTAAAT ATTATAAATA ATCTTTTCAA 300

ATTCCACATA GATATAGAGA CACTAATAAA CCTCTTTGTC TCGATATGAT AGTCTGCAAC 360

GATTCATGTT GTAGGCTTTT TAATTTTACA AATAAGGCTA AATATATAAG TTCTGGCACC 420

TAAAATATAG AAAATACATA AAAGTAAGTA TAGTTATTTT ATTATAATTA TTAAATTTTT 480

ATTAATTAAT TGTAAAAATG TATAATTATA ATTAATTAAC GTTTAATATT AAAATTAACT 540

ATCGTTTCAA TATTACTTAT AGGGATGGCT ATCAGTAATG TTTCGAAAGG GCAATACGCA 660

AAGAGGTTTT TCTATTTCGC TACTAGTTGT TTAGTGTTAa CTTTAGTTGT AGTTTCAAGT 720

CTAAGTAGCT CAGCAAATGC ATCACAAACA GATAATGGCG TAAATAGAAG TGGTTCTGAA 780

GATCCAACAG TATATAGTGC AcTTnCAACT AAAAAATTAC ATAAAGAACC TGCGACATTA 840

ATTAAAGCGA TTGATGGTGA TACGGTTAAA TTAATGTACA AAGGTCAACC AATGACATTC 900

AGACTATTAT TGGTTGATAC ACCTGAAACA AAGCATCCTA AAAAAGGTGT AGAGAAATAT 960

GGTCCTGAAG CAAGTGCATT TACGAAAAAA ATGGTAGAAA ATGCAAAGAA AATTGAAGTC 1020

GAGTTTGACA AAGGTCAAAG AACTGATAAA TATGGACGTG GCTTAGCGTA TATTTATGCT 1080

GATGGAAAAA TGGTAAACGA AGCTTTAGTT CGTCAAGGCT TGGCTAAAGT TGCTTATGTT 1140

TATAAACCTA ACAATACACA TGAACAACTT TTAAGAAAAA GTGAAGCACA AGCAAAAAAA 1200

GAGAAATTAA ATATTTGGAG CGAAGACAAC GCTGATTCAG GTCAATAATG CTCATTGTAA 1260

AAGTGTCACT GCTGCTAGTG GCACTTTTAT AATTTTTAGA TCACGATATG ATTTATTATC 1320

AATTCAGAAT TAAAAAAGTA AATAGTATCA AAAGTAAGTG TATTTAATAT TAGAAAATAA 1380

AAATTTTAAA TTTAGTATTA AAATGGAATG TTACTATATA GTTCAATGTG TATTATCACA 1440

GAAAATAAAA TAATGCTTTA CTTCTATATT TAAAAGTGTA TAATGAAAGT TAAGTAATAA 1500

AGAGCGTGAA GAAAAATGTG AGTTATTTAT ATAGAATATT CTCCTTTTCA TTTATGAATT 1560

TGTTACAAAA TATTTAGTGC AAAAGCACGA cGGAGGTATT CAATATGaAT AACGGTACAG 1620

TTAAATGGTT TAATGCAGAA AAAGGTTTTG GTTTCATCGa AAGAGAAGAT GGTAGCGACG 1680

TATTCgTACA CTTCtCAGCA ATCGCTGAAG ATGGATACAA ATCATTAGAA GAAGGCCAAA 1740

AAGTTGAATT CGACATCGTT GAAGGCGACC GTGGCGAGCA AGCTGCAAAC GTAGTTAAAA 1800

TGTAATTTTA ACTTATTCAA ACAGTCCTTA CTATAGGGCT GTTTTTTTAT GCTTTAAATC 1860

GATAACAGTT GGTGTGGTAA AAGCACTAGC CGTTATTTTT TTGTCCAATA AATTTAGTTG 1920

GAGATTTAAC AATATATAAT GGTTCTAAAA TAAATCGAAC TGATGGAAAA GTTTTTTACT 1980

TTTCATCTGT CCGACTTTTG ATTTTGAATA TAAAAAAGCG CCAATACAGA ACTTTAATAA 2040

TGACGAGAAT TAAAGTCTGT ATATGGCGAT AACAAGAAGT AATGTTAAAC ACTCAAAATG 2100

TTTAACAATA ATAGGATACC ACATCGCATA ATATCTTACT ACTTAATTAA TAATTTAACT 2160

AATCAACTTT TTGTTAATTT TTTATTAAGA CTGATTAATT ATTGAGAATA TTTATTGTTT 2220

TTAAAATCTC ATAATAATTC AGTAATCTTG TTTTCATTTA AAAGGCGAAA CATTAAAATA 2280

ATTAAATAAA AATATTGCGT TTAATTTACA GCGTCAAATA TACTTATTTC TAATGCTTTG 2340

ATTTCTGTGA GTATTTGGAA GCTACCATTA GGCAACGGTT TAACAATAGA CAATTGCTTT 2460

TCCGCTTGTT GTATTAAAAA AGGTTTTGTA GATTGATTAT TAATATGCCA TTCACTCATG 2520

TATGTTTTTC ACTCCTGCTT TAAAATAGGG TTAGAAAGTT TATAGTTGAG ACATTCATGT 2580

TCAACCAAAA TTTTGTTCGA ATTCAATAAA TGTCTTGTTT AAAATAGAAA TATTGTAAAT 2640

GTTATCGTCC AAAACTTCAC CAGTTAAGTA TTTGTTTTGA ATTAAAATTT GGCAGTTAGT 2700

TAAGAAGTCT TGATAATCAC GATCGCAAAA ATAGTTTTCA CGTGCATCTT TAGCATCGCC 2760

AAAAAAGTTA GCGACTGTTT CTGTTTCTCC TTTATTCGAA CGTTCAATAT ATAATTTGTA 2820

AAATTTAGCT ATTGTATACT TTTGTTCTTT AGTTAGTTCA TTCAAAATAT TGGGCCTCCT 2880

GAAATATCAT TTGTAATCTA TACCCAATTT ATTGCAAAAC AAAAACTAAT TTAACTATTT 2940

GATGAAACTG TGTTAATAAg CTTTAACAAG CCTTAGTTTG TATGGATCTA TAAAATTATC 3000

TTTAATTGCA TAGGGTGAAA TAATATGTAG TCCATAACTT TTAACTGATT TTTCACTTAC 3060

ACCAAATTTA TAAGCTTGGT AGATAATTTT AGTACAATAC GTAAATTTTT TGCTGTTCAA 3120

ATTTAATGTA ACTAGATAAC GATGATTTGT ATTCTCATAG TTTTTCTTAA CCCATTCAGC 3180

CGCTTTTTTA CCTGCACCAG GATAGCTGCA ACGATAAACT TTCATCCAAT CATTTTTGCC 3240

ACTTGCATAA TTATATTTAA AAGATTCGAA GGATTGTGTA GTTGGTTTGT CGCCAGGCCC 3300

CTCAATTTGT AAAATCGTTT TATCATCAAT CGCGATACTA CAATGACCAA AAAATCscCA 3360

CATGACAGGG CCTTTTGTAA CAATAATATC ACCAGGTTGT AATTGGAATT TGTCATCTTG 3420

AATTTCTGAA TACTTATTAT CTGCAATTGT TTTTGGTGAG TTTATTGGGG ATACGACAAC 3480

GAATAATATA AGTAAAATTA TCGTTCGTTT AATATAGTTC ACTTAAAAGC TCCTTGTTGA 3540

AGAAATATAT GTAAATAGTC TTAAATTAGA ATTGTAATCT TTAATAAGCT TGtAAGACTA 3600

AAACATATCT TAAATATTAA AGTATGAGAG TGTGAAATGT CTATTAAGAA TnAAAAACAG 3660

TCTGAAACAT CATTGAGACG TTCCAGACTG GATATAAAAT GAATTTCATT TATAGCACA 3719

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

TTGCGTTGCC GCACCAAGAT ATTGAATGCC TAGCGATTCC GAGTATGCAA ACTGAACGCA 60

CTCTTTAATA CGCGTTATCG CTTTTTGTAA ATCTGCATCA TGATAACAAA TCATAACGCC 180

ATAGCCACCT GCTGTCGGAA GATCATCTCC CGGCTTAATT ACTAACGGGA ATTCCCAATT 240

CTTAATCTCG TTTTCGAATT GCTCAATTTT TACAACTTTT CTTTTTGGTA AAAACTTCCC 300

ATTTGTCCAT TCAGGTATTC TTGCTTTATT ATTTAAAGCA ACAAATAACG TTTTATCTAA 360

TGCATAATAT TGCTGATTCA AGATTGTTTC ATCATGAATA TATTGAAAAT AAATCTTTTT 420

ATTTTCCTTA TGTGCCAATT GTTTGATCAA GTTTTCGTAA GATTGCTGAT TGTTAAATGT 480

ATAAATTGAG TTCGGtACTT CCTTACCAAT AACTTGAAAT AGCTGATGCA ATTTGTCTGT 540

CGCACTAGCT TCGTGAACAA TAACAGGTAA TTGATTTGCT ATTAATAACT CCCTACCAGT 600

TAAAAAATTA GATTGATGTT CGTCCGGTTT CAACCATGGA TTCGATATAT ACGAAGGTCT 660

TGACGTATAG ACAACATCTT TGTCATATAA ATCACTTAAC GTTAAGTTCG GCTCATTACC 720

ATTATTTGTC ATTACTTCCC ATTCCCTTTC AAATGCGCAT GCTCTTCAAT AATGTCTTGA 780

TAAACGTCTT GATTTGTAAT TAACTCTAAC CCCATCAACG CCATTATTTT AGCGCCTTTA 840

ATTAATGCTT CATCACCATG TACACTCGCA GCCGCTTCTC TAAATCTATG CGTATGTCCT 900

ACTAAATTAC GTGATCCTAT TTTAATATGA GGATGTATTG TTGGCACAaC ATgaCTTACG 960

TTCCCTGTAT CCGTAGAGCC ATAACCAAAA TCATCATCAA TAACTGCTTC ACCAACTTCT 1020

TCAGCATATT TAGCAAATAA ATCATCTAAT TTCGGCGTTT TAATGAATTC ATTCACACCG 1080

TTTTGAATTC GACCAAATTC ATAATCACAA CCAGTCTGTA TCGCAGCTCC ACGTGCGATT 1140

TGATTTACTT TTTCTGTTAA TATATCCAAT TCTTTACGCG TCATTGCTCT AGTATAAAAA 1200

CGAGCATGTG TATAGTCTGG AATAATATTA GCTGCTTTCC CGCCATCTAA AATCACACCA 1260

TGCACACGTT GATCTTTTTT AATATGTTGT CGTAGTTGTG CTACACCATT AAAATAACTA 1320

ATCATAGCGT CTAATGCATT TAACGCTTCA TCTGCATTTT CAGAGGCATG AGCACTTTTT 1380

CCGTAAAATT TAACATCTAA AACATCCACT GCCAAAGTAT CAATCGTTTT ATAAGTTTCA 1440

TTTCCCGGAT GAATCATTAA GGCAATGTCT ATTTGATCAA TCACACCAGC CTTGACATAA 1500

GAAGCTTTAG CGCTACCATT TTCCCCACCT TCTTCAGCTG GACATCCAAG AACGACTACT 1560

TTACCACCAA TTTGGTCAAT CACTTGCTTC AAACCAATTG CACCAAGAAC ACTTGCAGTT 1620

CCAATGATAT TATGACCACA AGCATGACCC AATCCTGGCA AAGCATCGTA TTCTGC 1676

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

TACAGTAGGA ATCATAAAAC CTAATACAAC AAATACAAAA CCATTTAAGG CATAACTAAA 60

TGTGTTCCAA ATTTGATGGT AATTCATTTG TAGTTCCGTT TGTGCTCTAA TTAAACGGTC 120

GCGTTCTAAA CCATGGATTA GACCTGCGAT TACAACTGCA ATGATACCTG AAGCATGAAC 180

TTCTTCTGCT AAAAAGTATA CGACAAAAGG AGTTAATAAT TGAATAAAAG TTAAGGTATT 240

GTTATCTTTT AAACCTTTAT TAGCGGTTAA GTCTATACGT ATTCTAACGA CAACGAATCC 300

AATAATTGCA CCAATAAGTA CACCTAGTAT TGTTGAAATG ATAAATTGTT CAACAGCTTG 360

GAATAATGAA AAGGTACCAG TTACTAATGC AGTAACAGCA ATTTTAAATG AAATGATACC 420

TGCTGCATCA TTGAGTAAAG ATTCACCTTC TAAAATCGTC ATAGAACCTT TAGGTAATAA 480

TTTTCCGCGT GTAATAGCAG ATACTGCTAC TGCATCAGTA GGACATAAAA TTGCTGCTAT 540

TGCAAAAGCG GCTGGCATTG GTAAGGCAGG CCAAATCCAA TGTATAAAAT AGCCAACACC 600

GACTACAGTT GCAAACACTA GTGCCATTGA CATTAATAGT ATAGGTTTAC GATATTCTAA 660

TAATTTTGTT CGAGAGACGT GGGTACCTTC CACAAAAAGT AGTGGCGCGA TAACGGCAAA 720

CATAAATACT TCAGAATTGA ATTGGAAATC AACTTGTATT GGAATAATGA AAATAACGAC 780

ACCTAATGCA ATTTGAATAA AGGCAGTAGG AATTTGTGGG AATCGATTAT TGATAACCGA 840

ACTAATAATC ACAGCAAAAA TAAAAATTAA AAATGCTTCT AATAGTGCCA TACAATACTC 900

CTCAAAATTT TAATAGTTAA TATTTTATCA CTTTTAAGGC ATAATGACAT AGATATATTG 960

ATAAAATGAA GTTATTTTCA AAAAAACTCT AGTATCGGTT GAACTGATAC TAGAGCGAGA 1020

TGTTTAAATT ATTGATTGTc ATATCTGAAA TGACCGCTGT CATTTTGTCG TTGTTCATAC 1080

GCGAGCTTTT CAGCATTCGT TTTGTATTTT TtATAAAAGa AAAATAaAAA TATnAACCaG 1140

AATGGCGAAA TATAAATAGC TGCTCTTGtT TCGTCACTAA AGAATAATAA AATGAATACA 1200

AAGAAGAAGA ACGCTAGAAT AATGTAAGCA ATAGGCTTAC CACCAATCAA CTTAAATTTA 1260

CTGTTTTTAT GTGCCTCAGG ATGCTTTTTC AAAT 1294

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1935 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ACATGATAAT GATGACGCTA TTAAAACACG TTTTTTATTT TTCATTGTTA TAACCTTCTT 60

TCGTATGATT GATATTTGTT GATATGTATC GACATGTGAA TAATATCACA AAAACAGAGA 120

ATATATATTT AACTATTTAT TAAATGATTT TGTTAATATT ATTAAATACT TTATCCTCTT 180

TAAAAATAAT GTGTGTACAA AGTCATTAAT TTAGCAAATA TTTTTATTTA GTAGTTAATA 240

ACCATCGATT TGAAATTTAT ATATAATTAT TAGCTAAATA ATATCCTGCA TCTTTCTCAT 300

ACAATTTACT ATAAAtTAgC ATATCCGATA TCAGCGTTAA TAAGATCGTT GATACTAGmC 360

AGTTAATTTC ATAGAACGAA ATCAAATAAC ACACTACTTT CTGCATTTTA AATTATGTTT 420

AAGAATCAnA ATTATGTTTA nATAAATATA TATACTACTT TGAAAGGTGT GAGCTTAATG 480

ACAACTTTTA GTGAAAAAGA AAAAATTCAA TTACTAGCAG ATATTGTTGA ACTACAAACT 540

GAAAATAATA ATGAAATAGA CGTTTGTAAT TATTTAACAG ATTTATTCGA CAAGTACGAT 600

ATTAAATCTG AAATTTTGAA AGTTAATGAA CACCGCGCCA ATATCGTTGC AGAAATCGGT 660

AACGGCTCAC CTATACTCGC ATTGAGTGGT CATATGGATG TTGTTGATGC AGGAAATCAA 720

GATAATTGGT CATATCCCCC TTTTCAACTG ACAGAAAAAG ATGGCAAATT ATATGGCCGA 780

GGCACTACAG ATATGAAAGG CGGTTTAATG GCTTTGGTCG TATCTCTAAT CGAATTAAAA 840

GAACAAAATG AATTGCCTCA TGGAACGATT AGATTACTGG CTACTGCTGG CGAAGAGAAA 900

GAACAAGAAG GTGCCAAATT ATTAGCTGAT AAAGGCTATT TAGACGATGT CGATGGCTTA 960

ATTATTGCTG AACCAACTGG ATCTGGAATT TATTATGCAC ATAAGGGGTC TATGTCATGT 1020

AAAGTAACTG CAACTGGTAA AGCTGTCCAT AGCTCAGTTC CATTTATTGG TGACAATGCA 1080

ATTGATACAC TGCTTGAATT TTATAATCTA TTTAAAGAAA AATATTCAGA GCTTAAACAA 1140

CAAGATACTA AACATGAATT AGATGTTGCG CCTATGTTCA AATCATTGAT TGGAAAAGAA 1200

ATTTCTGAAG AGGATGCAAA TTATGCATCT GGTCTTACAG CTGTATGTTC GATTATAAAT 1260

GGCGGcAAAC AATTTAACTC TGTACCAGAT GAAGCTTCAC TTGAATTTAA CGTAAGACCA 1320

GTTCCTGAGT ATGATAACGA CTTTATAGAA TCGTTTTTCC AAAATATCAT TAATGATGTG 1380

GATAGCAATA AGCTTTCACT CGATATTCCA AGCAATCACC GACCTGTAAC AAGCGATAAA 1440

AATAGCAAAT TAATTACTAC GATTAAAGAT GTAGCTTCTA GTTATGTAGA ACAAGACGAA 1500

ATATTTGTTT CAGCGCTTGT AGGCGCAACA GATGCCTCTA GTTTCTTAGG AGATAATAAG 1560

GACAATGTTG ATTTAGCCAT TTTTGGACCA GGTAATCCAT TAATGGCACA TCAAATCGAT 1620

GAATATATTG AAAAAGATAT GTATCTGAAA TATATTGATA TTTTTAAAGA GGCTTCCATT 1680

CAATATTTAA AAGAAAAATA AGAACGATGC TGTCAGCTGC CCTATTCGCG TGCTGGCAGT 1740

TCAAATATCA ACAAGCACAT TTTCATTGAT TAAGTGATGT AAAACTGAAA TTATTGTGCT 1860

GATTTGTCAT ACATATATTG ACTAATGGGC ATATAAAAAG ATAGCCTCTA ATAGTnACAT 1920

AAACTCGTAA AAnCC 1935

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

CCTTTnCCTA AACAATTTTT AGATTTAGAC AACAAACCGA TTTTAATCCA TACATTAGAA 60

AnATTTATTT TAATTAATGA TTTTGAAAAA ATTATTATCG CGACGCCACn ACAATGGATG 120

ACGCATACGA AAGATACACT TAGAAAATTC AAAATTTCTG ATGAAAGAAT TGAAGTCATT 180

CAAGGTGGTA GCGATCGTAA CGATACAATT ATGAATATCG TTAAACATAT TGAATCAACA 240

AATGGTATTA ACGATGACGA TGTCATTGTG ACACATGATG CAGTTAGACC ATTTTTAACG 300

CATCGTATTA TTAAAGAAAA TATTCAAGCT GCTTTAGAGT ACGGTGCAGT AGATACAGTG 360

ATTGATGCTA TAGATACGAT TGTTACATCT AAAGATAATC AAACGATTGA TGCAATTCCA 420

GtGCGTAATG AAATGTACCA AGGTCAAACA CCTCAATCGT TTAATATTaA TTTATTAAAA 480

GAaAGCTATG CACAGTTGAG TGATGAGCAA AAGAGTATTT TATCTGATGC TTGTAAGATT 540

ATTGTAGAAA CAAACAAACC GGTTCGACTT GTAAAAGGTG AGTTATATAA CATTAAAGTA 600

ACAACACCTT ACGATTTAAA AGTAGCGAAT GCTATTATTC GAGGTGGTAT TGCCGATGAT 660

TAATCAAGTA TATCAATTAG TTGCACCTAG ACAATTTGAA GTTACGTATA ACAACGTAGA 720

TATTTACAGT GACTATGTCA TTGTACGTCC TTTATATATG TCAATTTGTG CTGCCGATCA 780

AAGATATTAT ACTGGTAGCC GTGATGAGAA TGTCTTATCT CAGAAATTGC CAATGTCTTT 840

AATTCATGAA GGTGTTGGTG AGGTCGTATT TGACAGTAAA GGTGTGTTTA ATAAAGGTAC 900

AAAAGTAGTT ATGGTACCGA ATACGCCGAC AGAAAAAGAC GATGTCATTG CTGAAAACTA 960

TTTAAAATCG AGCTACTTCA GATCAAGTGG ACATGATGGG TTTATGCAAG ATTTTGTGTT 1020

GCTAAATCAT GATAGAGCTG TACCACTACC TGATGATATT GATTTAAGTA TTATTTCATA 1080

TACAGAGCTT GTAACAGTAA GTTTGCATGC TATTCGTCGT TTTGAAAAGA AATCTATTTC 1140

AAATAaAAAT ACATTTGGTA TTTGGGGTGA TGGTAACTTA ggTTACATTA CAGCCATTTT 1200

GAGTCACTTC TCATTTGTTG ATGATGTCTT CTTTATTAAT AAAATACCTG AAGGCTTAAC 1320

ATTTGATCAT GCATTTGAGT GTGTGGGTGG T 1351

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

TCATCAAGTC TACGATAAAT TAAGTCCATA TCTAAAGGCT CGGGGTCGAC AGTTTGTAAA 60

GTATAACCAA CTGCACAGTG GCTACAACGC ATATTACAAA GATTTGTAGT TGTAAATTCG 120

ATGTTACTTA AAGTTAATTG GCCATGTTCT TTAACATCGT TATATGCTTC CCATGGGTCG 180

TTTTGAATAC TTATTTTAGG CTTGTTATTA CGCATTTTAT AAACTCCTTA ATTGTTATTT 240

GATACCAATT TGATACCGTT TAATCAAATA TGCTCATAGC TTGATGTTTT TTATCAGTAT 300

ATAAATGAGA GTACGTTTGA ATTGTTTCTG TAATGTTAGA ATGCCTCATT AATTCCATTA 360

ATAAATACAT ATCTACACCA TTATTAATTA AaTAGCTAGC GTACGAGTGT G 411

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1639 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TCATTTTCAT AGGTTATTAC GCAGATCAGC ATAATAATCC ATTCCATATG AGTcCTTATT 60

TTGGTTATGC AGCACGTCTA TTGGCAACAA GTGGCATTGA CTATACGTAT GTAAGAATGG 120

CAATGTACAT GGATCCACTT AAACCATATT TACCAGAATT GATGnATATG CATAAACTGA 180

TTTATCCnGC TGGCGATGGT CGTATTAATT ATATTACTAG AAATGATATT GCTAGAGGTG 240

TCATTGCTAT TATTAAAAAT CCAGATACTT GGGGCAAACG CTACTTATTA TCAGGCTACA 300

GTTATGATAT GAAAGAACTT GCTGCAATTT TATCTGAGGC ATCaGGCACA GAAATTAAAT 360

ATGAGCCCGT TTCATTAGAG ACATTTGCAG AAATGTATGA TGAACCTAAA GGCTTTGGTG 420

CATTATTGGC ATCAATGTAC GACGCAGGAG CAAGAGGACT ATTAGACCAA GAaTCCAATk 480

TTAATAATAA AGGAGCGTTA TAGTGAATAT CATCTCAACA ATTtTAATCA TATTTGTGGC 600

ATTAGAGTTT TTCTATATTA TGTACCTTGA AACGATTGCT ACAACTTCCA AAAAGACTAG 660

CGAGACATTT AATATAAGCG TCGATAAATT GAAAGACAAA AATATTAACC TACTTTTGAA 720

GAACCAAGGC GTATATAACG GTTTAATCGG AGTTTTGCTA ATATACGGTT TGTTTATCAG 780

CAGTAATCCA AAAGAAATAT GCGCAGCTAT TTTAGTGTAT ATCATTGGCG TTGCTATTTA 840

TGGTGGCCTT TCAAGCAATA TTAGTATCTT TTTCAAACAA GGCACATTGC CAGTATTGGC 900

ACTCATATCA ATGCTTTGGT AAGTATTGGT GTTTGGGGGG GTGGAGATGT AGTCGGAGGT 960

TTGGAGGATT TGAGCGAATT GTGTGTGGAC TTTAGACTCA GAGTATTTCA TCCTAATTAT 1020

TTCAAGCAGA GGTGACAGTA GCGTTGCCTC TGTTTCCTTA TAAAAAAATT ATTTAATGAA 1080

GAAAACCCAT ATCTGATTTA ATTTTCAGCT GATAAATACT CCATATATTA GAATGGCTAC 1140

TTTATCTATT GCATCAATCC TTTAAAACAA AAAACCCATG ATTTCGAAAT TCCCGTATGA 1200

TGGGGTTCCT ACTCTCATGG ATCAGTTAAA TAAATATTAT CACTATCAGT TTATTATTTC 1260

AATATTATTA ACAATATATG TAGTCGTAAA AGGAAAGAGG ACATGAGAAC TTCGGTGTTG 1320

ATTGGCATTA CATAACGCTT CCAAACATAT TATTTGGTAA CAATAAGAAA CTATTTACAC 1380

AATATATTTT GTATAGTAAA ATTATTTTAT AATATTTAAA TCCAATTGCA CAAGGAGTGA 1440

TTATCaTGGT ACCAGAAGAA AAAGGTTCTA TTACTTTGTC AAAAGAAGCA GCTATCATAT 1500

TTGCAATCGC AAAATTCAAA CCATTTAAGA ACAGAATTAA AAATAACCCA CAAAAAACAA 1560

ATCCATTTCT TAAATTACAT GAAAACaAAA AATCTTAATC ACTTTtATTT ATAGcATTTC 1620

TAATCTCAGA AATGCTATA 1639

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1816 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

AAAATCGCAT ATAGTAATAT GAATAACCAG ATTGTATCTA CAAAAAAGTA TATTGAAAAA 60

CCAAGCGCAC CCATTAATAA TGCGAGAATA ATAATAATTT TTCTATTAAA GTGATGCGTA 120

TCCGAAAATC TAGCAATAAT TGAATTTACT GTAAACTGGC TAATCGCTGC AGATGCTAGA 180

AGTAATCCAT ACTGATTTGT TGTCATACCT AAATCTTTAG TTGCAAAAAG AACAAGATAT 240

TTCTyTATTT GTAaTAACGC TGCAAACATA TCCATAACCC CGCTTCTTAG AGCCCCTTTT 360

AATTnATnAA TTAGGGGCTC TTATGCAGTT GGTGCATTAG CAACCAACTG TATTCCTTTG 420

TCCCCTTTTA ATTTATTaAT TAGGGGCTCT TTTGCTGTTG GTGCATTAGC AACCAACTAC 480

GTTCAATTTA ACCGAATAGT TTAAAATTAA ATACAAACCT TAAATTAGTC TAAAACTACG 540

CCTTTGGTTG TTCAACAAAG CTCGCCATGA GATTTACAAA AGAATCAACT TGTGGCAATT 600

GCAACATGCT CGGATCATAA CTCATAAATG TCGAACGAAT CAGCGGTTCA TTATCAATTT 660

CTACTTTTTC AAACTCAAAT TGTTCTTTGC TGATATTTTT CATCATAATT TCTGGCAAGA 720

TTGTAACACC TACACCACTA ATCAACATTT CTTTGCAAGT TGCTACTTGA TCCACTGTAA 780

TAGTTGCATG GTAATCTTGT TCTAAATTAT CGTTATACCA TTCTTTTATT TGATTTATAT 840

AAATCGGATC AGCTTGAAAC TCTATAAATG GTAACTTTGT AACATCATCT CGTCTATTTT 900

TTGGAAAAAT AAAATAATGA TCATCATTAA ATAAATGTGT GTTAGCTAAA TTCATTACCT 960

TATTTCCACG AGTTATCATA ACATGATAAT CTCTATGATT TGCTTTAATT TGTTCAGTTG 1020

AACCAACTTG CACTTGTATT TCAACATTAG GAAATTGGGC ATTATATAGG CTCAAAACTT 1080

CAGGAAGTAA GGTTTGTCCA ATCAAAGAAG AACACCCGAT TGATATTGTT CCATTCACTT 1140

CACCAATATG TGCCTGCATT TTGTCAAAAA ATAATCGCTC TCTTTTCAAC ATGTCACGAG 1200

CATGCTCAAT AATCATTGTT CCTTCAGTTG TTGTAATCAA TTGTTTTTTT GTTCTGATAA 1260

AAATATCTAC TCCAAAAGCA TTTTCAATAG CTTTTAGTCT TTGTGTAACA GCAGGTTGAG 1320

ATATATATAA AATTTCAGCC GCTTTACGTA ACGTTTTCGT TTCGTCTAAT GTTATTAGTA 1380

AACGATAGTC TTCAATCTTC ATAATTTCCC CCCATAAATT ATTCAATTAT TGAACTTTCA 1440

TGGCTACAAG CATTCATGAG TTCATTACTA ACGAATAATT TCACCAATTT TATTGGTATG 1500

GCTGCAGCTT GAATTACTTA GTTTTTCTTT TGTTGTTGGT GATTTTTAGT TTGATTATAT 1560

TGCTTAGGCT TTATTTGTTT GCTTTTTTCA ATATTAGTTT TATTTTGTGG CTTTTGATGA 1620

TTTTTTTGAG CCTTTGCATT AATTTTATTA AAGCAGTACA TGATTTTCTT TTGGAATCCT 1680

TTAAAATCAT TTTCTAACTC TGCCATAATT TGATGTGCAA TCATATATGC TTCATGAAAT 1740

TGCTTTTTTG TAATTTGCTC ACTTTCTAAT GCAAACATTA AATCATCTTC ATCTACCAAC 1800

TCATaTcACC ACTTGG 1816

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9956 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

GCGTTGTCGT CGATGATTAA TAAAGTATGG GTATACCATT AAGAATAACG CTACCCAAAT 60

gAkTGCTAGT GACGTGCCGC CAATGACATC TGAAAAGTAA TGTGCATGAA AATAAAGGCG 120

ACAAAATAAT ATGCTAAGCC ATAATATTCC CATAACCAAC GCACTCAACA CTTTTGTTAT 180

TGTCTTAGCA GCAAGTGAAA TAATAATGAT CATTAAGGCG AAATATAATA ATGTGCTGGC 240

GTTGGAATGT CCACTCGGAA ATGAAAAGCC TGTATCAACG GCTAAATGAT TATATGGTCT 300

TGGACGTAAT ACAGTATCTT TAATTAATTT GTTCATGATG ACACCTGAAA CCAAATATGT 360

CACAAACCAA ACCGCTAAAT GCCTCTGTTT AATAAACAGT ATGATTGTGA CGATAATGGA 420

AATCAACACG ACACCTTTGA CATCTCCAAT TTCCGCACTA AACGTCATAT AGTAATTAAA 480

CAAATTGTTA ACATACTGAC GTTGTGGCTC ACCGAAATAA TCTGTAAACC ATGTTAATGA 540

TCCCATATCT ATATTTTTAA GCCATTCTTG ATTTGTCACT ACACTGTAAA ACATACCTAT 600

AAATACAATC AGCGCGATTA AAAATAAAGG CACTGTcATT TTCGGTGATG TTAATTTTTT 660

ATCTATCATC TTACAATCTC CTCGTATCAT CATTTTCATT TTACAAATGT TATCCATAAT 720

ATCAATGTGC CACAAATTTC ACTTTACCGA CAATATCAAA ATTATAAAGT TCATATTGTT 780

ATGTATATTG CAAATAAAAC ATTGTATAAT TGAAATAACA ATATTTTGCT ATTTTCAATT 840

TAGTACGATT TATATTTATT ATACAGAGGG GGTAAGGCGT ATCAATAGAG TTATTTTTGT 900

CTATATAGCG TTAATCATTA CATTAGTTAG ATTCTTTACC CCTATTCATC CATCATTTTC 960

AAATTTGATT TACTGGATAT TTGTATTATA TTTTATTCCT ATTATACTAT GCGTTATCGG 1020

TTTCAAGGCC GAAAAACTTA TTGCAACAAT GGTCATTATA CCTAATTTTT TAGGAATACT 1080

TTATCGATTA TATGCCTACG TCACACATAT ACTCTTTATG TAAAAGGATA GTGGGCATGT 1140

CTCGCAACAA ATATGCTTGC GTCGACTTGT CACCATTCGC AAATTTTATG ACATACGCCT 1200

TTCACGGGCT ATATTCAGAC CCACGCATTC ATCCACGTAA TAAACACATC ATGTAATAGA 1260

AAAACAGCAC ACCCAAATAT ATGGCGTTGC GCTGTTTAAC CAAGCATACT TCTATAGCTT 1320

TAATAAGCCA GCAGAAGCAT ACCTAACCTT CTTAAATATG CTTTTCCAAA TTATCCTCAA 1380

GTTTGAATAC GATAATACGT TCACCTGTAA CTGTACTTAA ATCACTATGG AAGCTCATCA 1440

CTTTGATACC TGTAATTTTA AAAATGATAT CATTCAAATC TTGCTCACCC GATTCAACTA 1500

ATTCAGAACG TGTTCGTTTA ATATTTAATA ATCCTTCATT CGTACTACAT ACACGATATT 1560

CAGCTGGCGT TAAGATACCT TGTAAACTAA TAATCACCAT ATCTCTTAAA ATGTCTGATT 1620

TTTCAGCTTC GATTTCACCT TTCGTTCTTT TCATATCACT AACTCCAATA ATATTAAAAT 1740

TGATTACTTC ATCTTTGTAT CGTTATCACG ACATCAACTA TTACATTAAG TTTATCATTT 1800

TTAGTATATT TTAAGAAGCT AGAACATTGT AGATATGATG ATATATTAGT TACTTAGCAT 1860

CGCAACATAT CATCGTTAAA TCCAACTTTT AAAACGCCCT TCCTCATTAA CGCTCATTAA 1920

ACGCAGCCAA TGATTAGACA CCTTCCTAGC GAAATGCTCA TTATTCGCGA GTAGTCTTGC 1980

TACAACATAG TCGGGTGCCT GAATAACGAC AAGTAAACGA ATTGGCGAAT GATACATCGT 2040

CCGATCAGCA GCCATAACAG ATTGCCATGA TAAGCCATAC ATCAGATCAC TCGCATTACC 2100

TTGCATGACA CCAACACCTG ACGTGACGGT TTGTGTCGCT TTATTCCCAC TTCCGTAAAA 2160

ATGCGGCGCA ACTGTCGACG CATAATATTG TAAATTAATC CATTGTGCCA CAAGTGCCGG 2220

ACCAGAAATG ATGGTATTTA ATAATGTGCC ATCTTTATCT TTACGCCAAT CATAATTGTG 2280

TAAAAATGTC CGCCCTTCTA AATCAATGCC TTTTGTTAAT TGGCGTCGTC CAATTATAAA 2340

TGATGCATTT TTAGCCAATC CCCATTCTGG ACGTACCTCA CTCCAATCAC TCGCAAACCG 2400

CTGCGCTTCT TCCACTGGAT GATTCACACG ACCAATCGTT GGCAGTTTGT CCAAACGTTC 2460

GCGATTCGcg TGtTCAGAAA TCATCGGCAT CGCGTCATTC AATGATTCAT ATGCATCTAA 2520

AGCAATAGAA GATAATGTGT CTGGCACATA TACCCATGCC AACGTATCAG TAGACGTATG 2580

ATGTTCTGCT ACCGCAAAAA CAGTTGTCTC TGGAATATAC ACACCTGATT GTTTTAATCC 2640

TTGTCTGACA TTTGGACGAT TACATATCAT CGCTAATAAC TTAGCATTAA AACCGCTTGA 2700

TGCGCCACCA CAAGCCCCAC ATTCAAGTGA TGCATGATGT GGATTATTGT GAGAATGACT 2760

AGCATGACCT GCTAACACAA CGAACGGCGC AAATGCTTCG GTTAAATCCA TCAATTTCAA 2820

CGCTTGTAAC GCGAAATCAA TTTGCTCTTG CTCAGTAAAT CCAACAGGTA AGTCTGATGT 2880

TCGGTCAAAC TCACGATCAA TCGTCAACTT TGTTTCAGGC TTTTTCAACC ACTTTTGTTT 2940

TATTTTTTGT AAAGACGCGC GACTTTTTCT AGGCATAATC GAATTGACAA TGGTACTTAA 3000

GCTTAAAAAT GGCCCACTTA ATTCAGGCAA TAACAGACTA GGCATGACAT TATTTTTCAT 3060

CAATTTAAAT GTGTAAAACA TCGATGACAT TGTCTGTTGC TGTTGTCGAT AAACATTCAT 3120

ATCGTAGCGG TCTGCAAATT CTTTAATGCG ATATGCCGGC GGTACCATGA CAGGTAATGA 3180

ATCATGTTTG AATTGTTCGT CTACGGCATC TTTTTGAATA GGTAATCCAA AGAAGCCTGC 3240

AATACCAATC GTTTCAAAGG GCCCTGCTGC TTCGATATGT CTACGAAATG GTTCTGAACG 3300

AACATCTATA CAAAATGCAA TTTGCGCTTT CGTTGATGTG CCCATCTGAT TTAGCTCGCT 3360

ATTATTTTCA TCAACTGCTT GTGTGTCATT TAACAATACT GAATGTGGCT GATTAGCGTT 3420

TGCTTTAATT TTTTGTTTTA ACTGAGATTC GTATGTCATT TCCCAGGCAA TTAGCCATAA 3540

ATTTTTAAAT ACATTTTTAT TCATAGTTGC TGCAAAATGA ATAAACGTTT GAATTTCATT 3600

GACGTCATGT TGTAGTAATA CATCGCTAGG CATATCACTG TAGTAACACC ATGATGCAAC 3660

AGTTTGCTTA AACCAATTTT CCGATCTACT TTCACAATCT TTAGCGACTG ACTTAAACTC 3720

ATCACCAACT AGCAATTGTT CGACAACTAA CCGAATTGCC AAATAATCCG TTAACAAATG 3780

TTGTTCAAAG TGATGCTGTT GTGAACGGTA ATACAACATA CCTGCCCAAC CCGGTAACGC 3840

CAAAAGATGT CCTTCAACAT AAGCTTGGTA GTCTTCCTGA TCTATTGAAA AATGAGTTAA 3900

TACTGACTCT ATCGTCATTT CAGGATCATT GGGTAAGCCT TTAATCACTT GGCGCTGTGC 3960

TTTAGTAAAA CTATGGTCAT GTTGCGCTAA ATGCAACCAT GCATGGTAAA AACTTTGcTC 4020

ACGCTTCGGC ATTGTCCAAC TCGATAGAAA TTGATCGATA TAAAGTTTCG TCCATTTAAT 4080

CATTTGACGA TTCACTTGTT CGCTAAGTGG CTCACCTTGT TCATCTATTA TTGCATCACT 4140

CATCGGACGT ACATCATAGT GATGATATGA TTCAGCCATA TCACGTTTTG ATTTTTCTAA 4200

TAGTAGATCA GCAACAACAT CAACATTTGA ATGATTCATA TATGATGCAG GTACGTCTTT 4260

TAATGTTTTA ATGTTATCAA TATAAAGATT GATGTAGTGT TGCGGGATAT TGTAGTGATG 4320

TTCAAGTAAC ATATCAGTAA CAAGTTGATT AAAGACACTT TCATCTAATT CACCACGTGC 4380

CACAGCGCTT TCTATTAATG CTTTATTTGG GAAAATATCC ACATCTCGAA CATCACGTAA 4440

CCATTTTGCG ACATCTTCAA ACGTATCCGC TTCTAATCCT TCCCATGGAT TTCGTGCTGC 4500

AAAAATCGAA ATTGGTGATA ATGGTGTAAT AACACGTTTC GCATTTTCAA TGACTGAATT 4560

GATATTTAAC TGTGTTGTCA TACCTTTCAC CTCCTATAAA TACTTCTTCA AATAATTCGG 4620

ATGACTTTCT ATCGCTTTCG AGCGTGCTTC ACCTAGATTA ACTAACCACA CGTACAATAC 4680

CGCAAAAGCC TTAGAGTATC GATGCCGCGC CACCCAAATA CTTAATAAAC TGCCAAAGAT 4740

TAAAATAACA ACACTAATGA TGACACTCAC TGTAGGCGGC GTTGTCGCAT GTGTTGTTAT 4800

ATTTTGTAAT ACAGCGTAAA AATAATTATG TGTGATGACG TAGATAAATG TCACGATTGC 4860

AATCAAAATC ATACCAACAA GACGTGCCAT GCGTCCTTTA CTAAAGGCTA CCATTTGATT 4920

CCAAGATACA AGTAATGACC ATCCTAGAAT GAGTGCACTT AACACTTCAT ATGCACTTCT 4980

GTCACTACTC ATCCAAAATA GAAATGCCAC GATAATAGCT AATACACGTC CCATGACAAT 5040

CCAGCCATAA GCGTCTTTAG CAGATGCTTG TTTTGGAATA TTGAATCGCT TCACGATAGA 5100

ACCTGATTGT AAAAATAATG TTGCTTTAAA AATACCGTGC AATATTAAAT GAATAATCGC 5160

TGCTGAATAT ACACCCAATG CACATTGAAC TAACATAAAG CCCATTTGAC TCATCGTAGA 5220

AGAAATACTA GAAAGGATAA GTAATAATGA TAACGCAAAT CCATTATCAA ATATCGGCGC 5340

AAAACGAGTT AGAATAACAC CACCTGCATT CACAATTCCT GCATGCATAA TTGCCGATAC 5400

TGGCGTTGGT GCCGTTACAG ATTCAATCAA CCATCGATGA AAAGGAAATT GTGCTGCCGG 5460

TATCATGACA GCTAATACAA GTAGTACATT CGTCAACAAT GACCATGTCG GATGAACTAT 5520

ATGTTGTGGT ACCCGCCACT CGCCAGTCGC AATATAAATA GTTACAATTG CTCCAACGAA 5580

TGCAAGCCAA CCACATAAAA ATGTCATGCT TGATAATTTC GCAGACTCAC GTGGCACTTT 5640

CCAAAAACGA TTAACGTTCA TCAGCAATGT TAAACATAAT AATGTAATAC CCCAGCAGAG 5700

TGCCATCAGT CTTAAGTCTT CAGACATCCA TGCTAAAGAT GCAAACGACG TAATCGCAGT 5760

GAACAATGGA AAGTAATGTC TATAATGATG ATCACCTAGT AAATATCGCA TTGAAAACTT 5820

TTGAATAATA AAGCCAAGCG CCATTACAAA GCCAGCTAAT AACCAAGATA AACGATCTAT 5880

TTTAAATGGA CCTAAGACAT GTTGACCATG AATACCGAAA AAGCCAATGA CTGCAAATAA 5940

TACTGGCATG ACTAGTATGT ATAAATGTAA TTTAATATAT CTCATTGGCA TAACTGGTGC 6000

TAAAAACAAC AAGCCACTTA TCAATGCAAT GATAAGCGCA ATAACAAACA GTGAAAATAG 6060

CAATTGAAAA CTTAACACTG CATAACCTCC TTATTTCTAA TCTCTCGCAT AATTGCTTAT 6120

GTATAAAAAT AAAAACCTAC AATAGTAGAT TCTGTACATA ATGGCAGAAA ATTTACTATT 6180

GCAGGTTTCA GTTTAACTAG ACACTGCATC ACGGTACGTT GATATACCTT GTTGCAGTGT 6240

TCTCTTTAAG CGTGCTCCCA TGCACATATG TATATAAAAT GTTACTTCTG TCTGTTCAAT 6300

TCATCTTCAT AAATATGCTT TGCCTAGACG AGACCTAACG TGTTATTCGT TTTAAACTTA 6360

TAACATAAAA TATAATTAAA TTTCTGCTTC ATGTCAAATT CATGAGCTTA ACCTCTATTA 6420

AACCAATGAT TGTAAAGATT TTGTAAATGC ACCTGTACAG TTAGGCAGTA TTTCCCGTCC 6480

TTTTAAAATA AAAAATTCGC AGTTATGATC ATAACAATTC AAGTTAGGAA AAAAATCAAT 6540

TACGCACAAG ATAACTATGT ACAATGAAGT TAACTCATAA GCAAAGGAGG TAATCTTAAT 6600

GGGTATCATC GCTGGCATCA TTAAAGTTAT CAAAAGCTTA ATCGAACAAT TCACTGGTAA 6660

ATAAGATTTC ATAACAAACA AAGGAGGTCT TTCACATGGG TATCATTGCA GGAATCATTA 6720

AATTCATTAA AGGATTAATT GAGAAATTCA CTGGTAAGTA AGTTATAAAA ATCTCATAGA 6780

TATGAACATC TTATTTGAAG GGGGCCATTC ACATGGAATT CGTAGCAAAA TTATTCAAAT 6840

TCTTTAAAGA TTTACTTGGT AAATTTTTAG GTAACAACTA ATCTCAAACA TTAACGATCA 6900

ACAACTCATC ACTATGTTAA ATCAACATAC AGGAGGACAA AACGATGGCT ATTGTAGGTA 6960

CTATCATTAA AATCATCAAA GCAATTATCG ACATTTTCGC AAAATAATTT AAGCGAATTG 7020

TTATTGATGT GAGGTGAGTC TTGTTAGTTT GTTGCAAATA AATGGTCTTG GTGTTTTTTG 7140

TATAGGACGT TCTTAGTGGG ACATACGGAA TATTCGTGAT CTTTGTAGTC TGACGCGTTA 7200

TATTTTTGTG GCGTGTTTTA TGTTTGATAC TCGAGTTCTG AGACATTCAT GATTTGGCAT 7260

GCGAAATCTT AATGATTTTC ATGATCTAGC GCAAGATATA TTGGCCACGT GCGGAATTGC 7320

GTTGCACGTT TAGACTGAAA CACTCGTGTG ACCGTAAGTG TTAATAGTAC ATTGATAGCT 7380

GCATTTACTT CACTCATTTT TATGACTGTT AAACAATGAT TGTACCTTCA ATTAACAGTT 7440

GGTACGATGG TTTTGCCATT TTTCATCAAC GTAAATATAA AAAGGACTAA GACACATACA 7500

TGTCCTAGCC CTATGGATAA AATGCAAATT TCTGCTTTAT CAAAACTATC ACACTTTAGA 7560

TAGATTGAAA ACAAAAAGAT CCTAAGAACA CCTTAACTTT TTATTAATTG TCATAAATTG 7620

CAAACAATTA AGCCACAATT CAAAAATGAT TATACTTCAT TCAACTTATC GTGCTGGTCT 7680

AATTTGCCAT TGATATGGAT CTTCAAATTG TTGCCAATCT GCATCAATTT CTTGCGCATT 7740

GACTAAGCAT GCGTCGAGTT CTTTTGTTAA TTTTTCTTCA TCTAATTCTG TACCAATAAT 7800

GACAAATTGT GTATGACGAT CGCCATATTC TGGATCCCAT TCAGCTGCGA CATCTTGACG 7860

TTCTGCTAAT ATTTGTGTTT GTTGCGCTTC AGACATACTA GCCACCCAAT ATGTAACTGG 7920

ATGAATATTG CAAGATGACC CTGCTTGAGA TAATAAACAT GCTACGTGAT TGTATTGTGC 7980

TAGCCATACG ATACCTTTTG ATCGAACGAC ATTATTTGGC ATGCTTTCTA ACCAATCATT 8040

GAACCTTTTA GCATGGAAAG GTAGACGACG TTTATATACA AACGATGATA TACCATATTC 8100

TTCTGTTTCA GGTGTATGCG ATGCATGCCC ACCAGACTCA AGTTCTTTGA TCCATCCTGC 8160

TGACTCGCTC GCTTTTTCAA AATCAAAACG CTGCGTATTC AAGACTTCTT TTAAATCTAC 8220

TTCAGAATTT GTTGTCTTAA TAATTTTAGC AGTCGGTTGC AATGCGCTTA ACATTTTTTC 8280

TAACTTCGCT AGTTCTTCTT CACTAATTAA ATCAATTTTA TTAATAATCA ATACATCACA 8340

AAATTCAACT TGGTCAATTA ATAAATCAGC AATCGAACGC TCATCTGTTT CGTCAACGCT 8400

TTGATCACGA TCCATCAATA AATCTTCTGA GTTGATGTCA TGTACGAAGC GGTTAGCATC 8460

CACAACTGTA ACCATTGTAT CTAAACGGCA AATCGCTGTA AGATCAATGC CAAGTTCATC 8520

ATCAATATAT GAGAAAGTTT GTGCAACAGG TACTGGCTCT GAAATCCCTG TTGACTCAAT 8580

AACAATTTGA TCGATGCCAC CTTTTTTCAC TAAACGCTCA ACTTCTTTTA ATAAATCGTC 8640

TCTAAGTGTA CAACAGATAC AACCATTAGA AAGTTCGACT AATTTTTCAT CTGTACGCGA 8700

TAGTCCCCCA CCATCTGCGA CAAGATCTTT ATCGATATTT ACTTCACTCA TATCATTTAC 8760

AATTACCGCG ATACGTCGAC CTTCTCGATT TTGTAAAATA TGATTTAACA ACGTTGTCTT 8820

ACTTCAATTT ATTTGTAAAT AGGAATAATT CTGTTTTACA TTATATAGGA GCGTTTCCTC 8940

TTTCGCAATC TTCGATAATA AAAAAATAGT ATACTTAATT AAATTATTGA GCGCTTTACT 9000

TTATAATGGA GACAAAGATA TATCTCACGA AAGAGAATCG AGGTGTATAA ACATGTTATT 9060

TGTCATTTTA GTTTTATATG TTACTGGTAT TGCATTTATT CTACTCAGTG TTTTTGGTTC 9120

AAAGACTGAA GGATTATCTA CGAAACATAC TTTATATACC ATTGGCAGTG CTATTATAAC 9180

GATTGCTATT TTCATTTCAA TTGGCTATGC CATTCAATAC TTAACTGCAG CGCTTTATGG 9240

TTTGTAAGGT GAAGGTGATG AGTAACGGGT AGTTCGGGAG AGGTTAACTT GCGTTGATTT 9300

TGATAAAGTG ATCATAGCTT TTAGTACTTG AGGATTTTTA TTGTTGCTGT TACGAATGTG 9360

GTCATGTTTA ATGCGGGACA GTAATTTAAG TTGTTTTTTT ACAATTGAGA GTGTGATATT 9420

TCGATTCGGT TCGAATTACT TTACATGGGA ATAATATAAA TTAAAAAGAA GCGGCCTAGT 9480

GTCAGTTGTG AATATACTGA ACATTGGTCG CTTTATTTAG TAGTATGATA TGTAGTTTAG 9540

CTATTAATTT TTTTCAGGTC ATCCTTAATG CTGTCTATCT CAGACATGGC ACTTTTAACC 9600

CAATCTCCTT GAGCTGCACC TTTAAAATTA GCTTTAAAAg ctTCGCAATG TTGCGCCATT 9660

TGTTCAATTA ATACTTTTTC TTCACCTTTT AATCCGTTTT CAATATCTTT GTATTTATGC 9720

TTATGTTCAG GTGCAATAAC TGTGCGAATA TTTTCTTTTT GCGCTTCCAT TTTAGATATG 9780

AGATTAAGTG TTTCTACTGT AGTACTTATA TCTGGCATTC TTAAGGTCAT ATCTGGTTCT 9840

ATTAGAGTCA TTTAATCTCC TCCAAATTAT CAGTCACTTA GCTTATCTAA CTGCTTTTCA 9900

TAAGACTTTT TTAAGTCTTC TTTATATTCT TCTAATTTCC CATTCTTGCT TTCTGA 9956

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2411 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

TTTCTTTTAA CAGaTTTATC cCATTAATTG TTCTACAAGC CCACGaTGAG CAATATCATT 60

TTTAGCAACC ATTAATAAAC CAGAAGTATC CATATCTATA CGGTGAACAA TACCTGGACG 120

AATTTCTCCA TTAATACCTG ACAAATTTTT AATTTGATAC ATTAAACCAT TAACTAATGT 180

ATTGGTATAA TGCCCTGGTG ATGGATGAAC TACCATGCCT TTCGGTTTAT ATACAACTGC 240

AACATCGTCA TCTTCATAAT AAATATCTAA ATTTAAATTT TCAGGTAGAA TATCAGCTTC 300

AACAACTTTA TCGTTTGCAA CGACTAAACC TGCTTTAATC CAATCTTGTA TCTGGTTACG 420

AGACCAATCA TTATTTAATT CAGGCAGCAA CTTATCTACA CGCATACCTG TTTGTTCTTT 480

ATCTGTAATG TTAAATTCAT AAGTCTCCAT TACTTAACCT CCTTCTCCTT TTTATTGGAA 540

GTATCCTTTA ATAAGGCAAT AATAATTAAT ATTACACCAA TTGTTAAACT TGAATCTGCG 600

ATATTAAATA TTGGAAAATC ATAACCAAAA ATATTTGTAT CAATAAAGTC AACAACTTCT 660

CCTGTTAAAA TTCTATCAAT AAAGTTTCCA AGTGCACCTG CAAAAAGTAA ACTAATAGCA 720

ACTTGCATAA ACAAATTATA TTGAGCATCT TTAATAAAGA AATATACTAA GGCTATTAAT 780

ATAATAATGG TAATAATAAA GAAAAATGTC ATTTTTCCAC TCAATATTCC CCATGcAGCA 840

CCATTATTTC GATGTGaTGT TATGTTTAAA AAGTGCGGTA TCACTTCAAA TGAATCTCCA 900

ATTTTCATTG TAGTAGCTAT AATATATTTA GTAACTTGGT CAAATATAAC GACAAATACT 960

GCTATTAAAA TGGAAGTGCC AATAAAATAT TTTTTGTGCA TTTTCGTTCC TCCAATCAAT 1020

CGTCCATGAG ACAACTCTTT ATATTATAGC TTACACCTGC TAATAAAAAA AGTAAGCATA 1080

TTACATTAAA TCTAATGTTA CTAACTCAAT ACTTGATAAA CTACTATGTT TTGACATTAA 1140

ATATGAACTT AATTATTCAT TTATCATATT TAAGATGACA TTAAAAATTA GGAAAGCAGG 1200

CTGGAACATA AATCCCTAAA AAGACAGTAG TAAGATATTT TCTAATTAAA AATTATCTTA 1260

CTGCTGTTCT CTATTTATAC AATACTTCGT ATTGAATGGC TTCGCTATGC CCATCTGGCA 1320

CATTACTGTA AAATTCTATA AATAGAATTT TTGATGATGG GTCCCTTCCT AGGGTGCCGT 1380

CTCAGCCTCG GtCTTCGACT GGCACTGCTC CCTCAGGAGT CTCGCCATTA ATACTACGTA 1440

TTAACATGTA ATTTTACTTT TAAATACTTT AAAAAAATAA GACATGAATC GTCTACACTT 1500

AATTGGACAA ATTCTATGAG AATAGATATT GTTAATTTAA GAAAGTAGGC TATTTTGAGT 1560

TtCACTCGAA TGTCAGTTCG AGGAATAAAT AAAGTTAAAC GAGAGCTAGG TTTTGTATTA 1620

ATGGCAATTA ATATAAGGAA AATAGCAGCT CAACGAGCTG TACATTATAA AATACATATC 1680

AAAAAAGCTG ATTTCTATCA AATAATTAAT AGAAATCAGC TTTTTTACAT TGCCTAAGAA 1740

CTTAATGTCC CAAGCCCTAA AACTTGTTGT TATTTATTTG ATTTAGCAGC GATACGTTTA 1800

TATCTTAAGT ACATAAATGC TAAAAGTATA AACCAAATCG GAATAAAATA AATTGCACGT 1860

CTTGTATCAA CATTAATAAA TAATAACCCG AACACAAAAA TGAAGAATAC AAATATTAAG 1920

TAGCCCATAT ATTTGCCACC TAATAGTTTG TACGTAGCAT TTTTATGTAG ATCTGGGTTT 1980

TTACGACTAT AATTGATATA TGCAATGATA ATCAGACCCC ATACAACTAA AAATAACACT 2040

GTAGAGATGG TAGTCACATA CGTAAATACT TTTGTCGCAT CTGGGAAAAT ATAGTTTAGT 2100

TTATTCGTCT TAGAAAAGTT CGGAGGTGCT TGTyGTTGAC TTGATAAACC GaAAAGCATA 2220

CGGCTATTTG AGAATATACC ACTGTTACAT GATGAAGCAG CAGCGGTTAA TACTACAAAA 2280

TTAATCAAGC CCGCAGCAAA CGGAATTCCG ATCAATGCGA ATrATTTTnC GAATGGACTG 2340

TTATCAGGAT CAACTTGCTG CCAAGGGGTA ATAGACATGA TAACCGCTAA CGCCCCAACG 2400

TTnnATATTA A 2411

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 605 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GnGAATTATT TTTAATAATG AAAGGATTAC TTnCATGGGT TTTTACTAGG AnTACCCAGA 60

AGGTCAAAAT ATTTTTGATG CGCTAAGTCA ATATGAAGTT AAGCGACGCG GCGATATGGA 120

AGAGGATCCA TCATATAAAC AACTCATTTC TTATTGTTTA CTTGAAAATG AGCATGGCGA 180

GATATTAGTG TATGAACGAT TATCTGGCGG TGGAGAAGCT CGATTGCATG GACAATCTTC 240

AATAGGTGTA GGCGGTCATA TGAATGATGT TCCAGGAGCA GAATCTATTA ACGAAGTATT 300

GAGAGTTAAT GCACAGAGAG AATTAGAAGA AGAAGTAGGT TTAAGTGAGC AAGATTCACA 360

AAATATGGAA TATATCGGTT TTATTAATGA CGATAATAAT GAAGTGGGCA AGGTACATAT 420

TGGTGTTGTA TTTAAAATCA CTGTAAGTAC GAATGATGTA GAAGCTAAAG AAACAGATAC 480

TTTACGAATA AAATGGGTTG AAAAAGGCAA CATAGAGTCA TATGATGATT TCGAAACGTG 540

GAGTGCATTA ATCCTTCAAG ATTTATAATC AAACGAGGTG ACATATATGT CAGATATTAT 600

TCCAG 605

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 668 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

TTTATTAGCA CATCCAAACT ATTCATATGT TGGACAATTT TTAAACGAAC TAGGATTTAA 60

ACAATTAGAC ACTGAACATT TAGCTGATTT AAATCCAGAG CGTATGATCA TTATGACAGA 180

TCATGCTAAA AAAGATTCTG CTGAATTCAA GAAGTTACAA GAAGATGCAA CATGGAAAAA 240

GTTGAATGCA GTTAAAAATA ATCGCGTGGA TATTGTTGAC CGTGATGTTT GGGCAAGATC 300

TCGTGGCTTA ATTTCTTCTG AAGAAATGGC TAAAGAACTT GTTGAATTAT CAAAAAAAGA 360

ACAAAAGTAA GGTGGAAGTA AATGGCTATA AAAGAAATAA GTAGCCAATC TGCCATAGAT 420

CATAAAAGAA AAAGACGCAC AACACTCACG TATATAGTGA GTTTGTGCTT TCTTTTTATT 480

TGTATATATT TAAATATGGC GATTGGTTCT TCGAAAATTA ATTTTAGCGA TATCATTCAC 540

TATGTTACTG GTCATACAGA TACGAAAGCA ACGTTTTTAT TGCATAATGT ACGTATGCCA 600

AGGATGATTG CAGGGTTATT TATTGGCGGT GCATTAGCGG TATCTGGTTT GTTAATGCAA 660

GCAATGAC 668

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 787 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

ATACAAAAAA ACATATCGAA AATAAAGCTA AAAGAAACTA TCAAGTTCCA TATTCAATTA 60

ATTTAAATGG TACATCTACA AACATTTTAT CGAATCTTTC ATTTTCAAAT AAACCTTGGA 120

CAAATTACAA AAATTTAACT AGTCAAATAA AATCAGTACT GAAGCATGAT AGAGGTATTA 180

GTGAACAAGA TTTAAAATAT GCTAAGAAAG CTTATTATAC TGTTTATTTT AAAAATGGTG 240

GTAAAAGAAT CTTACAGTTG AATTCAAAAA ATTACACAGC AAACTTAGTT CATGCGAAAG 300

ATGTTAAGAG AATTGAAATT ACTGTTAAAA CAGGAACTAA AGCGAAAGCA GACAGATATG 360

TACCATACAC AATTGCAGTA AATGGCACAT CAACACCAAT TTTATCAAAA CTTAAAATTT 420

CGAATAAACA ATTAATTAGT TACAAATATT TAAATGACAA AGTGAAATCT GTATTAAAAA 480

GTGAAAGAGG CATCAGTGAT CTTGACTTAA AATTTGCGAA ACAAGCAAAA TATACAGTAT 540

ATTTCAAAAA TGGAAAGAAA CAAGTAGTGA ATTTAAAATC AGACATCTTT ACACCTAATT 600

TATTTAGTGC CAAAGATATT AAAAAGATTG ATATTGATGT AAAACAATAC ACTAAATCAA 660

AAAAAAATAA ATAAATCTAA TAATGTGAAA TTCCCAGTAA CAATAAATAA ATTTGAAAAC 720

ATAGTTTCAA ATGAATTTGT GTTCTATAAT GCAAGCAAAA TTACmATTAA TGaTTTAAGT 780

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 534 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

AAAGTAAAAA TAAATCTCCC TTTTTAACTT TCGTTTCTGC CATAGCCATT GCTTCTTCTG 60

TGATAGTTGC TACAATATCT TTTCTTTCAC GGTTAAAATG TTCAACTTGT TCTGCTAAAA 120

ATGCAGCTTC TTCTTCGACG TCAGTCATCA ACAATTCGCa AGCTAATGAT GCGTCATCTA 180

AACGACCTAC AGCATTAAGT CTAGGTCCAA TAATAAAACC AATTGTTTCT TCATCAATAT 240

TGTCATTGTA TCCCGCTTCT TTTAGCAATG CTTTAACAGA GGTCGGACAT TGATCATTTA 300

AGACTTTTAA TCCTTGTtTC ACTAATGATC GATTTTCATC AGTTAAGGAT ACTAAATCCG 360

CAATGGTACC TATCGCAACT AATGCTTTAA AATAATCAGG TACATTTtCA ATCAATGCTT 420

GTGCTAATTT GTATGCAACA CCTGCACCAC ACAATTGTTG GAACGGATAA TTAAACGATG 480

GATGCATTGG ATGTACGATT GCATATGCTT CTGGTAATGT ACTACCAATT TCAT 534

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

GGTGAGTCAA ATTAAATGAA TCTAATAAGT CATAACTATC TATTTGTAAT GTGCAACGCT 60

TAACGCATAT ACAAAATGAA TGTGCTGATA ATGATTTACT CAAATTAAAA GGTGATTTTT 120

ATTCAATGAT GAATGAAAGT TGCCTTTTTA TTTTTGGTAA AAGTTAATGC GTCAGTGAAT 180

TGTGTAAGTT TTTCAAAAAG TAAAAAGAAA TAATAAAGGT GAATTATTAG AATTCCArAA 240

ATAATTCATT ACATTCATAA AGCATTTTAC AAATGGTAAG AAAATGAGTG TTACAAATCT 300

AAATATTGCA AAAGAAGCTG ATTTAGTCAC AAAAAATGTC CTATGTAATA ATTCGAGAAA 360

GATGCACTAT ATACGGTCTT CTTACTATTC AAATGTAAAA GTTGCTTATT TGCGTGGCTT 420

TTTGTTTTAT AAAAGTATAA AATTTTACTA TAATATATCT TGTAGAGAAC AATGAAATGA 480

ATAGCAAACT GTATTACTTT GATACAAAAA TGGTTGTAAT AAATATTTAT CGATATGACG 600

ACTTGAATAT GATAAAGTGA CATATTTATG TATATGACTA TTTCGCAAAA TGTAATCGAG 660

GTAGAATTTC TTGACAATTC TGTCAGTTTA TAAGATGTTA TAAATATGTA GTGTATAAGG 720

AGGCAAACAA GATGACTGAA GAATTCAATG AATCAATGAT TAACGATATT AAAGAAGGTG 780

ACAAAGTCAC TGGCGAGGTA CAACAAGTTG AAGACAAGCA AGTTGTTGTT CATATCAACG 840

GTGGTAAATT TAATGGGATT ATTCCTATTA GTCAACTATC TACGCATCAT ATTGATAGCC 900

CAAGTGAAGT TGTAAAAGAG GGCGACGAAG TTGAAGCATA TGTCACTAAA GTTGAGTTTG 960

ATGAAGAAAA TGAAACTGGA GCTTACATCT TATCTAGAAG ACAACTTGAA ACTGAGAAGT 1020

CTTATAGTTA TTTACAAGAA AAATTAGATA ATAATGAAAT CATCGAAGCG AAAGTAACAG 1080

AAGTAGTTAA AGGTGGTTTG GTTGTTGATG TAGGACAAAG AGGTTTTGTT CCGGCTTCAC 1140

TAATTTCAAC AGACTTCATT GAGGATTTCT CTGTGTTTGA TGGACAAACA ATTCGTATTA 1200

AAGTTGAAGA ATTGGATCCT GAAAATAATA GAGTCATTTT AAGCCGTAAA GCAGTTGAAC 1260

AAGAAGAAAA CGATGCTAAA AAAGATCAAT TATTACAATC TTTAAATGAA GGCGATGTTA 1320

TTGATGGTAA AGTAGCGCGT TTAACTCAAT TTGGTGCATT TATAGACATT GGCGGTGTTG 1380

ATGGTTTAGT GCATGTATCT GAACTTTCTC ACGAACATGT TCAAACACCA GAAGAAGTAG 1440

TTTCAATTGG TCAAGATGTT AAAGTTAAAA TTAAATCTAT TGATAGAGAT ACAGAACGTA 1500

TTTCATTATC AATCAAAGAT ACGTTACCAA CACCTTTCGA AAATATTAAA GGTCAATTCC 1560

ACGAAAAATGA TGTCATTGAA GGTGTCGTAG TAAGATTGGC AAACTTTGGT GCATTTGTTG 1620

AAATTGCACC AGGTGTACAA GGACTTGTAC ATATTTCTGA AATTGCACAC AAACACATTG 1680

GTACGCCAGG TGAAGTGTTA GAACCTGGTC AACAAGTAAA TGTTAAAATA TTAGGTATTG 1740

ATGAAGAGAA TGAAAGAGTA TCACTATCTA TTAAAGCAAC ATTACCAAAC GAAGATGTTG 1800

TTGAAAGTGA TCCTTCTACG ACTAAGGCGT ACTTAGAAAA CGAAGAAGAA GATAATCCAA 1860

CAATTGGCGA TATGATTGGT GATAAACTTA AAAATCTTAA ACTATAATTT AATATTTAAT 1920

AGTCAACTCC ACATGTTTAT GATTGcATGT GGAGTATTTT TATGTAACAA AATATACTCG 1980

GAATGATAAC GTGGgACAAA TTTAACTAAG TGTTTAAAAA GATArAGTTT TAAGTGCtGa 2040

tTTTTATCAT TACAGTAATA AACTCATTTT GAATACACAG TCTCATGTGA TATTATTAAA 2100

AAGATATaAG AAAGAGAGGA AGTTAGCTTA TGACTAAACC TATAGTAGCT ATTGTAGGTA 2160

GGCCTAATGT AGGTAAATCT ACAATTTTTA ATAGAATAGT TGGAGAACGT GTTTCGATTG 2220

TGGAAGACAC GCCAGGTGTA ACACGAGATC GTATTTATTC TTCAGGTGAA TGGTTAACAC 2280

AAATTAGAGC GCAGGCAGAA ATCGCCATAG ATGAAGCGGA TGTTATTATT TTTATGGTTA 2400

ACGTGCGTGA AGGATTGACA CAAAGCGATG AAATGGTCGC TCAAATTTTA TACAAATCTA 2460

AAAAACCGGT CGTATTAGCG GTTAACAAAG TAGATAATAT GGAAATGCGT ACAGACGTGT 2520

ATGATTTCTA TTCATTAGGA TTTGGTGAAC CGTATCCGAT ATCAGGGTCA CATGGTTTAG 2580

GTCTTGGTGA CTTGTTAGAT GCAGTTGTTT CTCATTTTGG TGAAGAGGAA GAAGATCCTT 2640

ATGATGAAGA TACAATTCGA CTATCCATTA TTGGACGACC AAACGTAGGT AAATCAAGTT 2700

TAGTAAATGC TATTTTAGGT GAAGATCGCG TTATCGTTTC TAATGTTGCA GGGACAACGA 2760

GAGACGCTAT TGATACAGAG TATAGTTATG ATGGACAAGA TTATGTTTTA ATCGATACTG 2820

CTGGTATGCG TAAAAAAGGA AAAGTATATG AATCAACTGA GAAATATTCA GTATTAAGAG 2880

CTTTAAAAGC GATTGAACGT TCAAATGTTG TTTTAGTGGT CATAGATGCA GAACAAGGCA 2940

TCATTGAACA AGATAAACGT GTTGCAGGAT ATGCACATGA ACAAGGTAAA GCAGTCGTGA 3000

TTGTCGTAAA TAAATGGGAT ACTGTGGAAA AAGATAGTAA AACGATGAAG AAATTTGAAG 3060

ATGAAGTACG TAAAGAATTC CaATTTTTAG ATTATGCACA AATTGCTTTT GTGTCTGCTA 3120

AAGAACGCAC AAGATTACGT ACATTATTCC CTTACATCAA TGAAGCAAGT GAAAACCATA 3180

AAAAACGTGT TCAAAGTTCA ACTTTAAATG AAGTTGTTAC TGATGCAATT TCCATGAACC 3240

CTACACCAAC AGACAAAGGT AGACGTTTGA ATGTCTTTTA TGCAACACAA GTTGCTATAG 3300

AACCACCGAC ATTTGTTGTA TTTGTTAATG ATGTAGAATT AATGcATTTT TCTTATAAAC 3360

GCTATTTAGA GAATCAAATC CGTGCCGCTT TTGGTTTTGA AGkTACACCA ATTCATATTA 3420

TAGCTCGAAA GAGAAATTAA CGATTGGGGG ATAACAATGA CTAAAATTAC CGTTTTTGGT 3480

ATGGGAAGTT TTGGGACAGC CCTTGCCAAT GTTCTTGCAG AAAATGGACA TGATGTTTTG 3540

ATGTGGGGTA AAAATCAAGA TGCTGTTGAT GAATTAAATA CATGTCATAC AAATAAAAAG 3600

TATTTAAAAT ACGCGAAATT A 3621

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 643 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CTTTCGGAAA TTAGGATCnG nGCTATCTTG GCCCCAATTA CCAAGGGAAC TAnTGGCACC 60

AATGCtTCTT TCATCTCCAT GCCCTGTTGC TCATTATTAA TAACACGGTC TATTAACACA 180

ATGGCATTTG TTACTACGAT TCCAATTAAC ATTAGCATAC CAATTAAACT TGGTACTGAT 240

ATTGTTTCTC CTGTGATTAA TAGTGCAATA ATTACACCGA TAACTGTAAA TGGTAAAGAG 300

AATAAAATTG TAAATGGTGC TAGGCCACCT TTAAATGTAA TAACTAGGAT TAAATATACG 360

ATAATGATTG CAGCTAACAT TGCAAAGGCT AATTGTGTCA TTGCATTGTT AATATCATCT 420

GATGCACCAC CGATATTAAC CTTTACATTA TTCGGTTTAT CCAAATTATT TATTTTAGAC 480

ATCACTTGTC GTGTTGTGCC ACCCACATCT TTATTTGTTA CTTTAGCAGA TACCGTCGTT 540

GCATAATCTC CTTGTTCTTG CGTCAATTTA CTTGGTGTCG TTGTTTTAAC TAACGTAGCG 600

ATATCTCCCA ATTTAATCGT ACCACCAGTC GGCTTTTTCA AAG 643

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2524 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

TTTCAGGCyG TGCAAGGGCT TTTTCTTTTG CTTTTAAGAT TATGATTTAT CGTGCAAAGT 60

TAAGTGGTCG TATATAGTTT TAGTTTTAAA AAGGTAATTA AATAAAATAG TTTGCCGAGG 120

GAGATGTCAA AATGATTAAA ATACCTAGAG GGACGCAGGA TATTTTACCT GAAGATTCAA 180

AGAAATGGCG TTACATTGAA AATCAATTAG ATGAATTAAT GACATTTTAT AATTATAAAG 240

AAATAAGAAC ACCAATTTTT GAAAGTACAG ATCTTTTTGC AAGAGGTGTT GGTGATTCAA 300

CCGATGTCGT ACAAAAAGAA ATGTATACAT TTAAAGATAA AGGCGATAGA AGTATTACAT 360

TAAGACCTGA GGGAACAGCT GCAGTTGTGC GTTCATATAT TGAACATAAA ATGCAAGGTA 420

ATCCAAACCA ACCAATTAAA CTTTATTACA ATGGACCGAT GTTTAGATAT GAACGTAAGC 480

AAAAAGGACG CTATCGTCAA TTTAATCAAT TTGGTGTAGA AGCTATTGGT GCTGAAAATC 540

CTAGCGTAGA TGCAGAAGTA TTAGCTATGG TTATGCATAT TTATCAATCA TTTGGATTAA 600

AACATTTAAA GCTTGTTATT AATAGTGTAG GGGATATGGC GTCTCGAAAA GAATATAACG 660

AAGCGTTAGT GAaACACTTT GAACCAGTAA TTCATGAATT TTGTTCAGAT TGTCAATCAC 720

GTTTGCATAC AAATCCGATG CGAATTTTGG ATTGTAAAGT AGACCGTGAT AAAGAAGCGA 780

TTAAGACTGC ACCTAGAATC ACTGATTTCT TAAATGAGGA ATCTAAGGCA TATTATGAAC 840

GTGGATTGGA TTATTATACA CATACAGCAT TTGAATTAAT GATGGATAAC CCTAACTATG 960

ATGGTGcCAT TACAACGCTT TGTGGTGGTG GCCGTTATAA TGGTTTATTA GAATTGCTAG 1020

ATGGTCCAAG TGAAACAGGT ATTGGTTTTG CGCTAAGTAT AGAACGATTA TTGCTTGCAC 1080

TTGAAGAAGA AGGTATCGAA TTAGATATTG AAGAAAACTT AGATTTATTC ATTGTTACAA 1140

TGGGTGATCA AGCAGATCGA TATGCTGTGA AGCTATTAAA TCATTTGAGA CATAATGGTA 1200

TTAAAGCAGA TAAAGACTAT TTACAGCGTA AAATTAAAGG ACAAATGAAA CAAGCAGACC 1260

GTTTAGGTGC CAAGTTTACA ATCGTTATTG GTGATCAAGA ATTAGAAAAT AATAAAATCG 1320

ATGTTAAAAA TATGACAACT GGTGAATCTG AAACAATTGA ATTAGACGCA TTAGTCGAAT 1380

ATTTTAAGAA GTAGAGAGGG CGTTAAAATA TGAGTAAGAG AACAACTTAT TGTGGATTAG 1440

TTACTGAGGC ATTTTTAGGA CAAGAAATTA CATTAAAAGG ATGGGTTAAC AATCGTCGTG 1500

ACCTTGGTGG ATtGATTTtC GTTGATTtAA GAGATAGAGA AGGAATTGTA CmAGTCGTGT 1560

TTAATCCTGC ATTTTCAGAA GAGGCaTTGA AAATTGCTGA AACAGTACGT TCTGAATATG 1620

TTGTAGAAGT TCAAGGTACA GTTACGAAGC GTGACCcTGA AACAGTTAAT CCTAAAATTA 1680

AAACTGGCCA AGTTGAAGTA CAAGTTACAA ATATTAAAGT GATTAATAAA TCTGAGACAC 1740

CACCATTTTC TATAAATGAA GAAAATGTTA ACGTTGATGA AAATATTCGA TTAAAATACC 1800

GTTATTTAGA TTTACGTCGT CAAGAGTTAG CGCAAACATT TAAAATGAGA CATCAAATTA 1860

CACGTTCTAT TCGTCAATAT TTGGATGATG AAGGGTTCTT TGACATCGAA ACACCAGTAC 1920

TAACGAAGTC AACACCTGAG GGTGCACGTG ACTATTTAGT ACCATCTCGT GTTCATGATG 1980

GTGAATTTTA TGCATTACCA CAATCACCAC AATTATTTAA GCAATTATTG ATGATTAGTG 2040

GATTTGACAA ATACTACCAA ATCGTAAAAT GCTTCCGTGA CGAAGATTTA CGTGCAGATC 2100

GTCAACCTGA ATTTACACAA GTCGATATTG AAATGAGTTT TGTAGACCAA GAAGATGTGA 2160

TGCAAATGGG TGAAGAAATG CTTAAAAAAG TTGTTAAAGA AGTTAAAGGC GTTGAAATTA 2220

ATGGCGCTTT CCCACGCATG ACATATAAAG AAGCGATGCG TCGCTATGGT TCTGATAAAC 2280

CAGATACACG TTTTGAAATG GAATTAATTG ACGTTTCTCA ATTAGGACGT GATATGGACT 2340

TTAAAGTATT TAAAGATACT GTTGAAAATG ATGGTGAAAT TAAAGCAATT GTCGCTAAAG 2400

GTGCAGCTGa ACAATATACT CGTAAAGaTA tGGGaTGCTT TAACAGAATT TGTaAACaTC 2460

ymTGGtGCTA AgGtTAGCGT GGGGTTAAAG TTGTGGGAAG GTGGTTTTGA CAAGGTCCCA 2520

ATGG 2524

(2) INFORMATION FOR SEQ ID NO: 361:

(A) LENGTH: 1507 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

TCGTTGAGTA AAAGTCCAGA AAATTGGATG AGTAAACTTG ATGATGGAAA ACATTTAACT 60

GAGATTAATA TACCGGGTTC ACATGATAGT GGCTCATTCA CTTTAAAGGA TCCAGTAAAA 120

TCAGTTTGGG CAAAGACTCA AGATAAAGAT TACCTTACCC AAATGAAGTC GGGAGTCAGG 180

TTTTTTGATA TTAGAGGTAG AGCAAGTGCT GATAATATGA TTTCAGTTCA TCACGGCATG 240

GTTTATTTGC ATCATGAATT AGGAAAATTT CTCGATGATG CTAAATATTA CTTGAGTGCT 300

TATCCAAACG AAACAATTGT GATGTCTATG AAAAAGGACT ACGATAGCGA TTCTAAAGTT 360

ACGAAGACAT TTGAAGAAaT TTTTAGAGAA TATTATTATA ATAACCCGCA ATATCAGAAT 420

CTTTTTtACA CAGGAAGTAA TGCGAATCCT ACTTTAAAAG AAACGAAAGG TAAAATTGTC 480

CTATTCAATA GAATGGGGGG TACGTACATA AAAAGTGGTT ATGGTGCTGA CACGTCAGGT 540

ATTCAATGGG CAGACAATGC GACATTTGAA ACGAAAATTA ATAATGGTAG CTTAAATTTA 600

AAAGTACAAG ATGAGTATAA AGATTACTAT GATAAAAAAG TTGAAGCTGT TAAAAATTTA 660

TTGGCTAAAG CTAAAACGGA TAGTAACAAA GACAATGTAT ATGTGAATTT CTTGAGTGTA 720

GCGTCTGGAG GCAGCGCATT TAATAGTACT TATAACTATG CATCACATAT AAATCCTGAA 780

ATTGCAAAAA CGATTAAAGC AAATGGGAAA GCTAGAACGG GTTGGCTGAT TGTTGACTAT 840

GCAGGATATA CGTGGCCTGG ATATGATGaT ATCGTAAGTG AAATTATAGA TAGTAATAAA 900

TAAGGATTCA ATAATGATAT TAAGACGAGT ATGAAAATAG TTAGATTCTA ATTATTTTCA 960

CTACTCGTTT TTATTTTGAA AATAAGTAAT AATTCAACAA TATTATAAAT TGAACAGATT 1020

GTTTGTGAAA TTTTTGATAA TATTAAAGTG AAAAAGTGTT ATAAATTGAT AAATATATGT 1080

AATTAACAAA AACAAATCAT TTTAAAAAGA AGAGAGTTGT AAGATGATGa AACGATTAAA 1140

CAAATTAGTG TTAGGCATTA TTTTTCTGTT TTTAGTCATT AGTATCACTG CTGGTTGTGG 1200

CATAGGTAAA GAAGCGGAAG TTAAGAAAAG CTTTGAAAAA ACATTGAGTA TGTACCCTAT 1260

TAAAAATCTA GAGGATTTAT ACGATAAGGA AGGCTATCGT GATGATCAGT TTGATAAAAA 1320

TGATAAAGGT ACATGGATTA TAAATTCTGA AATGGTTATT CAACCTAATA ATGAAGATAT 1380

GGTAGCTAAA GGCATGGTTC TATATATGAA TAGAAATACC AAAACAACAA ATGGTTACTA 1440

mTATGTCGAT GTGACTAAGG ACGAGGATGA AGGAAAACCG CACGACAATG AAAAAAGATA 1500

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

TACATGTTTC GGATGCTACT TTATTTAGTT TGAAGGGTGC ATTATGGACG TTAGCGCAAG 60

AAGTTTATCA AGAATGGTAT TTAGGATCGA AGTTGTATGA AGATGTTGAA AAGAAAATAG 120

CACGAACTAC TTTTAAGACA GGTTATATTT ATCAAGAAAT TATTTTGAGA CCAGTAGATG 180

AAGTTAAGGT ACTTCTGAAT GATTTAAAAG GTGCTGGTTT CGAATTAGGT ATTGCAACAG 240

GTCGTCCTTA TACTGAGACT GTTGTGCCAT TTGAAAATTT AGGATTGTTA CCATATTTTG 300

AAGCTGATTT TATTGCAACA GCAAGTGATG TTTTAGAAGC AGAGAATATG TATCCGCAAG 360

CACGACCATT AGGAAAGCCG AATCCTTTTA GTTATATCGC AGCTTTATAT GGTAATAATC 420

GCGATAAATA TGAATCTTAT ATCAATAAGC AAGATAACAT TGTAAATAAA GATGACGTAT 480

TTATAGTAGG CGATTCGTTA GCTGACTTAT TAAGTGCTCA AAAAATAGGT GCAACGTTTA 540

TTGGAACATT AACAGGTTTA AAAGGTAAGG ATGCTGCAGG TGAGTTAGAA GCGCATCATG 600

CCGACTATGT TATTAATCAT TTAGGTGAAC TTAGAGGTGT ACTAGATAAT TTGTAATTTG 660

ATTGTTGTTT GACAGCATAA CTTGTAGTGA ATGATTGAAC CAAAGGTTTC ATATTGAGTT 720

ACAATGAAAT TAATAATGAA AAAATGCCAA GAAGCAATGG AAGTAATCCA ATGTCTTCTT 780

GGCATTTTGA ATTTACATAA ATTGTTTATG ACTGTACCGT CAATTCAGTT GTGAAAATTT 840

GATTGTATTC ACCAACTTGT TTAAGTTCAT CAATTATATT GTTTGAAACA GGTTGATCAA 900

CGGATAAAAT CATTAGCGCA TCTCCGCCCG CTTCAGTTCT ACCTAAAGTC ATAGATGCAA 960

TGTTGATATT GTATTTACCT AACAATGCGC CAGTTTTTCC TACCATACCT GGAGTATCAT 1020

TATGATATGA CACAATTTGA TATTGATTTG GCTTTAAGTC TACAGAAAAA TTATTAATTC 1080

TAACAATTCT TGGACCGAAA CCTGTAAAGA CAGAAGCGCC AACTTTAACG GAATCGCnAT 1140

CGnTTGATAG TTCTACCTCT AAGTAGTTAC TAAAACCTGT CTCTGCTTTA TTATTTTCAA 1200

TATTTAATGT CACTTG 1216

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 867 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

ATCAAAATAT TTTAAATAAT ATTGATGGTC ACATTGTAAA TrmAATAGAA AATAAATTTG 60

ATCAAATATT ACAAGAACCA TTAAATCCAT TAAATTATGA TACTGTCAGT GGATTAGCTG 120

GGATAGGGAG ATATTTGCTA AATAGAGTAG ATGAGAATGA ATTTAATGTT AAAGCATTAA 180

AAAGCATATT AGTATACTTT AAAGATATTC AATATTCTAA AAATAGCTGG GTAGTCCCAC 240

AAGArAGTCA ATTTTTAGAG TCTGATAAAA ATTATTTTAC TGAAGGTAAT ATCAATCTTG 300

GCCTTGCACA TGGaGTGCTA GGACCGATGT CTTTATTTGC ATTATGCGTG ATTAAAGGAA 360

TTACGATTGA AAATCATCAG CACATATTAA AAGACATGTA CAAATTTATC ATGGACGAAA 420

AATTTTGTAA CCACGAAAGA TGGTTGCAGC GTTACGATTT AATTTCTGAA CGTAATCATT 480

TCAATTTTAT TCGGAATGGT TGGTGTTATG GCAATACGGG TGTAATGACG ACGTTGTTTT 540

TAATCGGCCA AGCATTACAA GATGATGAAA TAATTAAAAT GTCTAAAAAA GTGATGCTAC 600

AAGTAGTAAA TGATAAAGAT GAAAATTTAA TAAGTCCAAC TATTTGTCAT GGATTGTCAT 660

CACAAATATT AATGTTAACA ATTATGAATT TGAATTTTGA ATTAAATGAA GTGTCTGATT 720

ATATCACTGT ATTAATAAAT AAACTGATTT CTCATTATAA GGAAGATTAT CTGGTGAATT 780

TTATAGACAT TAATGAAAAT AAGCAAGATG TATTTAAAAG TAGGAAAGTT GGCCTTTTAG 840

AAGGTGAATT AGGGGTCATC TAACATT 867

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

TACCTTTTCT TtTAAATCAT TTTATATTTT CCCaCTAATA TCCGcTGtTA ATCaATCCtG 60

ACATCCtTGT ATCaCTATGA CAATTAATTG TTAAATACAT GAATTTCTAC ATTTTATGAA 120

AAAATCCATT TTTATTACAA TTCAACACTT TATATGACAA CTTCATTACA GTTACTTTTA 180

TTGTTGATTG CTTACATTGT TTTCTAAAAA AAATTTGTTA TCATAATTAA CGTTGAATAA 240

AGAAAAAAAT TAACTTGGGA GATAAAAATG GAATATAAAA AGATACTAAT TCGTTTATTA 300

CAATCGCATG CCGCAGTTAA TTATTATAGT AAAAACCAAT GTACATGGTG GGCATTTAAA 420

CGTCGCGCAC AAGTCGGTAA ACCTGTTTCT AATAGATGGG GCAATGCTAA AAATTGGTAT 480

TACAATGCAC GTAAATCAAA ATATGCGACT GGTCGTACAC CAAGAAAATT TGCTGTCATG 540

CAATCAACTG CAGGATATTA TGGACATGTC GCAGTTGTTG AACAAGTATA TAAAAACGGT 600

AGTATTAAAG TTTCAGAATA CAACTTTTAT CGCCCATTAA AATACAATAC ACGTGTACTA 660

AGCAAAAAGG CAGCACGTAA CTTTAACTAT ATTTACTAAT CAAAAAACTT CTATCACGAA 720

CGCTTCAATT TCCTGTATGC GTGTGATAGA AGTTTTTATT TTATGAAATT ATATTATTAC 780

TTCTACAAAT TTCAAATTGC CGTAATTGAA CGTATATTTC TTCTTCAACT ATTATTTCAT 840

CTTTAGCATA ATCTATATAT AAAATTTTAT GCTATTATTT AAATAATTCG CTATAACTTA 900

ACATACGTTT TCGATATAAA CCTTGTTCTA AATCTCAATA ATTTTTTGCT GTTTTCATCG 960

TCATTAGTTA AAAAAATAAT TTAACTGAGT TTTTGAGACC TGTTTAAATT GATGACTCAA 1020

AACCTTTATC CCCTTTTCAC TCGGTTTAAT TGCTTTAATA TTTAACACAG TCTCATTGTA 1080

ATTTTGCTAC TAAGTTTGAA ATATTTCGAT TCGAATGTGA AcATCATTTA TTATTACTTT 1140

CGACAGCTAG AAAAATATTG TTAAACCAAA ACTATAATTA CCACTTTTAT ATAGAACTAT 1200

ATATAAATTT TAACTTTGAG ACAGAACTGC TAGTCAGGTT TATGAATATA TTTCTTTAGT 1260

TTACTTGaTA TACTTATTGG TAAATCATTA TTTATTTGAA GAGCATTTAT AACAAAAAGT 1320

ATAATCCCAG TTATAGCGAT TCCATGACCA TTTTTATCAG TCAAAGATTC ATCAACAAAA 1380

ACTTTTTGAT AAATTTATAT ATTTGTATAA TTTATTATGG TAGATATCTA CACCCGTATC 1440

TATAACAGCT ACAGTTATCA TTGCGTCTTA TCCAAATAGT TTTTAAGAAA TAAATATAAT 1500

TCATTAATAT CATGGCTATT TGTAACGTCA GtGCTTaAGA CCTTGTCAAT TATTGTTTTA 1560

TCTGTTTCTA AGAGCCCCTG ATTTTCTGCA TACATATTTT GTATATCGCT GTTAATCTCA 1620

TTTAATTTTT TAAATTTTTT TCTAACCTTT TTCAAAATAA AATGCTCTTT AATTCCATCT 1680

CTTAAATACA TATAAATCTC TATTATAATC TCCATAAATG TCATATCTCC TCTCTCAAAA 1740

AACATTATAC TCAATATATT AAAAATAAGA AAGGTTTTTT CAGAATTTTT AGTATTTTCA 1800

GATATTTATT CTTAAGTATC TTATTATTAC TTCTTTTTAA CGCTAGTGGa ATAATTAATA 1860

ATAATTGTAT TTAAATGCAA TGCTGTTGTT CTTTCATACT TACAAGCAAG TCATAAGAAA 1920

TGAGAAATTA AATTCTTATA TGATGAATAA ATGATGACTG CAGAAGAAAT TGCTAAAAAA 1980

GGAGTGGAGT GAGGCATTCT ACTGTTCATA TTGTTAACAA ATATCAAAAT GATAGGAACT 2040

TGAAGAATCT AAGACTGTTA AAATCGAGAC AAGAAGAAAC TCGTTCCAAA TTTGAATCCT 2100

AAAACTTCTA TCACGAACGC TTCAATTTCC TGTATGCGTG TGATAGAAGT TTTTATTTTT 2220

GTTCATATTA ATTTATCTAA GCGCTACGAT GGaCTGACTT AAACTTTTCT TTAAAATCGC 2280

TATTCGCCAT TTACTATTGT TGTCTAATTT CTTGTAAAAT ATGTTCCGCT GCTTGTGTAT 2340

TTGCACGGGG TTCTTTTTTC AAAGCTTCAG CTACTTTAGC AATTTCATCA CCTTTTGCCC 2400

CTACAACGAT AGCTAATGAT TTATATTGTA AACTCATATG ACCTTGTTGA ATACCTTCTG 2460

ACACAAGCGC GCGACATGCT GCAAAGTTTT GCGCTAAACC AACGGCAGCA ACTACATGAC 2520

CTAATTCTTG TGCTGACTCT ACATTTAGTA GCTCTAATGA AGCTTTAGCA ATTGGTAATA 2580

CTTTTGTACC ACCGCCAACG ATTGCCAATG TCATAGGCAC TTCAATTGTA CCAATCAATC 2640

GTTGACGATC TTGATCGTAA CGCCATGTAG CAATACCACG ATACTGTCCG TCACGACTCG 2700

CGTATGCATG CGCACTTGCT TCTGCACCAC GCGTATCATT TCCTGTTGCT AAAACAACAG 2760

CATGTATGCC ATTCATAACA CCTTTATTAT GTGTTGCTGC ACGATGAATA TCTACTTGGG 2820

CCAATACAGA AGCACGTTCC ATTCGTTTGG CAACCTCTTC TCCAGTTCTC TCGCCCCTTG 2880

CTAAATCTTT AACATCAATT TCGCCTTGAA CTTTAACAAC GGACGCTGTT GCATGATTGG 2940

ATAAAATACT CATTAAAATG TCGCTTTGCG GAAATTCATT TTTTAAAAAT GCAGTTATGG 3000

CCTCTAAAAT CGTATTAAGC ATATTAGCGC CCATAGCATC TTTCGTATCA ACAAATACTT 3060

TTAAAGATAG TAACTGTTGC TCAGGAAATG TATCAATCGC TATACGTTGG TAACCACCAC 3120

CACGCGCTTT AATAGAAGGA TATGCCTCAT CCGCAATTTT ATGAATTTGC TTTTCTAAAG 3180

CTTTAATGTC TGCTGATAAT TTTTCAGTAT CGTCAACGCC ATCAAAGACG ATTTGACCTA 3240

TCATAATACG TTCAGAAGAT ACCGTTTTAA ATCCGCCAGT CTGATTCACT AGCTTTGCAC 3300

CATAACTAGC TGCAGCGACA ACTGAAGGCT CTTCCACCAT CATAGGTACA ACATATGCCT 3360

TATCGTCCAC AATGATATTC GGTAATAATC CAACGGGTAA TGCACCTTGC GCGATGACAT 3420

TTTCAATTAA ACTATTGGCT ACTTCTTCAT CGATTAATGG ATGATTCAGT AAAATGTCGA 3480

ATTGTTCTTC TGATAACCAT TGCTTATCAA CCAATTGTTG TAACTTTTCT TTACGAGATA 3540

AATGTCGAAA ATTCTTATCT AAATTTTGCA TGGACGTACT CCTTTTACTT CACATAATTT 3600

TTAACATTTC AATCACTACT ATTTTTACCA CAAAATAACG TCATTCGTCT TAAAATTCAA 3660

TTGAATAATT GTCGTTTTGA CTTTAAAATA AAACAAGGTA AATTAAAACG CTTACAAGAA 3720

ACGACAAATc ATTTTTAAAT TTAGTATATT TCTTTGTATA AAATTAGCAT ATTCTGATAT 3780

GATACAAGTG TTGCTTTTAT AAATTTGAAA GGATGTAAAA CCTTATGACA ATAGGTATCG 3840

ATAAAATAAA CTTTTACGTT CCAAAGTACT ATGTAGACAT GGCTAAATTA GCAGAAGCAC 3900

CTGTAAACCA AGACATCGTT TCAATGGGCG CTAACGCTGC TAAGGACATT ATAACAGACG 4020

AAGACAAAAA GAAAATTGGT ATGGTAATTG TGGCAACTGA ATCAGCAGTT GATGCTGCTA 4080

AAGCAGCCGC TGTTCAAATT CACAACTTAT TAGGTATTCA ACCTTTTGCA CGCTGCTTTG 4140

AAATGAAAGA AGCTTGTTAT GCTGCAACAC CAGCAATTCA ATTAGCTAAA GATTATTTAG 4200

CAACTAGACC GAATGAAAAA GTATTAGTTA TTGCTACAGA TACAGCACGT TATGGATTGA 4260

ATTCAGGCGG CGAGCCAACA CAAGGTGcTG GCGCAGTTGC GATGGTTATT GCACATAATC 4320

CAAGCATTTT GGCATTAAAT GAAGATGCTG TTGCTTACAC TGAAGACGTT TATGATTTCT 4380

GGCGTCCAAC TGGACATAAA TATCCATTAG TTGATGGTGC ATTATCTAAA GATGCTTATA 4440

TCCGCTCATT CCAACAAAGC TGGAATGAAT ACGCAAAACG TCAAGGTAAG TCGCTAGCTG 4500

ACTTCGCATC TCTATGCTTC CATGTTCCAT TTACAAAAAT GGGTAAAAAG GCATTAGAGT 4560

CAATCATTGA TAACGCTGAT GAAACAACTC AAGAGCGTTT ACGTTCAGGA TATGAAGATG 4620

CTGTAGATTA TAACCGTTAT GTCGGTAATA TTTATACTGG ATCATTATAT TTAAGCCTAA 4680

TATCATTACT TGAAAATCGA GATTTACAAG CTGGTGAAAC AATCGGTTTA TTCAGTTATG 4740

GCTCAGGTTC AGTTGGTGAA TTTTATAGTG CGACATTAGT TGAAGGCTAC AAAGATCATT 4800

TAGATCAAGC TGCACATAAA GCATTATTAA ATAACCGTAC TGAAGTATCT GTTGATGCAT 4860

ATGAAACATT CTTCAAACGT TTTGATGACG TTGAATTTGA CGAAGAACAA GATGCTGTTC 4920

ATGAAGATCG TCATATTTTC TACTTATCAA ATATTGAAAA TAACGTTCGT GAATATCACA 4980

GACCAGAGTA GTCGGTGTAT TTAAAACACA TATAATAAAA CCTAAAAGCA GCAGTAAGAC 5040

CACTTCTAAT TGAAATCGTC TTACTGCTGT TCTCTATTTA TAACACTTCG TATTGAATGA 5100

ATTCATTATG CCTATTTGAC ACATTATTGA AGTTTTCCTA ATGCCTGGAT CCTTTATACG 5160

TTACGGCTTC GTGCTATGTT TTGGTACATA AAGCTTTGAC ATATCGATAT TCTCCAACTC 5220

TAACAGCTTA ATTTTATTAT TAATCGTTCC ACCGAACCCT GTTAAGCTAC CCGTTTTACC 5280

GACAACACGA TGACATGGCA CGATAATAGA TAATGGATTA CTTCCGACTG CACCTCCAAC 5340

CGCTTGGGCT GACATTTTTG GCTTGTTAAG CAGCTTGCCT ACTTTTTTGG CAATAGCACC 5400

ATACGTTGTT AGAGTCCCAT AAGGAACCTG TCTTAATTCA TTCCAAACAC ACTGTTGAAA 5460

ATGACTACCT GTTGGCTTTA AAGGTATTGT GATTTCAGGA TTGTCACCTT TAAAATACGC 5520

GTCTAACCAC TGTGTCGCCT CTCTAAATAT CGCTAAAGAC GTATTTTCTT CCCTAGTACC 5580

ATCACCTTGT TGATTTTCAA ACAAAACAGC GGTCAGACTT ACCCCATCAC TCAAAAGTTC 5640

CAATCGTCCT ACAGGCGAAT CATAGTAACT CTTATACTCC ATAAAAATTC CCCCTTTTTC 5700

ATAAGTCGTC AATTACGTAT ATAAACACGT AATACCAGCT ATCACTTTGC TGCAATATAC 5820

AGTTACATAT CTTACTACAC GTGCTAACCT CTTACTTTGT AAACCAAATC TTAAATTAAA 5880

ATATTGAAAA TGCAATGAAT CCTTAATATT TTATTAAACC TATAATTACT TATTAAAAAT 5940

AACACACAAT ATTCATAAAG TTTTAAAAAT ATTCTGTTTT ATCACCTACT ATTAGTGGAA 6000

AAGTACAATT GCAATTGTAT ATAGTTTGCA TAACGCTTCA AAAGTAATTT CTTTTTTGTT 6060

TAGTTCAAAA AAATTTAGAG GTGATGTTAT ATGAATAACG GTTTTTTCAA TAGCGACTTT 6120

GATTCAATTT TTCGAAGAAT GATGAAAGAT ATGCAAGGTT CAAATCAAGT CGGAAACAAA 6180

AAGTACTATA TTAATGGTAA AGAAGTTTCA CCTGAAGAAC TAGCGCAACT CACACAACAA 6240

GGTGGCAATC ACTCTGCTGA ACAAAGTGCG CAAgcTTTTC AACAAGCAGC ACAAAGACAA 6300

CAAGGGCAAC AAGGTGGCAA CGGCAATTAT TTAGAACAAA TTGGTCGTAA CCTTACGCAA 6360

GAAGCACGTG ACGGTTTATT AGATCCAGTC ATTGGTCGTG ATAAAGAAAT TCAAGAAACT 6420

GCTGAAGTTT TAAGTAGACG AACTAAAAAC AATCCTATAT TAGTTGGAGA AGCTGGTGTT 6480

GGTAAAACTG CGATTGTTGA AGGTTTAGCA CAGGCAATCG TTGAAGGAAA TGTACCAGCA 6540

GCAATCAAAG ACAAAGAAAT TATTTCTGTA GACATTTCAT CATTAGAAGC TGGAACGCAA 6600

TATCGTGGTG CTTTTGAAGA AAATATTCAA AAATTAATCG AAGGTGTTAA ATCTTCACAA 6660

AATGCCGTAC TATTCTTTGA TGAAATCCAT CAAATTATCG GTTCAGGTGC CACAGGAAGT 6720

GATTCAGGTA GCAAAGGGTT ATCTGATATT TTGAAACCTG CATTAAGTCG TGGTGAGATT 6780

TCTATTATTG GTGCAACAAC ACAAGATGAA TATCGAAACA ATATTCTTAA AGATGCTGCA 6840

TTAACGCGCA GATTTAATGA AGTGCTTGTT AATGAACCAA GCGCTAAAGA TACTGTTGAA 6900

ATTTTAAAAG GTATTCGCGA AAAATTCGAA GAACACCATC AAGTAAAATT ACCAGATGAC 6960

GTATTAAAAG CATGTGTTGA CTTATCAATT CAATATATTC CACAACGATT ATTACCAGAT 7020

AAAGCAATCG ATGTGTTAGA TATTACAGCA GCACATTTAT CTGCGCAAAG TCCAGCTGTC 7080

GATAAAGTTG AAACTGAAAA ACGAATTTCT GAATTAGAAA ATGATAAACG TAAAGCAGTA 7140

AGTGCTGAAG AATATAAAAA AGCTGACGAC ATTCAAAATG AAATCAAATC ATTACAAGAT 7200

AAATTAGAAA ATAGTAATGG TGAACATACT GCTGTTGCTA CAGTTCATGA TATTTCAGAT 7260

ACTATTCAAC GATTAACTGG TATTCCAGTT TCTCAAATGG ATGATAACGA TATTGAACGT 7320

TTAAAAAATA TTTCTAATCG TTTAAGAAGT AAAATCATAG GTCAAGATCA AGCTGTAGAA 7380

ATGGTTTCAC GTGCAATTCG CCGTAATCGT GCTGGGTTTG ATGACGGCAA CCGTCCAATT 7440

GGCAGTTTCC TATTTGTTGG CCCTACTGGT GTTGGTAAAA CAGAGCTTGC TAAACAATTA 7500

GACACAACAG CTGTTTCAAA AATGATTGGT ACAACTGCTG GTTATGTTGG TTATGATGAC 7620

AATTCAAATA CGTTAACTGA AAAAGTACGC CGTAATCCAT ACTCAGTCAT TCTATTTGAT 7680

GAAATCGAAA AAGCAAATCC ACAAATTTTA ACATTGTTAT TACAAGTAAT GGATGATGGT 7740

AATTTGACTG ATGGTCAAGG TAATGTCATC AACTTTAAAA ATACAATTAT TATTTGTACA 7800

TCAAATGCTG GCTTTGGCAA TGGCAATGAC GCTGAAGAAA AAGATATTAT GCACGAAATG 7860

AAAAAATTCT TCCGCCCTGA ATTCCTTAAC CGCTTCAACG GCATCGTTGA ATTCTTACAT 7920

TTAGATAAAG ATGCATTGCA AGATATCGTC AACTTATTAT TAGACGATGT ACAAGTTACA 7980

TTAGACAAAA AAGGTATTAC GATGGACGTT TCTCAAGATG CGAAAGATTG GTTAATTGAA 8040

GAAGGCTATG ATGAAGAATT AGGTGCACGT CCATTAAGAC GTATTGTTGA ACAGCAAGTA 8100

CGTGACAAAA TTACAGATTA CTATTTAGAT CATACAGACG TTAAACATGT GGATATAGAT 8160

GTTGAGGATA ACGAATTAGT CGTAAAAGGT AAATAACGAC ACTTTAACAT ATCGCGCATC 8220

AAAAATGAGC ATCAGGTCGC CCTTGCCTGT GCTCATTTTT TTAATTATTT CCCTGGAAAA 8280

TGATTCGCTG TGTGCTGTTC TGTTCCACAA CAATCACGAT TAATGTCACA TGTACCACAT 8340

TTTCCTTGTT TTGAACGCTT GAAAAATTTT ACTAGTGTAT ATAAGGCATA TCCGAAAATT 8400

GCTAAAAAAA TTAAAATGTT AATAATGACT GACACTTTAA CCACTCCTTA AACAAATAAA 8460

TGTCCGACTT GATAAAAAAT GAATGTTAAG ACATATGCAG TGACTAGAGG ATAGGCAACT 8520

GCAAGTGCCG TCCATTTCCA TGAATAAGTC TCTTTACGGA TTGCTGCTAC TGTAGAAACA 8580

CAAGGAATAT ACAATAGTAT AAATATCATA AATGCATACG CAGATAGCGG TGTGAATTGA 8640

TTTTGAATCA CATTAACAAG GCCTGCATCA CCTGATGAAT AGATAATCGC CATCGAACTT 8700

ACGATAACTT CTTTTGCTAA AAATCCTGGC AcTAACGTAG CACCTGCTTG CCATGTTCCA 8760

AATCCGAGCG GTTGCACTAA CATACCAAAG AAACTACCAA CCATATGTAA AAAACTTTGA 8820

TTGATATTCA CATTGATACC ATGTGGTCCT ACATAACTTA ATAGCCAAAT GACTACTGAG 8880

CCGCCAAAAA TAAATGTACC TGCTTTACGA ACAAAGCCCT TAGCCTTTTC CCAAGTACTA 8940

CGCCACAACG TTTTAATGGA AGGCACACGG TATGTTGGCA ATTCCACAAT AAAGATTGCA 9000

TTATCATTTT TTAAAATCGT CTTAGTAAGT ACTGTACTGA CTAAAAATGC CATAATAATA 9060

CCTAAAACAT ACAGGCTTAA TACTACTAAA GATTGATTCT CTTTGAAAAA GATACCTACG 9120

AACAACGCAT ACACTGGCAG TCTAGCAGAG CATGACATGA ATGGTGCAAT TAATATCGTT 9180

GTTAAACGCT CTTTTTCATT TTCAATACTG CGCGCAGCCA TAATACTCGG TACATTACAA 9240

CCAAATCCGA TAATCATTGG TATAAAAGAC TTCCCGCTTA AACCGAACGA TTCCATAATA 9300

AAAAAGAGCA CAACAATTTG TGGTACAAAG ACTAATACTG ATCCTACACC AGCAATAATG 9420

CCATCTGTAA TTAAATCTTG TAAAAATGGT ATAACACCAA GATAATTCAT AATCGTCTTC 9480

ACACTATCTG TAAATGTACC ACCTATAAAT GCATCGAGTT GATCCGACAA AGGTGTGCCA 9540

ATCCATGTAA ATGTAGTTTG AAAGATCAAC CACATAATTG CTAGAAAGAT AGGCATCCCT 9600

ATATATTTAT GTGTTAATAT CTTGTCTATT CTAGAGCTGA AATATTGCTT ATCTTCATCT 9660

GGATACGTTA CCACGTCTTG CAATAACGTC TCAATATAAT GATTGCGTAT ACGCTCCATC 9720

TCTCGACGAA CAGATACAGC CCCTACTTGT TCAGCAACTT GATCACGTAA ACTCGACAAT 9780

TTATTTACAA CCTCTGAATT AAGTTCGTTT GCAATTTGCA TGTTATTTAA TAAGAATTGA 9840

ATCGCAATAA ACCTAGCTTG ATACTTATCA TGAGATGTCT CTGTCATTAT TATTTGACAC 9900

ATATTTTTAA TTGTCTCTTC AATCTTCTCA CCATAATTGA TTTTAAAATG CGGTTGATAC 9960

CCTTCCCCTA GATGCTTTAT TTCGCCAAGT AAATATTTTG TTCCTTTGCC TGTACGTGCC 10020

ACAACTGGAA AAATAGGTGT TTTTAACTTT TTCATCAATT TATGATAATC GATTTTTATC 10080

CCGCGCTTTG TAGCTACATC AATCATATTT AATCCGATGT ATATTGGTTG ATTAAGTTCT 10140

AACAATTGTA CTGTTAATTG CATATTTCTT TTTAGTTGAC TCGCATCAAC AATGTTAATG 10200

ATTCCTGAAA ATGAATCGTT TAATAAATAG TCTGTCACTA CAGTTTCATC TTTAGAAATC 10260

GGCGATAAAT CATATGTACC TGGTAAATCA ATTAATTGTC CTACATTTTC TTTAAGTTTC 10320

CCTACTTTTT TCTCTACCGT TACGCCACTC CAGTTGCCTA TATATTCATA CGAACCAGTT 10380

AAAGCGTTAA ACAAAGATGT TTTACCAACA TTAGGATTTC CTAAAATACA ATAATTTTCC 10440

ATTCGTCCGG CTCCTATTCT TCTAATGCAA TAGAACAAGC ATCGCAATGT CTAATACTTA 10500

ACTGTTGTCC GTTTACTTCA ATAATACATG GCCCTTTAAA TAAACATTTT TGTTTAATCG 10560

TTATGATAGC GTCATCTGTT AACCCAAAGG CACTTAGACG ATACAACATA TTCTCATTAG 10620

CAATATCCAT TCGCTTTATT TTATAAGCCT TATTCATTTC ACCATTTTTA ATGTTTAACA 10680

TACTATTTCG CTCTCCTATT AGAAATAATA ATCATTATCA CTTAAAAATC ATAACCCTTA 10740

AAATTGTAGC TCGCAATACT TTATTTAAAT AATTTTCATT TTTCATGTAA AATTTGTGAC 10800

ATTGCAAAAA TGT 10813

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6804 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

TGATGGATTA GCAGACATTT TACGAGCGAA TGGTTTCAAA GTGTTTGGTC CAAATAAGCA 60

AGCAGCTCAA ATCGAAGGCT CAAAATTATT TGCTAAAAAG ATAATGGAAA AATATAATAT 120

TCCAACTGCT GATTATAAAG AAGTTGAGCG AAAAAAGGAT GCTTTAACAT ATATTGAAAA 180

CTGTGAATTG CCCGTTGTTG TCAAGAAAGA TGGGTTAGCT GCTGGGAAAG GCGTTATTAT 240

TGCAGATACT ATTGAAGCAG CCAGAAGTGC TATTGAGATT ATGTATGGTG ATGAAGAAGA 300

AGGTACTGTT GTATTTGAAA CGTTTTTAGA AGGTGAAGAG TTCTCGCTAA TGACATTTGT 360

TAATGGTGAT TTAGCAGTAC CTTTCGACTG TATTGCACAA GATCATAAAC GCGCATTTGA 420

TCATGATGAA GGACCAAATA CTGGTGGTAT GGGGGCTTAT TGTCCmgTAC CACATATTAG 480

TGACGATGTT TTAAmACTTA CAAATGAAAC AATTGCACAw CCCATTGCAA AGGCAATGCT 540

TAATGAAGGT TATCAATTCT TCGGTGTATT ATACATTGGT GCTATTTTAA CTAAAGATGG 600

TCCAAAAGTA ATAGAATTTA ATGCCCGTTT TGGTGATCCT GAAGCTCAAG TATTATTAAG 660

TCGCATGGAA AGTGATTTAA TGCAGCATAT TATTGATTTA GATGAAGGAA AACGTACTGA 720

ATTCAAATGG AAAAATGAAT CTATTGTAGG GGTCATGTTG GCATCAAAAG GATATCCTGA 780

TGCATATGAA AAAGGGCATA AAGTAAGTGG CTTTGATTTA AATGAAAACT ATTTTGTTAG 840

TGGATTAAAG AAGCAAGGTG ATACCTTTGT TACTTcAGGT GGTAGAGTTA TACTTGCCAT 900

CGGAAAAGGT GACAATGTAC AAGATGCACA GCGAGACGCA TACAAAAAAG TATCACAAAT 960

ACAAAGTGAC CATTTATTCT ATCGTCATGA CATTGCGAAT AAAGCACTAC AACTTAAATA 1020

AGTAAATTTA AAATACTAAG aTTAGCTATG AACGAATCTA TAACGATAGA TTTTTTCATA 1080

GCTTTTTTAG TTGTAGAGTC TAGGACATTG ATTTCTGTAC CAAATTTGTG ATTATGCATA 1140

TGTAATACAA AAGAGGCGCC ACAACATGTT TGGATGAACA AAATAACATG TTTGTGGCAC 1200

CTCTTTTGTT TAGTATGGAA TAAATGGTTT TCTTTTTCTA TACAATGAAT TTCTAATTTA 1260

GTATCTATAC AATTATGGAT AAAATTTAAC CTACACGACC AAGACGAACA TCATCTATGC 1320

CCGTGATGGG TAAGGTGATT GAACAATAAT ATGCCATAGT AATAATGGCA ATTAAAACTA 1380

TAATAAAGAT TATATCTTTA TATGAGAAAG GTACGTTGTA ATAGTAAGTA CGAGGACCAT 1440

CTCTAAATCC TTTCGACTCC ATCGCAACTG ATAATTGATG TGCCTTTCTA ATATTTTGGC 1500

TTAATAGAGG TATAATTAAA TGCTTAAATC GCTTTAACCC TCTATAATTT GCCGCGTCTA 1560

TCATCTGATA GCGCATTTTT AAAGATCTGC GAAgcTGTAt TAAAGAACTA ATCATTAAAG 1620

GTATCATACG AATGGCAGCC ATGAATGCAT AAGCAACTTT TGATTTAACC TTTAAATGTT 1680

ATGAAATAGC AATGGTTCTT AATGATACAT GTAAACCACG AACTAAACTT TCTGTTGTAA 1800

TATGGATAAA TCCGAATTTC AAAATTGTAT GGCTACCATT CCCGTATAAA ATCATGAACA 1860

GGGAAGAGAG TAATGCAAAG CCAATACTTA TAGTTATAAA AATTGCTGTA ATTTTAAACT 1920

GAGTACCATT AAACATCAAT AAGAAAACTA ACATTAAGAT AGTGATATAA AGCATAAAAT 1980

CGAAATTATG CACAAATATA ATAAAGAAAA ATAGTATAAT TCCAAGAAAT AGTTTCGTTA 2040

TAATGTTGAC ATCATCAACA AATGATTGCC GAACTTTCCA TTGCTCATAC ATTCGTATCA 2100

CCATCACAAT CTAGTAACGC ACCATCTGAA ATTTTAAGTC TTCTTGATGG ATAACGTTCA 2160

ATTATTTCAT CGTCATGTGT AaCCATGACA ATACTTTGTC CCAAATTAAT TCGCTTTTGG 2220

AAAAGTTTGA TCAACTGGAA TGTATTATGG CTATCAAGTC CAAATGTCGG TTCATCTAAA 2280

AAGATAATAT CAGCTTTAGA ACTTAGTGCG GTAgcTACGC TAAGGCGTCG TTTTTGACCA 2340

ATAGACAACT CATAAGGATG TTGATCTTTT ACATTTTGTA AATCTAAAAG TTTTAAAAGT 2400

TGTATCGTTT CATCATCACT TTGATCTTTA GAAAGGTGAT TAAAATGAAT GTTAATTTCA 2460

TCATAAACCG AATTTGTTAT AAATTGTAAT TCTGGGTTTT GATAAACTAG GTACATGTGT 2520

TTTGCTGCAT GTTTAATTTT TGTTAAACGC TGATTTTCAA AATAAACATC ACCTTGATAT 2580

TTAATCAATT GCATAATTGA TTCAAGCAAG GTTGTTTTAC CACTACCATT TGCCCCTGTA 2640

ATTGTAATCC ACTCACCTAG ACCAATTTCT AAATCTGAGA ATGAGAGCAA TGTTGATTTA 2700

CCGCGAATAA TACGTCCATT TTTAAATTGT AATAAGTGTG AGTTTGTTGT TGGAAAGTCA 2760

ACACGACTTG GTGCGAATTC CCATGCACGT GGATGCCACA CACCATATTC ACTGAGTAAA 2820

TGAACATACT TCTGTAATAT GATTTCAGGA CATTCATCGG CAATGATATT TCCGTTATAA 2880

TCCATCAAAA TGACGCGGTC GACATGATTC CAGATGTGTT TAACTTTATG TTCAACGATT 2940

ACAACCGTTT GATCTTCCCA AAGTTCAATT AGTTTAGTCC ATAAATCTTC TGTTGCTTGA 3000

ACATCTAACA TTGCTGTCGG TTCATCTAAA AACAATGTTT TTGATTGTTG AAGAATGGTT 3060

TCAACAATTG CCAATTTCTG TTTCATCCCG CCACTTAAAT CTTTGATATA CGTTTCAGGG 3120

GTAACATTTA AATTGACCAT ATTTAAAGCA TTGATAATTA ACGCATCCAT GTCTTCACGT 3180

GGTAATTGTC TATTTTCTAA AACGAATGCA AGTTCTTCGT ATACTTTTGG CATACAAAAC 3240

TGGCTATCAG GGTCTTGGAA AATAACGCCA CTTAATGGGT CAACGATTAG TTCATCATAT 3300

TTCATAGGTA ATTCAATTAA ATTAGGAACA ATACCACTTA ATACATTCAG AAGTGTACTT 3360

TTACCGCAAC CAGAAGGACC GAGTAAAAGT ACTTTTTCTT TGTCTTGAAT AGTGATATTT 3420

AAATGATCGA AAATTTTACG TTGACCACTT GGATATTTTA ATCGTAAATC ACTTACTTTT 3480

ATTTTGTTAC GCCTGTCTTA TCTAAAGCTT TTACTAAAAG GTAAGATAGG ACGCCGGCGA 3600

CTACTGCACC ACTAATTAAT CTAAATACGA TGAATAATGT TAAGTTCCAA CCTGCAACTT 3660

CATTTAAATA ACCATAGAAA TAATCTATCG GGAAAGCCGC GATTGCTGTA CAAAAACCTG 3720

CTAACATAGC TACCATAACT GAACGTGATT GATATTTAAA AATTGCAAAG ACAAGTTCAC 3780

ACGCTAAACC TTGTATAAAA GCGTAAACGA TTGTCGGAAT ATCGAAACGA CCCATAATGA 3840

TAGTTTCGCC GGCACCTGCA GCAAATTCAG CCAGTAAAGC AATACCTGGT TTTGGAATAA 3900

TTAGATAGCA GACAATCGCT GCCATGAACC AAACCCCGTT TGTTAATTGT TCGAGGTGAA 3960

GGCCTGTAGC TTGCACACCA TTGTAAACAA ACCACCATAA ATTGTAAATA ACTGCGAATA 4020

CTACTGAAAT AAGTACGGTT ACTAGTATTT CAGATAGCTT TAAACCTTTT GACATTTTTA 4080

CATCCTCCTA ATAAAAAAAC GCACAACCAT CCATAGGAAA GTTATGCGTT CACAATATAT 4140

ATTAGTAAAA CATATGTATA GTAACACTTT CCTACGCTAG TTCAAGCTAG ATCAGGTTCA 4200

AAGGGTTTGA GGGCAAGCCT CATCTCAGTA TAAAACACCC CTAGTGTGTG CGATTTATTT 4260

AATTAATTAT ACTGTAAGAC GTTTGTAAAC TTATGTCAAT AGGTTGTCTT CATGAAATTT 4320

CGTTTAATTC GATTTAAAAT TTATAATATT AGCATTGGAT TTAAATTGAA GATGTAGTAG 4380

GAATGTTAGT AATTAAAGAT ATAAAAATAT GTGACATGTA ATAATATTGA GCTGATAAAT 4440

GAAGAGGGAT ACTTATCAAT CATACCTCTT TAACAACAGT GAAGAACCCG TGCATAATGG 4500

CTTACGAATT ATAGTTTATA AGGAAGAAGA GGGATACATG CGCCGAGCAC ATGCATAAAA 4560

GCCCCTAACA ACTAAAAGTT GTAAGGAAGG AGAGGGATAC ATGCGCCGAG CACATGCATA 4620

AAATCCCCTA ACAACTAAAA GTTGTAAGGG GATTTAAATT AATTTAGTGT ATCTTGGATA 4680

TCTTGTTTTG kTTGaTTAAT ATCTTCTGTT TTTTCTTCTT TTTTATCTTT TAATTTTTCT 4740

TCAACTTCTT TAGCTTTTTC TGCTGCTTTT TTATTTTGAT TTTCATTAGA CATGATTAAT 4800

TCCTCCCAAA TTGGATAATT ATTTATATAT AAATCTTACC CGGTTGTACT TTCGTTAAAC 4860

TTTTCTAAGT CTATAGCACT ATTTATTCAT TTATCTAAAG ACAACAACAT TAGATTAATA 4920

TATAATGATT TTGAGGTGAA CATAATGTCT TTTCTTAGGA AACACGCCGA AATTATTTTT 4980

AGCTATTTAA TCGGTmwCGT TcACTCTTCA CTGGkcTCAT TATTTTAATT AACTTGCCAT 5040

TAATTAAACA ATTAAATGGT GGTAAAAAAG TTGATACACA TGTTCATAAT GTGTGGGAAT 5100

TTCTGAATGC ATTTTTCAGT GAAATTATTA AAGTAATGAG TCGATTTATA GGTAATTTCC 5160

CtATAGTTAG TGCAATTGTG ATAATTATAT TCGGTATTTT AGTTATGTTG ATTGGTCATA 5220

CATTACTTAG AACTATTAAG TATGACTATG ATATTTCTAT CTTTTTCTTA GTTATCGGTA 5280

TTTTCATTAT TCCATTTACA ATTCATATAG GATATATCGT CTATAAAGAT GAATTGAATC 5400

AGGAAAATGT AAAAAATCAT TTCATGTGGA TAATTGTGAG TTATGGTATA AGTTACTTAA 5460

TTACACAAAT TGCATTGTAT GGCAGAATTG ATGCTAATGA AATAGAGTCA ATTGATATCT 5520

TAAGTGTCAA TGCTTTCTTT ATAATTATGT GGTTACTTGG TCAAATGGCT ATTTGGAATT 5580

TCTTGTTCTT GCGCCGAGCT TTACCTTTAA CAAAGCAAGA ATTAGGTGAA GAGGAGCCAG 5640

AATTATCAAG AACAAGTAAA GGGAATGTCA CGAATCAAAC TAAAATTCAC TTGAAACAAC 5700

TCCAAGATAA GACTACAGAA TATGCACGTA AGACAAGAAG AAGTGTCGAT TTAGATAAAA 5760

TTAGAGCTAA AAGAGATAAA TTCAAAAAGA AAGTTAATGA TATTATCGAT ATTCAAGAAG 5820

ACGATATTCC TGATTGGATG AGAAAACCGA AATGGGTTAA ACCAATGTAT GTCGAACTAT 5880

TTTGTGGTGT CGTCATCTTT TTATTCACAT TTTTAGAATT TAATAATCGT AATGCATTAT 5940

TTGTATCTGG TGATTGGAAA TTATCACAGA CACAATATGT TATTGAATGG GTTACATTAT 6000

TAATTCTGTT ATTCATTATT ATCGCATATA TCGCTACAAC GTTAACTTTC CACTTGAAAG 6060

GTAAGTTTTA TTATTTACAA TTATTTATGG GGAGCATTTT ATTCTTTAAA TTGTTAACGG 6120

AATTTATAAA TATAATGATT CATGGACTAT TACTTTCAGT GTTCATTACG CCAACATTAC 6180

TATTAATGTT ATTGGCAATC ATCATTTCTT ATTCGTTACA ATTACGAGAG CGACCATAAT 6240

TAAAAGCATT ATAAAAGTAC TATCTATTAA ACATTTTGAT GTGTACGCTA TAAGTTAGAT 6300

ATATCTCTAA CTTACTTAGA TACAGGTCAA TGAAGTTTAT GGATAGTACT TTTTTTGTAA 6360

CTAGATTTGA TTGATTCAGG TGATGTGAAT TAAGTATTGA rAATTGTATA CAAAGTTTTA 6420

GTGCAAATAA AATAGTTGAA AAGTTATCCA TTTGTAAAAT CAAGAAAACT AGTAAATAGT 6480

TGAAGCGACT TATGGaATTT GCGAAACGAT ATATAGTATT TCCTTTGTAG AAATTTmACA 6540

TATATCATTC AAATTACTAA TTTGTTAAAA TCAACAGTAA GATTAGAAGT AGATGATATT 6600

GAAATTTGGC AAACAaTtTA ATCTATATAA AACTACAACG AAACACAGAA AGGAAGTTGT 6660

CAGATGAAAA TAGCAACTCT GAACAAAGGC AAAGAAACAA AATATTTTAA TGGATATCCT 6720

TTAATTGAAG AAGAGGATAT CTATTCACAA GATCATTTAA AAGAAGGAGA TATTTTTCAA 6780

ATTGTGACTG ATAAATCACA ATAT 6804

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

aaaAGAGACG CATTaAAACA AGCTATACAA ATTATCGATA AATTAACATG GGGTGTTTAG 60

TGGTGGTTAA AGAAATTTTG AGACTATTAT TCTTACTAGC GATGTATGAG CTAGGTAAGT 120

ATGTAACTGA GCAAGTATAT ATTATGATGA CGGCTAATGA TGATGTAGAG GCGCCAAGTG 180

ACTTTGAAAA AATCAGAGCT GAAGTTTCAT GGTAATAGCT ATTATCATTT TTGAATTAAT 240

TATATTAATG TGTGTAGCAA TAGCACTGGA GGTGTTGTAA ATATGTGGAT TGTCATTTCA 300

ATTGTTTTAT CTATATnTTT ATTGATCTTG TTAAGTAGCA TTTCTCATAA GATGAAAACC 360

ATAGAAGCAT TGGAGTATAT GAATGCTTAT CTTTTCAAGC AGTTAGTAAA AAATAATGGT 420

GTTGAAGGTT TAGAAGATTA TGAAAATGAA GTTGAACGAA TTAGAAAAAG ATTCAAAAGC 480

TAAAGAGAGG CGTTGGCTTC TCTGCTCTAT CyAAAATAAT GAAAGGAGCC saACATGTTA 540

GaCmAAGtCA CTCAAATAGA AACAATTAAA TATGATCGTG ATGTCTCATA TTCTTATGCT 600

GCTAGTCGTT TATCTACACA TTGGACTAAT CACAATATGG CTTGGTCTGA CTTTATGCAG 660

AAGCTAGCAC AAACAGTTAG AACTAAAGAA GATTTAACTG AGTACAATAA AATGTCTAAG 720

TCTGAACAAG CCGATATAAA AGATGTTGGC GGATTTGTCG GTGGATATTT AAAAGAAGGC 780

AAACGGCGTG CTGGTCAAGT CATGAATCGT TCAATGCTAA CACTTGATAT CGATTATGCA 840

GCCCAAGATA TGACTGACAT ATTATCTATG TTTTATGATT TTGCATATTG TTTATATTCA 900

ACACATAAGC ATAGAGAGAT AAGTCCAAGA CTGCGTTTAG TGATTCCTTT AAAACGAAAT 960

GTAAATGCAG ATGAGTATGA AGCTATTGGG CGTAAAGTCG CAGATATCGT TGGCATGGAT 1020

TACTTCGATG ATACAACTTA TCAACCACAT AGGTTAATGT ATTGGCCTTC AACTAGTAAC 1080

GATGCGGAAT TTTTCTTTAC CTATGAAGAT TTACCTTTGT TAGACCCAGA TAAAATATTA 1140

AATGAATATG TTGATTGGAC TGACACATTA GAATGGCCAA CGTCTTCAAG GGAAGAGAGT 1200

AAGACTAAAA GATTAGCAGA TAAGCAAGGC GACCCAGAAG AAAAGCCGGG AATTGTTGGT 1260

GCATTTTGTA GAGCCTATAC GATAGAAGAA GCTATAGAAA CTTTTATTCC TGATTTATAC 1320

GAAAAACATT CTACTAACCG TTATACCTAT CATGAAGGTT CAACTGCAGG TGGATTGGTG 1380

TTATACGAAA ATAACAAGTT TGCCTATTCT CATCATAATA CGGATCCCGT AAGCGGTATG 1440

CTTGTGAACA GTTTTGATTT AGTACGCATA CACTTATATG GTGCTCAAGA TGAAGAAACT 1500

AAAACAGATA CTCCGGTTAA TCGACTACCT AGTTATAAAG CAATGCAGCa AAGAGCGCAA 1560

AATGATGAGG TTGTTAAAAA GCAATTAATT AATGACAAAA TGTCTGATGC AATGCAGGaT 1620

TTCGATGAAn GAGAAAATAG CGATGATGCA TGGTCTGAGA CGTTnGAAAT TACTTCGAAA 1680

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1847 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

AAGATTAGGC ATCAAGACAG GGTCGCGATT GTTTGAAATC CCACATAGnA ATGATATTTa 60

CaTTATCAAT CCaAGTATGC GTAAATATCT TAATGTTTCA GTTGCTATTT CTAAGATTGC 120

ATTGCGTTAT ATTCCACCTG AAGATTTACA CCAATATAGT ATTGACGAAT TTTTTATGGA 180

TGTTACTGAT AGCTATCATA GATTTAGTTC TACAGTACAT GCATTTTGCG AAAGACTTAA 240

ACGTGAAATT TATGAAGAAA CAGGCATTTA TTGTACTGTG GGCATTGGTT CTAATATGTT 300

ATTAAGTAAA ATTGCTATGG ATGTTGAAGC GAacATAGTc AAAATGGTAT AGCTGAATGG 360

CGATATCaAG ATGTACCAAC GAAATTATGG CCAATTCmGC CCtTGCGAGA TTTTTGGGGT 420

ATTAATCGTC GAACAGAAGC CAAATTGAAT AAAAGAGGAA TTTTTACTAT AGGAGATTTA 480

GCGAAATATC CATATAAATT TTTAAAAAAA GAGTTCGGTA TTTTAGGTGT TGATATGCAT 540

CTACATGCGA ATGGGATAGA TCAGAGTAAA GTACGTGAAA AGCACAAGAT CAGCAATCCA 600

TCGATATGCA AAAGTCAAAT ATTAATGAGA GATTATCATT TTGATGAAGC AAAAGTAGTA 660

ATGCAAGAGT TAATTGAAGA TGTTGCTAGC AGAGTTCGAG CAAGAAAAAA AGTGGCAAGA 720

ACGATACATT TTGCCTTTGG CTATAGTGAT GAAGGCGGTG TACATAAGCA ATATACTTTG 780

AAAGATCCAA CAAACTTAGA AAAAGATATT TATAAAGTAG TAATGCATTT CGCAGATAAA 840

TTATGTAATA AACAAGCACT ATATCGTACG CTAAGTATAT CTTTGAGTCA ATTTATTAAT 900

GAGGATGAGC GACgTTAAGT CTGTTTGAAG ATGAATACCA ACGCAAACGT GACGAATGTC 960

TAGCTAAAAC GATAGACCAA TTACATTTGA AATACGGCAA AGGTATTGTG TCCAAAGCAG 1020

TATCGTTTAC AGAAGCAGGT ACAAAACACG GCAGATTAGG TTTAATGGCT GGACATAAAA 1080

TGTAATGACT ATACGGTTTA AGTAATATAT AACTGTGATT CGTATAAAAT AAGTCTCTAA 1140

AGATAAATAT TTCATATATC ACAATAGATT TTCACAATAA TATCTAAGAA TACATGGAAT 1200

TTATCAAAAG AGACTTAATA ATTATTGGAT ATAACAATCA AAATCACTCA ATGCTTGCAT 1260

ACCGCGTTCT CGGTCAGTAG GGTTTTTGAA ACTAATTTTT AAAGCACCGT ATATATCTTC 1320

GCGTACTTCT AAGATTCTTA AGTTGCTTAT AGATATGTTA TGTAAACTCA GGATATAAGT 1380

TAGTCCACCT AGTTGTTTAG CGGGTAGTGC GTCGCGATAC GATTTAGCTT GGGCAAAAAA 1500

TGATAACAAT TTTTCAGAAT CATTGCTTTC AATTAGTCTt TCTAAATCTT GAAACTGACT 1560

TTTTAGCTGT CGAATCATTT CTAAAATATA CGTTTTATTA CTCAAGGTGA TATCTTTCCA 1620

CATTTGTGCA TTACTACTAG CTATACGAGT GATATCACGA AAACCACCAG CTGCAAGTTT 1680

ATTAACTAAA TGATGTTCTT GACCGTTCTT TTGACTAACA TGAACTAAAC TAGATGCAAC 1740

GATATGAGGT AAATGACTTA CGACGCTTGT TACGTAGTCG TGTTCTTCAG CAGTAGTTAC 1800

AATAAATTTA GCAAGAGTAG GTGATAACAG TTCTTTTAAC GTGTTTG 1847

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

AACAAAAGGC ATAAGTTCGT GAATTAATGC GTATACAAGG ATAAAGCTTA TAACAGTAGT 60

AATTGTTGCT ATCAAACGAA CAACATATAT TCTATTTTCA GATAGCAATC GATTCACTAA 120

TCGATAATTT ACGTATACAA GAATTAACAA CAGCACAATA TAAACAATAA TCATATTTGG 180

CCCCATTTAA TTTTTAAATT TGTTTTCACA TCATTTTCTA CTTTATTATC ATACTAATTT 240

TAAAGGCAAA GGTGGACATC GGCAACCTCT CGTAAACTAT TTATCAAAAA TAAACGTATC 300

TCATTGTTAT GATATTTATA AATCAATTCG TTTTTATTAA AGTCTTTTTC AACAAGTTTG 360

TCACTATCTA TTAAATAATC ACGCATGCAT CCTTTTAAGA AATCATCTTT ATAACTTGGT 420

GTGTACCATT TTCCATCCTC TTCAATGACA ATGTTGCCAA TATCAAATTC AAGGACCTTG 480

CCGTCCTCTG AAGT 494

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2518 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

GTCCATATTT CCCGTCCAAC CAACTAAAAA TGGGTAAATC CCTGGATTTa AATCTACTTC 60

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GATAATTTCn AATGTAGCGA CCATCATTAC GAGATGATTT GATATAAGCA CAGTTTGGAT   180
GTTGACCAAT ACTATCGCCT TCTTCTTCGA TGATATCTAT TTTAATACCA TCATCAGCTG   240
CAATTTCTAA TGAAGATTTA ATTCGGTTAT CAAATGTTGA ATATCCCATT GCTCCACCCA   300
CAATAGCGAC ATCTGTACCA TGTCCTTGGT GTGTTTGAGC AAATGATTCA TAATAATGTA   360
TTTCAATATT TTTAGGAATA TCTCCCAATA TTGCGCGTGC TGAATTCCCA ATCTTTACTG   420
CACCAGCCGT ATGAGAACTT GAAGGGCCCA TCATAACTGG TCCGATAATA TCGAAAGCAC   480
TTTGATAATC ATAGCTCTTT GCCATAATTA AACACTCTCC TTAATATGAT TCTTTTTGCT   540
CGGCATTTTA AAGTTGATAT TCATTAAATT AAACTTATTA ATTAGTGTTC CAATAATATA   600
GGCTAAGACA ATGCTGACAA TAATCACTGT TGCGATTGTT ACAATTGATG TCACTGCATT   660
ATTAAAGCCA AACAATACGA TGGCGCCTGC AATTGGTGTT GCCATACCTT TGACACCTAT   720
TACTAGTCCG CTAAATGTCA CGATACATGC GTTGACGACC CCAATCAGTG CATTTGTACC   780
ATATAGTTGT ACTGGATATT GCGCTATTAA ATCAATTTGC GTCAATGGCT CAATACAAAC   840
TGCAAATGCT TTTGACGGTC CACCAATGTT TAATTTTCGG AATAAAATAA GGTTAACAAA   900
TGAGCTACCT GTACATGTTA GTGCTCCAAT AGCCATAGGA ACACCTGTCA GTCCTAATAA   960
ACTTGTTAAT ACCATTGAAC TTAGCGGTGT CATACCTGTA ACAGGAATCA CTAGTCCTAA  1020
AATGACCGCT AATGCATATG GATTGTTATC ACCTACCGCA GTGACAGCAC TACCTATTTG  1080
TTTTAATGTT GCTAGCACAC CAGGTGTAAT GATTGATGCA AGTCCGAAAG CAATTGCTGG  1140
TGCAAATAAG ATCACCACAA TTAAGTCCAA GCCTTCTGGA ACTTTCTTTT CAATCCATTT  1200
AATTAAAAAA GcTACGCCAT AAGCTGCGAT GAATGCTGGT AATAATTTAA AGTCATGTAA  1260
TACTAAACCA ACAATGACCG CAAATACTGG TGCAACGCCT AAGTTTAAGC ACGTTAGAAT  1320
ACCTACTGcG ATACCGCTTA AACTTCCTGC TAAATCCCCA ATATCTTGTA GAAATTTAAT  1380
ATCAAATACG CCACCAATAG CATAACTTAA GAATGCTTGT GGTAGAAATG TCGCACAAGC  1440
TGCACCGGAT AATGCTTGTA GTCCTTGTTT ACCGTACGGT GCATACTTTA AAAATAGCGT  1500
CATGATCACT AAAACCAAGA CTAATGTGCC TACACCTAAC AGAATATCCA TTTCCCAAAA  1560
ACCTCTCTCT ATGTTTATTT TATTTTCAGA CCATAAACAT CGTACACCCT TAAGAAAACG  1620
TTTTCAACTT TTATCTGTTA TCAAATCaAA TATTTAAGTG AAATATTTCA TATTTGTGAA  1680
AGATTTTTAA AATGGATTGT TTCAAAAACT ACTTATGTTG TCGTTAATAT TTACTAATTA  1740
ACTTTTTACT CTATATTTCA AACAGTTGTG TGACAGTTTT TTGATAACTT TTTTACATCT  1800
GAAAGTAAGT AATATTTCTA AAAACTTTTA ATATTTATAC ACTTTATCTT TCGAGCTATT  1860
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ACACATATAT TTGCAATAAG ATAATTAAAG TAGGATATTA TTTTTAGTTT TCTGATAGGA 1980

ATGATGATAG TCTATAGGTT GAATCTTTAC TTTTTTTTAA AGCTAAATTT ACATCAACTT 2040

AACAATGGTT GGTTATACTG AAGATGAAAA TATTTAGTAT AACTTAGTGG AGGCGATAAA 2100

GGTGCAATTG AGTCATTCCG TTAAAGTTGC AATTTCTATC TATTTAGCAC TTATCTTTAT 2160

AACGTTCACT TCTTATTTAG TCATTATTTT ATATACGAGT ATGACTGGAC ATGATGTATC 2220

ACATTTCGTG TTAGATAGTC AGCATTCTCA TCATGGATCT CTTACGCAAA AACATTTGAG 2280

TCTTCCTGAA ATCTCATTTA AATAGTTTAT CCTCTGTGTT TCAACATTCA TTTCCCATAT 2340

CGATTCATTT ATCTATCATC TAGACCACTA CATCTTAGAT GATTTTTTTA TTTTCTCATT 2400

TCACTCTTTC TTAAAAGTCG ATATAATGAA TTAAATCATT ATCATACACC GACATATTTT 2460

ATGTTGTTGG TGTTAAGTTT aAAGGGGTGA GATACTTGGC GAATaATCaT TCAGCTTT 2518

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 790 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

ATACTACTGG ACCGTCnACC AATTGACAAA ACCTGAAAAC TGGATTTTTA TTGCAGGATT 60

ACATCGAACC TGGAAGAACA ATCCCCAGGA GTTGATGATA TTCGAGATAT GGCATACAAT 120

CAAGGTAGTT TAGATAAGAC AATTTATGAA ATTTCTAAAC GCACAGTACT ATTTTTAATA 180

CAGAAAGATA TTACGGTATA TAATAAGACG ATTGACTGTT TAAATTATTA TAACTATAGT 240

GACGAAAGAA TAAAGGATGA TTAAATGAAT TCACAAGAAT TATTAGCAAT TGCTGTGGAT 300

GCAATTGACA ATACCCCAGG CGAAGATACG ATTTCTTTAG AAATGAAAGG TATCAGCGAT 360

ATGACAGATT ATTTTGTTGT AACGCACGGA AATAATGAAC GACAAGTTCA AGCGATTGCT 420

AGAGCGGTGA AAGAAGTAGC CAATGAACAA AATATAGAAG TAAAACGTAT GGAAGGATAC 480

AATGAAGCGC GTTGGATATT AATTGACTTA GCTGATGTTG TGGTACATGT TTTCCATAAA 540

GACGAAAGAA ATTATTATAA TATTGAAAAG TTATATCAAG ATGCACCATT AGAATCATAT 600

AGTCAGGTTG CGTATTAATT ATGTCGCAAT ATGCAGAAAT GAGCCTAGTG TACGATCAAT 660

TGACTCAAGA TCAACCATAT GAAAAATGGT TTGAAATTGT AAAAAATCAC TGCAAAGATG 720

AATCAAATAT TTTAGATATT GGATGCGGTA CTGGTAGTTa ACAGTTCAAT TAGAAGCTTT 780

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1823 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

ATAGATGAAG GTGCAAATAT TGAAaTAGGT TATTTACCTG GACGCTTGAA ATGGTTAGTT 60

GCTGATTTAT TAACTAAACA AGGATTAAAA GTAGTTAACG ACGATATGAC AGGAAGAACG 120

TTAAAAGATC GTAAATTATT AACAGGTGAC AGTCCTTTAG CTTCAAATGA GTTAGGAAAA 180

TTAGCAGTTA ATGAAATGTT AAATGCAATA CAAAATAAAT AATTAAATAT TAATTAGAGG 240

AGCCTCATAT GTAAATGTAT GAGGGCTCTT TTTTTTGGCA AAATTTAAGT GATACTTGTA 300

AAATAGAACC TATTATGAGT ATGATTTAAG AAAACGCTTG CAAAACTAAT AACCGCAACT 360

AGCGATATGG AGGAAACATG ATGTCTTATA GCATTGGAAT TGATTATGGA ACTGCTTCAG 420

GCCGTGTGTT TTTAATTAAT ACAACTAACG GTCAAGTAGT ATCAAAATTT GTGAAACCAT 480

ATACACATGG TGTCATTGAG AGTGAATTAA ATGGTTTGAA AATACCACAT ACATATGCAC 540

TTCAAAATAG TAATGATTAT tTAGAAATTA TGGAAGAAGG AATATCATAT ATAGTACGTG 600

AATCAAAAAT AGATCCAGAC AATATAGTAG GTATTGGTAT AGACTTTACT TCATCTACTA 660

TTATTTTTAC TGACGAAAAC CTTAACCCGG TACATAACTT AAAACAATTT AAAAACAATC 720

CACATGCGTA TGTGAAACTT TGGAAACATC ATGGTGCATA TAAAGAGGCA GAGAAATTAT 780

ATCAAACTGC TATTGAAAAT AATAATAAGT GGTTAGGCCA TTATGGATAT AATGTTAGTA 840

GTGAATGGAT GATTCCCAAA ATAATGGAGG TCATGAATCG AGCACCAGAA ATTATGGAAA 900

AAACGGCTTA TATTATGGAA GCGGGCGATT GGATTGTAAA TAAATTAACT AATAAAAATG 960

TACGCTCGAA TTGTGGATTA GGTTTCAAAG CATTTTGGGA AGAAGAAACA GGGTTTCATT 1020

ATGATTTATT TGATAAAATA GACCCCAAAT TATCAAAAGT AATTCAAGAT AAAGTATCTG 1080

CACCGGTTGT TAATATTGGT GAAGCAGTAG GGAAACTGGA TGATAAAATG GCACAGAAAT 1140

TAGGATTATC AAAAGAAACT ATGGTAAGTC CTTTTATTAT TGATGCCCAT GCTAGTTTAT 1200

TAGGTATTGG GTCTGAAAAA GATAAAGAAA TGACTATGGT GATGGGAACA AGCACATGCC 1260

ATCTTATGTT AAATGAAAAG CAACATCAAG TGCCAGGTAT ATCAGGTTCT GTAAAAGGAG 1320

CAATTATTCC AGAATTATTT GCTTATGAAG CGGGGCAATC AGCAGTAGGT GATTTGTTTG 1380

CTGTATTTGA ATTAATGAAT GAAAAGATAA AACATCAAAT GCCAGGTGAA AGTGGGCTCA 1500

TTGCTCTTGA TTGGCATAAT GGAAATCGAA GTGTATTAAG TGATAGCAAT TTAACAGGTT 1560

GTATCTTTGG ATTAACTTTA CAAACTAAGC ATGAGGaTAT TTATAGAGCm TATTTaGaAG 1620

CTACaGCATT TGGTACtAAG ATGATTATGC mACAGTATCA AGATTGGCAT ATGGaAGTAG 1680

aAAAGGtATT TGCaTGTGGc gGTAtACCtA AAAAGAATGC TGTTATGATG GATATCTATG 1740

CGAATGTACT GAATAAAAAA CTAATTGTTA TGGATAGTGA GTATGCACCA GCAATAGGCG 1800

CAGCAATATT AGGTGCAGTC AGT 1823

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1600 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

ACGATCATCT GCATCAGCGA ATTCCGATGc AaTTcATATG tCCtAATAAC AAAAGAATAG 60

GTTTTaAAAG ATATGCATAC CGTAATGaTA GATATAGTTT TAAACGTGAC TTCAAGCTAT 120

ATGaATGTGA TGACTGTTCA TCATGTTCTT TGAGACATCA ATGCATGAAG CCAAATTCGA 180

AATCCAATAA GAAAATTATG AAGAATTATA ATTGGGAATA CTTTAAAGCC CAAATTAATC 240

AAAAGCTTTC TGAACCAGAA ACGAAAAAAT CTATAGTCAA AGAAAAATTG ATGTAGAGCC 300

TGTTTTTGGA TTTATGAAGG CTATTTTGGG TtTCACTCGA ATGTCAGTTC GGGAATAAAT 360

AAAGTTAAAC GAGAGCTAGG TTTTGTATTA ATGGCACTTA ATATAAGGAA AATAgcaGCT 420

CAACGAGCTG TACATTATAA AATACATATC AAAAAAGCTG ATTTCTATCA AATAAATAAT 480

AGAAATCAGC TTTTTTACAT TGCCTAAGAA CTTTAAGGAA CTTAATGTCC CAAGCTCTTT 540

TTTGTTATAT CTAATTCGTA ATTTATGATT GTTTATTCGG TCCTTTGATG TTCACTAAAT 600

GTGACTTTAA ATCTTGTTCT AATTGTTGTA ATTCTTTTTC AGCTAATTGT CGTTCTTCGC 660

GACCGTGTTG TTGAATAATT AATGTTTCTT CAATTGTCTC AATAATGTTA CGCTGTGTAC 720

GTTTCAATGT ATCAAGATCA ACAATGCCAC GCTCATTTTC TGTTGCAGTT TCAATCGCAT 780

TTTGTTTCAA CATTTCAGCA TTTGCTGTTA ATAAATCATT AGTTGTATCA GTGACAGCTC 840

GTTGTGCAGC AACTGCATTA CGCTGTCTCA TTAATGTAAG CGCAATGGCC ATTTGATTTT 900

TCCATAGTGG AATACTTGTC AAAATTGAAC TTTGTATCTT CTCGGCAAGT GCTTGATTAA 960

AGTCATATAT GCGTTTATCT AGTCTATCTA TAAATTGCTG CATATCTGCA ACTTGTTGAA 1080

TATCCATTTG ATTAGTGGAt TgtGCGCTTG CTGTTGCAAT TGTGGTAGCT TTTCATTTTC 1140

TAATTGCAAC TTTTTTTGcT GTGCAGCAAT GATATGCAAT GATAAGTCAT CAAAGTATTG 1200

TTTGTTTTTA TCATATAGCG TATCTAATAA TTCAATATCT CTTGTTAAAT GTGTTTGATG 1260

TTTCTGCAGT TGAATCGTTA TGCGATCGAC TTGAGCACTA ACTGATTGCA TTCTTGAAAA 1320

GATTTCATTG ATAGACGACT TTGCTCTGCT AAAAATTCTT TTTAACATAG ATGGTTTATC 1380

AGTATTTAAC TCATTTGGAT TAACTGACTT TAGTTTTGAC ATTAGATCTG ACAAAGTATC 1440

TCCAATAGGA CCAACATCTT TACTTTGTAC TTCATCCAAC ATTTGATGTG AAAATTGAGA 1500

CATTTGTTTC TGkAAATCAG AACCAAACGC TAATAAACCT TCATTGTCTA AAGGGTTAAT 1560

TTGTTTACTG ATTGTGTCTA CCTGTTTTTG TTGTTCAATT 1600

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

ATGTTGATAA TGGTAGCTTC TACAAGAATA AAGACCAACA AGTTGGTGCA ACAATTCTTG 60

aTAGTAAAAC TGGTGGTTTA GTTGCTATAT CTGGTGGACG TGATTTCAAA GACGTCGTTA 120

ACAGAAACCA AGCAACAGAT CCTCACCCTA CTGGTTCATC TTTAAAACCT TTCTTAGCGT 180

ATGGACCTGC CATTGAAAAT ATGAAATGGG CAACAAACCA TGCGATTCAA GATGAATCTT 240

CATATCAAGT TGATGGTTCT ACATTTAGAA ACTATGATAC GAAGAGTCAC GGTACTGTAT 300

CTATTTATGA TGCTTTACGA CAAAGTTTCA ATATCCCAGC TTTAAAAGCT TGGCAATCAG 360

TTAAGCAAAA TGCTGGTAAT GATGCACCTA AGAAATTCGC TGCCAAACTT GGCTTAAACT 420

ACGAAGGCGA TATTGGTCCA TCTGAAGTAC TTGGTGGTTC TGCTTCAGAA TTCTCACCAA 480

CACAATTAGC ATCAGCATTT GCTGCAATCG CTAACGGTGG TACTTATAAC AACGCGCATT 540

CAATTCAAAA AGTAGTTACT CGTGATGGTG AAACAATCGA ATACGATCAT ACTAGCCATA 600

AAGCGATGAG TGATTACACT GCATACATGT TAGCTGAGAT GCTAAAAGGT ACATTTAAAC 660

CATATGGTTC TGCATATGGC CATGGTGTAT CTGGAGTAAA TATGGGTGCT AAGACAGGTA 720

CTGGTACTTA CGGTGCTGAA ACTTATTCAC AATATAATTT ACCTGATAAT GCAGCGAAAG 780

AAGTTAAACA ATATGGTGAA AACTCATTTG TrGGACATAG CCAACAAGAA TATCCACAGT 900

TCTTATATGA AAATGTGATG TCAAAAATTT CATCTAGAGA TGGCGAAGAC TTTAAACGTC 960

CTAGCTCAGT AAGTGGTAGT ATCCCATCAA TCAATGTTTC TGGTAGTCAA GATAACAACA 1020

CTACAAATCG TAGTACACAC GGTGGTAGTG ACACATCAGC AAACAGCAGT GGTACTGCAC 1080

AATCAAATAA CAATACTAGA TCTCAACAAT CTAGAAACAG CGGTGGATTA ACAGGTATAT 1140

TCAACTAATC CACTCAACAT AAAATCCTCA GTTATACCAT ATTTATGGTG TAGCCGAGGA 1200

TTTTnTTAGG TTCTTCATCT TTTATGG 1227

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1953 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

CCATATGGtG CAACATTCTT CGTATTTAGT GATTATTTAA AACCAGCGTT ACGTTTATCA 60

TCAATTATGG GATTAAATgC aACGTTCATC TTCACACATG AyTCaATTGC AGTAGGTGAA 120

GATGGTCCTA CTCATGAACC AATTGAGCAA TTAGCTGGAT TAAGAGCCAT TCCAAATATG 180

AATGTTATCC GTCCTGCTGA TGGTAATGAA ACAAGAGTAG CATGGGAAGT TGCCTTAGAA 240

TCTGAATCTA CACCTACTTC ATTAGTATTG ACACGTCAAA ACTTACCGGT ATTAGATGTA 300

CCAGAAGATG TAGTTGAAGA AGGCGTTCGA AAAGGTGCCT ATACAGTTTA TGGCTCTGAA 360

GAGACACCAG AATTCCTATT ATTAGCTTCA GGTTCAGAAG TTAGTCTTGC AGTTGAAGCT 420

GCTAAAGATC TTGAAAAACA AGGTAAATCA GTACGTGTTG TTTCAATGCC TAACTGGAAT 480

GCATTTGAAC AACAATCTGA AGAATATAAA GAATCAGTTA TTCCATCAAG CGTAACAAAA 540

CGTGTTGCGA TTGAAATGGC TTCACCGCTT GGATGGCATA AATATGTAGG TACTGCAGGT 600

AAAGTTATTG CTATTGACGG CTTTGGCGCA AGTGCACCTG GCGATTTAGT AGTTGAAAAA 660

TATGGATTTA CAAAAGAAAA TATCTTAAAC CAAGTTATGA GCTTATAAGA ATAATTTATA 720

AAGCGAGTAT GTTTAGAAGT CTAGGATGCA TAATCTTAGG CTTCTTTTAA AGTGTTGAAA 780

TTTAGAGTAT AGCACTTAAA CTACATCATA AGTGATAAGT TATGAAAGTA TACTATTTCA 840

GATTAATCTT TAAAAGCTCT GTTATAACAG CATGATTTTT GATATTATTT TTAGTATCGA 900

TATTAAAATA CTTGAATAAA CTAGTTCTTG AAATAATGTG ATGAATTTAG TAAAATTCAG 960

TGCATTAATT TTAGGTTTAA TTGGAGGTTT CCTTTTAGCT AGAAAATATA TGATGGACTA 1080

CTTGAAGAAA AACCCACCAA TCAACGAAGA AATGCTTCGT ATGATGATGA TGCAAATGGG 1140

TCAAAAACCT TCTCAGAAGA AAATTAATCA AATGATGACG ATGATGAATA AAAATATGGA 1200

TCAAAATATG AAGAGTGCGA AAAAGTAAAT TCGCAATTGA TAGAGGCTAT TTTCCAGATA 1260

TGGAAATGGC CTCTTTTTAT AATCAAATTA ATAAGAATAA ATATGTTTAT TAAAATTAAA 1320

GTTAACAAAA TGACGAATAG ACTGAGAAAT GCTATAATTC ATTTTGTATG ATTTACAGAG 1380

AGTTTATTTA ACGAGAAGGT GTCyGCGTGC TCTATTTAAT ATTTTCAATC ATTGTAGCTT 1440

TATTTATGGG AACTATAGTT ATAGTTATTC GTATGAAAGC TCAAAATTAT CCGGTAAAkG 1500

AGAAAAAAAT AGTTTTGCCa CCgTTTTTTA tGGCgACCGG TGCATTGATG TACGTCGTTC 1560

CaTATTTTAG GCTAACAGGA TCGGAAATGC TAGAAGCCTT TATAATTGGT TTGCTTTTTT 1620

CtACAGTTCT AATTTGGACT TCTCGATTTG AAGTCAAAGG TACAGAAATT TATATGAAAC 1680

GATCTAAAGC ATTTCCAGTT ATTTTGATTT CATTACTTAT CATTCGTACT GTGATGAAAA 1740

TATTCATTAG TAATGAAATA GATCCTGGAG AATTAGGCGG CATGTTCTTT TTATTAGCAT 1800

TCTGTATGAT TGTTCCTTGG AGAGCAGCAA TGCTATATAA ATACAAAAAA CTAAAGAAAA 1860

CATTAATCAA TTAATTACTT TTaAAACCAC TTGTGATCGA CTTCTAAATC AGTCAATGAG 1920

TGGGTTTAAT nTTACTTGGA AAAGGnGGAA AGG 1953

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3787 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

ACATTTGATC AAnTTATCGA CATTAAAGAT GAATTCAnTT GATCGTnTCA ATGATTATCC 60

TGTTGAAGTA GCACGTTTGC TTGATATAGT GGAmATaAAA GTACACGCAT TACATTCAGG 120

TATCcACGTT GATTAAAGAT AAAGGGAAAA TAATTGATAT TCATTTATCT GTAAAAGCCA 180

CTGAAAATAT TGATGGCGAA GTGCTGTTCA AAGCAACACA ACCTTTAGGT AGAACAATGA 240

AGGTTGGTGT TCAAAATAAT GCAATGrCAA TTACTTTAAC GAAACAAAAT CAATGGCTTG 300

ATAGTTTGAA GTTTTTAGTT AAGTGCATTG AAGAAAGTAT GAGAATCAGT GATGAAGCAT 360

AAAGAAGCAT TTAATGGCGT TGTCGTGTTA ACTGCTGCAT TAATTGTCAT TAAAATTCTG 420

CAACAAGTGT ATCCAATTGT AGCATTAGGA ATGATATTAT CGATGAATGC CATTCCTAGT 540

GCAATTACAC AAAATATAGG GAAGTATCAT AGTGACGAAG CATATGCAAA AGCAGTCGCT 600

TATATACAAT TAGTTGGTAT ATTATTATTT ATTGCTATTT TTGTGTTTGC GAACAATATT 660

GCACATATGA TGGGTGATGG CCATTTAACA CCAATGATTC AAGCTGCAAG TTTAAGCTTT 720

ATATTTATAG GTATGCTTGG CGTGTTAAGA GGTTATTATC AATCTGCAAA TAATATGACA 780

GTTCCGGCTA TTTCCCAGGT TATAGAACAA GTTATACGAG TAGGTATTAT CATTGTTACT 840

ATTGTTATTT TTGTAGACAG AGGTTGGACG ATATATGAAG CGGGAACAAT TGCTATTTTA 900

GCATCAACGA TAGGTTTTTT AGGTTCTTCA ATTTATTTAG TAGCGCACCG ACCTTTTAAG 960

TTTAAAATGG TAAATAACAC TGCAAAGATC GTTTGGAAAC AGTTCGCACT TTCGGTTTTG 1020

ATTTTCGCTA TCAGTCAATT AATCGTAATT TTATGGCAAG TGATTGATAG TGTTACTATT 1080

ATTAAGTCAC TTCAAGCGAT ACGCGTGCCA TTCGATGTTG CCATAACTGA AAAAGGAGTC 1140

TATGACCGTG GTGCATCATT TATTCAGATG GGATTGATTG TAACTACAAC ATTTAGTTTT 1200

GCGCTCATTC CTCTGTTAAG TGACGCAATC AAAATGAATA ATCAGGTACT TATGAATCGT 1260

TATGCAAATG CGTCATTAAA GATTACGATT TTAATAAGTA CAGCAGCGGG AATAGGATTA 1320

ATTAATTTAT TGCCTTTAAT GAACGGTGTG TTTTTTAAGA CGAATGATTT AACCTTAACG 1380

TTAAGTGTTT ATATGATTAC GGTCATTTGT GTATCGTTAA TTATGATGGA TATGGCATTA 1440

TTACAAGCGC AACATGCTGT GAGACCTATT TTTGTTGGTA TGACGGCAGG ATTGGTTATT 1500

AAATTTATAC TTAATATCAT TTTGATTCGT TTAAGTGGCA TTATTGGTGC GAGCATTAGT 1560

ACTGTTGTAT CATTAATTAT ATTCGGTACG ATTATCCATA TTGCTGTCAC GAGAAAATAC 1620

CACTTATATG CGATGAGACG ATTTTTTATC AATGTTGTTT TAGGTATGGT ATTTATGTCG 1680

ATTGTTGTTC AATGCGTGTT AAACATAGTG ACAACACACG GTAGAATCAC TGGACTCATT 1740

GAATTATTAT GTGCAGCAGT ATTAGGTATC ATTGCATTGT TTTTCTATAT TTTTAGATTT 1800

AATGTTTTGA CATATAAAGA GTTAACTTAT TTACCATTTG GTTCAAAGTT GTATCAAATT 1860

AAGAAAGGAA GACGTTGATG GCACATACCA TTACGATTGT TGGCTTAGGA AACTATGGCA 1920

TTGATGATTT GCCGCTAGGG ATATATAAAT TTTTAAAGAC ACAAGATAAA GTTTATGCAA 1980

GAACGTTAGA TCATCCAGTT ATAGAATCAT TGCAAGATGA ATTAACATTT CAGAGTTTTG 2040

ACCATGTTTA TGAAGCACAT AACCAATTTG AAGATGTCTA TATTGATATT GTGGCGCAAT 2100

TGGTTGAAGC TGCTAATGAA AAAGATATTG TCTATGCGGT TCCGGGTCAT CCTAGAGTTG 2160

CTGAGACAAC TACAGTGAAA TTACTGGCTT TAGCAAAGGA CAATACTGAT ATAGATGTGA 2220

ATGATGGCTT CACACTGTTA GATGCGACAT CATTACAAGA AGTAACACTT AATGTTAGAA 2340

CGCATACATT GATTACGCAA GTTTATAGTG CAATGGTTGC TGCTAATTTG AAAATCACTT 2400

TAATGGAACG ATATCCTGAT GATTACCCTG TTCAAATTGT CACTGGTGCA CGAAGCGATG 2460

GTGCGGATAA CGTTGTGACA TGCCCATTAT ATGAATTGGA TCATGATGAA AATGCATTCA 2520

ATAATTTGAC GAGTGTATTC GTACCAAAAA TCATAACATC GACATATTTG TATCATGACT 2580

TTGATTTTGC AACGGAAGTG ATTGATACTT TAGTTGATGA AGATAAAGGT TGTCCATGGG 2640

ATAAAGTGCA AACGCaTGmA AcgCTAAAGC GTTATTTACT TGAAGAAACA TTTGAATTGT 2700

TCGAAGCTAT TGACAATGAA GATGATTGGC ATATGATTGA AGAACTAGGA GATATTTTAT 2760

TACAAGTGTT ATTGCATACT AGTATTGGTA AAAAAGAAGG GTATATCGAC ATTAAAGAAG 2820

TGATTACAAG TCTTAATGCT AAAATGATTC GTAGACACCC ACACATATTT GGTGATGCCA 2880

ATGCTGAAAC TATCGATGAC TTAAAAGAAA TTTGGTCTAA GGCGAAAGAT GCTGAAGGTA 2940

AACAGCCAAG AGTTAAATTT GAAAAAGTAT TTGCAGAGCA TTTTTTAAAT TTATATGAGA 3000

AGACGAAGGA TAAGTCATTT GATGAGGCCG CGTTAAAGCA GTGGCTAGAA AAAGGGGAGA 3060

GTAATACATG AGATTAGATA AATATTTAAA AGTATCACGG TTAATAAAGC GACGTACGCT 3120

AGCAAAAGAA GTAAGTGATC AAGGTAGAAT TACAATAAAT GGTAATGTTG CTAAAGCTGG 3180

ATCGGATGTT AAAGTTGAAG ATGTGCTGAC GATTCGCTTT GGTCAAAAAT TAGTAACAGT 3240

TAAAGTAACT GCATTAAATG AACATGCATC TAAAGATAAC GCGAAGGGTA TGTATGAAAT 3300

CATTGAAGAG CGTCGACTTG AAGAAGCGTA AATTGGAGGT GACAAGCAAT GAAAAATAAA 3360

GTAGAACATA TAGAAAATCA GTACACGTCG CAAGAGAACA AGAAAAAACA ACGTCAAAAA 3420

ATGAAAATGC GTGTTGTTCg TAGGCGTATT ACAGTATTTG cGGGCGTATT aCTTGCGATA 3480

ATTGTTGTTT TATCaATCTT GCTTGTTGTC CAAAAACATC GCAATGATAT TGATGCACAG 3540

GAGCGAAAAG CGAAAGAAGC ACAGTTTCAA AAGCAACAAA ATGAAGAAAT TGCGTTAAAA 3600

GAAAAGTTGA ATAATCTGAA TGACAAAGAT TACATTGAAA AAATTGCGCG TGATGATTAT 3660

TACTTAAGCA ACAAAGGTGA AGTGATTTTT AGGTTGCCAG AAGACAAAGA TTCGTCTAGC 3720

TCAAAATCTT CGAAAAAATA AATCCAAATT GATTCAAAAT TATCCGAGTA TAGACATTGT 3780

GAAAAAA 3787

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1644 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

TAAACCATTT CAAACTGAGG AACGCnAAGA CGGsACgTTT CCAGATTTAG AAGTATTTAA 60

AAATGAATGT GATTTAAGCT ATGACATAAC GTCACTTTAT ACTTTTAAGC AACCTGTATC 120

ACCACACCTT GCATTTAAAA TGACAGATCA AATTTTTCTA AATAAGCAGC GTGTATTAGA 180

TAAGGTAAAA GTTTTAGATA AGGAATTTGA TTTTATCTTA ATTGAGGGTG CTGGGGGAAT 240

TGCCGTACCA ATATATGAAG GTACAGATGA TTTCTACATG ACTAAAGATC TAATCAATGA 300

TTGTGCAGAT TGTGTCATCA GTGTGTTGCC ATCAAAATTA GGTGCTATTA GCGATGCCAT 360

TGTTCACCAA GATTATGTTA ATCAGAATGT ATCGGCGAGT AATTTTTTAA TAATGAATCG 420

CTATACAGAC AGCTATATTG AAAAAGACAA TCAAATGACG ATTGGAAAAT TAACAAATAA 480

AACAGTCTAT ACATTTGAAG AACATGCCAC GTATGAAAAT TTCTCAGAAG CATTTTTAAA 540

ACAATTAATA GGAGTTAAAA ATGAATTACA CACAACAACT TAAACAAAAA GACTCAGAAT 600

ATGTTTGGCA TCCATTTACA CAAATGGGTG TATATAGCAA AGAAGAAGCA ATCATCATTG 660

AAAAAGGAAA GGGTAGTTAC CTTTACGATA CGAATGGCaA TAAATATTTA GATGGTTATG 720

CATCGTTGTG GGTCAATGTG CATGGTCATA ATAACAAATA CTTnAATAAG GTAATTAAAA 780

AGCAACTCAA TAAAATTGCC CATTCTACGC TGCTAGGATC ATCAAATATT CCGTCAATAG 840

AACTTGCGGA AAAATTAATC GAAATCACGC CAAGTAATCT AAGAAAAGTA TTTTATTCTG 900

ATACAGGCAG TGCGTCTGTT GAAATCGCAA TAAAGATGGC ATATCAGTAT TGGAAAAATA 960

TTGATAGAGA AAAATATGCC AAGAAAAACA AGTTTATAAC GCTAAATCAC GGTTATCATG 1020

GGGATACGAT TGGTGCGGTA AGTGTTGGTG GTATCAAGAC CTTTCATAAA ATATTTAAAG 1080

ACTTAATATT TGAGAATATT CAAGTAGAAA GCCCATCTTT CTATCGCAGT AATTACGATA 1140

CTGAAAATGA AATGATGACA GCTATTTTAA CGAATATAGA GCAAATTCTA ATTGAAAGAA 1200

ATGATGAAAT CGCAGGGTTT ATATTGGAAC CGTTGATTCA AGGTGCGACA GGCTTGTTTG 1260

TTCATCCTAA AGGCTTTTTG AAAGAAGTCG AGAAATTGTG CAAAAAATAC GATGTCTTAT 1320

TAATTTGTGA TGAGGTAGCA GTTGGTTTTG GGAGAACTGG AAAGATGTTT GCATGCAATC 1380

ATGAAGATGT TCAACCGGAT ATTATGTGTT TAGGTAAGGC GATTACTGGT GGCTACTTAC 1440

CACTTGCAGC TACATTGACA TCTAAAAAAA TATACAATGC ATTTTTAAGT GATTCGCATG 1500

GTGTGAATAC CTTTTTCCAT GGTCaTACAT ACaCCGGAAA TCAAATcGTT TGTaCGGTTG 1560

cATTaGaAAA TATaAGaCTT TATGaAAAAC GTaAGTtnAT TGTgCACATa TTGaAACGaC 1620

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

ATGATTTTtA aAAATCATTA AGTTAAGGTr GATACACATC TTGTCATATG ATCAAATGGT 60

TTCGCCAAAA ATCAATAATC AGACAACAAA ATGTGCGAAC TCGATATTTT ACACGACTCT 120

CTTTACCAAT TCTGCCCCGA ATTACACTTA AAACGACTCA ACAGCTTAAC GTTGGCTTGC 180

CACGCmTTAC TTGACTGTAA AACTCTCACT CTTACCGAAC TTGGCCGTAA CCTGCCAACC 240

AAAGCGAGAA CAAAACATAA CATCAAACGA ATCGACCGAT TGTTAGGTAA TCGTCACCTC 300

CACAAAGAGC GACTCGCTGT ATACCGTTGG CATGCTAGCT TTATCTGTTC GGGCAATACG 360

aTGCCCATTG TACTTGTTGA CTGGTCTGat ATCcGTGAGC AAAAACGGCT TATGGTnTTG 420

CGAGCTTCAG T 431

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2006 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

TTTnTATAAC GTATTATAAA TCGTTAAAAA TTTTGGTTGT GTTTGCGTCA CGTAGACAAC 60

CTCCATAAAG TTACTTAATC ACTCTCATCA TACAATAATT TTTACTCAAA TTGGAAnAAT 120

TATAAAAATT AAATATAGAT AGGCTTTGAA AATTAGTTTT ATACAAGGTT AGTAGCTGTA 180

ACTGTAAAAT GTTCTTAATA TTGTCAAAAT GTAATGCTTG AAAGCGCTTT TAAAaAATAT 240

TATTATATAC ATGGTTAGAC AAATAGACAA ATCACTATAC AAATATTGGG AGGAATATTT 300

TATGAAATCA ACACCACACA TTAAACCAAT GAATGACGTC GAAATTGCAG AAACGGTTCT 360

ATTGCCAGGA GATCCGTTAA GAGCTAAGTT CATTGCAGAA ACTTATTTGG ATGATGTGGA 420

ACAGTTCAAT ACAGTGCGAA ACATGTTTGG TTTTACCGGA ACATATAAAG GTAAAAAAGT 480

TTCTGTCATG GGTTCAGGTA TGkGTATGCC ATCTATTGGC ATTTACTCTT ATGAATTAAT 540

CATTGATTTA TATGATGTGA TTaTTkCACA AGGTGCCTCT ACTGATTCAA ATTACGTTCA 660

ACAATATCAA TTACCAGGTC ATTTTGCGCC AATTGCTTCT TATCAATTAT TAGAAAAAGC 720

AGTTGAAACA GCACGTGACA AAGGTGTACG TCATCATGTA GGTAATGTGT TATCAAGTGA 780

TATTTTCTAT AACGCGGATA CAACAGCGAG TGAACGTTGG ATGCGTATGG GTATTTTAGG 840

TGTAGAAATG GAATCaGCTG CaTTATACAT GaATGCAaTT TACGCTGGTG TCGAAGCATT 900

AGGTGTGTTC ACAGTGAGCG ATCATTTAAT TCATGAAACG TCAACAAcAC CTGAGGAAAG 960

GGAACGTGCA TTTaCAGATA TGATTGAAAT TGCACTGTCA TTGGTGTAGA TGATTATGAA 1020

TGTTGAATAT TCTAAAATAA AGAAAGCAGT ACCTATTTTA TTATTCTTAT TTGTATTCAG 1080

TTTGGTTATA GACAACTCAT TTAAATTGAT TTCTGTAGCC ATTGCTGATG ACTTAAACAT 1140

ATCTGTAACG ACAGTAAGTT GGCAAGCGAC ATTAGCCGGT TTAGTAATTG GTATTGGCGC 1200

TGTAGTATAC GCTTCATTAT CTGATGCCAT TAGTATACGC ACACTATTTA TTTATGGCGT 1260

GATATTAATC ATTATCGGAT CAATTATTGG TTACATTTTC CAACATCAAT TCCCATTACT 1320

TTTAGTTGGA CGTATTATTC AAACTGCCGG TTTAGCTGCT GCAGAGACAT TATATGTGAT 1380

ATATGTTGCA AAGTATCTTT CTAAAGAGGA CCAGAAGACT TACCTTGGCT TAAGTACGAG 1440

CAGTTATTCC TTGTCATTAG TTATCGGTAC ATTATCAGGT GGATTTATTT CTACGTATTT 1500

ACACTGGACA AATATGTTTT TAATTGCATT AATCGTAGTA TTTACGTTGC CATTCCTATT 1560

TAAATTATTA CCAAAAGAAA ATAATACGAA TAAAGCTCAT TTAGATTTTG TTGGCTTAAT 1620

TCTAGTGGCA ACTATTGCTA CAACAGTCAT GCTGTTTATT ACGAACTTTA ATTGGTTATA 1680

TATGATTGGT GCCTTAATTG CGATTATCGT TTTTGCGCTA TATATTAAAA ATGCGCAACG 1740

TCCATTAGTA AATAAATCAT TTTTCCAAAA TAAACGTTAT GCTTCATTTT TATTTATAGT 1800

ATTTGTAATG TATGCTATCC AATTGGGTTA TATTTTTACG TTCCCATTCA TAATGGAGCA 1860

AATTTATCAT CTGcAACTAG ACACAACATC ACTGTTATTA GTACCGGGgT TaTATAGTAG 1920

CAGTCATTGT TGGtGgCACT AAGTGGgTtA AAATCGGgCG rAATATCTGG AATTCCAAAA 1980

CCAAGCGGAT TATCACAGCC AATTAA 2006

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4858 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TGGGGAAAAA AAGACCCAGC AGTATTAGAA GAATCGTTAA ATATTTCTAT TGAAGAAATG 60

AATCGTATCA TAAAATTAGT CGAAGAATTA CTTGAATTGA CTAAAGGAGA TGTAAATGAC 120

ATTTCTTCTG AAGCACAGAC CGTGCATATT AATGATGAAA TTCGCTCGCG AATACACTCA 180

TTAAAACAAT TGCATCCTGA TTATCAATTT GATACGGATC TGACATCTAA AAATCTAGAA 240

ATTAAAATGA AACCTCATCA ATTCGAACAA TTATTTTTAA TCTTTATTGA TAATGCAATC 300

AAATATGATG TGAAGAATAA GAAAATTAAA GTTAAGACAA GGTTAAAAAA TAAGCAAAAA 360

ATAATTGAAA TTACAGATCA TGGAATTGGT ATTCCAGAGG AAGATCAAGA TTTCATTTTT 420

GATCGCTTTT ATCgAGTGGA TAAATCTCGT TCAAGAAGTC AAGGCGGTAA TGGACTCGGA 480

TTATCTATTG CTCAAAAAAT CATTCAATTA AACGGAGGAT CGATTAAAAT TAAAAGTGAA 540

ATTAACAAAG GAACAACGTT TAAAATCATA TTTTAATCAT GACTGAGACG TCAATCAAAG 600

TCATAGGATC AATTTTTTAA GTACACATTA GCTGTGACTA ATGTATAAGA ACAACTATAA 660

AACAAATAAA CAGTGGTTCT TTATCATTTC TGTTGTACTC CCAAAATTTA CAATAAAATA 720

CATCTATAAA CCTAGAAGAA TCAACGCTTT TGTTGATTCT TCTTTTTAGC AGATAAATAG 780

GTAAATCTAC TTTAACAAAT AACTAAATAG TGATATTATT ACATTGTAAG CGTTTCAACA 840

TTTTTGTGGA GGGTGTAAAA TGACTAACGA AAGAAAAGAA GTTTCAGAGG CTCCTGTAAA 900

CTTCGGTGCG AATTTAGGTC TAATGTTAGA TCTATATGAT GACTTTTTAC AAGATCCATC 960

ATCTGTACCA GAAGATTTAC AAGTCTTATT CAGCACAATT AAGAATGATG ACTCAATTGT 1020

ACCAGCTTTA AAAAGTACAA GTAGTCAAAA TAGCGACGGC ACAATTAAGC GTGTCATGCG 1080

TTTAATTGAT AATATTCGCC AATACGGGCA TCTTAAAGCC GATATTTATC CTGTAAATCC 1140

TCCAAAAAGG AAACATGTAC CTAAATTAGA GATTGAAGAC TTTGATTTAG ATCAACAGAC 1200

TTTGGAAGGT ATATCAGCAG GAATTGTTTC AGATCACTTT GCCGACATTT ATGATAATGC 1260

TTATGAAGCA ATTTTAAGAA TGGAAAAACG TTACAAAGGA CCAATTGCAT TTGAGTATAC 1320

ACATATTAAT AACAATACCG AACGTGGTTG GTTAAAAAGA AGAATTGAAA CGCCATATAA 1380

AGTAACGTTA AATAATAACG AAAAAAGGGC ACTATTCAAA CAATTAGCGT ATGTTGAAGG 1440

GTTTGAAAAA TATCTTCATA AAAACTTCGT TGGTGCAAAG CGTTTTTCAA TTGAAGGGGT 1500

AGACGCACTT GTACCGATGT TACAACGTAC TATTACGATT GCTGCGAAAG AAGGTATTAA 1560

AAATATACAA ATAGGCATGG CTCACCGTGG ACGTTTAAAC GTTTTAACGC ATGTCTTAGA 1620

AAAACCGTAC GAAATGATGA TTTCAGAATT TATGCATACA GATCCAATGA AATTCTTACC 1680

TGAAGATGGT AGCTTGCAGT TAACTGCTGG ATGGACTGGT GATGTGAAAT ATCACCTTGG 1740

AAGTCACTTG GAAATTGTTG CACCTGTTGT TGAGGGGCGT ACGAGAGCAG CACAAGATGA 1860

TACACAACGA GCTGGGGCTC CGACGACTGA TCATCATAAA GCAATGCCAA TTATTATACA 1920

TGGCGATGCT GCTTATCCTG GTCAAGGAAT TAACTTCGAA ACAATGAACT TAGGAAACTT 1980

GAAAGGCTAT TCTACGGGTG GTTCATTGCA TATTATTACT AACAATAGAA TTGGATTTAC 2040

TACAGAACCA ATTGATGCAC GTTCAACAAC TTATTCTACA GATGTGGCCA AAGGTTATGA 2100

TGTGCCAATA TTCCATGTCA ATGCAGATGA CGTTGAAGCT ACTATTGAAG CAATTGATAT 2160

TGCAATGGAA TTTAGAAAAG AGTTTCATAA AGACGTCGTT ATTGATTTAG TAGGTTATCG 2220

TCGTTTCGGA CATAACGAAA TGGATGAACC ATCAATTACT AATCCaGTTC CTTATCAGAA 2280

TATTCGCAAA CATGACTCTG TTGAATATGT GTTTGGTAAA AAGCTTGTTA ATGAAGGTGT 2340

CATTTCAGAA GATGAAATGC ATTCATTTAT AGAACAAGTC CAAAAGGAAC TAAGACAAGC 2400

TCATGATAAA ATTAATAAAG CTGATAAAAT GGATAATCCA GATATGGAAA AGCCTGCAGA 2460

TCTTGCATTA CCGTTACAAG CAGACGAACA ATCATTTACT TTTGATCACT TGAAAGAAAT 2520

AAATGATGCA TTGTTAACAT ATCCGGATGG CTTTAACATT TTGAAAAAGT TAAACAAAGT 2580

TCTTGAGAAG CGTCATGAGC CGTTTAATAA AGAAGATGGT TTAGTTGATT GGGCACAAGC 2640

AGAACAACTT GCATTTGCGA CAATTTTACA AGATGGTACA CCGATTCGCT TAACTGGTCA 2700

AGATAGTGAA CGTGGTACAT TCAGTCATAG GCATGCCGTG TTACATGATG AGCAAACAGG 2760

TGAAACATAT ACACCTTTAC ATCATGTTCC TGATCAAAAA GCGACATTTG ATATACACAA 2820

TTCTCCGCTT TCAGAAGCAG CAGTAGTTGG TTTTGAATAC GGCTATAATG TGGAAAACAA 2880

AAAAAGCTTC AATATTTGGG AAGCACAATA TGGTGATTTT GCAAATATGT CACAAATGAT 2940

TTTTGACAAC TTCTTATTCA GTTCTCGCTC AAAATGGGGA GAACGTTCAG GATTAACATT 3000

ATTCTTACCT CATGCATATG AGGGTCAAGG GCCTGAACAT TCATCAGCAA GATTAGAGCG 3060

ATTTTTACAA TTAGCTGCTG AAAATAATTG CACAGTTGTC AACTTATCTA GTTCAAGTAA 3120

TTATTTCCAC TTATTGCGTG CACAAGCGGC TAGTTTAGAT TCTGAACAAA TGCGACCATT 3180

GGTTGTTATG TCACCAAAAA GCTTACTGAG AAATAAAACA GTTGCAAAAC CAATTGATGA 3240

ATTTACTTCT GGTGGATTTG AGCCAATTTT GACAGAATCA TATCAAGCGG ATAAGGTTAC 3300

AAAAGTTATT TTGGCAACTG GTAAAATGTT CATTGATTTA AAAGAAGCAT TAGCTAAAAA 3360

TCCAGACGAA TCAGTATTAC TCGTTGCGAT TGAAAGATTG TATCCATTCC CAGAGGAAGA 3420

GATTGAAGCA TTACTAGCAC AATTGCCAAA CCTTGAAGAA GTGTCATGGG TACAAGAAGA 3480

ACCTAAAAAT CAAGGTGCAT GGTTATATGT CTATCCATAT GTTAAAGTGC TAGTTGCAGA 3540

AGAAATTCAT AAACTTGTTC AAAATAAAAT TATAGAAAAT GCATTAAAAA ATAACTAGGG 3660

GGAAATAAGT CATGCCAGAG GTTAAAGTTC CAGAATTAGC AGAATCTATT ACAGAAGGTA 3720

CCATTGCAGA ATGGTTGAAA AACGTAGGGG ATAGCGTAGA AAAAGGTGAA GCTATTCTTG 3780

AATTAGAAAC TGATAAAGTT AATGTCGAAG TTGTATCTGA AGAAGCAGGT GTATTATCTG 3840

AACAACTTGC AAGTGAAGGC GACACTGTAG AAGTTGGACA rGCAATTGCT ATCATCGGCG 3900

AAGGTAGTGG CAATGCTTCT AAAGAAAATA GTAACGACAA TACTCCACAA CAAAATGAAG 3960

AAACAAATAA TAAAAAAGAA GAAACAACAA ATAATTCGGT AGATAAAGCT GAAGTAAATC 4020

AAGCAAATGA TGACAATCAG CAACGTATTA ATGctACGCC TTCTGCGCGT CGATATGCTC 4080

GTGAAAATGG TGTGAATCTT GCTGAAGTAA GTCCGAAAAC AAATGATGTG GTTCGTAAAG 4140

AAGATATTGA TAAGAAACAA CAGGCACCGG CATCAACACA AACAACACAA CAAGCATCTG 4200

CAAAAGAAGA GAAAAAATAC AATCAATATC CTACAAAACC AGTGATTCGT GAAAAAATGT 4260

CACGTAGAAA GAAAACAGCT GCCAAAAAAT TATTAGAGGT ATCTAATAAT ACAGCTATGT 4320

TAACAACATT TAACGAAtTG AcATGACAAA TGTTATGGAA TTGCGTAAAC GTAAGAAAGA 4380

ACAATTTATG AAAGATCATG ATGGTACTAA ATTAGGATTT ATGTCATTCT TTACTAAAGC 4440

TTCTGTAGCA GCTTTGAAAA AGTATCCAGA AGTTAATGCA GAAATCGACG GCGACGACAT 4500

GATTACGAAA CAATATTATG ATATTGGTGT AGCTGTTTCT ACAGATGATG GATTATTAGT 4560

ACCATTTGTA AGAGATTGTG ATAAAAAGAA TTTTGCAGAA ATCGAAGCAG AAATTGcTAA 4620

TTTAGCAGTT AAAGCaCGAG AGAAAAAACT TGGCTTAGAT GATATGGTTA ATGGTTCATT 4680

TACGATTACA AATGGCGGTA TTTTTGGATC AATGATGAGT ACGCCAATTA TCAATGGTAA 4740

TCAAGCTGCA ATCTTAGGCA TGCATTCAAT TATTACAAGA CCAATTGCGA TTGATCAAGA 4800

TACAATCGAA AATCGTCCAA TGATGTATAT TGCATTAAGC TATGATCATA GAATTATT 4858

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

ATCAGTCACA CGGTAGGCAT ATAAAATGAG TCGTTTCTAC AACATTTTTA AACAGTTCAT 60

TCAATATTAT TTTTATCTAA TAATnATATT GGGAGGATTA TACCTTTATA CACACCATGC 120

ATGCTATTTA GCTAAAGCTA AAAGACCAGA CACTATGCAT ATTTCAACTG GAAATATGTG 240

GCGATACTTA GTTGCAATTA TTGCCTGTAT GATTTGGTAC CTTAATAAAG CGCATGTAAG 300

TATCATCGGT ATAATTATTG GTTTAATGAT TTCATATGTT GTAGTTATCA TACGTCCTTT 360

ACTAAAGGTG AGCAAATAAA TTAAGAAAGA GGTGAGATTA TGGATCACAA ATCCCCGCTC 420

GTGAGTTGGA ATTTATTCGG TTTTGaTATC GTTTTCAATT TATCAAGTAT ATTGATGATA 480

CTTGTTACGG cGTTTCTTGT TTTTCTACTT GcTATCATTT GTACGCGTAA TTTGAAAAAA 540

AGACCAACTG GCAAACAAAA TTTCGTTGAA TGGATTTTTG ATTTCGTGAG GGGAATCATT 600

GAAGGTAACA TGGCTTGGAA AAAAGGTGGT CAATTCCACT TCTTAGCAGT AACGCTGaTT 660

CTGTACATTT TTATAGCTAA TATGTTAGGT CTTCCGTTTT CTATAGTAAC GAAAGATCAC 720

ACATTGTGGT GGAAATCACC GACAGCnGAT GCAACAGTGA CTTTAACGTT GTCTACAACG 780

ATAATACTGT TAACTCACTT TTATGGAATT AAAATGCGTG GTACGAAACA ATATCTTAAA 840

GGTTATGTAC AGCCGTTTTG GCCATTGGCA ATTATTAATG TTTTTGAAGA GTTCACTTCA 900

ACATTAACGC TTGGTCTGCG TTTGTACGGT AACATATTTG CAGGTGAGAT ACTATTAACA 960

TTACTTGCTG GCTTATTCTT TAACGAACCA GCATGGGGTT GGATTATTAG TATCCCAGGA 1020

TTAATTGTTT GGCAAGCATT TTCAATATTT GTAGGAACAA TCCAAGCATA TATCTTTATT 1080

ATGCTTTCGA TGGTTTATAT GTCACATAAA GTGGCAGATG AACACTAAAA ATTTCAATAA 1140

TTATATACAA TCACAGGAGG AAATTAAATT ATGAATTTAA TCGCAGCAGC AATCGCAATT 1200

GGTTTATCAG CATTAGGAGC AGGTATCGGT AACGGTTTAA TCGTTTCAAG AACAGTTGAA 1260

GGTGTAGCAC GTCAACCAGA AGCACGTGGT CAATTAATGG GTATCATGTT CATTGGTGTA 1320

GGTTTAGTTG AGGCATTACC TATCATCGGT GTAGTAATTG CATTCATGAC ATTTGCTGGA 1380

TAATTAACAG ATAAAAGAGG TCGGGACAAA GCGCATAGGA CATAATTCAT GATGCATATA 1440

TAGTAATATC TTTGAACTTT ATTAAATAGT TGAGATATGA ACGCACCATG CCTATCGCAT 1500

AAATTCAGTA GGTCCTAACC TCGTCGTTTT TTTCTATATA ACACTAGCGA TTATTTTAAT 1560

GAAAGGAGTG TCATGAACCC GTGACTGAAA CAGCTAACTT ATTCGTTCTT GGTGCAGCTG 1620

GAGGCGTTGA GTGGGGTACT GTGATTGTAC AGGTCCTAAC TTTCATCGTG TTAcTTGCGT 1680

TACTTAAAAA GTTCGCATGG GGTCCATTGA AAGATGTAAT GGATAAACGT GAAAGAGATA 1740

TTAACAGAGA TATCGATGAC GCAGAACAAG CTAAGTTAAA TGCACAGAAA CTTGAAGAAG 1800

AAAATAAACA AAAACTTAAA GAAACACAAG AAGAAGTTCA AAAGATTTTA GAAGATGCTA 1860

AGGTTCAAGC ACGTCAACAG CAAGAACAAA TTATTCaTGA AGCAAACGTA CGTGCAAACG 1920

TTAATAATCa AGTATCTGAA CTATCAGTGT TAATTGCTTC TAAAGTTCTT AGAAAAGAAA 2040

TTTCTGAACA AGACCAAAAA GCATTGGTTG ACAAGTATCT AAAAGAGGCA GGCGATAAAT 2100

AATGGTAAAA GTAGCTAACA AGTATgcTAA AGCATTATTT GACGTGTCAT TAGATACAAA 2160

TAATTTAGAG ACTATTAATG AAGAATTAAC AGTTATAAAT GAAGCAGTAA AAGATAAAAT 2220

TG 2222

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

TAACAATTCC TaTATTCATG TTTAATACGA AACACTACAT TTACATTGTA ATTCACTATC 60

TTTTGAAGTA ATAAAGTGAT TTGTTCAATC GATAGCTCAT TGCTTGTGTC GATTGTAACA 120

ATTATATGCA AGTTTTCAGG ATTAACACCT AATCTTTGAA TGATTTGTTT AATAGTATAA 180

TAATCCATCC AATAAAAATT ACTTCCTTTA ATATAAATGT TTTTAGGTTG ATACATTTGA 240

CTCCTTTTTG TAGGCTCAAA AGGTATATCA ATCTCGCGCA TACTTGAAGA ACTTTGATTA 300

GTATCATCAA ATAATTCAAT TATATTTTTA TCAATTTCAA CTAATTGGGA ATGGTTAATT 360

GAATGAGATG TTGGACTATA TCTTTTTCTA ATTAATTTAG GAGTGTTACC ATACGTTTCT 420

TTAAAGAGGT GTATAAAACG AGAATAATGA TTAAAACCAT GACTACTTGC GATTTCTTCA 480

ATAGGCTTCT TAGrAGTTAA AATATCAATT AAGCAATGCT CCAGTCTAAT ATGATTTAAA 540

TATTGAATAA AATTACTATA AGGTGTCGCT TTAAACATGT CACTTAAAGC TTTGTTTGTA 600

ATACTAACTT GATTAATGAC ATCTTTCCTA TTTATCTTTT TATGGTGGTT GTTTGTTAAA 660

TAATCGTGCA CTTCTTCGGC TACTAAATGA CGACTACCAT CGTATGTATT TAATGACATT 720

AATTCAACAC ACATGTAATT AATAATCTTA TCATTAGCAT TATAAGACTG TTGTTTAATT 780

TTGCTGTAGA TTAAATACTT AATCAAGATT CTAAAAGTGC TAGCAACCTC ATTTGTTAAT 840

ATCTTGCCAC GCATCATATA GTTTGCATTC ATAAACTTCA AAAATGTCTT TGCACTTACT 900

TCAACAACAC AACATACACT ATCATCATTA CCATCAATTT GATACAAATC ATTCAACATA 960

ATAATGGTGA CATCATTTCT TTTTACATCA TATTGTTGTA GATTGATTGA AACTACACCT 1020

GTACCTTGTA GCCAATATAT AATTTTtAAG TTCGCTTCCT TCACACTACT CATTTTCATA 1080

ATT 1143

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

GGACCACCTT TTTTACCTGT ACGACTAAAG CCAACTGTTT TAAAGGCACC AACAGCATGC 60

CACACTTGAA TAATTTCTTG TGATGGTCTA AAGCGAACCG TATAAATTAA TGGATGGAAA 120

TCATCAACAA AAATATAATC GGCCTTACCA AGTAAATATG GCAATCTAAA CTTGTCTCTC 180

CATTTGCGTC TATCCGTAAT ATTCTCCTTA AATACCGTTT TAATATCATA ATCAAAATCT 240

ACTTTTTGGC GTAGTAACTC ATCATATACA TACTTGAAAT TCCCTGATAA ATTCGGACGC 300

GAATCTGATG TGAATAATAT TGTTTTGCTT CTTTTAATAT GTAGTAACTT TGTAATATTA 360

AAAATAGCTT TAAATAAGAA ACTTCTACTT TCAAATGAAG CTTTATGaCC TTGTTTaTGA 420

AGCCAGTGTG cACTTgTCGC AATGaCCCCT GaTTTCyCyT GagGtAAGGk GaTTTCmATA 480

TCAAATACAA ATTCGTTAAC GTCACT 506

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

AGCATCTGCA AtGAGTcTCT AATACAACGA TACGTTTTGC ATCTTTAGGT ACTTTTACTG 60

TACCATTTTC ATCTTTTACC GAAATAGTAT CTTTAGTTGA TGATTCTTTT TTACTTGAAT 120

TATCCGTATT ACCACAAGCT GCAACTAAAA GTAAGGCAAC TATTAATCCC AATATACTAA 180

AAGTTTTTAG ACCTCTCATC GTTCCACTCC TTAATATGTA TAACTTCATT TATTATTTTA 240

TTGATAACAA TTATCATTGT CAAGTAGCGT TCAATCTTTT TTATATTTCT AAAATGTATG 300

ACTATATATT TCCTCTAATA ATTATGACTA CAATTAGCAC ATTTCCTTAG ACAAAATACT 360

GATAATGTAT CATTGCTATA TCATCTTTGC ATTAATACAA TTGACACCAT TTAGCATGAC 420

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 862 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

TGCACTTGAT ACTTTAGCAC ATGAAATTGC TAATCGATTA GTTGCAAATG ACAAGAATGA 60

AGCAACTTTG GAAATGACTA ATAAAATGGC AACGATTCGT TTTACAGAAC CTACGCTGAT 120

TGCATTAGCA GGGGGTAATG TCAAAGCTTA CACTGAGCAT ATGACTATAT CTCCATATAA 180

ATTGTATTTG TTAGATAAAG GCGATGTTTT AAAGTTTAGA GAAACAAGTT ATACATCGCG 240

AGTGTATTTA GCTGTgGGAG GCGGATTTGA ATTAGATGCA TGGTTAGGAT CTAACTCAAC 300

CGACTTTAAT GTAAAAATTG GTGGTTTTAA AGGTAGAACA TTACAAGATG GCGATGAAAT 360

AAAGCTTAAG AGAGATTATA CAGCTCGTCA TCATAAGTTA TTTGAAAACC TTGCTCACAC 420

GAAACAAACA GATTGGGGTA TTGATGGATA CGCCTTGTCA TTTAATTATA TGTCTGATGT 480

ATTTCATGTC GTTAAAAATA AAGGTACGGA AGATTTTAAA GAAGATGCCA TTCAAAGATT 540

TGTGAAACAT GATTATAAAG TAACGAGCAA AGCAAATCGC ATGGGGATGA TGCTTGAAGG 600

TGAAAAAATC AAAGCTTTTT ATGAAGATAT GCCACCGTAT CAGACTGTCA AAAAAGGAAC 660

GATACAAATT AAGCGTGATG GCACACCTAT TATCCTATTA AATGATCATT ATACGCTAGG 720

TAGCTACCCG CAAATCGGTA CAATCGCAAG TTATCATTTA ACGAAATTAG CACAAAAACC 780

GCAAGGATCA CGTTTGAAAT TTCAATTTAT AGATATTTTA ACGGCTGAAA AGAACCTTGT 840

TAAgTATAGT AACTGGTTAA AC 862

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1027 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

AAATGAGTTG ATGATGGCTC CTATTCCATC TATCTCTAGG TATGACAGAA sATAAACGGT 60

CTTCTACCTG TCTsACATTA TCTTTCCAAC GATTAATACC TAAGCGTTTA GAAACACGTT 120

CAGTTTTACG TCCTACACCT GCTAAACTTT CTAATTCCTT ATGTGTTTGT GGTATTTCTC 240

CATTAAATTG ATCAATCAAA GATTGACAAA GTTTCTTAAT ATTCTTAGCT TTGTTACGAT 300

ACAGACCGAT AGAACGAATA TCATTCATAA GTTCTTCATC ACTGACTGCC AAATAATCTT 360

CAGGCGTTTT GTATTTTTTA AACAGCTCAG TTGTTACTCT ATTTACTAGA ACGTCTGTAC 420

ATTGCGCTGA CAATAATACA GCAATAGTTA ATTCGAACGG ATTATCATGT TTTAATTCAC 480

ATTCTGCATC CGGAAACATA TTTGCTATAA CATCAATCAT TTCTAATGCT TTTTTCTTAC 540

TTACCATCAA GGTTCTCCCC GTTTAACCAA TCAAATTTAG GTACCGTTTT AACTGTGTGC 600

GTCATTTTCG GTTTATTGAA TTTTTCTCTT ATTTTTCTAG AATCGTCAAT TGTTTTGACA 660

TTGTTTTTCT TCCAATTAAG TAAAATACGA TCTATATATT TAAAGCTAAG TTTATTCAAA 720

CTATTCGCCT CGTCTAATGC CGCTTGTATA ATTGCAGTAT CGTGTTTATC AACATCAATC 780

CATTGATTTA ACGTTTCTAT TTCATATGGA GATAACGGCC TTGCAAATGT ATCCTCTAAA 840

ACTCTAAATA ATTGTTTAAA TTTTTCTTTA CTATTTAGCT CTTTCGTTTC CATACTTTGT 900

TGCTTCAATA TATGACTTAA TTTTTCGAAA AAAGGATCTA GATTCATATA TTCGGkAAAT 960

CTACCTTCyT CATCyTTTTG aACTkGtAAT tCTAGCAATT CACGTgTATC AAATTTTGGA 1020

TACCATT 1027

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1006 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

AAGGnTTGGA GGGAATTAAT nGATGGCAAA TCCCAGaTAA AGTACACaAC GCATGGAATG 60

TGATGCATTT AATATTTCCA GTAGTTAGTA CGACGTTTGC AAGCTTTAAA TCTATGTATG 120

GGGGCATACC AAAAGATTTC ATAGACTACT TATTTATTGA TGAAGCAGGA CAAGCAATAC 180

CTCAAGCAGC TGTGGGAGCA TTATATCGTT CAAAAAAAGT TGTAGCTGTA GGTGATCCGA 240

TTCAAATAGA ACCGGTTGTG ACTTTAGAAA GTCATTTAAT TGATAACATT CGTAAAAATT 300

ATCATGTTCC GGAATATCTA GTTTCTAAAG AAGCTTCTGT GCAGTCTGTT GCAGACAACG 360

CCAATCAATA TGGTTTTTGG AAATCTGATG CTACTGATAG TAATCAAAAA ACCTGGATAG 420

GCATACCTTT ATGGGTGCAC AGACGATGTT TAAAACCTAT GTTCACGATa GCTAaCCAAa 480

GGTATGACGT TAAAGGAAaC GCAGTTCAAA AACAATTTGT GAAAGAGCAT GGTGAAAAaG 600

TAGTGGGATT ATTAGCTGAT GATTGGATTG AAGCAATTAA GGAAGGTAAA AATGAACCGA 660

GCTCATTTGT AATATCGCCT TTTTCAGCAG TACAGCAACA GATTAAACGT ATGTTAAAGC 720

AACAACTACC GACTAGAATT GATATTGAAC GTACAAAAAT TAATCAATGG GTCGATAAAT 780

CCATTGGTAC TGTTCATACT TTTCAAGGTA AAGAGGCTCA GAAGGTGTAT TTTGTAATAG 840

GTACTGATAA TACCCAAGAT GGTGCTGTGA ACTGGTCATG CGAAAAACCA AACTTGTTAA 900

ACGTTGCAGT GACAAGAGCT AAGAAAGAGT TTaTGTAATT GGCGACATGC AAAGAATACA 960

GATGAaACCA TTTTATGAGA CGATTTTTAn AGnAAGAAAT GTAAAA 1006

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 662 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

CGTTTCATCA AGTnATCGAT CCTAATTTAC AAAATATTCC GGTTAGACTT GAAGAAGGGC 60

GTAAAATAAG AAAAGCCTTT AAACCAACTT CAAAAGATAG CGTTATATTA TCAGCAGATT 120

ATTCTCAAAT TGAATTGCGT GTATTAGCAC ACATTACACA AGATGAGAGT ATGAAAGAAG 180

CATTTATCAA CGGCGATGAT ATTCATACAG CAACTGCTAT GAAAGTATTT GGTGTAGAAG 240

CTGATCAAGT CGATAGTTTA ATGCGTCGTC AAGCAAAAGC AGTTAACTTT GGAATTGTTT 300

ATGGGATAAG TGATTATGGT TTAAGTCAAA GTTTAGGTAT TACTCGTAAA AAAGCAAAAG 360

CATTCATTGA TGATTATTTA GCTAGTTTCC CAGGTGTAAA ACAATATATG TCTGATATTG 420

TAAAAGATGC CAAAGCTTTA GGTTACGTGG AAACATTGCT ACATCGTCGA CGCTATATTC 480

CTGATATTAC GAGTCGTAAC TTTAATTTAC GCGGCTTTGC TGAACGTACT GCTATGAATA 540

CGCCAATACA GGGCAGTGCT GCAGATATCA TTAAACTGGC AATGGTTAAA TTTGCTCAAA 600

AAATGAAAGA GACAACATAT CAAGCTAAAC TATTATTACA AGTACACGAT GAATTAATTT 660

TT 662

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 669 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

TCATCCAAAT TTTGGAAATT CCACATTTTA CATATCGTAA TTTTTTAGGA AACTAGTGAA 60

TATAACAAAT CCCTCCTCTC ATTTTTAAAA TAGATATATC ACTTCCCCAC TTTTACTTAA 120

CTAAACTGCA ACGGTTCCTA ATACCAAAAT CCTGCCCTCT ATTTTTATCA ATTCAAGCAT 180

ACTTATTGAA AAATGTTAAC GTTTTCTTGA TAATCATTGT AAGCGCATTT ATTTTATAAA 240

CTAACGTTTG AAATATACTA CAGGAGTGAC ACGTAATGAC TCAAATTACT GAAAAAGAAT 300

TAAAAAAGAA GTATTTAGAT TTACTATCCC AAAATTTTGA TACTCCAGAA AAACTTGCAA 360

CTGAAATTAT CAATTTAGAA TCAATTTTAG AATTACCTAA AGGTACGGAA CATTTCGTCA 420

GCGATTTACA TGGTGAATAT GAAGCTTTCC AACACGTATT ACGCAACGGT TCTGGGAACG 480

TGCGAGCGAA AATCAATGAT ATTTTCAAAG AGAGACTTTC AACTAAGGAG CTTAATGACT 540

TAACTGCTCT TGTCTACTAT CCAGAAGrCm AATTtAAAAT TgATTAAAAG TGATTTCCAA 600

AATTgCGGtC mACttAATGt CyGGtATATC ACaACmATCG aACATTTAAT TGAGTTAATT 660

AAATATTGT 669

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

CACATGGCTG TTAGAGATAT GAATGGCCAT GCGTTACCTT TAACAAAAGA TGGCAATTTT 60

TATCAAACGA ATGTAGATGC AAATGGTGTT AATCATGGTG GTAGTGAAAT GGTGCAAAAT 120

AAAACAGGTC ATATGAGTCA ACAArGCCAT ATGAATCAGA ACACACATGA ACCAACAGCC 180

ACACATGCAA CAAGGTCATA TGCAATCATC AAACCATCAA ATGATGAGTC CAAAAGCAAA 240

TATGCATTCA TCAAATCATC AAATGAACCA AAGTAACAAA AAAGTTTTAC CAGCTGCTGG 300

TGAAAGTATG ACATCAAGTA TTCTTACTGC AAGTATTGCC GCACTACTAT TAGTATCTGG 360

GTTATTCTTA GCATTTAGAC GACGTTCAAC AAATAAATAA ACATAATACG ATTAATAATA 420

GAAAAATCGT GTGATTATCT GaGGGAGCCT AGGACATAAA TCAATGTCCT AGGCtCnCTA 480

AtGTTATATT GGCAGTAGTT GACTGAATGA AATTGCGCTT GTAACAAGCT TTTCCATTTC 540

CGATTGTCTT ATACGTGTCA GTGTTAATTC AGATATTTCC TGTGGAATAT ACCACTTATT 660

AATCATAATT GGATAAGGTG tTTGTGCGTA CAGTGTTTCA ATAATCAGCC AACAATGTGT 720

ATCACCaTCA AACACGTGAC TATGATTTTk GAAGTGGGGC GCTTTGGTAA TAGACATTTT 780

TAAATCTGAT TGATATGCAT TGCTATAAAT CGTTTGCTCA ACGAATGTCT TCATGTCGTC 840

TTCGTTTTGT GTATTCACTT TAAATGTGTC AATGACATTT AACGGTATAA AGGTAAAGCA 900

AAATGCATCA GCTTGCTTAG AATGATTGTC CTTTTTTTGA TAATAGCGTT CCATTGCAAT 960

GACGGCAGAA GGATGGTTTG CAAACAAATG ATTTGTATAT TCACTTTCTA AATCAACACG 1020

ATAATTAATT GATGACATAG ATACGCGAGC TAGCAATATT TGATCAAGTG GATGCTTAAA 1080

TTGATCCATA CTTGAAGCGT GTTGGGCATT TGTTTGTGGA ATAACAAAGT GTCCCTTCCC 1140

TCTTGTACTC TCTACGATGC CATCTTCGGC TAACAATTTt ATAGCTTGGC GCAAAGTCAT 1200

ACGACTGGAC ATCAAAGCGC GCACAAAGTT CCTTTTCAGT AGGTAATGC 1249

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1788 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

AATGATGATT CATTCAAAGA AATTAACGCT CGGTATATGC TTGGTATTAC TCATTATATT 60

GATTGTAGGT TATGTCATTA TGACAAAAAC AAATGGTCGA AACGCCCAAA TTAAAGACAC 120

ATTTAATCAA ACATTAAAAT TATATCCAAC CAAAAATCTC GATGATTTTT ACGATAAAGA 180

AGGCTTTCGA GATCAAGAAT TTAAAAAGGG TGATAAAGGT ACTTGGATAG TTAATTCTGA 240

AATGGTAATC GAGCCAAAAG GTAAGGATAT GGAAACGAGA GGAATGGTGC TCTATATCAA 300

TCGCAATACT AGAACCACAA AAGGGTATTA TTTTATAAGT GAAATGACAG ATGACAGTAA 360

CGGCAGACCA AAGGATGATG AAAAAAGGTA TCCGGtAAAA ATGGAACATA ATAAAATCAT 420

ACCAACGAAG CCACTACCGA ATGACAAGTT AAAAAAAGAG ATTGAAAACT TTAAGTTCTT 480

TGTACAATAT GGCAACTTTA AAGATATTAA TGATTATAAA GATGGTGATA TTTCATATAA 540

TCCTAATGTA CCAAGTTATT CGGCAAAATA TCAATTGAAT AATGATGATT ATAATGTCCA 600

ACAGTTaAGa AAAAGATATG ATATTCCAAC CAAACAAGCG CCGAAACTAT TATTGAAAGG 660

CGATGGAGAT TTAAAAGGTT CATCCGTAGT TcTAGAAGTC TTGAATTTAC CTTTGTCGAA 720

AGGTATGAGT CAAACTGAAT ATCAAATAAA ACCTGGTAAT ATAACAAGTA ACTCTGAAGA 840

AACAAGTTCG ATATCTAAAG TGAGCTGTGA AATATAGGTA GCCATTTCAA AAAATTTAAA 900

GGTGAATTTG ATAATGTAGC TCAAGGAGAT TGGGTTAAAA AGGCGAAGAA TGAACTGGAT 960

GATATTAGTA AGAAATTAAA AAATATTCAA AGAACGGAAG TTTAATAGCT TATATGATTC 1020

TTGGAGCTAA GACAGCATGC GTTCATTCAT GCCATTATTA ATATAAGCAC CGCAACAAAA 1080

AAGCTTCTAA TGTGATACAG GAACCTCATA TTCCGTATCA TGTTAGAAGC TTTTAATGTC 1140

TAAAGAACAT CTACATTTTA TCATATTTTC TGACTTATTA AACTTTTATA TAATTAAATA 1200

TTTCTTAATT TTCCAAAATA GTGATAAATT TGTGAAATAC ATCACAAATC CCTTTATTTA 1260

TTTGGAAATT CATGTAATAT TAGACTTGTA AGAAGTTAAT AAATAGAGAG AGACGAGAGA 1320

GTTTATATAA ATACTATATA AACATTGGAG TGATGATTAT GAGAAAAGAG ATTGAAGCGC 1380

TTATTTTCTC AGACGTAAtA GCTATGATAT TTACGTGAAC ACTGGTGTAA ATCAAGGATT 1440

AATTGGTGAC ATCAAAGATG GTTACCTAAC TATTGATTCT ATGCCTTACA TTGATGCTGA 1500

GCGTTTGTAT CACTTTGCTA TGGAACGTAA ATCGTTAGTC ACTAACTAGT TCTTATTGCC 1560

AATGATTACT ACCCCTAGTC GGCGGCAATT GAAGTGTGAT TGATGTAACT TGCCCTCGTT 1620

GGTGAGCAAT TGAGGGCAGA CCCCTTTAAT TAAGTAAACC CTAACTCCCC ACAAATCTGG 1680

AACGATACTA AAAGCCACGT CCTATATTGG ATGTGGCTTT AGTCAkACTT ATATTATTTT 1740

tAAAACGATT ACCTACAAGA TTTACATATA AAATTCTATC ATGnCTGC 1788

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2407 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GCAAGTTTAG TTAAACAGAT ATTAAAACCA GATCAATATA CAGATGCAAA TTCTCTATTA 60

GAGATTAGTT TGCAAACAGG TATGTTTATT GCAGGTGGAT TATCAGGAAT ATTATATAAA 120

ATAAATGGAT TCACTCTAAT TATAGCGATG ACTATAATGA TGTTTCTAAT CAGCATTTTT 180

ATGTTATTTA GATTGCATGT AGATAAACCA ACTCATTCAG AGGAAGAATC AACAAATAGC 240

TTATTGCAAG AATATTTATT AGGATGGAAA TTTTTAAAAG ACAACATGAT GATATTTATT 300

TTTGGAGTTA TTTCAATCAT ACCAATGGTG TTTACAATGA TCTTTAACAT ATCATTACCA 360

TATGGCATTG GAGGATTATG TGCAGGTTTA ATTTCAGCTA TTCTTTCGAA GAAAATCTCA 480

ACTAAAGTAT TGATATTTTT GTTATATTTC ATATTAGTCA TAAATTCAGC ACTATTTATT 540

TGGATAAACT CAGCATTTTA CTTATTCATA GGATCATTTA TACTAGGCTA CTCAATTTCA 600

TCAATCAGAA TTTATATGAA TACAGCTATA ATGAACACTG TTTCAGATAA ATATGTCGGT 660

CGCTCATTTA CGATATGGAC GTCAATTTCA TTGTTACTGC AAAGTTTAAT TGCTCCATnT 720

TTAGGAAGAT GGATTAATGA AATTAATGAT AAATTCGGTT TCTATATTAT ACTCATTTTA 780

TCCTTACTCA TATTTGTaCA CTGCTGCTTG TTAACAAAAC AGACAAAATA AAATATGCAC 840

ATAAAGAAGA GTGACCGTCA CTCTTCTTTA ACAAGCGACC ATTTATCGaT GGGCTTAGTT 900

CTCTCTGCAC CCACACTTCA CTACTTCACT TTTTCAAATC ATTTTTTATG GTCTTAAATA 960

AATCAGTGAG ATTTGTTGCT TCGGTAAAGT CTAGAATTAA TATCATTTCT TTAGAACCTG 1020

GATATGGCGA AACTAATGTA TTATCTTGCA ATTTCTGCTG GGCACTTTTA GTCGCCTTGA 1080

CCAATAATCT ATTATCATAC AAACCACCTA TAACCACGCC ATCATAATAA ATAATATATT 1140

CTCCCATCAT CTTTCTTGTC TTAACCGCGT TTGAATTCAC ATGATTTAAA AATAAATCAT 1200

GTACATCTTT CTTAGTCGCC ATTGTAATCG CTCCTTCAGT TTTATGTTTA ATCACATTCG 1260

TATTAATGAT TCATTTCGTG TTGCTCTTAA TTTTATCTAT AATTATATGC GTAGTTAAAA 1320

TCAAACCTAT GGAAAAGAAA ATAATGATAA CAATGTTAAG AAATATAGTT ATAAAATTAT 1380

AGTTTGGAAG GTATGCGAAT AGCAGAAAAA TAGGTATCGC AAAAAATAAA TCCCACCAAC 1440

CTAAACTTTT TAAAGAATGC TTTAAACCTT CCATAATATC ACCTTTATAA ATTTGTCTTT 1500

GTTATAAGAT AACTAAAAAA TCGCTTTACT GTAAAAGTAG CCAAAGAAAA TTCTGAATCA 1560

TATTCATAAG TAGTGTATCA TTAATAATGA ACAATTTAAT ACTATAATCC TTGATCTTTG 1620

TATTGATCAA CTTACCACAA CATTTATTTT AGACTACTCT TAGACTTCCC TTTCAAATGG 1680

TTGCATCTAT TGAAATTCCT TTTGTATAAG TTAGGCTTTT GTGGTAATAT CATCATGCAT 1740

AAAAAATCGA GATACTAATT ATAAAGAGGG TATAAATATA TTATGAAAGA AAATTTTTGG 1800

AGTGAATTAC CACGTCCATT TTTTATTTTG GCGCCAATGG AAGACGTTAC AGATATCGTC 1860

TTTCGACACG TTGTAAGTGA AGCAGCTAGA CCGGATGTGT TTTTCACTGA ATTTACAAAT 1920

ACTGAAAGCT TTTGCCACCC TGAAGGCATA CATAGTGTGC GCGGACGCTT AACTTTTAGT 1980

GAAGATGAAC AGCCGATGGT CGCTCATATA TGGGGAGATA AGCCAGAACA GTTCCGTGAA 2040

ACGAGTATTC AATTAGCTAA AATGGGCTTT AAAGGCATAG ACTTAAATAT GGGATGTCCT 2100

GTAGCAAATG TTGCTAAAAA GGGTAAGGGT TCCGGCTTAA TCTTAAGACC TGACGTTGCT 2160

GGCTACTATG AAATCGATGA ATGGAAAGAT TGGTTGAAGC ACGTCTTCGA ACAAGACATT 2280

GCCAATTTAT CTATTCATCT TCGTACACGT AAAGAAATGA GTAAAGTAGA TGCACATTGG 2340

GAATTAATCG AAGCTATTAA AAATTTACGT GACGAAATTG CACCAAATAC ATTGTTAACA 2400

ATTAACG 2407

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2424 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

ATGATGnATG GCnCCGCCAA GAAGTTGAAC CAGTCTATTG GCTAGAATTG CTCAAAAAGC 60

GAGAcaTGTG GTATTCaTAT GTTaGTAgCt ACGCAAAGAC CATCTGTCAA TGTAATTACA 120

GGTTTAATTA AAGCCAACAT ACCAACAAGA ATTGCATTTA TGGTATCATC aAGTGTAGAT 180

TCGAGAACGA TATTAGACAG TGGTGGAGCA GAACGCTTGT TAGGATATGG CGATATGTTA 240

TATCTTGGTA GCGGTATGAA TAAACCGATT AGAGTTCAAG GTACATTTGT TTCTGATGAC 300

GAAATTGATG ATGTTGTTGA TTTTATCAAA CAACAAAGAG AACCGGACTA TCTATTTGAA 360

GAAAAAGAAT TGTTGAAAAA AACACAAACA CAATCACAAG ATGaATTATT TGATGaTGTT 420

TGTGCATTTA TGGTTAATGA AGGACATATT TCAACATCAT TAATCCAAAG ACATTTCCAA 480

ATTGGCTATA ATAGAGCAGC AAGAATTATC GATCAATTAG AGCAACTCGG TTATGTTTCG 540

AGTGCTAATG GTTCAAAACC AAGGGATGTT TATGTTACGG AAGCAGATTT AAATAAAGAA 600

TAATTATGAG TAAGGAGTTT TATATAATGA CACACTATCA TTTTGTCGGA ATTAAAGGTT 660

CTGGCATGAG TTCATTAGCA CAAATCATGC ATGATTTAGG ACATGAAGTT CAAGGATCGG 720

ATATTGAGAA CTACGTATTT ACAGAAGTTG CTCTTAGAAA TAAGGGGATA AAAATATTAC 780

CATTTGATGC TAATAACATA AAAGAAGATA TGGTAGTtAT ACAAGGTAAT GCATTCGCGA 840

GTAGCCaTGA AGAAAtAGTA CGTGCACATC AATTGaAATT AGATGTTGTA AGTTATAATG 900

ATTTTTTAGG ACAGATTATT GATCAATATA CTTCAGTAGC TGTAACTGGT GCACATGGTA 960

AAACTTCTAC AACAGGTTTA TTATCACATG TTATGAATGG TGATAAAAAG ACTTCATTTT 1020

TAATTGGTGA TGGCACAGGT ATGGGATTGC CTGAAAGTGA TTATTTCGCT TTTGAGGCAT 1080

GTGAATATAG ACGTCACTTT TTAAGTTATA AACCTGATTA CGCAATTATG ACAAATATTG 1140

TGGCACATAA TGTTAAAAAA GGTATTATTG CTTGGGGTGA TGATGAACAT CTACGTAAAA 1260

TTGAAGCAGA TGTTCCAATT TATTATTATG GATTTAAAGA TTCGGATGAC ATTTATGCTC 1320

AAAATATTCA AATTACGGAT AAAGGTACTG CTTTTGATGT GTATGTGGAT GGTGAGTTTT 1380

ATGATCACTT CCTGTCTCCA CAATATGGTG ACCATACAGT TTTAAATGCA TTAGCTGTAA 1440

TTGCGATTAG TTATTTAGAG AAGCTAGATG TTACAAATAT TAAAGAAGCA TTAGAAACGT 1500

TTGGTGGTGT TAAACGTCGT TTCAATGAAA CTACAATTGC AAATCAAGTT ATTGTAGATG 1560

ATTATGCACA CCATCCAAGA GAAATTAGTG CTACAATTGA AACAGCACGA AAGAAATATC 1620

CACATAAAGA AGTTGTTGCA GTATTTCAAC CACACACTTT CTCTAGAACA CAGGCATTTT 1680

TAAATGAATT TGCAGAAAGT TTAAGTAAAG CAGATCGTGT ATTCTTATGT GAAATTTTTG 1740

GATCAATTAG AGAAAATACT GGCGCATTAA CGATACAAGA TTTAATTGAT AAAATTGAAG 1800

GTGCATCGTT AATTAATGAA GATTCTATTA ATGTATTAGA ACAATTTGAT AATGCTGTTA 1860

TTTTATTTAT GGGTGCAGGT GATATTCAAA AATTACAAAA TGCATATTTA GATAAATTAG 1920

GCATGAAAAA TGCGTTTTAA TATGTTTATA ATAGAGTAGT ATGGGTATTT ATTATTAATG 1980

ACATTATTAC ATGTTAATTA GGAGGCGTTT TTAATGGATT GGATTTTACC AATTGCTGGA 2040

ATTATCGCTG CGATTGCATT CTTAATTTTA TGTATCGGTA TCGTAGCTGT ATTAAATTCT 2100

GTTAAGaAAA ACTTAGATTA TGTTGCAAAA ACACTTGACG GTGTAGAAGG TCAAGTTCAA 2160

GGTATTACTC GTGAAACAAC AGATTTACTT CATAAAGTAA ACCGTTTAAC TGAGGATATC 2220

CAAGGTAAAG TAGATCGTTT AAACTCAGTT GTAGATGCTG TTAAAGGTAT CGGTGACTCA 2280

GTACAAACGT TAAACAGCTC TGTAGATCGT GTAACAAATT CAATTACACA TAATATTTCT 2340

CAAAATGAAG ATAAAATCTC ACAAGTTGTT CAATGGTCAA ATGTTGCAAT GGAAATTGCA 2400

GACAAATGGC AAAATAGACA CTAC 2424

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CnATAATATT CnTCAAnCCT TTAAATAGAG GAATAGACTG CCGACAGAGT CCGAGACTTT 60

GTGGGTAGTT TTTTTAGTTT TGATAACGGA AGTTAGAGGC TCTCTGTCAA ATTGGGCAGA 120

AGTGTAAAGT TTTCAACATA ATACTATTAG TTCGGTCATG TATCGGACTG ATGGAAAAGC 240

GTTTCACTTT TAATGACTCA TTAAGAACGG CCTGAAAATG TTTGGCGTAT TAAGTGCAAT 300

GATAGTTTTG ACATTTAGTT TCTAATTGGT CATTACTGCC GAGCAAATCT AGTAGAGTAA 360

TCATGTAAAT CTTTAATGTG CCATTTGATT CACTAGCGGT GTTAATAACT ACGGAAATTG 420

CATTTCCGAC TGAAATTTTT GAAAAATATC AACGTACGCT ACAAATAAAA TTTTAAACTG 480

TTATAAATGT GTCTCAATTT CATATGTTCA TCGACGATAT GAAGCGTATT ATGGTAAAAT 540

GAAGAAATAA TAAACTTGTT AATAAATAAA ACATCACGAT TTGACTAAAG CACTTTATTA 600

TTGTGTAGAT AATAGTTTTT TAACGAAATA AAAATGGCGA CTGGTTTTAA TAAATCAGCT 660

AATGAATCAC TACACCTATA AGTATGAATA TAGTGATTAG AATGCTTTGT ATAGTTGGAT 720

TTTGCAAAAT TGATGTTA 738

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

AAAAGTTGTA ATTAAAAGTG GGATTTTACT TAAGnnAGAA GGAAACTATT TATATGACTA 60

ATAAAAGAGn AGATGTCCGC AATATAGCAA TTATTGCTCA CGTTGACCAT GGTAAAACAA 120

CTTTAGTAGA TGAGTTGTTA AAACAATCTG GTATATTCAG AGAAAATGAA CATGTCGATG 180

AACGTGCAAT GGACTCTAAC GATATCGAAA GAGAGCGTGG AATTACGATT CTAGCCAAAA 240

ATACGGCTGT TGATTATAAA GGTACACGTA TTAATATTTT GGATACACCA GGACATGCAG 300

ACTTTGGTGG AGAAGTAGAA CGTATTATGA AAATGGTTGA TGGGGTTGTC TTAGTAGTAG 360

ATGCGTATGA AGGTACAATG CCTCAAACAC GTTTTGTACT TAAAAAAGCG CTAGAACAAA 420

ACCTGAAACC TGTTGTTGTT GTTAATAAAA TTGATAAACC ATCAGCACGT CCAGAGGGTG 480

TTGTAGATGA AGTTTTAGAT TTATTTATTG AATTAGAAGC AAACGnTGAA CAATTAGAAT 540

TCCCTGTTGT TTATGCTTCA GCAGTAAATG GTACAGCTAG CTTAGATCCT GAAAAGCAAG 600

ATGATAATTT ACAATCATTA TATGAAACAA TTATTGATTc ATGTACCAGC TCCAATTGAT 660

AACAGTGATG AGCCCATTAC AATTTCCAAG TAGCATTGTT GGACTACAAT GATTATGTTG 720

GACGTATTGG TATTGGTCGT GTATTCAGAG GTAAAATGCG TGTCGGAGAT AATGTATCAC 780

GATTAAAACG TTTAGAAATT GAAGAAGCAC AAGCTGGAGA TTTAATTGCT GTTTCAGGTA 900

TGGAAGACAT TAATGTTGGT GAAaCTGTAA CACCACATGA CCATCAAGAA GCATTGCCAG 960

TTCTACGTAT TGATGAGCCT ACTCTTGAAA TGACATTTAA AGTTAACAAT TCTCCATTTG 1020

CTGGCCGTGA AGGTGACTTT GTAACAGCAC GTCAAATTCA AGAACGTTTA AATCAACAAT 1080

TAGAAACAGA TGTATCTTTG AAAGTTTCTA ACACAGATTC TCCAGATACA TGGGTAGTTG 1140

CTGGTCGCGG TGAATTGCAT TTATCAATCC TTATTGAAAA TATGCGTCGT GAAGGTTATG 1200

AATTACAAGT TTCAAAACCA CAAGTAATTA TTAAAGAAAT AGATGGTGTA ATGTGTGAAC 1260

CATTTGAACG 1270

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

AAGACCAGGA GAACAmGTAA AACAATATAC AGTTGaAATC GCTCGTAAAT TAATGGAATT 60

TGATATAAAA TGCTCGTGAT TGCTTGTAAA TACGCAACTG CTGTnGCTTT AGAATATTTA 120

CAAAAGACCT TATCAATCCC CAGTGATTGG CGTAATTGAc CAGGTGCTAG AaCAGCAATA 180

ATGACTACTA GAAATCAAAA TGTATTAGTA CTAGGAACGG AAGGCACAAT TAAATCTGAA 240

GCATATCGTA CGCATATTAA ACGTATCAAT CCACATGTAG AGGTACATGg CGTTGCCTGT 300

CCAGGTTTTG TGCCACTTGT AGAACAAATG AGATATAGTG ATCCAACAAT TACAAGCATT 360

GTCATTCATC AAACACTGAA ACGTTGGCGT AATAGTGAGT CTGATACTGT CATTTTAGGA 420

TGTACCCACT ATCCATTGCT CTATAAACCT ATCTATGATT ATTTTGGTGG TAAAAAGACA 480

GTGATTTCGT CTGGATTAGA AACGGCTCGT GAAGTTAGTG CATTGCTAAC ATTTAGTAAT 540

GAACATGCAA GTTATACTGA ACATCCAGAT CATCGATTTT TTGCAACAGG TGATCCTACT 600

CACATTACTA ACATTATCAA AGAGTGGTTA AATTTATCTG TCAATGTGGA ACGTATATCA 660

GTGAATGACT AGGAGGATTT TTAATGAAAG AGATTGTTAT TGCATCGAAT AATCAAGGGA 720

AAATAAATGA CTTTAAAGTA ATATTTCCAG ATTACCACGT AATAGGTATT TCAGAACTAA 780

TACCAGATTT TGATGTGGAA GAAACAGGAT CAACATTTGA AGAAAATGCT ATATTAAAAT 840

CAGAAGCTGC TGCAAAAGCA TTGAATAAAA CGGTCATAGC TGATGACAGT GGACTAGAAG 900

GCGATGAAGC AAATATTGAA AAATTATTAA ATAAGCTTGG TAATACAACT GATCGTCGTG 1020

CGCAATTtGT TTGTGTCATA AGTATGAGTG GCCCTGATAT GGAAACAAAA GTATTTAAAG 1080

GTACTGTTTC AGGTGAAATT GCAGATGGAA AATATGGCGA AAATGGTTTC GGATATGATC 1140

CGATATTTTA TGTACCGAAA TTAGATAAAA CCATGGCTCA ACTTTCAAAA GAACAAAAAG 1200

GGCAAATTAG TCATAGACGA AATGCGATTA ATTTACTTCA AGCTTTTCTT GAAGGTGATA 1260

AAAATGTCTA AATGGATTAT TGTGAGTGAT AACCATACTG AATCAGGCGT TTTATATCAA 1320

ATTTATGAAA TGCACCCAGA TGCAGATGTA TATTTACATT TAGGA 1365

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

AATTCCTGGT GCAATAATAA ATAGGATGAA AAAGATTCGG AAAATATGAT AACTCGTAAT 60

CATAGCAACA TCGGCACCAG TAGCTAATGC AACTAAAACT ATCTGATTAA CCCCTCCTGG 120

TGCTGCACCA AGaAACAATT CATTAATAGG ATTATTATCA AAGAAATGTA TGATATAAAC 180

CATGATTAGC GCACCAATTA TCAACATAAT ATTTTGAATT GTAATTGCGA TTGCTAGTCT 240

ACCTTTTAAA TCTGACAATA AATGCGCAAT TTGAACTCCA ATTCTAATCA TATATATTAG 300

TTGTGCCATG TTCAACAACC AATGATCTAG TGTAAATGTT AAACCTGTAG AAAAATTCCA 360

AACAATTAAT ACAATGAGTG GTGCTAATAA TTGAAATGTT GGAAACTTTA TTTTAGACAT 420

AATTAGATAA ACTATAAAGA TAGCTATCGC TAAAATAACT ATTTGCCCTA TGTTTAATAC 480

TTGTGATAAA GGCAAGACTT TTGTTAACTT TCCATTCGCA TGCATGTTAC CATCATGAAA 540

AAAATATGAA ATGAACGGTA CTAAAACAAC AACAAATATA ATTCGTGATG TTTGCGTTAA 600

GCTAACAACT AACAAATTAG CACGTTTGTC TTGTTCAGCC ATGACCAGCA TTTGTGTTAG 660

TGCTCCTGGT ATAACACTTA AAATAGCTGT TTCTGTATTA ATACGTGCAA TTTTTTTAAA 720

AACAAATGCC ATTACTATTG CAATTAATAA TATCGAAATA GATACAACAA TAATCGAAAG 780

CCAATTGTTT TTAATATCCA TAACGACATT TTTCGTAAAC GTTGATCCGA TTTGCACACC 840

TAATAGTACA ATACCTAATT CACTAAGTAA GAATGGCCAT TTAATATCAA GTTTGAAAAC 900

TTTTACACAA ATGATTGATG CGATAATAGG ACCAAACATA AATGGAAGTA ATACGTGCGA 960

TATCATTGCC ATGTTTTCCA CTTCTTTCAA TAAAAAATAA AATGACTAAA TTGCTGCTTG 1080

AGCTTCACGT TTGTTAAGAT AACAATATCC GCTAGCAGTT tTGACTACAA AGCATATATG 1140

GaCTTTCACT ATCAAGTCGC CGCCCATGCC TTATATACAT TTAAAAnGAG CCTGAACAAA 1200

GTTCAGGCTC TCAATTTGTC CGTATATTTA TTTTACAATA CGACTTAAAG CCGTATCAAA 1260

TGCTTGAATC GTTTTTCAAT ATCTTCTTTC GTGTGTGCCG TAGATAAGAA TGTACCTTCA 1320

AATTGAGATG GnGGnAAAAA CACACCTCTT TGnCATTCTC GGTACATTTC TGCAATAATT 1380

TCC 1383

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 415 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

TCCACTAAnA TGATTACAAT TGCATTAGTT TGGTGGAGTG CATTTACAAT CTTAACGGGT 60

ATGATTAAGA ACCACGGTTT AATTaTTTAG TGAGATTCTT ATTTGGTGTA GGTGAGGCGC 120

CAATGTACCC TTCTAATGCT GTGTTTAATT CATTTTGGTT CTCTAAAAAT GAAAAAGGTA 180

GAGCATCAAG TGCATTATTA GCAGGATCAT ATTTCGGACC TGTATTAGCA CCAATAGTTA 240

CAATTGCTAT TGTTAACGCA TTTAACTGGC AAGCAGTATT TTACATTTTT GGTGCAGTAG 300

GTATTTTAAT GGCkGTATtA TGGGCGATTA TTGCCAAAGA CTTACCTGaG CrACATAGwa 360

TGGTTAATGA AGCGGAGAAA CGTTTCATTA TGGAAAATCG TGATATCGTA GCTAC 415

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

TTTTAGaTaA aTyCAATTnT CyATaCTaAA TgATTnTCTT ATTaCGTCAA TTcGCCTTTT 60

aTTTTATCGT AATCTTTCCa CTGCAAAGCT AAAGCTTCTC CTATTCTAAG ACCAGAATAA 120

AATAACAGTC TAGTTAGCTG ACGAGAAGTA TCATTTGTGA TTTGTTCTAC TTTTTCATCA 180

AATGTGGGGT CGTATAAGAG CTTGTAATGC TTTTTGGCGT AATTGATAAC TGCTTTAAAA 300

CCTGCCCACA CAGATCGTGC ATAGTCAACA GAAAGACCTG CATCGTTTAA CAAATAATTC 360

CTGAAAGCAG TACATTGCGT AGTAGTGATT TTGCCAATAG GGATATTTCC GAACCTTTCT 420

TTTATGTGAG TATTATATTC TGTAGTTCGC TTTTCTATTG AGCGTGCAGA AAGATTTTCA 480

TTTTTTAAAC GATCAAAAAA TATATATTCA AAGGGTTGAT TGTCCGAGTA TCCATATTTA 540

ACATTTTGTA TAAATTCGCT TTCAGCTAGT TTGGCATCTT TCTTACGTTC AAACCCACGC 600

TTCATTTTTC GTTTGTTATT ACCGTATACA TCTTTATATC TAATGGAAAA ATACCATTTA 660

CCTGTATTAT CATCCTTATA TACTGGCATT TTGCTTCTCC CTCCTCAAAA TTGGCAAAAA 720

ATAATAAGGG TAGGCGGGCT ACCCGAAATT TAGTACTAGG TACTAAATGT GATATAATAA 780

AATAAAAAGT AGGTGATGTT ATGACATTTA AAAACAATCA TAATTTCAAT GAATTAGTTT 840

TAACGAATGA AGACATTAGA ATTTTAAAAA ATGTCTTAGA AGATGCAGTC AGTGTTTATG 900

ATGAATATTC GGTATGTAAT GAAGAATCCG ATTTTGCTTA CTGTTTATTA AGAGACTTAT 960

ATACATTAGA CAGCTTAGCT ATTTCGTCAA ATAATGTTTG AATTATCGAA TTGTACTCTT 1020

CGATTTTAAT ACCATGCATA ATAGAGTTTC TGTGTTCAAT AGCAGCTTTG ACTGAATGTk 1080

TTAAATGTTC TTCTATTAAA TCGTTGTTTk CCAtTTCGtk TAaAAATGTt CyTATATTCC 1140

T 1141

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 706 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

ACTGTGGTAG GTTTTTTATT TTGAAGTATT AATCATAACA GACTAATAAT CATGAGGTAA 60

CTAATAACAC ATATTTAACT TGTATTCTTA AACTGGTATA ATAAATTTAT GTTGAAATGA 120

ATATTGTATG ACAGGGTATT CACTTTTATT AAAAGGTAAA ATTAAATAAA GGTTTTATAG 180

AACGTATTTA AATATATGAG GAGTAAACAA ATGGCTGATA GAACGAATAA AGAAATTAAA 240

ACAGGACGCT TTATTGCAAC TGCATCAATC GTATTCTCAA TATTATTGAT TATTCATTAC 300

TTTGTTTCGT TGGATAATGC GACTGCCAAA GCATTACTTA ATTTAACGAA TCAAAACACT 360

TCAGATAAAG CGATTGATTA CATTTTAAAC AGCTTTAGAT TCACTGGTAT TATGTATATT 420

ATGTTTGCAG TTTATGTATC AAATAGTTTG TTTACGTTGA TTAATTTATC AATCACAATT 540

CAAGCAATAA AAGCTGCACA CGGTGCGTAC TTAACATTGC CAATTTTAAT TGTTATTATA 600

GGTTCGGTTG CATTAGCGAT TTATATGCTT GTTGTTTCTA TCAAACGTAA AAGTACATTT 660

AATCGCTAGA AAATTGATTT TAACAATAAA AATATGAAAA AAAAnn 706

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

ACACAATCTG AAGATTCACG TTGTGGTGCT GGACATGATC GAAAAATTAG AGCTGAACAA 60

ATGAnAGAAA TCAGTGATTT TGTTAAAAAG AAAAATATCC CTAAAGATGA AACGGTATAT 120

ATAGGTGGCG ACCTTAATGT CAATAAAGGC ACTCCAGAGT TCAAAGATAT GCTTAArAAC 180

TTGAATGTAA ATGATGTTCT ATATGCAGGT CATAATAGCA CATGGGACCC TCAATCAAAT 240

TCAATTGCGA AATATAATTA CCCTAATGGT AAACCAGAAC ATTTAGACTA TATATTTACA 300

GATAAAGATC ATAAACAACC AAAACAATTA GTCAATGAAG TTGTGACTGA AAAACCTAAG 360

CCATGGGATG TATATGCGTT CCCATATTAy aCGTTTACAA TGATTTTTCA GATCATTACC 420

CAATCAAAGC CTATAGTAAA TAGTGCTCAA CTAACTAATA ACTTGCTtCG TTCTAAAAGG 480

ACGAAGCGAG TTATATTGTT AAAATTTGAA TTGACTTACA TTTTAATAAA ATCATCTTAA 540

CAACTTTAAT TTTTCaTTAA TACAaGTCTT TACTCTACAC TCAAACnAGA TTCATACACT 600

GCACGTCATA ATAAATCTAT CTATTCAAAT ATAAATAAAA GTTACCTACT ACATTCTATG 660

TAGCAGGCAA CTTTTATTAC TTATTTCTTT TCATTATCAT TAAGTACTTT TACAAACTTC 720

ACATTATGTG TCTTCCAATC AACTTCATAT AATGCTGATA ATTTTTCTTC TTTTTTATCT 780

ACATGGTTTT CACCAGACCA ATAGCCCCAG AAACCATGGC GATTCCAATC TATTTTAAAC 840

TCATCCATTG ATCTTTTATA ATGAACAACA AATTGTGATT TACCTTTGTC TTTTTTATCA 900

TGTGACATAA CAGCTAAAAA TTCTGGATTA AACCCTTCAG ACACAGTTAC AGGCATTTTG 960

TCTTTAGGTG TGAAATTATC TTTCGCCCAT AAATTTCCAT TTCGTGTTAA AGAAAAAATT 1020

TCACTTTTAG TTCTATTATC ACTATCATTA GTTAATTGTC TCGTATGGTC ATGTCCCATA 1080

TTATTTATCA AATGTGCTTC TACTTTCCAA CCTACACCTT TATGTGACGT AGATTGATCA 1140

(2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 847 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

CCAGAATTAT TTTTTCAAAA AGGACAATTT AACAATGTCG ATAACGTTAT CATAAGCAAA 60

CCGATGAAAG GGACAATGCC TAGAGGTAAA ACGGAaGCTG AAGATCAACA GTATTATAAA 120

ACATTGCAAA CTTCTTCGAA AGATCGTGCA GAAAATGTCA TGATTGTTGA TTTACTAAGA 180

AACGATATAG GGAGAATATC ACAGAGTGGC TCAATTAAGG TGTATAAACT ATTTTTTATT 240

GAGGCATATA AAACTGTATT TCAAATGACT TCGATGGTAA GTGGAACTTT AAAAAATAAT 300

ACAGACTTAA CTCAAATTTT AACATCGTTA TTTCCTTGTG GTTCGATTAC AGGTGCACCG 360

AAACTGAATA CAATGAAATA TATTAAACAA TTAGAAAGTT CACCTCGTGG TATATACTGC 420

GGACAATTGG ACTATTACTT CCAACTGAAG ATGATAAAAT GATTTTTAAT ATTCCGATTC 480

GCACTATTGA GTATAAATAT GGACAAGCGA TTTATGGAGT CGGAGCAGGT ATTACAATTG 540

ATTCTAAGCC AAAAGATGAA GTGAATGAAT TTTACGCAAA AACCAAGATT TTGGAGATGT 600

TATAATGCAA TTATTTGAAA CAATGAAAAT TGATAATGGA CATATCCCTA GACTTACTTA 660

TCATACTAAT CGCATAAAAT GTTCTTCTGa GCGATTAAAC TTTAAATTTG ATGAACATGC 720

ATGGCGAAAT GAATTAAACG ATGTAACAAC AAAGTATCAC AGTGGTCAAT ATAGACTTAA 780

AATCGTATTA AATGCTGAAA GCAAATTTGA AACGATAGTG TCACCTTTAC CTGAGAAAAG 840

TAGTTTT 847

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 740 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

TGAAGATGAA GCAGAAGCAG AAGACAATCT GCTACGAGTA CAATCGAAGA AAGAAGAAGT 60

GTATCGTCGA TTACTTGCTT CTAACTTAAC AAGCGTTCCT GAAAGtTTAT CATCATGAAA 120

GTTAAACAGT TAAAAGATAA AGTGTCTAAA ATTGTGATTC AAATGAATAC ATTTGAAGAT 240

GAAGCAAATG ATGTTCTTGT TAATGCTGTT TATGCAGAGA AATTAATTCA ATATGGAAAT 300

AGATATCGTA AGGACTATAG CAATGTTGAT AAGAGCTTAA ATGAAGCTGA ACGATTATTT 360

AAAAATAATC GCTATAAGCg TGCGATTGAA ATTGCAGAGC AAGCTCTTGA AAGTGTTGAG 420

CCAGGTGTTA CTAAACATAT TGAAGAAGAA GTTATTAAGC AATAGAAACT AGTATGTAGT 480

TATACTTAAA TAATATGAGC ACTCTGTCAA ATTGGACTGA TGAGTTTAAT AATTGAAGTT 540

AGCCAACGAT ACGTTGTCTA GCTTCTTTTT TATATGGATA AATGaAAGGG ACAATAAATA 600

TAAATAGCAA TTGTTTAAAG ATAAACGTAA TCAAATGTGT TGTTTTAATT AATATAAGTA 660

GTGAAAAAAG CATAATCACA CAGCTGTTTA AATAGAGTGA AATAGTCTAA TTCTTATTTA 720

ATAAGTAGAA ATAAGATTAT 740

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 630 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

ATGCCAATAA TTAAACCATG TAATAAATAT ACGTATAGCG TACGACTACC AATATAAGTA 60

TATAATTTTT TCTTTGTTGA CATTAAATTT AGAAACGCAG TCATTGCGAT TAATATAATT 120

CCATATAATA TAAGTCGTTT AAAAGGACTG AATATACTCT GTCCTTCATT TTCAAGTGAA 180

GTATATGGTG AACTTCCCAA TAACCAATCT GCATTGATAG GATGAATCAC GTAAACGATA 240

AAAAACAAAA TAAAGGTAAT GATAGATACT GGTATTAGTT TTTTATTTTT AAAAATAGCC 300

GTATGTTTTT TGGTGAAAAT GTAACCTAGA TAAAATATTG GGAAAAATAC GATTGTCCTT 360

GAAATGCTTA AGTAGCTATC GATGTTATCT GAAAAACCTG CTCCAATAGA TATAATAATT 420

GAAACTGATA GCACTTTATA TGGATTAAAT CTTCTAACTA TTACTAAAAT GACATGAAAG 480

AAAAATAGCG TGATCAAAAA CCATAACGCA AATACTGGGT TAAAAGGATC AAGTTGTAAT 540

TCGTCACTTT TACCTGTTAA GAAATAATAA ATTGAAAAGA ATGCAAAAAA TATCATATAA 600

GGTACTATCA AACGTTTTGA AATTTTTTCT 630

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6254 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

ATTTAAACGT TCAGTTTCTA AAAGTGGAAC AATCCAAGAA GTACGTAAAC GTGAATTTTA 60

CGAAAAACCA AGCGTAAAAC GTAAAAAGAA ATCAGAAGCT GCACGTAAAC GTAAATTCAA 120

ATAATTAATA CCTCTGTTGA CTCCCTCAAC ACGAATATTA ATTATATAAA ACAAACATCA 180

CAAGTTAGTG TCTGACACTA ATATGTGATG TTTTTTTGTT GTCAATTTTT AATTAAAAAA 240

AGTTATATAG TTTATAAATA ATCAAATTGA TATTCTATAG GTTCTTATAA CTATAAAGTA 300

TATTCAATTT CATGTATAAT TAATGTGAGG GCGAGGTGAA ATTGTGAGTT ATAATAATTT 360

TTTACAAATG ACAACTATCT TGGAATCAAC GGCTGGAGAT ACTTGGGTTG AACAAGTTAG 420

CAATATAATT GTTCAACCTA TTTTTACGTT AATATTAACC TGTTTGACAT TCTTAGGATT 480

TGTATATCAA CTTTACTCTA AAAAAATCAA TGCAGCTGGT ATTATCGCCA CATTATCATT 540

ACTTATTTTA TTTTTGGGAT TTCTAATCCA AGGAAATGTC AATATGCATT CTATCTTAAT 600

ATTCTCAATT GGCGTTATAT TAGTTGTAAT TGAATTATTT GTAGTTGGTG CAGTAATTGG 660

TATTATTGGC ATGATACTGA TAACTATAAG CATAACAACG CTCGGTGATA ATTTGCTATT 720

TATGCTTGCG AATGTTATCG TTGCCTTGAT TTTAACGATT GTAGAATGGG TGATATTAGT 780

GAAGATTTTC AACAGAAAGA TTCCGTTTTT GGATAAAGTT ATCTTAAAAG ATTCAACTAA 840

TTCTGAGTCA GGTTACAATT CTCATGATAA CCGCTCGCAC CTCGTAGGAA AGACTGCTCA 900

AACAGTTACA GATCTTCGAC CTGCAGGGAT TATTTTTTGT GAAAATGAAC GTATTGATGC 960

TGTTTCAGAT GGCAACTTTA TTTTGCGCAA TAAAACGGTA AAAATCCTTG AAGTTGAAGG 1020

AACAAGAGTA GTTGTGAGGG AAGTAGATTA ATTAAAAGGA GCGATACCAT GTTTAGTTTA 1080

AGTTTTATCG TAATAGCAGT TATTATAGTA GTTGCATTAC TTATTTTATT CTCATTTGTA 1140

CCCATTGGTT TATGGATTTC AGCGTTAgcA GCTGGCGTTC ATGTTGGTAT AGGTACATTG 1200

GTTGGTATGC GTTTACGTCG TGTATCTCCA AGAAAAGTTA TAGCGCCATT AATTAAAGCG 1260

CACAAAGCAG GACTAGCATT AACAACAAAC CAATTAGAAT CGCATTATCT AGCAGGAGGA 1320

AATGTTGACA GAGTTGTTGA CGCTAATATT GCTGCACAAC GTgcTGACAT TGATCTTCCT 1380

TTCGAACGTG CTGCTGCAAT TGaCCTTGCA GGACGTGACG TATTAGAAGC GGTTCAAATG 1440

TCTGTTAATC CTAAAGTCAT TGAAACACCA TTTATCGCAG GTGTAGCAAT GaACGGTATT 1500

GAAGTGAAAG CCAAAGCTCG TATCACAGTT AGAGCTAATA TTGCTCGACT TGTTGGTGGT 1560

AGTAAGCATC ATACAGAAGT ACTTGAAAAC CCAGATAATA TTTCTAAAAC AGTTTTAAGC 1680

AAAGGTTTAG ATTCAGGTAC TGCATTTGAA ATTTTATCAA TTGATATTGC TGACGTTGAT 1740

ATTAGTAAAA ATATTGGTGC AGACTTACaA ACTGAACAAG CATTAGCAGA CAAAAATATT 1800

GCACAAGCAA AAGCTGAAGA ACGTAGAGCT ATGGCTGTAG CAACTGAGCA AGAAATGAAA 1860

GCGCGTGTAC AAGAAATGCA TGCTAAAGTA GTTGAAGCCG AATCTGAAGT ACCATTAGCT 1920

ATGGCTGAAG CATTACGTTC AGGTAATATC AGTGTTAAAG ATTATTATAA TTTGAAAAAT 1980

ATCGAAGCTG ATACAGGCAT GAGAAATGCA ATTAATAAAC GAACTGATCA AAGTGATGAT 2040

GAGTCACCTG AACATTAAGT CGAGAGGTGA TTAAATGAGT GTCGGTATTC TAATTTTTGT 2100

CATATCAGTG ATCATTTCTA TCATTACTAC TATGCGCGAA AATAGTCATA AAGATAGACA 2160

AAATCAAAAG CCACCTCAAA AAACATCTAC CGATAATGAA CCAAAAAAAG GTGGCTTTTT 2220

TGAAGAAATT GAGCGAACGT TTAAAGAAAT AAGTGAAGAA TTAAATGAAG AAGAAAAGAA 2280

ATCATCGAAA CGAAAATATG ATGATACGTT ACCACCTTTA TTCGATGAAC TTCCAAAGGA 2340

AGAGCCTAAA TCGAAACCTG TTGTAGAACC TATGGCACCT AAAAAACAAC AAGAAACAAA 2400

ACCGATGACA GAGAAACCAA TCACAGTGCC TAAAGCAGAA CCGGTGGAGC AGAAACATAG 2460

ACCTTCTAGA CAAGATAATT CTGACGAAAT TAGACGTCAA TTAGAAAAAT CACTTAGAGA 2520

TGATATTAAA ACGATTCGTA CTGACATTGA TAGAGAAAAA GAAAAGCAAA TTGCTAAAAT 2580

GGAAAAACGT GCTAGAGATA TTATTGAGGA TAAATACTTA TCTGAACGTA CAAAACGTTT 2640

GAAATTAAAG CAGCTGCTTA ATTCTCAAAA TGTCGAAAAA GATTTGACTA AATCAGCGTT 2700

CCAATTTGAT AAAGATGAAG TAATCAATGG TATGATATGG TCAGAAATTT TAGCTAAACC 2760

AAAACAATTA TAAAATTTTT TGAAAACAAG CACTATCGTA ATGGTAGTTG CTTGTTTTTT 2820

TACGTTAAGG AAAATTAAAA AACAAAGAGA ATTTTTCGAG AAATATTAGT TATTTAAATT 2880

ACAGCAAAAA ATTGATTAGT CTAAAATTGA ATCTGCTTTT ATGACAAGGT GAAAAGTATA 2940

AATGATTATT TTAAATTAAA GAAAAATGAG TAAGTCAATG CAAAGATGTT TAAATCAATC 3000

AATTGCATGA TATAATTAAG TAGATATTAA AGCATCATAG AATGAATATA AATGATATAT 3060

GAAAAGGAGC GCGTGTATGC CTGGAATTAT ACAAATAGAC GATATGAACC AATCTCAAGC 3120

TTTAATTGGA AATAATGATG AACATTTAAA AGCAATTGAA GAGAGTTTCG ATGTTGTCAT 3180

CCATGCAAGA GGACAAGaAG TTGCCGTTAA AGGTACAAAA ATAGAAAACG TAGAAAAAGC 3240

GGAATCAGTA TTAATCAATT TGCTGAAGGT TATTGATTTA GGTAATAATA TTACAATTAA 3300

AGATGTTGAA GCAGCTATTA AAATGGCGCA TAATAACACA ATTCAACATC TGTTAGATTT 3360

GCAACGTATA TATGTTAATG CCATGAAAAA TAATGATTTA GTATTTGGTA TAGGTCCTGC 3480

TGGTACAGGT AAGACATTCT TAGCTGTAGT TTATGCAGCA AAGCAACTCC GTAAAGGTGC 3540

TGTTAAACGT ATTGTATTAA CAAGACCTGC TGTTGAAGCA GGAGAGTCAC TTGGATTTTT 3600

ACCAGGAGAT TTGAAAGAAA AGGTAGATCC ATATTTAAGA CCTTTATATG ATGGTCTATA 3660

TACTGTTCTT GGGCGTGAAC AAACAGAGCG ATTTATTGAA AGAgGCATTA TCGAAATAGC 3720

GCCACTTGCA TATATGCGCG GACGAACATT AGAAGATGCA TTTGTAATTC TTGATGAGGC 3780

GCAGAATACG ACACATGCGC AAATGAAAAT GTTTTTAACA AGACTAGGTT TTGGCTCAAA 3840

AATGGTAGTT ACTGGTGACC AAACTCAAAT CGATTTACCT AAAGGTGTTA AAAGTGGACT 3900

TAAGGAAGCG GTCAGTAGGT TACACAACGT TAAAGGTATA AGTATATTGA AATTAGATCA 3960

GAGCGATGTA GTCAgACATC CATTGGTAAG TAAGATCATT GAACATTATG AAGGAGAGAA 4020

TTAAATGTTT ACGATAGATT TTAGCGATCA CACAGGCTTA GTTAAAGATG CTTGGTATAA 4080

ACAAATTGAA GATTTATTAG AATTTGCTAA AAAAGAAGAG CATATAGAAG ACGATGCTGA 4140

GCTTTCTGTT ACATTTGTAG ATAAACAAGA AATACAAGAA ATTAATCGAA CATATAGAGA 4200

TAArGwTAAr GTTmCaGATG tAaTCyCaTT tGCTTTAGrA GrAGATGAGC CmGaGATkGA 4260

TtTTAGTGGT CTTGATATAC CACGTGTTTT AGGGGATATA ATTATCTGtA CGGATGTAGC 4320

GCAAGrACAA GCAAACAATT ACGGACATTC TTTTGAACGA GAATTAGGAT TTTTAGCATT 4380

ACATGGATTT TTGCATCTAT TAGGTTATGA TCATATGACT GAAGCGGATG AAAAGGAAAT 4440

GTTTGGTCGA CAAGATACAA TATTAAACGC ATATGGATTA ACACGAGACT AATTATGAAA 4500

AGGTTTAAAT ATGCACTTGA TGGGCTGAAA ATCTTAATTC AAAAAGACTA TAAATTTCTT 4560

TTACATGTGT TTGCAATGAT TGTTGCTATT GTCTTTGGTC TCGTACTAAA TATTAATCGG 4620

ATTGAGTGGA TATTTATACT CATTGCTATT GCATTAGTTC TCACTGTTGA AGCTTTAAAC 4680

ACTGCTATTG AATATGTTGT CGATTTAGTG ACCGTTGAAT ATCATGATTT AGCTAAATAC 4740

GCTAAAGATA TTGCGGCTTT TAGTGTACTT ATAGTTTCAA TATTAGCATT TATTATAGGT 4800

TTAATAGTAT TTTTACCACA TTTTATAGCG TTATTTTAGG GAGGCATATA TGAGTTATCA 4860

ACCTCATTAT TTTCAAGAAG TTAGAAAAGC ACAACAAGAA TCATATTCGC CATACAGTCA 4920

ATTTAAAGTA GGGGCTTATT TAAAAmCGAA AGACgGTAGA ACTTTTTATG GTACCAATGT 4980

AGAAAATGCT TCTTATCCAT TATCGATATG TGCTGAACGA GCTAGTTTGG TATCGGCAAT 5040

TTCTCAAGGA TACAGACCAG GTGATTTTGA ATCAAtAACT GTAACCGTAG ATGCAGATAA 5100

ACCGTCATCA CCTTGTGGTG CATGTCGTCA AGTTTTGAAG GAATTATGTG ATGATGATAT 5160

ACCATTTGGA TTTTCAGGAA AGGATTTAGA ATAAATGACA GAACATAAAT CAGGATTTGT 5280

TTCAATTATA GGTAGACCAA ATGTAGGAAA GTCAACATTT GTTAATAGAG TGATCGGCCA 5340

TAAAATAGCA ATCATGTCCG ATAAAGCTCA AACAACTAGA AATAAAATTC AAGGTGTTAT 5400

GACAAGAGAT GACGCGCAAA TTATATTCAT TGATACGCCA GGTATTCATA AACCTAAACA 5460

CAAATTAGGT GACTATATGA TGAAAGTCGC TAAAAATACA TTATCTGAGA TAGATGCAAT 5520

CATGTTTATG GTTAATGCCA ATGAGGAmAT TGGACGAGGC GATGAATATA TTATAGAAAT 5580

GTTGAAAAAT GTTAAGACAC CAGTATTTTT AGTATTAAAT AAAATAGATT TAGTGCATCC 5640

AGATGAATTA ATGCCAAAGA TTGAAGAATA TCAAAGTTAT ATGGACTTTA CAGAGATTGT 5700

ACCTATTTCA GCATTAGAAG GGCTAAATGT CGATCATTTT ATTGATGTTT TAAAGACGTA 5760

TTTACCCGAA GnACCTAAAT ATTATCCAGA TGATCAAATT TCAGACCATC CTGAACAATT 5820

TGTAGTGGGT GAAATCATTC GTGAAAAAAT CCTTCATCTT ACAAGTGAAG AAATCCCTCA 5880

TGCGATTGGT GTTAATGTGG ACCGTATGGT TAAAGAAAGC GAAGATCGTG TTCATATCGA 5940

AGCAACTATA TATGTTGAAA GAsGTTCGCA AAAAGGAATT GTCATTGGAA AAGGCGGTAA 6000

AAAGTTAAAA GAAGTAGGaA AAcGTGCGAG ACGTGAtATA GaAATGCtTC TAGGCTCTAA 6060

AGTTTACTTA GAATTATGGG TCAAAGTTCA AAGAGACTGG CGAAACAAAG TTAACTTTAT 6120

TCGCCAAATT GGTTATGTTG AAGACCAAGA TTAATCTTAA AAGTGGTGAA GATAATTGTT 6180

AATGCGCCAA AAAGGGATTA TCATCAAAGC AGTTGATTAT GGTGAATCTG ATAAAATTAT 6240

CACGATTTTA AATG 6254

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3710 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

GTTGTTCTAA ATGTTTCTTG nATGAAACGA GTCAATGTAA ACTGATATTG CTGTATTTGT 60

TGCAGCAATT CATATTGGTC TGGTGTTGCA ATAACAGCAG CTTGAGTTGG AGTCGCAGCT 120

CTGATGTCTG CAGCAAAATC ACTTAATGTA AAGTCTGTTT CATGACCAAC TGCTGATATA 180

ATCGGTGTCT TACAATTATA TATTGCACGG ACGACAGCTT CTTCGTTGAA ATTCCATAAA 240

TCTTCTATGG ATCCACCGCC TCGACCTACA ATAATGGTAT CTACACCTAA ACTATCTGCA 300

TGTATTTGTT CAGCTAATGG AAAACGACTA TTTATCGTTG AATGGATATC TCGAATTGCG 420

GCACCTGTAC TCGCTGTTAA AACTGCAATT TTTTTAGGAA ACTTAGGTAT TGATTTCTTA 480

TTCGCTTTAT CAAAACAACC TTCTTCAGTT AATTTTTTCT TTAATGCTTC TAATTTTTGA 540

TATAAGTTCC CTATACCATC TAATTGCATT TTATTTACAT AAATTTGATA GTTTCCACGA 600

CGTTCAAAAA CAGAAACACG TGCTTCTAAT AAGACTTCAT CTCCTTCTTT AGGTTCGAAG 660

TTTAATTTAG AAGCACTACC TTTGAACATC ATGGCACTTA TAACGCTTTC TTTATCTTTC 720

ACATTAAAGT ATAAATGaCC ACTTGaATGc TTTTTGAAAT TTGAAAGCTC ACCTTTAATC 780

AATACAGATT GGAGATGTGG ATCTTGATCA AATTTATATT TAATATATTT CGTTAAAGCT 840

GAAACACTTA AATAATCTGA CATATAACAT CACTCAATTT TATTTTTTTA TATTACTCAA 900

TACACCATTT ATAAATTTAT AATGATCATC ATCACTGAAT TGTTTTGTTA ATTCAACTGC 960

TTCATTCATT ACGACTTTAG CAGGTGTATC ACTGTGTAAT ATTTCATATG TTGCCATTCT 1020

TAAAATAATA CGATCCGTTT TTAATAAACG TGCAATAGTC CAATCTTTTA AATAAGGACT 1080

AATTGTCTCG TCTAATACAG GTTCGTGATC TTTAACGCCA GAAACTAGCC AATGAATAAA 1140

TTCGAAGTCT AAATCTGGAT TATCGTCTTT AATAAAGCTT ATCGCTTCAT TTATCGTTAA 1200

ATCACTGTCC TTCATTTCTA ATTGAAATAA AGTTTGAAAA GCTTGCACTC GGGATTCTTT 1260

ACGACTCATT TTTAACTCCT TCAAACGTTT GTATTTTTCT TTATTTAATT ACTGAATTAG 1320

GTATGACATT ACTTTTCAAT AACGATTTGT GTAATGTGAA TATTAATTTG CTTAGGTTCT 1380

ATCGCTGTCA TATTAGAAAT TGAATTAAAA ATTGACGTTT GAATTTTGTT TGCAGTTTTT 1440

GAAATATTAA CACCATGTTT TAATGCACAA TATACATCTA TATATATGCC ATCTTCTTTA 1500

CTCTCGATTT TTAAATCACG GCTTAAATTT TTACGACTAA CTTTTTCTAA ATTTGTTTCT 1560

TTTAATTCAG CAAAATGGCC AGTGATGCCT TCGACTTCCG AAGTAGCTAT ACTTGCAATA 1620

ACAGATAGCA CTTCTGGCGC TATTTCTACT TTACCTAATT TTGAATTTGA ATAATCAGTT 1680

ACTTTGACCA TGGATTGACC TCCTATTAAC CTTCATCATT CATAATGCTA TTTTGCTCTA 1740

AAAAGTTTGT ATTAAATTTA CCGCTTCTAA ATATATCGTT ATTCAATAAT TTAATATGGA 1800

ATGGAATAGT TGTATCAATA CCAAGAACCA CAAATTCACT TAGTGCACGA ATGCCAGCCA 1860

TAATCGCTTC ATCTCGTGTC GGTTCATGTA TGATTAATTT CGCTACCATC GAATCATAAT 1920

ATGGCGGTAT CGTATAATTA GTATAACATG CTGACTCTAT TCGAACACCA TATCCACCTG 1980

GTGCAAGATA TTGCTCmATT TTACCTGGTG ATGGCATAAA GTTCTTGTAA GGATTTTCAG 2040

CATTAATTCT AAATTCAATT GCGTGTCCTG TTAATTTAAT ATCTTCTTGT TTATACGGTA 2100

CAGTTACAGG ATGTTCTACT TGAATACGTG TATTCATTTC CATAAAATAA AATTTATTAT 2220

CATTTAAATC ATATATAAAC TCAATTGTTC CCGCATTTTC ATAATTTACA GCTTTCGCTG 2280

CACGAACTGC GGCATTTCCC ATTTCACGAC GTGTTTCATC ATCTAAAATT GGGGAAGGTG 2340

CTTCTTCCAC TAATTTCTGC ATACGTCTTT GAATTGTACA ATCACGTTCT CCTAAATGAA 2400

TTACATTACC ATAGCTGTCC CCAACAATTT GGATTTCAAT ATGGCGGAAG TTTTCGATGA 2460

ATTTCTCCAT ATAAAGTCCA CCATTACCAA ATGCAGTTTG AGCTTCTTGT TCTGTCATTC 2520

GGAAGCCAGT TTCAAGTTCT TTTTCATCAC GAGCAACACG GATACCTTTT CCGCCACCGC 2580

CAGCAGTAGC TTTAATGATG ACCGGATAGC CAATTTTTTT GGCGATTTTC TTAGCTTCTG 2640

AGACGTCTTT CATTAAACCG TCACTACCAG GAACAACTGG AACATTGGCT TTGATCATTT 2700

CTGCCTTAGC AACATCTTTG ATACCCATTT TTTGGATAGA TTGATAACTT GGTCCAATGA 2760

ACTTCAATTG GcATgctTCG CATAATTCTG CAAAATCAGC ATTTTCAGCT AAAAAGCCAT 2820

AACCCGGATG AACGCCATCA CAACCTGTAG AAGTTGCAAT AGATAAGATG TTCGGAATAT 2880

TTAAATATGA ATCTTTAGAC AAAGTGGGAC CTACGCAATA TGCTTCATCA GCAATTTGAG 2940

TATGTAGCGC ATCTTTATCC CCTTCAGAAT AGATTGCAAC AGTTTGGATG CCTAAATCAC 3000

GACAAGCGCG AATAATCCTA ACTGCGATTT CACCGCGGTT TGCAATTAAA ACCTTTTTCA 3060

TTATTTCACC TTAAATAACG GTTGGCCATA CTCTACCATT TGTCCGTCTT CTACTAAGAT 3120

TTCAACAATT TCACCTGAAA TTTCTGCTTG AATTTCATTA AATAGTTTCA TTGCCTCTAA 3180

AATACACACT GTTGTTTCAT TTGAAACAGT GTCCCCAACT TGCACATATG CTTCTTCGTC 3240

TGGAGATGGC GATTTGTAAA ATGTACCTAC CATAGGTGCA TTAATTGTTT TGTGATTATC 3300

TGAAGTTGGC TTTGGAGCTT CAGTTTTATT GCTATCAGTT GATTGTGCTT GAGGCATAGG 3360

CATTGCCGCA GCTTCAACTG GCATTTGTGA GATTTGTGGC GTGATAATCT CAGTTTCTTT 3420

TTCTTTCTTA AGCGTCACTT TGCCTTTAGT ATCTTCAATA TTGATTTCCG TTAAAGTTGA 3480

TTTATCCAGA ATTTCAATTA ATTCTTTGAT TTCTTTAAAG TTCATTATTA CTGACTCCTT 3540

CAGTTTGTTT TCATCTACCC GTCTATTTTA CTTGAGACAA CTCTTCAATT CAAGCATGTT 3600

CATATTGCTG GCGACATTAT AAGTCTATCC CAAAGTTATA ATAAAACCAC ATTTTAAATT 3660

AAAAACACTT GTGTATTTAT TACTTAACAT TGACTCATCT TAACTCTTGA 3710

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1705 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

GCTGATGTTC GTTGCCTTTn TCCACCAGAC AATTCAGAGG GATATTTATC ACTAATATCC 60

AATATATTTA ATGCTTCTGC TACTTTTTCA TAACGATTTA ACATATGTTC TTTATCTAAC 120

TTCTGTACCG TTAGTGGTAA CATTATGTTT TCTTTAACAG TCAATGTATG CAGTAAATTA 180

TACTCTTGAA AAATAAAACC AATATCATGC TTGCGTATAT CAGATwATTC CTTGTTTGAA 240

AGCTTTTCTA ATTTTTTTCC TTTTAATGTA ATAGAACCTT GTGAAATATA ATCAATTGAA 300

CTTAAAACAT TTAATAATGT CGTTTTCCCA GATCCAGAGG GACCCATAAT AGCAATAAAC 360

TCGCCTTCTT CAATAGACAT ATTGATATCT CGCAACACTT CTTGTGCCAT TTTTTTAGTT 420

CCATATATTT TTGTTAATTG TTTTACTTCT AAAATTGCCA CTTTAACACT CCTATAATTT 480

ATCTTAACTT CATTTCCTTT AGGCTTTGGC ACTTGTATCT TCAATTTAAC ATATGACTAA 540

CATCTATCTT ATTATAACGT TGAAGCTGCA TTGATGTATC AATTCTAAGT AACAAAACGC 600

ATGTTTAAAA TGACAAATTT GTCACTTCCG ACATGCGTTC AACAATTTCA TTTTGTAATG 660

GGAAAATCAA TCTGACAGTT GTCCCCTTAC CAACAGTCGA CGTGACTTGC AGGTGAATAC 720

CTAATTGATC CTTTACACTA TTTACTAAAT ATAGACCCAT ACCTGAAGAC GTCGTTTCAT 780

TTCTGTTAGC CGTTGACGTA AATCCTCGTT CAAATATTCG CGGCATATCT TTTTTACTAA 840

TACCTCTGCC ATAGTCTTTA ATATATAACG AAACATGTTG ATCATTTAAT TCTGTCCCAA 900

TTTCAATATT AAAATTCTCA CTATATTTCA ATGCGTTTGA CAAAATTTGT CTAATAATCA 960

TACGACACCA TTTTATATCT GTATAAACAT AATCATCCAC TTTAAAGTCA ACATCAAAAC 1020

CAATACCTTT AACCTGACTA ATATGTCTTG TTAATTGTAT TTCATCAATG ACCATGCGTT 1080

TAAGTGACAC GTAATCAAAA TACATATCTT TACGTTGAGA TTCTAATCTA GTAATATACA 1140

GCTGTGTATC TAGCATCGAG TTTATACGAG ACCATTCATA TAGTAATGCT TGTwTTCTTT 1200

CTTGATTTTT TTCTTGATCA ATTAATAATT TCATAGCTGT CACAGGtGTT TTTATGTCGT 1260

GCACAAATTC TGTAATGGTT TGTTCATGCA TGTTCAATTG CAACTGTTGC TCAACAACCT 1320

TTTCTTTGTG CGCTGAGATT TGACGATATA AATAATCAAC TGTATGACGT TGAAATGGCG 1380

TTTCCGCTAA ATCTTTATGT TTAATTTCTT CTATTTCTTT ATCTTTGTCA AAATGCTTAT 1440

ATAATTTTAC TTCTTTAAAA TATGTCAATA AAAGAAAAAT CATTGTTAAA CTTAAATTCA 1500

AAGAAACAAT ATAAAATAAA CTGTCTATTG GAAAATCATA ATCGATTAGA CTArTGCCTA 1560

ACATAAGGAA GTTTAAAAAC AATATCCAAA AtATCCAGTT CATGCGAGAT TTCAAAAAAT 1620

GCACTATCCA TACTAATTTC AGATA 1705

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1722 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

TCAATATATC TTAAAATTCA ATGATTAAAT CnATTATCAC TAGACATnAA ATACATAAAT 60

CCTATTCCCC ATTTTCATTT nTTAATTCAT AAATGAATCA ATAACCACCT AATAACAAAT 120

CATATTATAC ACCTTTGTTC TCTATTTTTC TAAGGTTTAA AAAATATTTT TAGGTAAACC 180

TAAAAATAGA TGTAATAAAA ACGCCTCCTC AGATATTTAT ATATCTATGA AGACGTTTAA 240

ATACATTATA GATGGTCTGG TTCTGGGTGA ACGTATACTG AGGAAAtACC TTTTTTGTGC 300

AAATGATGTT CGACATTGTC ACAAATTTGA TGCGCTTCTA CTAAGGAAAG GTTAGCATCT 360

ACAACAATTG TGACATCAAT AAACACACTA CTTCCATGGT AACGCCCTTT AATACTTTTA 420

ACTTCTTGTA CTTCATCAAC TTCTAAAATA TCATTGCGAT ACGCTTCTAA TTCAGTTTCA 480

TTGAAACCAT CACTCAACAT AAAAATTGCT TCTTTAAAAA TACCAAAACC AGTATAAACG 540

ATTAGTAAGC CTAGTAATGT TGCTAAAATA ATATCGACAA TTGGGAAACC GATTTGCGTA 600

AAAATTAATC CTATCGCTGT TCCAATGCTG ACTAAACTAT CCGATAAATT ATCTTTGGCA 660

GCCGAATTTA AAGAACTACT TTTCGTTCTT TTCGCTAGTC TTTGATTGAC TGCAAATACA 720

ATCAACATTA CAAGACCACT GATTAAGCTG ACGATAATTG TTATTGCGTT AGGTACAACG 780

TCATCTTCTT TGAACAAACG AGGTGCATTT TGAATAACTA CTTGGATACC TACAAACATA 840

ATGACAAATG ACACCAATAA TGAAGAAATA TTTTCAGACT TCAAATGGCC ATAAGGATGA 900

TTTCGATCGG CAGGTTTAAT TGAAATTTTC AATCCAATAA TAACAGCTAA AGAAACGATA 960

ATATCTGTCA TATTGTTTAA TGCATCGGCT CTTACAGCTG CAGAGTTAAA GACAAAACCC 1020

GTGACATACT TAACAATAGA TAAGATTATA TATACAATTA AACTCAAATA AGCACCGCGT 1080

TGCGCCAATT TAAGATTTTC ATTATGAGAC ATGCGTTGAA CCACCTTGAA TTAGTATAGT 1140

AACAATATTA TGAATGATTC ATTTTAATTT TACAACGTTT TTAATTTTTA TAAATTTTTA 1200

TAAAATTAAA CTAATTTATT CATTCGCAAC CCCTAAAAAT AATTTTTAGC CTTTCTGCGA 1260

ATTTTATGAG CTAGAAAGGC GCCCAACTCT CCCTGTTTGT TAACTTTCGC CTCGAAAGTT 1320

CGAAwwTTAT GAGCTAGAAA GGCTTATGCA GTTGACGTTT TACGTCCAAC TGCGTTCCTC 1440

CGTCTTCTTC AAATTTATTT GTnAGAAAGG CACCCAACTC TCCCTGTTTG TTAACTTTCG 1500

CCTCGAAAGT TTCTATGTTA GAACCCTATG CATGAGTTGC GAAnTATCTA ATGTCGTGAA 1560

CTAATTATAT AGAAGAAAAA GTGCATCAAT GACAAATTAA ATGAGATTTC TACTCTACCA 1620

AACTCTCTTC GAAAGACAAT TTTCTCCTCT ATTTATTAGC AACTATTGCA TTTCTCCATA 1680

TAGTACTTCC TTACTTAAAA TACGCTGAAT GTCTGAATTA AA 1722

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

GCGAGACCCC CTGAGGGAGC AGTGCCCAGT CGAAGACCCG AGGCTGAGAC GGCACCCTAG 60

GAAAGCGAcC ATTyCAATAC GAaTTgTGAt AAATAGAGAA CAGCAGTAAG ATATTTTCTA 120

ATTGAAAATT ATCTTACTGC TGTTTTTTTA GGGATTTATG TCCCAGCCTG TTTTTTGTGA 180

TTTTTAATAA TTTGAATATG GAAAATGTAT TATTCTCTCA TTTGTATAGA TTGTATTTAA 240

TAAGTTAATG TAATCCTTGA GCTCACGATT AATAAAATTC TATAACCTTA ATTATTTTCT 300

CGATACAAAG GGTTATTAAC TTTAATATAA GTATAATGAT GTGCCTCATC TTCAAGACGC 360

ATTGTTGTAA CACACTTATA ATCTATAAAT GGCGCGAACA TGGTATCTTT AATTTCaTTT 420

ATGCGATTCT CATTTACTTG ATTAGATTTG TGTGTCGAAA GTACAAGTTG ATCaAAAATG 480

TTATCTAGTA CATCACGAAC GATATACCAC ATATGTCTTT CTAAGTTTGA ATCATTTGAT 540

GCTTTAGAGA TTGTAAGAAT TAATTCGCCT AAATGGTTTT GAACGGTAGA ATAAAAGGCT 600

TTGTTAAACA CAGACGTTTT TGAATCAGTA AGAATTCTTG ATTTTTCATG GAAATGAGAT 660

GTACTGTATA CCATTTCATT TAGTTGTGCT TTATCAATTC TTAAACCTTC AAAGTCTCTA 720

ATATACATCG TGTCCAATAG ACCATCTTTC CGAAATGTTG CAATAGCATT TTGCAAGTGA 780

GCCTCTAATG CAATGCCATA TTTAGTAACT AGTGGGATTA CGAGACCAAG CAATGCTTTA 840

CTATAAGTTT CAACCCACGA TTTCGCCGAT GATTCAAAAT CAGACAATGA TGCAGCTGAT 900

TGATAACGTT TAATCAATGT CACGATAGGT GATTCATTGT TAAATGGGTA GGTTGCAACT 960

AAGCTTGAAG GAATCAATGG TGTGACTTCT TGTGGAATCA TTTGGTATAT ATTTTTTCTA 1020

AAAAATGAAT ACCAGCAACT TCATCAATAA TTGTTGATGC ATAGGACTTA AATATGACAT 1140

CTTTCTCCAA AATATCATTT AAAATACGTG TCATTAGTGG ACCATTGTGC GTCGTTTGTT 1200

CTGATAATGT ACGAATCTCA CCTGTAATAT GAACGTTTGT CGACAATTTG ATGTGTGGCG 1260

ACATAGCTGG GTATTTAGGA ACTAATGTTC TGAAAGATAA ACCAGCATAA TAATCCaACG 1320

TATGTTTTGC TTCAATGATT AATTCTTTAT CTACTTCTGC TTGATAATCA GAATGTAATA 1380

CGTCATCTAA TTGCCATGGA TGAACAATCA TAATGTGATA ATCATTAAAG TTAAACTTTG 1440

GCGTAAATTC ATTTTCTAAT TGTTTAATTA AGTCCGGAAA TAGTTGATGA ACAGTTGTAT 1500

CATAATCTTT AGACAGTGAC ATAGTACGGC TTAATTTACT GTGAATCAGT ACTATTTTCA 1560

ACTTAATAGG TTGATTGAAT TCTGAAGAAT ATAGGAATGT TTGTAATGCA TTTAAACCTT 1620

TACGTAATTT AGCCCCAGGA TGTAGCGGAT GACCTTCAAT AACGGCTTGC TCTGAACGCA 1680

AGTAACTATC TTCGCTATTT TCGATAATAT TAAATAAAGG TGCAGAATCA TGTTGCATTG 1740

ACAGTGCTTG ATAGCTAATT GCAAATGTCA TATtAGTtGC ACTGTTTATT AAATCTTGCT 1800

GAAATTGATC ACTAGCAGCA TTTTTTAAAT CTGGTGCTTC AATTAAAATA CACTCAAGAA 1860

TTTCATTTGG ATGGTGTACT CGTGTAATCG TATTTGTAAT GTCATCTTTA ATGTAGAAAG 1920

GGCCTTCAAC ATCAATTCGA TCAAAGGCGT GTTCTCCAGT GATAGGAGCA TATAATGTTT 1980

GCTTAGCTTG TGGGAACTGG ATTTCTAGTA TATGAGTCGT TGAGATATCT AACATAATCA 2040

AATCACGACT CAATATTTTC TTACTTTGAG TGCGCGCTTT AACTAAGTTT TCGCGATGCA 2100

TTGATGTGAC CAATCTCTGA GTGACTTTAT CTCTTCCTTG TAAAATCATC TCTTTAAAAA 2160

TATTAGCCCA ATCGCTATTA TGTTGTTGTA AAAATAAATA TGTTTCTTGT TCTTCTTTGT 2220

TAAATTTTAA TGTCTGTTCT TTAAAAATTA AGTTCAAGTT CATAATTCAC CTCTATGAAA 2280

TATTTTACAA AAGCAAGATA GATTTGTATA ATCCATATTA ATGATAATGA yTCTTATTAT 2340

CAACAGAATG CGGGTGTAAG TTTTATGACA AAATATTTTT TTAGCAGTTC TTTTCTACTA 2400

TTTCTAGGTA ATTGGATTGG ACAAATAGGG CTAAATTGGT TTGTACTTAC CACTTATCAT 2460

AACGCAGTTT ATCTGGGGAT TGTCAATTTT TGCAGACTTG TACCAATATT ATTACTAAGT 2520

GTGTGGGCAG GGGCAATTGC CGATAAATAT GATAAAGGGC GATTGCTGAG AATTACAATT 2580

TCATCATCAT TTTTAGTAAC TGCAATTTTA TGTGTGCTCA CGTATAGTTc ACTGCAATTC 2640

CAATTAGCGT CATTATTATA TATGCGACAT TAAGAGGGAT TTTAAGTGCG GTTGAAACAC 2700

CTTTAAGACA AGCAATCTTA CCAGATTTAT CAGATAAAAT ATCTACTACA CAAGCTGTmw 2760

CATTTCATTC ATTCATCATT AATATTTGTC GTTCAATAGG GCCTGCCATT GCTGGTGTCA 2820

CAGTTTTATT ATGCTTACCA TTACATTTTA AAGTAACTAA AATACCTGAA GaTGCATCAA 2940

GaTACATGCC GTTAAAAGTT ATTATAGATT ACTTCAAATT ACATATGGAA GGTCGACAAA 3000

TATTTATAAC ATCATTATTG ATTATGGCGA CAGGTTTTTC ATATACGACA CTTTTACCAG 3060

TTTTGACAAA CAAAGTATTT CCGGGGAAAT CTGAAATATT TGGTATCGCT ATGACGATGT 3120

GTGCCATTGG TGGTATTATT GCAACGCTAG TTTTACCTAA AGTACTTAAA TATATTGGTA 3180

TGGTAAATAT GTATTATTTA AGTTCATTTT TATTTGGCAT TGCTTTGTTA GGTGTGGTAT 3240

TTCACAATAT TGTCATCATG TTCATTTGTA TTACATTGAT TGGGTTATTT AGTCAATGGG 3300

CACGTACGAC AAATCGCGTT TATTTTCAAA ATAATGTTAA AGATTATGAA CGTGGTAAAG 3360

TACTGAGTAT TaTTATGATG GgATAGAGGT ATGaTTCCAT kGGGAAGTCn ATTAATGAGT 3420

ATATGTGCAG ATGTGTTTGG CATTGTTAGA ACTTTTTCAA TAATGGGAAT AAGTACTATA 3480

TGCATTACAA TGGTATTCTA TTTTATAAAT AGAAAGTTGA AGTTAAAGTT GGAGGAAAGT 3540

AATCATGGTA TATCTTGAAT GGGCAAAGGC AGATAGAAAT ATTCAATATC GTGTAATTAA 3600

CGCCATTATT AAAGAACGTA TTTACCCCGA GCAAACATTT ATTTCGCAAA AAGGATCTTT 3660

AATTGAAATT CAGTATCATA TGCATGTGTT GACTATTGAA GTTGTTAGAA AAAGTGCATT 3720

AGAACGCTAT GAGTTTACAG GTGATATTAC TTATTTAAAT AAAGGTGAAA CGTCATTAAT 3780

TATAACTTTA GAAGGTTTAT TAGATGTGTT GAATCATGAC TTTGATATCC CTATTTCAGA 3840

GCGACTACGC GAAGAGTTAA TACACAGTCG AGATAGTTTA GTTGAAACAT ATAAGCAAAT 3900

GTCTCACAGA CAAACGTTAA TAAGTCmAAG TTTTAAATTT TCAAGGTTAC CACAAGATAT 3960

TAACTTTTTT TCakGGTtAC AACATGTAAA AGATAGTGAT AAGACAGATG ATTTAACTTA 4020

TTCTGAGAGT TTGGTACCAG AGGGGCATCC AACACACCCT TTAACCAAAA CGAAATTGCC 4080

CTTAACTATG GAAGAAGTAC GAGCATATGC ACCTGAGTTT GAAAAAGAAA TCCCTTTGCA 4140

AATTATGATG ATTGAAAAAG ACCATGTTGT GTGCACAGCT ATGGATGGTA ATGATCAATT 4200

TATTATTGAT GAAATAATTC CCGAATACTA CAATCAGATT CGTGTGTTTT TAAAGAGTTT 4260

AGGTTTGAAA AGTGAAGACT ATAGAGCGAT TTTAGTACAT CCTTGGCAAT ATGATCATAC 4320

GATAGGGAAA TATTTTGAAG CATGGnTTGC TAAAAAAATA TTAATTCCAA CGCCGTTTAC 4380

AATACTTcCA AAAGCaACTT aTCatTTaGG ACGATGTCTT TAATTGATAA ACcATACCAT 4440

GTTAAgTTGC CCgTCGATGC aCAAGCAACA AGTGCCGTTA GAACAGTCTC AACTGTGACT 4500

ACTGTAGATG GACCAAAGTT AAGTTATGCT TTACAAAACA TGTTGAATCa ATATCCaGGA 4560

TTTAAAGTTG CTATGGAACC GTTCGGTGAA TATGCAAATG TTGATAAAGA TAGGGCACGT 4620

AGTGCAAGTC TAGTTAATAA AAATCCAATA GATCAAAAAG TTATCGTGGA TAGTTACTTA 4740

GAGTGGTTAA ATCAAGGAAT TACTAAAGAA AGTATTACGA CATTTATTGA ACGATACGCT 4800

CAAGCATTAA TCCCGCCTTT AATTGCTTTT ATTCAAAATT ATGGAATTGC TTTAGAAGCA 4860

CACATGCAAA ATACAGTAGT GAACTTGGGG CCACATTTTG ACaTTCAATT TTTAGTGAGA 4920

GATTTAGGTG GTTCTAGAAT TGATTTAGAA ACATTACAAC ATCGTGTATC AGATATTAAA 4980

ATTACAAATG ATAGTTTAAT AGCTGATTCT ATAGATGCAG TGATTGCAAA ATTCCAACAT 5040

GCTGTTATTC AAAATCAAAT GGCAGAATTA ATCCATCATT TTAATCAGTA TGATTGTGTT 5100

GAAGAAACCG AATTATTTAA CATAGTACAG CAAGTAGTAG CGCATGCCAT TAACCCAACA 5160

CTACCACATG CAAATGAGTT AAAAGATATT TTGTTTGGAC CAACAATTAC TGTCAAAGCG 5220

TTGTTAAATA TGAGAATGGA AAATAAAGTA AAGCAATATT TAAATATTGA GTTAGATAAT 5280

CCGATAAAAA AAGAGGTGTA GTACTACATG GCACACGTTA ACATAAATAT ATCGAAGATT 5340

AAaTATAACG CCAAAGTACT TCAAACAGTT TTTCAAAGTA AAAATATGCA ATTCACACCA 5400

GTAATTAAGT GCATAGCTGG TGACCGTACA ATTGTAGAAA GCTTAAAAGC GTTAGGTATC 5460

AATCATGTTG CAGAATCCAG ATTGGATAAC ATAATTAGTA TTGCAGATAC AGGATTTAAC 5520

A 5521

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

AGGTCGTCTr GCaGmAGmGm TATTTGACGA TCTTGCTTTC CCAAAACACG ATGATGATTT 60

TAACATACTG TCTGATTATA TTGAGACACA TGGTGATTTC aCATTGCCAA TGTCTGTATT 120

TGATGATTTA TATGAAGAAT ATACGGAATG GCTAAAATTT TAATATAATT TTTAATAATA 180

ATAGTTAGAA CCAGGGTGAT GCAATTCGTT ATCCTGGTTT TAATTTAAAA TAAACTAAGT 240

TGTGACTAAA AATTAATCAA TTATAGTGAA ATATGGTGCG CTATCTTGCA TAAATTGATA 300

TGATTAACTA CACAGAATTT AAAAGTACAT AATACATAAT AAGGAAGTGA TACAATGGAT 360

GATAAGCAAC ACACATCTTC ATCCGATGAT GAACGCGCTG AAATTGCAAC AAGCAATCAA 420

GACCAAGAAA CTAATTCATC GAAACGCGTT CACTTAAAAC GTTGGCAATT CATATCAATA 480

CAAAAAATAA GTGGTTTAAA CAAAACTGAT CAAGCAAACT TAAATAAAAT TGAAAATGTG 600

TATAAAATCT TAAATAGTGA TTATTACAAA AAACAGGACT CTGACAAGTT AAGTAAAGCT 660

GCAATTGATG GCATGGTCAA AGAATTAAAA GATCCTTATT CTGAATATTT AACAAAAGAA 720

CAAACGAAAT CCTTTAATGA AGGTGTTTCA GGTGATTTTG TAGGTATTGG TGCAGAAATG 780

CAAAAGAAAA ATGATCAAAT TATGGTTACT AGTCCTATGA AGGGATCTCC AGCAGAACGT 840

GCTGGCATTC GTCCTAAAGA TGTCATTACT AAAGTAAATG GAAAATCAAT TAAAGGTAAA 900

GCATTAGATG AAGTTGTCAA AGATGTTCGT GGTAAAGAAA ACACTGAAGT CACTTTAACT 960

GTTCAACGAG GTAGTGAAGA AAAAGACGTT AAGATTAAAC GTGAAAAAAT TCATGTTAAA 1020

AGTGTTGAGT ATAAGAAAAA AGGTAAAGTT GGAGTTATTA CTATTAATAA ATTCCaGAAT 1080

GATACATCAG GTGAATTGAA AGATGCAGTT CTAAAAGCTC ACAAAGATGG TTTGAAAAAG 1140

ATTGTTTTAG ATTTAAGAAA TAATCCAGGT GGACTACTAG ATGAAGCTGT TAAAATGGCA 1200

AATATTTTTA TCGATAAAGG AAAAACTGTT GTTAAACTAG AnAAAGGTAA AGATACTGAA 1260

G 1261

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

AAATATATTG AAnAGAnAAT TACTAAGATT AAATCnTCTT AAAATATCCC TGAAATAACG 60

TCCTAAAGAT TAAAGGAAAG AGGTTATAAG TTATGCCAAA ATTAATTTTA TGTCGTCATG 120

GACAAAGCGA GTGGAATGCT AAAAACTTAT TTACTGGATG GGAAGATGTT AATTTATCTG 180

AACAAGGTAT TAATGAAGCG ACTAGAGCAG GTGAAAAAGT AAGAGAAAAT AACATTGCCA 240

TCGATGTAGC TTTTACATCG TTATTAACAC GTGCTTTAGA TACAACGCAT TATATTTTAA 300

CTGAATCTAA ACAACAATGG ATTCCTGTAT ATAAAAGCTG GCGTTTAAAT GAACGCCACT 360

ATGGTGGATT GCAAGGCTTA AATAAAGATG ATGCTAGAAA AGAATTTGGA GAAGAACAAG 420

TACATATTTG GCGTCGTTCT TATGATGTGA AACCACCTGC TGAAACCGAA GAACAACGTG 480

AAGCTTACTT AGCTGATCGT CGATATAATC ATTTAGATAA ACGTATGATG CCTTATTCTG 540

AAAGTCTGAA AGATACTTTA GTTCGAGTGA TACCATTTTG GACAGATCAT ATTTCACAAT 600

TTAAATATCT TGAAGATGTG TCAGATGAAG ATATCATTAA TTATGAAATT AAAACAGGTG 720

CACCGCTTGT TTATGAATTA ACGGATGATT TAGAAGTTAT AGATAAATAC TACTTATAAA 780

AaAAGAGCTG CATGTACACA AGGAGTGAGT GTATATGcAG CTCTTAAAtA TGTGAAGTAA 840

TGTAAGGAAA TAGTTAAGTA TAGAGTTTAT ATTAACGAGC TAGGGATACT CGAAAATATA 900

GTTAGACATA CAATATAGTC AAATTAAAAC AATTATTTCG CTCTTTTATG TTGCTTAATA 960

ATCTTTAAAG CACGCTTTCT TGTTTTAATG TTAGGGCTAT TTAAATTACG ACGAGCAGTC 1020

TGTAAATCTA ATTTCATCTC TATCCCTCCT TGTAAATATA TTATGACCGA TAACTACTCA 1080

TATGTAAATA GTAATGATTA CGTTTTAAAG AAATTGTAAT AAAGTCGTGC TAATTTTTTG 1140

GAAAATGGGT ATAATTACCG GATATCTAAA AATGTGTGTC GTTTTTTAGA TGGTGAGGGG 1200

GAAGCTTTAA ATGTCGAAGA AACAAAAATT AACGATGATT ATTACTATGC TGATGGGTGG 1260

ATTTTTTGGA TTATTAAATG AAACACTATT AGTGACGGCT TTACCAAGTA TTATGAAAGA 1320

TTTTGAAATT TCATATACAC AAGTTCAATG GCTGACAACA GCTTTTTTAT TGACTAATGG 1380

GATTGTTATT CCTTTGTCCG CGCTTGTTAT ACAACGTTAT ACAACAAGAC AAGTGTTTTT 1440

AGTGGGTATT TCTATCTTTT TCTTAGGTAC ATTACTCGGC GGCTTGAGTC CGCACTTTGC 1500

AACATTATTA GTTGCTAGAA TTATTCAGGC GTTAGGCGCA GGTATTATGA TGCCATTGAT 1560

GATGACAACG ATTTTGGATG TTTTCCAACC ACATGAACGC GGTAAATATA TGGGGATATT 1620

TGGTTTGGTA ATTGGTTTAG CACCAGCTAT TGGACCTACT CTTTCAGGTT ACCTTGTTGA 1680

ATATTTTAAC TGGAGATCGC TTTTCCATGT TGTCGCTCCA ATTGCAGCTG TGACATTTTT 1740

AATTGGaTTT AAAAcGATAA AAAATGTTGG AACTACAATT AAAgTACCTA TTGATTTTAT 1800

TTCTGTCATT TTTTCTGTAC TAGGTTTCGG cGGGTTATTG tATGGAACGA GTTCaATTTc 1860

AGAAAAAGGT TTTGATAATC CTAcGtATTA GTATCTATGA TTGGAGGCGT TGTTTTAGTC 1920

GCATTATTTG TAwTACGTCA ATATCGGCTA TCAACACCAT TATTaAATTT TGCTGTATTT 1980

AAAAATAAAC AATTTACAGT TGGTATCATT ATTATGGGTG TCaCAATGGT ATCGATGATT 2040

GGTTCGGAAA CGATTTTACC TATCTTTGTG CAAAATTTAT TGCATCGTTC AGCTTTAGAT 2100

TCTGGATTAA CTTTATTACC AGGAGCAATT GTTATGGCAT TTATGTCGAT GACTTCGGGT 2160

GCTTTATATG AAAAGTTTGG TCCTAGAAAT CTTGCTTTAG TAGGTATGGC GATTGTTGTT 2220

ATTACTACGG CTTATTTTGT TGTAATGGAT GAACAAACAT CAACAATCAT GTTGGCAACA 2280

GTTTATGCGA TTCGAATGGT TGGTATCGCG TTAGGATTAA TTCCAGTAAT GACCCATACG 2340

ATGAATCAAT TAAAGCCAGA AATGAATGCA CATGGTTCAT CTATGACAAA CACAGTACAA 2400

AACTTTTCTC CAACTATGTC AGACTATA 2488

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

TTTTACAATT TCAGATATCT CTAAAACACA TACCGATCCA ATGGCCAAAA TTATTCGTCA 60

AAAATTGAAA AAACTAGGAA TTCGTAAAGG GATTCCAGTT GTATTTTCAG ATGAAAGTCC 120

AATTGTCATA AGAGAAGATG TAAAAGATAT AGTTGGAGAT AAAAATGCTA TCAATCGAAA 180

AGGACAAATG CCACCTTCTT CAAATGCCTT TGTGCCAAGT GTTGTTGGAT TAATTTGTGC 240

AAGTTATGTG GTGAATGACG TATTAAAAGA TATTCCAGTT CGTCGCATTA AAGACAAAGG 300

GCAATAATTC ATTTTGAAAG GGATAATTTT CAACGTAAGG CAAGTGTAAC CACACCATAA 360

AACTAAAACT GACTAGTTCG CAAGCATAGT AGAATATGCC TCGTGTACTA GTCAGTTTTG 420

ATTTGATTAT AGCTAAAATA TCAAAGGTAA TCGATTTAAT CTTATTTTTA CGGCCTTTGT 480

TTAAGTAAGT TGTTATATAT TTCTTTGAGT TGTTGTTCAC TTTTAGATGT CGTTTTTGGT 540

TCGTAATAAA TTTTGTTTTT TAGTTTATCA GGTAAATATT GCTGTGAAAC ATAGCCATTA 600

ACATATTGGT GTGGATATTT GTAACCAATA GATCGGCCTA GATCTTTAGC ACCTTGATAA 660

TGTCCATCTT TTAAATGGTT TGGAATTTGG CCCACATGAC CGTTTCTAAT ATCGGACAAT 720

GCACTATCAA TGGCACTCAT TGCTGAATTT GACTTAGGTG ATAAGCATAG TTCGATTACT 780

GCTTGGCTTA GTGGAATTCT AGCTTCTGGT AAACCTAGAC GTTCTGCTGA TTCAATAGCA 840

GCAAGTGTTC TCTGACCAGC ATTAGGTGAG GCTAAGCCTA TATCCTCATA GCTAATTACA 900

AGTAATCGTC GAACTATTGT AGGTAAATCT CCAGCTTCAA TTAATCGTGC TAAATAATGT 960

AAAGCGGCAT TGACGTCGCT ACCACGGATA GATTTTTGGA AAGCGCTCAT AACATCGTAA 1020

TGCATGTCAC CATCCTTGTC ACTTACAAAT GCACCTTTTT GTAAACAGTC TTTAGCATCT 1080

TGCAATGTAA CATGTCGATA ACCGT 1105

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

TAACGTCGAA CTTGAGCTGT TACGTTATGA CTCATAATTA TTTTAGCATA GTCATTTAAA 60

TAAACTTCTG TTCTGTCTGT TGGATAAGCA AATTCAAGCA ATTGACTGTA ACTATCATTA 120

ATGACTTCTT GATCAACATG ACTATCAAAA TATACAGCAT AATAATAAGT ACCATCAACC 180

ATATATAACA AATCTTCAAA CTCTGTAGTT ATTGGATTGC TATGATATGC ATAATTAATA 240

ACATCTTCTA AATCGTTAAA TTTCACAATG ATTGTTCTTG TATTTTTACG TGCTGAAGAC 300

TTTTGACGTT TAGAACCTTG AGCTTCTTTT TCTTTTGTTC GTTGCTCGAA TAATTCTTCT 360

AATTGATCTT CACCTTCTAA TGTTTGAGCT AACAATTCTT GAACTTGTTC ATCAAATkGA 420

TCAGTTGCAT CATCATCAGA CATATTCATC ATATCTTCAT TTTTAGATTT AGAAATTGTG 480

ACTTCGACAC CTTTTTCAAA GGCATGTACT TGAATCCATA ATGGACCTnC TACAACAAAA 540

TCTTCTACTT CGTTAATTTC ATCCATCATT GAnCAAAAG 579

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

GTGGTGAAAC TTCTTGCTTT GTAATTTTAT AAAGTGGATC AATATCACTC TGACTTACAT 60

CAGGTTGAAC TGTCATCTTT TTAGTTACTT TGTTTTCAAG CGTAATATTT GCTAATTcTA 120

GGtTTTACAG AATAATGAAT GTCATCAGCT AmCCCTTTmm CtTGATACTy CTCTTGATAT 180

TTTCCAGCTT TAGCATTTGA TAAATCAATC ACTACTCTTA AATCTTCTGG ATTTTCAATT 240

TTTATTATCT TTGATTGTGG TCCTGAAATA GTCACATTAA CTGTTTCAGG CGCTTTTGTT 300

AAATGCAAAT CTTTAGTGTT ATAAAGAATT TCAACGGGTA CATCTTGAAT CGTTTTACTA 360

GACTTTTGAC CAAGATTACC AGTGTTAAAG ATATTTCCAA AAACATTGTT AACAGATAAA 420

AAGAAAAACA ATGCCAAAAG AAAGGCAATA AATCTCAAGC CCCATTTACT TTCTAGCATA 480

TTATTTCACA CCTTTCTTTT GAAAGCGTGT GCCAAACCAA TGTTCAGCAA GCAACTCTTC 540

AAAAATTTCG TTTGAAATGT CTCGTCGTAA TTTTCCATCA AATGTTACCG AAATATCACC 600

AGTTTCTTCA GATACAATAA CGGTAAATGC ATCAGATACT TCTGAAATAC CAACCGCAGC 660

TGCTGCTGCT GCAATCTTCG TGCCTTGAAT AATCATTGCA CCATCATGTA AAGGTGTGTT 780

AGGTATAAAG ACATTAATTA AAAGTTCTTG CGAAATATTT GAATCCATTG CAATACCTGT 840

TTCAATATAA TCTTGAAGAC CTGTTTCTTT TTCAAAGACA ATTAATGCAC CTATACGTCT 900

TTTAGCCATA TATTGCACAG CCTTTGAAAC CGATTGAATC AATTTCTCTT CATCTTTACT 960

ATACGTATTA GAAGTATAGC GTTTTAAAAA GCTACCTCTA CCAAGTTGTT CTAACGCACG 1020

TCTAATTTCT GGTTGGAATA TTACTATTAA AGCTAATACC CCCCATTGAA TAACGATATC 1080

GAATAATTTA GATGTTGCAG TCAAGTTCAA TATCATACTT ATCTGCTGAC CAATAACAAT 1140

TACTAATATC CCTTTAAGTA ATTGTATCGC TTTAGTTCCC TTAAAGACCG TGATGAGAAG 1200

ATAAAGTACA TACCAAACTA TCAGTAAATC AAGGATACTC GTTACAATTT TTAACGTACT 1260

GAGGTTTTGA AAAAAGTTGG AAAAATCCAT AACATCTCCT CCGGGTAATA TTTTTCCATA 1320

ATACCCATTA TACCAATCAT TT 1342

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1073 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

CTGTATAAAG ATGGAGGTGT TTTGCATGGT AAAACGTACT TATCAACCAA ATAAACGTAA 60

ACATAGTAAA GTTCATGGTT TCAGAAAACG CATGAGCACA AAAAATGGCC GTAAAGTTTT 120

AGCGCGCCGT CGTCGTAAAG GCCGTAAAGT TTTATCTGCA TAAGATCACT GACTCATCAG 180

TGAtCTkTTT TTTCGTTTAA ATTAAGAATA AATAGAAATT TATGTTATAA GCTCAATAGA 240

AGTTTAAATA TAGCTTCAnA TAAAAACGAT AnATAAGCGA GTGATGTTAT TGGAAAAAGC 300

TTACCGAATT AAAAAGAATG CAGATTTTCA GAGAATATAT AAAAAAGGTC ATTCTGTAGC 360

CAACAGACAA TTTGTTGTAT ACACTTGTAA TAATAAAGAA ATAGACCATT TTCGCTTAGG 420

TATTAGTGTT TCTAAAAAAC TAGGTAATGC AGTGTTAAGA AACAAGATTA AnAGAGCAAT 480

ACGTGAAAAT TTCAAAGTAC ATAAGTCGCA TATATTGGCC AAAGATATTA TTGTAATAGC 540

AAGACAGCCA GCTAAAGATA TGACGACTTT ACAAATACAG AATAGTCTTG AGCACGTACT 600

TAAAATTGCC AAAGTTTTTA ATAAAnAGAT TAAGTAAGGn TAGGGTAGGG GAAGGAAAAC 660

ATTAACCACT CAACACATCC CGAAGTCTTA CCTCAGACAA ACGTAAGACT GACCTTAGGG 720

TTTAGATACA ATTACGAGTA TTTCAACACC AATGGGTGAA GGGGCAATTG GAATTGTTCG 840

ATTGTCTGGA CCGCAAGCCG TTGAAATTGC TGACAAATTA TATAAAGGAA AACATCTTTT 900

AAATGATGTT CCATCACATA CGATTAATTA CGGTCATATT ATTGATCCAG tCTAAAGAAG 960

TGGTTGAAGA AGTTATGGTG TCTGTGTtAA GAGCGCCAAr AACATTTACA CGCGArGATA 1020

TTATAGAgAT TAATTGTCAT GGTGGtATTk TAACGATTAA TAGAGTGCTG GGA 1073

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

CTTTACCAAT GCCAAATCCG AAGTAAAGTA TAGCAATAAA GATTACTAAT ACAATTCTGT 60

AAATGGCAAA TGGAATTAGT TTGATTTTGT TAATTAGATG CAAGAATGTT TTGATTGCAA 120

TTAGTCCAAC AGTAAATGCA GCTAAAAAGC CTAAAATATA AAAAGGTATA TCAGCAATCT 180

GAATATCTTG ATAATGTTTT AATAAAGATA AACCACTAGC TGCTAACATA ATTGGAACAG 240

CCATAATAAA TGTAAAGTCC GATGCTGCTT TATGATTTAA TTTCATTAAT ACCCCAGTTG 300

AAATTGTTGA GCCTGAACGG CTGAAACCAG GCCACATAGC TACTGCTTGA gAAATACCAA 360

TTACAAATGC TTGGAAATAA CTGATTTGAT CTACTGTTTG TGGGTTTTTA ACTTTAGCTG 420

AGTATTTATC AGCAATAATC ATATAGATAG CACCTACGAA TAAGCCAATC ATAACAGTTG 480

GCACACTAAA TAAATGTTCT TCGATGAAAT CATCAAATAG TAAGCCTAAA ATACCTGCTG 540

GCACCATACC CACTAATACA TGTAATAAAT TTAAACGTCT TGGCTTTGAA CGTCTTTGTT 600

GATCGTTATC TCCTTCAACA TGTTTGTGTT TACCAATATG TAAAATCTCT AAGAAGCGTT 660

CGCGGAACAC CCATGCTGCT GCAAAGACGG ATCCTAATTG GATGACGATT TTAAATGTAA 720

ATGCTGACTG AGAACCTAAA AATTCAGATG ATTTTAACCA CATATCATCA ACTAGGATCA 780

TATGTCCAGT AGAGGAAACA GGTGCAAATT CTGTTAATCC TTCGACGACC CCTAAGATAA 840

TACCTTTTaT TAATTCAATG ATAAACATAA TGTACCCACT TTCATTACTC AATTTAATTT 900

ATTTAAATAT CAAAATTACC ATATCATGAT AGCATATTCA TTTAAAGACA TGCTAGTTAT 960

AGTTATAATA CTAGACTAAA GATGTATATA TTCATTTTCT TTTACATGTA AAACTACAAT 1020

ATTTTATTGA GCTATTTAAT TTGATTTTAA GGAAAACCTT TTATAATAGG TTTAGGTGAT 1080

TTCTTGGTCA GTACTGGTCT CGGCATAATC GTTATAACGC AAAATATTTT AATAGCAGAT 1200

TTTTTAGCTA AAATTATAAG ACATCAATTT CAAGGTTTAT GGATTGTATT ATTTATTTTA 1260

TTAGGTGTTT TACTTTTAAG AGCAACTGTG CAATTTCTAA ATCAATGGTT AGGTGATACA 1320

TTAGCATTTA AAGTTAAGCA TATGCTTAGA CAGCGGGTTA TTTATAAAAA TAATGGTCAT 1380

CCAATCGGTG AACAAATGAC TATACTCACA GAAAACATTG ATGGTCTAGC ACCTTTTTAT 1440

AAGAGTTATT TGCCTCAAGT GTTCAAATCA ATGATGGTTC CGCTCATCAT AATCATTGCA 1500

ATGTTTTTCA TCCATTTCAA TACCGCATTA ATTATGTTAA TAACTGCACC ATTTATTCCT 1560

TTGTTTTATA TTATTTTCGG TTTGAAAACG CGAGATGAGT CAAAAGATCA AATGACTTAT 1620

TTGAATCAAT TTAGTCAACG GTTTTTAAAT ATTGCTAAAG GTTTAGTGAC GTTAAAGCTA 1680

TTTAATCGTA CAGAGCAAAC AGAGAAGCaT ATTTaCGACG ATAGTACTCa GTTTAGAACT 1740

TTAACAATGC GCATTTTaCG CAGTGCTTTT TTATCGGGAT TAATGCTCGA ATTTATAAGT 1800

ATGTTAGGTA TTGGATTGGT TGCATTGGAA GCAACGCTAA GCTTAGTAGT ATTTCATAAT 1860

ATTGATTTTA AAACTGCGGC AATTGCGATT ATTTTAGCGC CTGAATTTTA TAATGCAATT 1920

AAGGACTTAG GGCAAGCGTT CCATACTGGA AAACAAAGTG AAGGTGCCAG TGACGTTGTG 1980

TTTGAGTTTT TAGAACAACC GAACTATAAT AATGAATTTC TATTAAAGTA TGAGGAAAAC 2040

CAAAAGCCAT TTATTCAGTT AACAGACATA TCATTTCGAT ATGATGATTC TGATAGATTG 2100

GTATTAAATG ATTTAAATTT GGAAATATTT AAAGGTGATC AAATTGCACT TGTAGGTCCA 2160

AGCGGGGCAG GTAAATCCAC TTTGACACAT CTTATTGCAG GTGTTTATCA GCCAACAATA 2220

GGTACTATAA GTACAAACCA GCGTGATTTA AATATAGGAA TACTTAGTCA ACAGCCATAT 2280

ATTTTCAGTG CTTCTATAAA AGAGAATATT ACGATGTTTA AAGATATAGA AAATAATACT 2340

ATTGAAGAAG TGCTAGACGA AGTAGGTTTA TTAGACAAAG TGCAATCTTT CACAAAAGGC 2400

ATTAACACAA TAATAGGTGA AGGAGGCGAA ATGTTATCTG GTGGACAGAT GAGACGCATA 2460

GAACTTTGCC GTCTTTTAGT TATGAAGCCA GATCTCGTTA TATTTGATGA GCCTGCAACT 2520

GGTTTAGATA TTCAAACAGA ACACATGATT CAGAACGTTC TGTTTCAACA TTTTAAAGAT 2580

ACAACGATGA TTGTCATTGC ACATAGAGAT AATACAATTC GCCATTTACA ACGACGCTTG 2640

TATATAGAAA ATGGAAGACT GATTGCTGAT GATCGCAATA TTTCAGTAAA TATAACAGAA 2700

AATGGTGATG ACTTATGAAA ACACGACTAA AATTTCAAGT AGATAAGGAT TTATTGTTAG 2760

CTATAGTTGT TGGTGTTTGT GGAAGTTTAG TTGCGCTCGC CATGTTTTTC TTAAGTGGTT 2820

ATATGGTGAC ACAAAGTGCA CTTGGTGCGC CACTATACGC TCTGATGATT TTAGTCGTTA 2880

ATAAAGCTAC ATTTACAATG CTACGTGATA TTCGGGTACA GTTTTTCGGT AAATTAGTAA 3000

ATGTCATTCC TAATGTTTAC CGTAAACTGA GTTCTAGTGA TTTAATTTCA CGTATGATTA 3060

GTCGTGTTGA GGCATTACAA AATATAkATT TACGTGTTTA TTATCCACCA GTCGTCATCG 3120

GTTTGACAGC GCTAGTTACA GTCATAGTTT TGGCGTTCAT TTCAATCGGC CATGCG 3176

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

TCTTTATTTC AATTTCCAAT TGAATTTTTT TATTATTTAC GCATAGCTCT TAAAATTAAC 60

GTTACGATTG CAATTAAGAT AATTGAACCA ATTAATGCTG GCAAGATGTA AATACtTCCT 120

AATTCAGGAC CCCATTGTCC GAATAGTTTG CCACCTACCC ATGATCCAAT AATACCTGCG 180

ATAATATTGC CTAAAATACC ACCTGGGATA TCTTTACCCA TAATAGCACC AGCAGCCCAT 240

CCAATTAAGC CACCGACAAT TAACATTCCA ATAAATCCAA ACATAATTTT CAGTCTCCTT 300

TTTCTATTTA TTTTGCGTTA TTCTAAGTAG TACCCCTTAT TTACAATTCT AAAACAAATT 360

CAAATTATTT TTATCCAAAT ATTTTTAAAA GTAGTAATTG AATATCAATT TTATTCAATG 420

TAGCTATCGT TATTTAAAGT CTCTGTACCG ATAATATCAT ATACATTTAC ATTATTTTTT 480

CTGCCGAATT CATAGCTTGA TTATTTTATG TTATAGGACT AgAATATACA CATATTATTA 540

GAGCATCTTT GAATTTTAAA TCAAGAAGCG AGGTTAATGA ACAATGAATA TGCATATTTT 600

ATATaACTTA CGAACTAAAC ATAATTTAGA AATTGACGAA TTAGCACAGC AATTAAATGA 660

GAAATATGGT ACTAAATATG AAGCACATCA AATTTGGGAA TGGGAGAATC ATCACCATGA 720

ACCTAAATTT AAAGATGCCA TGCATTTAGC TGACTtCTTT GATGCACCAT ATGAAATGTT 780

TTTAGAAAGT AAGGTTAAAG AATATCAGAA ACATTTAGAA GAAGTCGATA TTCGCATGGA 840

TAAATAGATG CAAATAAACC CTCACAACAC GTTTGGCATA TATCCTTTCA AATCTATACT 900

GGATATATTA CATTACGTTG TGAGGGTATT TTATTAATTA ATATGAATTA AGACATTTTA 960

CAAGCGTTAA TGCAACGAAT CTTTTTAGTG ATCTTGCTCA CTCTTTAATA CTTTACCGTT 1020

CTTAGCATCA ACAGTAACTT CTTGTTTTTT ATTACCTTTT TTCAAATCGA TATTGTAAAC 1080

AAGTTTGCCA TCATCTTTTT CAAGTGACCA TTCTTTAATA TCACCATCAA ATTCTTTTTG 1140

ATTCATTGTA TCTTCTTTTT CAGTCTTTTT GTTAATCACT TTTTTATTTT TATCAGCAAC 1260

AAGTACTTCT GACTCTTCAC CAGATTTTTG TTGCGTCACT TTATAAGCCC ATTCACCATT 1320

AGAATTTTCA AATGAAATTC CTTTCAACTT TTGGCCTTTG TAAGTTTCTT CAGCTTTTTT 1380

CACAGCATCT TCTGGGCTTG TTTTAACATC TTTTAAAGCA ATAACATCTT TTGTTGTATT 1440

AGTGTCTTGA TTAGTATTTG ACTCTGTTGA TTTTGTTTCA TCTTTTGGAG TATCATTGCC 1500

ACATGCAGTA AGCACCACCG CTGACATTGA TAACACTGCT AATGATTTTA ATTTCATAAT 1560

ATCACTCTCT CTTCCTATTT TTGAAACTCA TAACAAAAGC TTATATGCTA TATAGATTGT 1620

ATTACCCCTT GTTTTTTAATT TTATTCATAA TTATTACAAA TATTTTTAAA TTAATCGTCA 1680

TGCGTTACTT TCGTTCGTAC TCCTTTTATA AATGAACCAT GTAATATAAG CATGCTATTA 1740

TCGACTCAGT TTGTCTAATG CTTTCTTTGG TACTTCTTCC TTTTCAACTT CTTCAAAAGT 1800

TTCTACATGA TGACCTTTAT GTGTAATTTT CAAGTATCTA TGCGGTTTAA CATCAAATGT 1860

AGCAGTATAC ATTAATTGCG TCTCTTTCCC TTCTTTATTA AAAACACTTT GACTATAACT 1920

TCGGAGTTGA TCATCCATTC TAGTAGACAC CTCTGTCGTT TTAACATAAG AATCATCCTT 1980

CTTTACTAAT GGGTTAAATT GATCTGTTAT ACCATGGGAG TCTATTGTTT TTAAAATGAA 2040

TAAAGCAgCA TAAGCGCCAA TGATAGTAAG TACAAGATAt GTkATTGTTT TTAAAATCGT 2100

TTCAAAAGA 2109

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

GTTACATAAA TGAAAACAAA AAAGATAATT TTACTGCTTA TGCTACACCA GAACATAATT 60

ATCAATTTGG TGGTGCTATG ATAGAAAGTG AAAAATTAAG CGAGTTACTA AAGCCAGCCA 120

ATCAGTTAAA ATCACCAGAT GATATAAAAA AAGAACTAAA TAAAAAGAAG AGTCACTAAA 180

GTTAGGAGTT ACTTTAATGT CCAAAAAACA TGTTTTTATA ATTATTGGTG TCATATTGTG 240

TATATGTACA GTTTCTACGG TCATGCATTT TAAAATGAAA TATGATGAAA AAGAAAAACA 300

AAAAGCGATT TACTACAAAG AACAACAAGA ACGTATTACA CTCTATCTTA AGCATAATAC 360

TAAAGAAACG AACACGATTA AATCTGTACA TTTCACAAAC TTGGAAACAA GTCCTATGGG 420

ATCGCCTGAA CATAATTATC AATTTGGTGG CGCTATGATA AAAAGTGAAG GAGTAGATAA 540

ATTATTAAAA CCAGCACATG AAAGAAAATC ACCAGAAAAA ATCAAAGAAG AATTAGATAA 600

AAAAGAAGGC CACTAGGGTC TTCTTTATTT TTGATTTAAT CTTCCAATAA TCTATGTCAT 660

TGCTATCGAA GGTGTTTCGC AATTAATATA AATCACTTCA TCATCACCAA TACTTCCCCA 720

GTTTTGTACA GTACATTAAC ACAAACGAAC CACGTTAATT TAAATGGAwT AaTAGTTTGG 780

CCATTATAAG AACAATATAT ATCGAnTAAC AAT 813

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 640 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

AAAAGCAATC GTTGGTGGTG CTAAATTCAT CGGCAACTCA TATGTAAAAG CTGGTCAAAA 60

TACACTTTAC AAAATGAGAT GGAATCCTGC ACATCCAGGA ACACACCAAT ATGCTACAGA 120

TGTAGATTGG GCTAACATCA ATGCTAAAAT CATCAAAGGC TACTATGATA AAATTGGCGA 180

AGTCGGCAAA TACTTCGACA TCCCACAATA TAAATAAGCA ACATGAACAT AGGATCAAAA 240

GTCATCCCCC ACTATCAATC ATGGGGGATG ACCTTTGATC CCTTTTTTAT ACATACACAA 300

GCAAAAATAG CGGTGATTGT TTACCATCAA TTTTAACAAT CACCGCTACT TTTGCTTGTA 360

ATTCATGATT CAATTTTTGT TGTGTGCACA ACGACACTAA ATTATGTGTT TGCTATTGTC 420

GTGTTACAAC GATATGCGTC GTTGATTTAA CTTATCAAGT AATTGATTTA AATTGTCTAA 480

TTCGACTTCC GATAAACATT GACATCTTGC TTCAATCAAT TCGCAACGTG CATTATTTAT 540

TTGTGAAATT AATGTACGTG CTTGATCAGT CAAAATTAAT TCTTTACATC TTAAATCTTC 600

GCTAGATTGT TGACTTGTGA TGTACCCnnT CAAAACTAAT 640

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

TTCTTGGATA CGTAATAAAT TACCTTTTGT CATAGGATTA AACATAGATC CAGGTAAAAC 120

ATAAACATTT CTATTTTGCT CTAATGCAAA ATCTATCGTG ATGTGACTGC CACTTTGTTC 180

CTTAGCCTCA GTAATTAAAA CCCCTTTTGA CAAACCGCTG ATAATTCTAT TGCGCTCAGG 240

AAATCTATAT TTAGCGATTG GTGTATGTGG TGGATATTCA GATATAACTA AACCTTTTTC 300

TTCTATTTTA TTTCTTAATG CTAATGTACT TTTGGGATAA TGTGTTTGAT GGCCAAAGGC 360

TAAAACTGCA ATTGTAGGGA GATTGTATTT TAAAGCTATT TGATGTGCCA TTGCATCAGC 420

TCCTTGAGCA AGGCCGGAAA CAATTGTTAA ATATTTGCTT TTATCATTTG ATAATAAAAA 480

TTCTAAAGAC TGTTGGGTAT AACTTGTAGA ATCTCTTGCA CCTACTACTG CCAAATGATG 540

CATATTATTT ATTAATTTGA TGTTCCCTTT ATAGAAAAGA AGTAATGGAA ATTGATATAT 600

TTCTTTTAAT AGCACTGGGT ATTCAGAATC CATATATGTA ATGTAACTTA CTTTTAATTT 660

CTGCAGTTCT TTAATAATAT CGTTATGATC AAGTTTTATA AAAGCATAGT ATTTACGTAA 720

TAAATGAACA TTTTCTTCCC TATTCACCCA TTCACATAAA TAACTATCTT TTTTTCTTCC 780

CTCCTCTTTA ATTACATTAG GATATGCCAT TAAAAATTGA TGAATTTGTT TAGTCGAAAA 840

GTGTGCCCAG TATAACTTAA GCAAAAATAG TTTAATCAAT AAATCAACTC CTTTTTGTAA 900

TCATACAAAA TCATATTCTA TTTTTGTTTT ACATTTCTAA TACAAAAACA TTGTCGATGT 960

AATGTTATTT TAAGGAGTAA AAATACTGAC TTAAAAAGTG AAAAGTATGT TGGAAAGAAT 1020

TTAAAATTTC AATTTCCAAC ATACTTTATA ATTAAACCTT ATAAATAAGT TTTGCAAATT 1080

TATATAGAAT TGGTCTTACT GGTTTGATGA AATCACCAAT TAATTCTTCA ACATGTGCAT 1140

TAAAACCCTT TTTAAATTG 1159

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1879 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

TCAATCAGCG ACTACAAGAA GTGCGGGTCT TCAAACAATT GATGTGACAA CACTAAGTGA 60

CCCCACTAAT ATTATCATGG GTATTTTAAT GTTTATAGGA TCTTCGCCAA GTTCGGTTGG 120

TGGCGGTATT CGTACAACAA CTTTCGCTAT TTTAATTTTG TTTTTAATTA ACTTTAGTAA 180

TAATGCCGAT AAAACATCCA TTAAAGTTTA CAATAGAGAA GTACACATTA TGGATATTCA 240

ATCAGCTACT GAAAATGGTA AGCTTACATT TTTACAAGTA TTTTTTGAAG TCATGTCTGC 360

ATTTGGAACT TGTGGACTAT CGCTTGGTGT CACAAGTGAT ATTAGTGATA TTTCTAAGGT 420

CGTACTAATG ATACTCATGT TTATAGGACG TGTTGGCTTA ATATCATTTA TCATTATGAT 480

AGCAGGACGT CGAGAACCAG ATAAATTCCA TTATCCAAAA GAACGTATTC AAATAGGATA 540

ATATAATAGC AATCTAAGTT TAGTTAATGT AGATTTTAAC TGGAACTTAG ATTGCTTTTT 600

TAGTTTGTAT TTTTAACTTA TTTTATAAGA CGATTGGTTT CGAAAATGGT AAACTAGTAA 660

CAATGAGAGG TGTAACATGA TGGAAAAAAA TGAAAACATT AATGTAGAGA TTTTAACTAC 720

GTCAGATATG CATAGTCATT TCTTAAATGG TGATTATGGT TCAAATATTT ATAGAGCTGG 780

TACTTATGTT AACCAAGTAA GAGCACAAAA TCATCGCGTC ATTTTATTAG ATAGTGGCGG 840

AAGTTTAGCT GGCTCGTTAG CGGCCTATTA TTATGCTATT GTTGCACCTT ATAAACGACA 900

TCCAATGATA AAGTTAATGA ACAGAATGCA TTATGATGCT AGCGGTGTGA GTCCAAGTGA 960

ATTCAAGTTT GGTTTATCAT TTTTAACTCG TTCAATTGCT TTGGCACGTT TTCCATGGTT 1020

ATCAGCAAAT ATTGAATACA ATGTTACTAA GGAGCCTTAT TTTTCAACTC CATATTGTAT 1080

TAAACATTTT GGTGACTTAA AAATTGCTAT CGTAGGCGTC ACAGCAGATG GTTTAATGGA 1140

AAATGAGTAT TCTGAAATGG AGCAAGATGT ATCTATTGAA AAGACATTAG TGGCATCAAA 1200

ACGTTGGATT AGATATATCC ATGAAGTTGA AGAGCCAGAT TTTTTGATTG TAATTTATCA 1260

TGGTGGATTG AATAAAATTA GTAATAGTAC GAAAAATAAA AAGGCAAGTT CGAATGAAGC 1320

TGAAAAATTA ATGGAAGAAC TCGGTGTTAT AGATTTAATG ATTACAGCTC ATCAGCATCA 1380

AACAATAGTA GGTCAAGATC ATGAAACGTA TTATGTTCAG GCTGGTCAAG ATGCCAAAGA 1440

GCTTGTACAT CTTTCGATTA ATTTTAAAAA GAGAACAACA ACTTATGATG TTGAAAGCAT 1500

TGATTCTAAA GTGATTGACT TAAATGAGTA TGAAGAGGAT CAAGAATTAT TAGATTTAAC 1560

ATTCTATGAT AGAAAAGCAG TGGCTTATTG GTCACAGGAA ATCATAAGTG ATAAAGGTTT 1620

GATGTTATCA GTAAATGGGT TACAAGATTT AGTCTGTCAA ACACATCCAT TTTCGCAATT 1680

ATTACATGAT GCAATTCACC TTGCATTTGA TAATGATATA ACATGTGTCC ACGTGCCTAT 1740

GaACGGAGAG AAGGGGTTGA GTGGACAGAT TCGAAATGAA GrTTTGTATC aTGCATACCC 1800

ATaTCCAGAT aAGCCAtGGG tATGACAATT aGTGGTCAAA ATaTCAAGGT ATnTTGGGGT 1860

ATAGTTATTC ACCATTAGG 1879

(2) INFORMATION FOR SEQ ID NO: 421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2710 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

AATTCCCCCT TTTTCCCCAT CCATTTTnCC ATCCACTGGT CCTTACGGGA CCATATTATT 60

TnAAATTGGA nAAAATTATt TTAAAGaTTA TwACtACTCT TtAATCATTT TrGTGAATTA 120

AAAAAAGTAG TGCAAAAAGC AAAATATACT TTATACACTA CAAATCATTT ATTTATAATA 180

AAGTTTCACC AAAAAATGTT CCAACTAATG AAACCGCTTG TTCAGCAGTA TGATTATTAC 240

TGTCAATCAA TGGATTTACT TCAACTAAAT CCATTGAGGA AATTAAATGT GATTGATGCA 300

GTAATTCCAA TGCAAAATGG CTTTCTCTAT AACTAAGACC ACCCAAAACT CTAGTACCAG 360

TGCCTGGCGT TTCAAGCGGA TCTAAAGCAT CAACATCTAA AGATAAATGA ACGCCATCAA 420

CATTGCGTGA CTTCAAATAT TCTATTGTAT TTTCAATTAC TTCCTTTATC CCCAATTTAT 480

CAATATCTGA CATAGTAAAT GTTTTAATAT TATGATCTTT GATAAATTGT CTTTCACCTT 540

TATCTAAATC TCTCATACCA ATTAGTACGA TGnTTTCTGG CTTGATTACA TTACnATTTA 600

ATTCTAAAAG TTCTTTGGGA CCTTCGCCTG TCAAAATCCT TAGAGGCATA CCATGAATAT 660

TTCCACTTGG TGACTCTTCA GGTATATTTA AATCACCATG TGCATCATAC CAAATAACAC 720

CTAAATTATT ATAATGTTTA CTTATTGCTG ATACTGAACC TACCGCAATA GAATGATCTC 780

CACCAAGAAC TAGAGGAAAT CTGTTATTTT CAATTGATGC TGAAACCTCT TTATTTAATT 840

TTTGATTAAC ATCTATAATT TCATCATAAT TTCTTAATCC TTTTTGTTCA CTATGAAATT 900

TTTCAATGTT CACAGCAGGt ACCTTAATAT CCCCCTTGTC ATATACATCA AGGTCTAATT 960

GCTTTAATCT TGAAATTAAT CCAGCATATC TAATTGCTGT TGGTCCTAAA TCAACACCTA 1020

ATTTTCTTTG TCCAAATGTT GATGGTGCAC CTATAATATC AATTGCTTTT GTCTTTGTCA 1080

TAAGCGTCCC CCTTTGCTCT ATGTAATTAA AGAATAATGT ATGCGCTTAC CATTATCAAG 1140

CAATAGCTAC ACATATAATC TGTTTATCTT ATTACTTCAT AAAAAAAGGT TCTTCATCTT 1200

TTATGGTGGG AAGGTAAAAC TTCCTGCTTT TTTTAATACA CAAAAAGCGC AATTGCCTCT 1260

ATAATTTAAA GTGACCAAAC CCAAACTAAA GGAGACAAGT GCGCCTATGT GTAATGATAC 1320

CTTAGAATTA CTAAGAATAA AAGATGAAAA TATAAAATAT ATAAACCAAG AAATTGACGT 1380

CATTATCAAA GGAAAAAAAG CAACAGTGGT TAATGCTGTA CTAACGTATA AGCCTTCGGC 1440

CTGTTATTGT TGTGGAGTTA AAAATGAAGG ACAAATTCAT AAACATGGTA AGCGTGTTTC 1500

TCGTATTACT TTACTTAAAA CTCAAGGGTA TAACACATAC CTCAACTTAG CTAAACAACG 1560

GTGTTTTATC TCAAGATGTG TTACTCAAAA AGTTATAGAA GAAGCTACTA AAGTTAAAAC 1680

AGAGATTGAT ACTGCAGAAG ATAACTGTAT CTCTCCATCT ACTGTAAGTC GTATTAGAAC 1740

TAAAGCGGCT AATTCATTAC GAATTAAACC CTTTAATTGT TTGCCAGAAC ACATCGCTAT 1800

GGATGAATTT AAAAGCGTTA AAAATGTAAC TGGATCAATG AGTTTCATTT TTATAGATAA 1860

TGATACTCAT GATGTTATAG ATATTTTAGA AAATAGAACT ACAAGATTCT TGCGTGCCTA 1920

TTTCGAGCGA TTCGATTTAA AAAATCGACA ACAAGTTAAG ACGGTTACTA TTGACATGTA 1980

TGAACCCTAT GTCCGATTAT TTCGCGACCT ATTTCCTAAT GCAGCTATTA TTTTTGACAG 2040

ATTCCATATC GTTCAACATT TAAATAGAGA ACTTAATAAG TATCGTGTAC AAGTTATGAA 2100

TGAATACCGT AATAAAAAAG GACCTGATTA TACAATTTTT AAGAATAACT GGAAAGTCCT 2160

ATTGATGGAT ACTAGTAAAA CCATATTTAG TAAATACAGA TGGAATAAAT CTTTTAAGGC 2220

TTATAAACGC TCATCTGACA TTGTAGAATT CATGCTTTCA AAAGACGATA TACTACGACA 2280

CTCCTACGAA CTTGTCCAAG GATTACGAAA AGACCTAAGG TTATGTAATT GGCCTAAATT 2340

TATTAATCGT TTAAATTCAG TTAGTAAAAA GTCTGTGAGT AAGGGTGTAT GGAAAGTGGT 2400

TAAATATTAT AGAAAACATC AAAGGATGTT AAGAAATACA ATTTATTACC CAGCATTTAA 2460

TAATGGTGCT ATAGAAGGAA TTAATAATAA GATAAAATTA ATCAAGTGAA TTTCTTTTGG 2520

TTACAGAAAT TTCAACAACT TTAAAGCACG TATAATGATG aTTTTCAGCT TGTACAAAGG 2580

AGaAAAAAAG AAGACAACCA AGCCCAATAA TGGACTGGCC GCCTAATAwA nGGGskCTAA 2640

AAGTTgTATT TTTAAAAATA GTTCCTTTAA ATTATATACC CnCCACATTT GGGGGAGGAC 2700

CTAAAAAAGC 2710

(2) INFORMATION FOR SEQ ID NO: 422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1027 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

CATTTTAATT GtTaAAATTC CAAAAAAtGT ArGTGGATTw AAAGrAAACC CtGTGTTTTT 60

AAAAGGtACC ATTaAAATAg TTCCGATTGT ACCATCCCAC GTGAAAtTTT TAgTAtTGCC 120

GGTGaGAGAA AATGCCAATG CAATCATCGC AGTTCATAAT CATCCATCCG GTGATGTAAC 180

GCCCTCACAA GAAGATATCA TAACAACAAT GAGGTTGAAG GAGTGTGGTT TGATTTTAGG 240

GGGTTACTTT GATGAAAATG ATTGAAGTTG ATAGAATTAA TGACGTATCT TGTGTATAAT 360

ACCTACGAAG TACTTTCATT GGAGGAAAAA TAGTGACTCT ATTTATTATT ATCGGGGTTC 420

TCGTGCCAAT GGTTTATACC ATGCAGTTAA ATATTAAAAA TGAACCTGTa ACAAAGCGCA 480

ATCTTTTAAT AACATTAGCT TTATCTACGT TAGGTATTTT AGTAACCGCG TTAGCAGGTG 540

TAATCGTTAC GAAACAAGCT TTTCCTTTAT TAAGTGTAGC AATTGGCTCA ATTTTTACTG 600

GAATCGTTTG GGGCCTTTTA CTAAGTGGTA GcTACGCGCT GATACGATTT TTATCTAACG 660

CATTTGGGCG TAAGTAATAG TAATCTGTTC ATCAAGTAGT ATCCGTGCTT GAAAACAAAC 720

TAAAACTCCT AATGTGGAAC TAGTTAAAAA ATTCTAAACT AGTACATTAG GAGTTTTGTT 780

ATGCAGAATA AATTTAATTG TTAAATTGAA AGTGCGGTAA AAATCCACTA TTTATTTGAA 840

AAAAATCGAG CAACCAAATT AAACCTTGAT ATCCTAAGTA AATACATAAT AAAACAAGTC 900

CGACATAAAT TAAAAATCGC AAAATAGAAA GTCCAACTCT AAAAAGGAGG ATGACTAATA 960

GTGCTATTAA AATAATTGTt AGTATACTCA ATGCTACAAA CCTCCTArTA CGCTTTTAAA 1020

TCCATAA 1027

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 569 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

CGGCACATTT TTAATTTATA CATATTTTAA AACTAAGTAA CAGTTTGAAG AAATCGTAGT 60

TCAATAATGT TAATTGTGAA AATGTATATA AACATAAAAA AATCATGTAT AATATATGTT 120

GTTAATTAAA CAGTTCGAAA GCGAGATGAC ATTATGGGAC GTAAATGGAA TAACATTAAA 180

GAAAAAAAGG CCCAAAAAGA TAAAAACACA AGTAGAATAT ATGCGAAATT TGGTAAGGAG 240

ATTTATGTTG CAGCAAAATC TGGTGAACCC AATCCAGAAT CTAACCAAGC TTTAAGGTTG 300

GTGCTTGAAC GCGCTAAGAC ATATTCAGTG CCGAATCATA TTATTGAAAA AGCAATAGAT 360

AAAGCTAAGG GTGCTGGAGA CGAAAACTTT GATCACCTAA GATATGAAGG ATTTGGCCCA 420

AGCGGATCAA TGCTAATTGT TGATGCGTTA ACAAATAATG TAAATCGTAC TGCCTCTGAT 480

GTGCGAGCTG CTTTTGGTAA AAACGGCGGT AATATGGGTG TATCTGGATC AGTTGCTTAT 540

ATGTTGTCAT GTGGCCACAT TTGGTATTG 569

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

TGGACCTATA AAATGGATGC ATCCAAATAT GGATGnGGGG TAnGGCGGGa AAATAGGaGG 60

TTATATAGTA AGTCATTTAA GTCGAATAGC CATCCTTTTT AAAATGAAAA AAATAGAAAG 120

CTCAATAGTT TGTTAAAGCC TTTAAATAGC GTCGTTACGC AATTTTAGAA TGCTAAAAAT 180

TGTCACAAAT TTCAAATTAC GTGCTAAAGC TTGAGATATC AATATTTATT GGCGATAGAG 240

TGTAATTTGA CTCCGCTTAC ATCTCAGTTT TATGTTTGTA ATTTGGTAGC ATAATATTAT 300

AATAAAATAA AATTGTTAAT CTTTAATTTC AGTATAGATA TTTTTACGTG TAGTCACGTG 360

TAAAATAAAT TCAATTAGGT TAGGAGACAT AATTATGAAA ACATTTGGTA AAAAGGTTGT 420

ATTAATCGGA GATGGATCTG TAGGATCAAG CTATGCCTTT GCAATGGTTA CGCAAGGTGT 480

TGCTGATGAA TTTGTAATTA TTGACATTGC AAAAGACAAA GTAAAAGCAG ATGTTCAAGA 540

TTTAAACCAT GGTACAGTCC ACAGTCCTTC ACCAGTTGAT GTGAAAGCAG GTGAATACGA 600

aGaCTGTAAA GATGCAGATT TAGTTGTTAT TACAGCTGGT GCACCTCAAA AGCCAGGTGA 660

AACACGTTTA CAATTAGTTG AAAAAAATAC TAAGATTATG AAGAGCATCG TTAAGAGTGT 720

TATGGATAGT GGCTTTGATG GATATTTCTT AATCGCGGCA AACCCTGTAG ACATTTTAAC 780

AAGATTTGTA AAAGAATATA CTGGATTACC AGCAGAGCGT GTTATCGGTT CAGGTACTGT 840

ATTGGACAGT GCACGTTTAC AATATTTAAT TAGCCAAGAA CTTGGTGTTG CACCTTCAAG 900

TGTTGACGCT AGTATTATTG GCGAGCATGG TGATACTGAA CTTGCAGTTT GGTCACAAGC 960

AAATGTAGCA GGTATTTCAG TATATGACAC ATTAAAAGAA CAAACTGGTA GCGAAgcTAA 1020

AGCGGAAGAA ATTTATGTGA ATACACGTGA CGCTGCTTAT GAAATTATCC AAGCTAAAGG 1080

GTCAACATAC TATGGTATTG CATTAGCATT GATGCGCATT TCAAAAGCCA TTTTAAATAA 1140

TGAAAATAAT GTCTTAAATG TTTCTATACA ATTAGATGGT CAATATGGTG GTCACAAAGG 1200

CGTTTACCTA GGTGTACCAA CATTAGTTAA CCAACATGGC GCAGTTAAAA TTTATGAAAT 1260

GCCATTAAGT GCCGAAGAAC AAGCGTTGTT CGATAAATCT GTTAAAACAT TAGAAGATAC 1320

ATTTGATTCA ATTAAATATT TATTAGAAGA CTAAGCCTAT TTTAAGTATT AATTAGAAAT 1380

ATATTAATGG TAAGAGGATC TATTAGTGTT GCAGTAACAC GTGGCACTGA TAGGTCCATT 1440

TATGACTCGT GAAAATTTAG TGACATGAAT AAAAATGTTG AGGCGTCATT GAGTATAAAG 1560

GAAAGTAGTT CTGCATTAAT CACGAaGTAG AGCATGACmA CGAGGAATAA CTATAGGGaG 1620

ATGGTTTTGG AATGACGAtG TCTTGTATCA ACATGGTACA TTAGGTACGT TAATGGCTGG 1680

CTTACTAGAA GGCACAGCTA CAATTAATGA ATTGTTAGAA CATGGGAATT TAGGGATTGC 1740

AACGTTAACA GGGTCTGATG GCGAAtAATA TTTTTAGACG GAAAGGCATA TCATGCTAAC 1800

GAGCATAAAG AATTTATAGA ATTAAAAGGC GATGAGAAAG TACCGTATGC ATCGATTACT 1860

AATTTTAAAG CGAGTAAGAC ATTTCCATTG CAACAATTAT CACAAGATGA TGTATTTGCA 1920

CAAATTAAAA ATGAAATGTT AAGTGAGAAT TTATTTTCGG CTGTTAAAAT TTATGGCACA 1980

TTTAAACATA TGCATGTACG AATGATGCCT GCTCAGCAAC CGCCATATAC ACGTTTGATT 2040

GATTCAGCAC GCAGACAACC TGAGGAAAAA AGACAAGATA TTCGTGGTGC CATTGTTGGA 2100

TTTTTTACAC CAGAATTATT TCATGGCGTA GGGTCTGCTG GTTTTCATAT ACATTTTGCG 2160

GATGATGAAA GAGCTTATGG TGGACATGTT CTTGACTTTG AAGTGGATGA CGTTGTCGTT 2220

GAGATACAAA ACTTTGAAAC ATTCCAACAA CATTTCCCGG TAAATAACGA GACGTTTGTT 2280

AAAGCGAAAA TAGACTATAA AGATGTGGCA GAAGAAATTA GAGAAGCTGA ATAGTCTAAT 2340

ATAATTAAAA GACCTTAGCG ATATTAGGAA CAGGTGGTTC TAAATGCATC GTTAAGGTCT 2400

TTTTATATTA TATATGTGCT TACATATTTT GTTGATACGC GCGTAAAAAG CTATAAATAG 2460

TATCAAGATA TGGGGTGTCA AGAATGTGTT CACGTGCACG TCGATAAATA AAGCCTTGAA 2520

TCGCTTCGAC TTCAAGAGGT TGCTGATGCG CAATGTCGTA ATACATGCTC GTTCCCATTT 2580

CGTCGGGATA ACCTTGATAT ATAGTCATAA TAGTATCGAC AGTTTGTTCT GAAAAGTTTA 2640

ACCCCTCTGC CTGTGCAACA CGACAACCAT CTAGTAATAG CTGTCTACAC AGTGTACGTA 2700

TTTCAGGATT ATGCATGATT GCAACGGTCT GTCTACCGAG TGCTGTGATA GAATTAATGC 2760

CCAAGTTAAC TAACAATTTA TACCAAATAG CTTGTTGAAT ATTTGCTTCT AATACAATGT 2820

CGATTTGACT GTCTTGGACC AAATCTCTAA ATTGTCGAGT TAATGCATTA TCTTGTATAC 2880

GTAATTGATA ATCTCTGAAG TGCGTAACAA CATCGCCTTT CTTTTGACCA CTTATATAGA 2940

CAACTGCTTG GCATACGTTT TTAAATGAAA TATGTTCGAG TTGACCATAA CCATTTTGGG 3000

CTAAAATGAT GAGCGTGTCC TCATGTGCAA GATGAGTTAA ATGAGGAATA ACTGCATCAA 3060

GTTGATGTGT TTTGACTGCA ATAATAATAA CATCAAATGT GTTTGTGACA TCTTCATAAC 3120

CTTTCACAAC AATATCTTGT GCAGGTGCAT GTGGTACAGT ATAATATGTT ATTGTTTTGG 3180

CGTGTCTCCC GATAAGCGTT GTATGAGGCA ATGATTGTTG TAATTCATAG GCAATAGTTG 3240

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 796 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

AGAACGAACC TTTAATACGT ACGTGTCGAC CACGAACTGT CATGACAAAT TGATAAAACG 60

AATAGTTTTT CATTAGTTCA TTGTCACATC AATCACTTTT GTkTCACCTT TAATCACAGC 120

ATTTTCATCA TAAATATTAA TTGAAGCTGC TTGATCAGTG TTAGTAATTA TAATTGGTGA 180

AATTACAGAT TTAGCGTTAT TATTAATATA TTCAAGGTTG AATCTTACTA ATGGATCTCC 240

GACGTTAACT TCGTCACCAC TAGACACTAA CACTTCAAAT CCTTCACCGT CTAATTGAAC 300

TGTGTCTAAA CCGATATGAA CTAATAATTC TAATCCGTTA TCTGCTTTTA ACCCAATCGC 360

ATGCTTAGTT GGAAAGACAT TGTCAACACG TCCTGCAATT GGAGACACAA CTTCTCCTTC 420

AGTTGGATTA ATACCAAAAC CTTCGCCCAT CATTTTTTGT GCGAATACAG GATCTGGAAT 480

ATCTTCAATT TTCACGAATT CTCCAGTTAA TGGTGCATAA ATTGCGATAT CTTTCTGAAC 540

TTCTTTGCCT TTTCCGAATA ATTTTTTAAA CATACTTTCC ACTCCTACTT ATCAAAATGT 600

GATATTAAAT CGCCATAACC CAATTCTTCT AACTTTTCAT ATGGAATAAA TTGAATTGCA 660

GCGGAATTGA TACAGTATCT TAAGCCGCCA CTTTCTTTAG GTCCATCATT AAAGACATGT 720

CCTAAATGAC TATTTGATTC TTCTGAACGC ACTTCAGTTC TCAACATACC AAATGATTTG 780

TCGACTAATT CTATAA 796

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

ATCCAGCAAA TCTTTCTTAT CACGTTCTGT AATTTTCTTA GTATCCATCT TGATTAGCTT 60

TGATAACTTT TCAGCCGTAT CCAACATTTC CGATTGTGTT GTTTTTCGAC CCCTAGTATA 120

TGTAATAGCC ATTTTAGAAG CATTATCAAC TAAAACTTTC CCATTTCTGT CTAAAATACG 180

ATGTGAGCCT TGTGCGATTT GTAAATAACC TAAACGTAGT ACTAGTACTG CAAAAATAAA 300

TACAATCACA CCAAATATAA AGTTAATTCT CTTGTTAATT GTATTTTGAA CGATTTCATC 360

ATTTGATTTT TCTTTTAGTC TTTTTAACAA AACTACCTAC CTCTATTCAA AGTCTTTCAC 420

TTTAAATCAT ATATGAATTT AGAAATTATT TCTATCTTTT TGACAAAAAA ATAACGGTCT 480

CATTtAAGAG ACCGAACAAG TAATCATACT TTATTTTGTT GCATTATATA ATTCGTCAAC 540

TTTTTCCCAG TTAACTACAT TCCAAAATGC GCCAATGTAG TCAGGGCGTT TGTTTTGATA 600

TTTTAGGTAA TAAGCGTGTT CCCATACGTC TAAACCTAAA ATAGGTGTTT TACCCTCAGT 660

TAATGGATTA TCTTGGTTTG GTGTAGTCAC AATTTCTAAC TGGCCATTGT TTACGACTAA 720

CCAAGCCCAA CCTGAACCAA AGCGTGCAGC TGCTTTGTCA GCAAATTCTT TTTTAAATTC 780

TTCTAAAGAA CCCCATTGTT CTTTAATTTT TTCTACTACA GTACCTTTTT CTTCTGAGTT 840

TGGTGAAAGT AACTCCCAGA ATAATGAATG GTTTAAATGT CCACCGCCAT TATTACGTAC 900

AGCAGTTTGG ATGTTAGCTG GTACACTGTC TAAATTAGCA ACAATTTCTT CAATAGATTT 960

AGATTCTAAA TCTGTACCTT CTACTGCAGC ATTTAATTTC GTAACATACG TGTTATGATG 1020

TCTGTCATGG TGAATTTCCA TAGTTTCTTT GTCAAAATGT GGTTCTAATG CATCAAATGC 1080

GTATGGTAAT TTTGGTAATT CAAAAGCCAT AAATAATCAT CCTCCTAAAA TGTCTGTAAG 1140

TAAATAATAA CAAGCAGTGA CTGGTTCAAC AAAGAATTTG CTTAAATTCT ACTACTTATT 1200

ATTTTCTCTA CTCATTTAAT ATAACTCAAA TCAAAAATAA TTAAACATTT TGTATATAAA 1260

AAGTTAACAG ATTTGCCATA AAATCATACG AACGGAGTAT GAAATGAACC TTTATCTTCT 1320

ATAATTTAAA AAATGAGATT TATGCATACA TCGGACCAAA TGTGCATAAA TCTCATTTCT 1380

TTATATTAAT CTTGGcAAGA CTCACATACA CCATAAACTT CAAGTTTGTG TTTGTGAATA 1440

TTAACACCAG GTAGTGATAA TTTTATCTGA TCTATTGGAC AATAATCTAT TACCTTTGTA 1500

TCTCCACACT TTTCACAGAT AAAATGATGA TGATGATGGT TTGTACAAGC GATTCTAAAC 1560

TTCATTTCAC CATCAAGTTC TGTATTTTCA ATAATTCCTA AATCTTTAAA TAAGTGCAGG 1620

TTTCTATATA TTGTGTCGAA TGAAATTCCA GGATAATTTT CATCCATAAC TTGTTGTATA 1680

TACTTTGCGT TTATATACTT ATCTTCTTCG ACAAAAATAT CTAACATATC TTTACGTTTA 1740

TCTGTATATT TTAAACCGTT CTCTTTTAAA ATTTTAATAG CATCATTTGT ATTCATTGAT 1800

ATTAGCTCCC TTTTTAAACT TCATTCGCAT TTTCTGATAA GCCATTGTAA TCATAAGTAA 1860

AATAACAAGT AGAACTACAA TTACACCACC CGGAGAAATG TCCATATAGA AAGCTAGGAC 1920

TAAGCCTAAT ATTACTGATA ATTCACCTAA AAATACACTT AGTAATATCA ATTGCTTAAA 1980

TATCCCTACA ACACGCATTG AGGCAGAAAT AACCATCGCT ACAATAACAA TAAATAAAAA 2100

TTGAATCCAT TTAGGAATGC CAATGACTTT ACTATATTCC TCATCAAATG ACAATATAAA 2160

TAATTCTTTA TAAAACAATG TAATAAACAG AACAACTATG ATGGCAATGA CAATAATCGT 2220

TGTTAAATCA CTTATATTCA CTGCGCTTAT TGAGCCAAAT AGCAATCCAA CAATTTCTTG 2280

ATTGAACCCA TCAGCTAATG AAATGAAGAT TGCACTCAAG GCGATACCAG CACTCATTAT 2340

AATTGGAATA GCAATTTCTT GGTAAGCAGT GTATGACGTT CTTAATTTTT CAATTAGAAG 2400

CGCACCTACT ATTGCGAATA AGATTCCAAA CCACATTGGA TTAATAAATA CTAGTGTTGG 2460

CATAATAGTA AGTAAAAACA TACCGAAAGA TATACCACCT AAAGTTACAT GACTTAGAGC 2520

ATCAGCTwTA AGTGATAGTC GTCTAACAAc GATAAAAGCA CCGaTTAGAG GCGCAATAAA 2580

ACCTAtCAAG ATAcCACTAA TTAAAGAGTA CCTCATAAAA TCAAAATTCA ATAATGCATC 2640

TATCAATTGT GACACGCCTT TCCATTTTAA ATAAACTCAA ATCTTTATTA ATTACAACAT 2700

TCTCGATTAT GCTGATGATC GACAAAACGT ACAGGATGTC CATAAATTTT TGAAATTTCA 2760

ACTTCATCAA GTGATTTAAA CTCATCAGTT GTACCATGGA AATGCAAATG CTTATTTAAA 2820

CATGCTACTT CAGTAGCAGT ATCTGCTACA ACACCGATAT CATGAGTAAC TAAGATAATG 2880

GTGATACCTT CTTGTTTTAA TTGATCTAAA GTATTATAAA ATTCACTTAC ATGTTTTGCA 2940

TCAATACCAT TCGTTGGTTC ATCAAGTACT AATACTGcAG GTTCTGAAAT CAATGCTCGA 3000

GCAATCATTa CACGTTGTTG TTGACCACCT GATAATTCTG CTATATTTTT ATGAATTAAA 3060

TCACTTATAT TCAGTCTTTC TAGTACTTTA ATCACTTTTT CATTATCTTT GCTATTAAAT 3120

GTTTGGAAAA GACGTTTTGT CTTTGTTAAT CCGCTTAAAA CAACTTCTTT AACACTTGCT 3180

GGGAAACCTG AATTAAAGGC ATTTGCTTTT TGTGATACAT AGCTTAATTT AATTGATGTT 3240

TcTTATTTTT AAAATCAATA CCTTCAACAA AAATCTCACC ACTTTGTAAA GGTAATAACC 3300

CTAGAATCAA CTTCAATAAT GkTGATTTAC CAGCACCATT TGGkCCAACA AwTGCtAAAA 3360

ATTCACCTTT ATTTATTTTG AATGnnnTAT ATT 3393

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

CCCTGTTTCT TAGCCTTTTC GTATATGCGT TCATAAGAAG AATTCTTTTT GATTTCAGAT 120

TGTAAAGCAC TGTTTTCACT TGATTGTTTA TCTATTTTAT AATCTAAATC TGCAATCTTT 180

CCTCGCGTAT CATACGCATC CATTTTTAAA GATAGCATAT AAATACTTAA CATAGCAATT 240

ACAGTAATCA AAGTTATGTA TAAAACTTTT TCAAATTTAG TTAATTGTAC AACCACTTTT 300

CTCGAAACAG TCTTCTTTTC GGGCTTAGTT TGTGGTTGTT GCTTCGGTAT ACTATTATAA 360

ACTTGTTCGT CATATGGTTG GTACACTTTT TCTACAGCCA TTATAAATTG CTCCTTATTT 420

AAGTATTTCA GCTACACGTA ATTTCGCGCT TCGTGCTCTG TTATTGTCAT CTAAATCTTC 480

TTCTGTAGCG GTAATCGGTT TACGATTAAC ACGCTTTAAC TTAGGTGTAT ATGCTTCTGG 540

TATAACTGGT AATCCTCTTG GTACCTCTGG ACCTTTTTCA TATTCTTGGA ACACCTGTTT 600

ACATAAACGA TCTTCTAAAG AATGGAAAGT GATTACCGAA ATCCTGCCAT CTACTTTCAC 660

TAATTCAATC GCTTGTTCTA TTGAATCTTC AAAAGCTGAC AATTCATCGT TTACTGCAAT 720

TCGTAGTGCT TGAAATACTC GTTTTGCAGG ATGTCCGCCT TTTCTTCTTG CTTTTGCAGG 780

AATACCTTCT TTTATAATGT CAACTAATTC TAATGTTGTT GTTATTGGTT GTTGTTCGCG 840

ATGTGCTTCG ATTCTTCGAG CTATCTGTTT TGAAAATTTC TCCTCGCCAT AGCGATAAAA 900

AATCTTCACT AACGCTTCAT ATGACCAATT GTTAACAATT TCATATGCTG TTAGTTCTTG 960

TGTTTGGTCC ATACGCATGT CTAATGTTGC GTCATGGTGA TAACTGAATC CTCGTTCTGG 1020

AATGTCGAGT TGTGGGCTTG AAACACCCAA GTCGTAATAA ATTCCATCTA CTTTTTCAAT 1080

GTTTAAGTCT TTTAATATTT GAGTTAATTC ACGGAAGTTG CTA 1123

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 838 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

TATATCCTCC AnACCATAAA AATGGAATTA TAGTGAAGAC CGCTATGATC CAGGATGACC 60

ACGTATTATA GAATCTTTCg ATAGAGAAAC GAATCaACGT ATCCgACATC aCGAAATGAA 120

ATTAGAAGAT TATAAAGATG AGTTAAGAAG AGAATATCTA AAACAATCTG ACAGAATTGA 180

AGGAGATGAA TAAGCGTGGG ACTTGATTTT AGTGGTTTAC CAGATTTAGC AGTATTGGAA 240

CAAATGAAGG AAAAAGAACA GATTAGTGAG GTTATTGCGC CTGAACATGT TCGTATGCAT 300

CATTTCAAAA AATTTGAAGA TGATTTTAAA AATGCGGCAC AAGGGGCTTG GGTGAAAAAT 420

GCCACAGACG AATTAAAAGA TATTAGTAAT GATTTAGAAA AAATTCAAGA TATTAAAGTA 480

TAAAAAGGTA TTAAGAAACA CAATAAGTAT ATAATCCATT TAATAATAAA TGAATTATAT 540

AGTTCATAAT TTCGACTATA AGTGGCTATT AGCCATTATT TTTCGGGATC TATGTCAAAT 600

CGGACTAATG AATTCAATAA TGGAAGTTAA GCAACCAATC TTTGTTTAAC TTCTTTTTTA 660

TTTTTTGGAA AATAAAGTTT TGAACATAAT AAAATTTGAT TATGTTTTAA CGAATTTTGA 720

TGTTTCTTGA ACTATATATC ATCTAGTCGT CATTTACAAT TGGTAAATAT GACTTCAAAC 780

TGkATGAAGG TGATGGCGAT TAAAAGGCTC ATCCGTAGGT TCTAAAGAAC TAGAnTTT 838

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

nGTGTTCAAA TAATAGAATG GCTAATACCC CAACAATAAA TAGGAATAAA TATGTTGATG 60

TCGTAATTTT AGTAAATAAT GAAAATCTAA AATTAGTAAC CCTATTTTGA ATATAAGCTT 120

TAACTTCTAA TAATACTGGG AAGCCGATTG ATCCTAAAAT TATTAAAAAT ATAACTATCG 180

CTTGTACAAA ATAATCATGT GCATAAGGAA TTAATGACTT ACCTGTAATA TCTAATCCAC 240

CATTGGTAGT GGCAGAAATA GAAACAAAAA CACCTTGCAT GATTGCATAT TTTAAATCTG 300

GATTATCTCG ATAAAAGTAA AATGCTAATA ACATGGCTCC TACGAGTTCG ATTACAAATA 360

TTGATTTTAC AATATCAATA ATCAATTTGA CGGTACCACT CATTGTGTTT TTGTTATTAT 420

CTAACATAAT TAACTGACGT TCTCTAATTC CAATATGTTT ACCTAGTACC ACCCATAACA 480

TCGTACCAAT TGCCATGACG CCAATTCCAC CAATATTTAA TATCACGAGG ATAATTAATT 540

GTCCAAATGT AGAATAGGTA TCGACAATAC TTATCGGAGA CAATCCAGTA ACACTAATTC 600

CGGATACGGC AACAAATAAT GTGTCAATTG GATTTACTTC TACACCTGGT TTATGaACAT 660

ACGGTAAGTT TAATAATAAA AATGCAATGA CAATTGCGAC GATATAGTAC AATACAATAC 720

CTTGTTGAGG GCTTGATCTT TTTAAAAACT GGCTAAAAAT TGACACGTTG TTCACCTCAA 780

CATTATTTTA GTTTAATATT AATTTCTTTC TCTTTACCAT CTCTATAAAT CTTCGCTGTA 840

ATTGATTTCA AGTCATCTTT ATGACTAAAT ATAATCTGCC TAAAGCGTAA ATCATCTTCT 900

AAACCATTGT TGTCAACTTG ATCTACAACA ACACCGTTCT TAACTTTTCC TGGCAATTTA 1020

ACTGCTTGTC TTTCAAAACT ATTTAGACTG ACAATATTCT TCATTTTAAC ACCTACATCG 1080

GGATAGTCAA TTTTACCTTT tGTTTCTAAA TCTTTTACAA TCTTTtGTAC TTCATTAaCA 1140

GGtATTGCAA 1150

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 797 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

AAGAATATTT AGGATTTTAT GTTTCGCAAC ACCCAGTAGA TAAAAAGTTT GTTGCCAAAC 60

AATATTTAAC GATATTTAAA TTGAGTAACG CGCAGAATTA TAAACCTATA TTAGTACAGT 120

TTGATAAAGT TAAACAAATT CGAACTAAAA ATGGTCAAAA TATGGCATTC GTCACATTAA 180

ATGATGGCAT TGAAACTTTA GATGGTGTGA TTTTCCCTAA TCAGTTTAAA AAGTACGAAG 240

AGTTGTTATC ACATAATGAC TTGTTTATAG TTAGCGGGAA ATTTGACCAT AGAAAGCAAC 300

AACGTCAACT AATTATAAAT GAGATTCAGA CATTAGCCAC TTTTGAAGAA CAAAAATTAG 360

CATTTGCCAA ACAAATTATA ATTAGAAATA AATCACAAAT AGATATGTTT GAAGAGATGA 420

TTAAAGCTAC GAAAGAGAAT GCTAATGATG TTGTGTTATC CTTTTATGAT GAAACGATTA 480

AACAAATGAC TACTTTAGGC TATATTAATC AAAAAGATAG TATGTTTAAT AATTTTATAC 540

AATCCTTTAA CCCTAGTGAT ATTAGGCTTA TATAACTTTy ATCAACTAAT AAATTATGAT 600

ATAGTAAACT GATGGTTAGA TATTTyTyAA CCATCAGTTT GCGTktATAT TAGTTTTTTA 660

TGCTTATTAT TTTTATGAGT TTCACTTTAC ATTATTGATT AATCCATAAG AATAATTAGC 720

ACAAAAAGCA GTATACATAA ATTGAGTAAA GAATTTTGTC GATATAACCG nGCGGAAAAA 780

TAATAACnTT TTGGATn 797

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1466 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTTCCAAGAG AAGTTGCGGA AGTAATTAAT AAAACGCATC ATAATAAATT GGTCATTTCG 60

ATGATTTCGk CACAAATCGA TGCGGATAGA ATGGATTATT TACAACGTGA TGCGTATTTC 120

ACAGGTGTAT CATATGGTGC TTTTGATATG GAGCGTATTT TAAGATTAAT GCGACCTTCT 180

AAAGATGAAG TACTAATCAA AGAAAGTGGT ATGCATGCAG TTGAAAACTT TATTATGAGT 240

CGTTATCAAA TGTATTGGCA AATTTACTTC CACCCAGTTA GTCGTGGTGG AGAAGTGCTG 300

CTTAATAATT GtTTGAAACG CGCAAAACAG CTTTATAATG AAGGCTATGA ATTTAAGTTG 360

CATCCACATG ATTTTATTCC ATTTTTTGAA GAGACAGTTA CGATTGAACA ATATGTTGAA 420

CTCGATGAAG CGGTAGTTAC GTATTATTTG GAAAAATGGA CAAAAGAAGA TGATGCTATT 480

TTAAGTGATT TAGCAAGTCG ATTTATTAAT CGAGACTTAT TTAAATATAT TCCATTTGAT 540

GGCTCAATTA TTACAATATC AGAACTGCAA GAACTGTTTG AAGCAGGTGG TATTAATCCA 600

GATTATTATT TTGTGAGTGA AGCATTTTCT GATTTGCCAT ATGACTATGA TCGACCGGGG 660

TCAAATCGCA AACCGATTCA TTTATTAAGA CAAGATGGTA CGATTAGAGA AATAAGCAAT 720

CAATCATTAG TCATTCATAG TATTACAGGC ATTAATCGCC AAGACTATAA ATTATATTAT 780

CCTAGAGAAA TGGTTGCAAA GATTAAAGAT AAGACAATTA GAGAAGCTAT TGAAAATTTG 840

ATTAATGAGC TTAATTAAAC AGGGCTAAAA TTGTTATCGT TAAATATGGA GGTTATATCA 900

TTGTCTGAGA AAAAAGGCTT TAATTTTAAT ATCATAAAAA ATGACCCTCT AGATGGTCAT 960

AAAGGTACAA ATATTGGTTC AATTAGCTTA GACAATATTG CACCAGTTTT TATCGATGTT 1020

GCTAACAAAG AAGCATTTAT TGATATTGGA GGCATGCATG CTCGTGCCAA AGTTGAAAAA 1080

GGTGTGAAAT GGATTACTGA TAAAGCTGCT GTTGAAGGCG ATGAAGCTAA AGaATATTGG 1140

TTGTGTTGGG TAACAACAGA ACGTAATGAA CAAGGACCAT ATTACGCTGG TTTAACAGCG 1200

TGCTATTTAT TAGTGAATAA AGCAATTCGT CGTGGTTATA AAAGTATGCC TGAACATGTT 1260

AATATGATGG ATAAATCAAT GAAACATCAT ATTATCATAG ATCAAATTGG TGACGAGAAT 1320

AAAGCTATTT TAAAAGACTT TTTAATGAAC CATGATGAAG GTATGTGGAA GCATTCTTCT 1380

GATGCTTTAC ATCAAGCATT TAATTAAATA TTAGAAACTA AAATTTCCCA ATTAATCTAT 1440

AAAGATATGA TTCATTTCTC AATGAC 1466

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

TTGTACGAAT ACAAAGTTGC ATTAATATAG AATCATTTAT GCTTTTTAAT ATCACAAAAC 60

AAATTGATTA AACTAGCTAA AATAGTCAAA ATTGGAATCA AGATTACATA AATATCATAA 120

CCTCTAGATA TTAGTATACA TAATATAATT AGCGACCCTA TTATAATTGC TAAATTATAA 180

GCCAAACTAA TTTTATATTT CATTTCAATT CCCACCTTAA TAGCATTTAT TAAAATTCTA 240

TAATGTTTAC ATAGACTTCT TAACAAACTT TAACCCAGCT AAGCTAAGTA TTGAAATAAT 300

TACACCTCCT AATATAAATA TATTACTTAA GCTTAGTAAA GGTATAATTA TACTTATCAG 360

TCCTAAAGAC AATGTATCCG CTGcATAATT CGaTGtAGAT GAGATACTAA ATACTTTCCC 420

CATCAAATGA TTTGGCGTTT TTATTTGAAT GGCAACTGAT CTTGTTAGTC CCTCTATAGA 480

TTGTCCAAGT CCCAATAATG TTGCACCTAT ATATAATATC GCCACACTTG GAAACACATT 540

AATAATCGAT AAGCCAATTC CCCAAACTAA AACACCAATA CTAAATTTAA AGATTAATCG 600

CTTTTCTGAC AGCAAACCCA TAATCAATGA CATTAATAAA GATGCTATAC CTAAACATGA 660

TGTAGCTAGT CCATATACAC CAACGCCCTC TTTTAATATA TTGGAAATAA ACAATGGTAA 720

TACAACACGC CAAAGGCCAG TATTAATCAA TATGCAGGCA AATTGGATGA TTATAATAAA 780

TGGAATTTCT TTAGATTGTT TCAAGAATTC CCAAGTTTCA GAAAAATCTT CTTTTGAGTG 840

TCTATCAATC ATGTTGTTAT TTGTATATTT TAAAAGTGCA TTAAAAATAA ATCCTAAAAA 900

TAGCAATATA CTACAAATAA AAAAGACGCC AACATTACCA ACTAGTATTA CAATGACACC 960

AATTAAAGCA GGTAAAATAA TATTTGAGCC TCTTTGCAAA CTATCGATTA ACGCATTACT 1020

TGTTGCTAAA TGCTCCTCAT CAATAATTTC AGGAAGAATT GCCCTAAACG CAGGATCCGT 1080

ATAGCAGTTA ATAATGGTGA TAGCTGTAGA TATGGTTAGA AGCGTCAGAT AATTTAAATT 1140

TGATGTTATT GCAAGTAAAG GAATAATTAT TATAATCAAA CTTAGTATAA GATCAGATAG 1200

ATAAAGTATT TTCTTTTTAT TATGTTTATC AGAATATGCG CCACCGAAAA TACCAAATAT 1260

AATAAATGGA AGTGTTTGAC TCATAACCAT CATTGATAAT TTTAAAGATG ATTGGTTTGT 1320

CAATTCAACA GTAAACCAAA TTATTTGTAA CGAAAACAGC ACAAAACAAC TCCGACGTAA 1380

GArATTACCA ATCAATAAAT ATGTAAAGTT TCTATTTTTC AAAACTTCTA AATACAACAT 1440

ATTTATCACC TCTCATAAAA ATAATTGAAT GCATCCACCA GCTTTTTTAG ACCTTCTTCT 1500

AAACTCTCTT TATCCAAAGC GCAATTAATT CTAATATAAT TTAGTCAGTT AAATATCAAT 1560

TATTTCGAAA TATACATACT ACTTGAAACA CCATACATAA CCCCCAAAAT GACTACTCAG 1620

AGGTTATATT CTACTAATTA TGATTATATT AAATATGAAA ATATTATCAA AAAAATCAAA 1680

TCATTCTCAT CATATTCTAG GTTGTTTTTA ACAAACTAAA TATAGTGAAT GCAAATCAAC 1800

TATTATTTAA ATTATGAATT ATTTTAATTC TTTCTTCTAC GAGCCAATAA CATTAATCCA 1860

GCAATTCCAA TTATACTACT AAAGATCAAA CCTTTTTGCG TGCTTTCTAA ACCTGTTTTT 1920

GGTAATTCTG CTCGTTTTTT CTCTTGATTA GCTACTGATT CTTTAGCAAT TTTAGATTTT 1980

TTAACTTTAT CATTTTTATC CATTGAATGA ACTGGGCCAT TTGGTTTTGC TCTGTCTTTC 2040

GATAATCCTG GATTGTTAGG ATTTACTGGG CCACTTGGAT GAGTTGGTCT GCTCGGCTTC 2100

TCTGGGTTTT CAGGTCCTTT TGGATCTTTT GGTTTCTCTC CACCGAACTC TACAATCTTA 2160

TCTACTGGTT GTTTtGTGAT CTCTTCTGTT GGTTGACCCT CGCCAACTTT TTCACCTGTT 2220

AATGGGkTCA CTGTGAwTGG TGkTGTGAwT GTCyTACTTC CTGGkTGTCC TTCTTGTTTC 2280

ACTCGCTCTT CACCAGGTTG TAAT 2304

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4733 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

GTCTTAATAT TTTACAAGAT ACAGCCTGAC AATATTTATA TTACAAACCA ATATGGTAAA 60

GAGGCTGTGT CTCGATTAAA AAGAATTTTA GAGCAAAGTA TACCTAATAA AGAATATATT 120

GATTTATCAG AGATATCATT AATTACATTT TTTAAACCAG AATATAATAA ACAACATGTG 180

AATGAGGAGT TTAATTCTTT ATCTTCTTCG AAAATAAAGA ATTTAGCCAA AGAAAATGAT 240

GGTATTATTA TTTATTTAAA TTTTAAGGAT GTTAATTATC AACTGaTAaG TGAAGGCAAT 300

ACTTTTTTTT CTGCAAAACC ATATTTGCAT TGTGTGTTCA ATAAAGATAT TTTAAATATG 360

GATAAAGTTG ATATAGAAAA TTTTTTCAAA AGTATAGAAG TCAAATACAG TAAATAAGAT 420

CAATTATTGA ATCCACCGAC CAGCAGATTT TTTTAAAAAA TTAATACCCC GTTAATACCC 480

TTTGCTTCAA TTTGATGAAA ATCAATGAAA TTCAAAATTG AAGAAATCCT TTAATATCAA 540

GGTGTACGAC AGTCTATATA ATCATGCGAA ATTCTAAAAT TTTCtGAcGT AAAAAAACAA 600

ATTCyTAAAG CAGCTCGTCG TTCACCTCAA TTCTCAAAAC GTTAATTGTC GGACGATATA 660

TATACAAAAC ACCTCGATGT TATGTCGAGG TGTTTTTTTG CGTTTGTGTG GGGAATATGG 720

AATAGAGTAT AAATGAATTA ATGTCTCAGG TATAGAATTA ATTCAACTAT GAATTATTGA 780

TTAGCTTGCG GAGACCGTAC GATAGTGTTC TAATAATAGA TATTCAAGGG AAAGAGCTAT 900

CGGATGATAA CCAGATGATA ACTCAAGAAC CATGrTTTAA GAGTGTTATC AAAATAAGGA 960

GTGACTTAAT TGAAAGATTC TATATTTTGG AAGAAAGCTT TTATTyCTGT TTATTTTATT 1020

GTTGsGATGC TGGTGTTTCT ACTTTTTAGG TTTTATATTA AaACAGATAA CTTTTCTATA 1080

TATTTAATGA GTATCTTCTT AATTTGTTTA GGAACTGCTT CTATCATTTA TAACTATAAA 1140

ACCAATCGAT AAATATAAGT ATGAAATGTA TAAGTCACAG TTAGATCTAA GTCTTGCTGT 1200

GGCTTTTTAT ATCTCCATAA AACGACAAAT TCAAGCCCGA CATAAAACAG CATTTTCAGC 1260

CCACCATAAA ACGACAATTT CAGCCCGCCA TTGACTAAAC ACCACATCCC AAAAATATCG 1320

TAACAATCCT CTACATCAAT CAATCCAACA TCCCTCATAA TCACAACGCA CAAAATCTAT 1380

TCATGCATTT TTGGAATACT TAGTATTACA AATAACGATT TTTATTCATC TAACAAAGGT 1440

TATATAATGT ACTGAAGGCA ATTTTTATGT ATTACAAATC TAATCGTACA TGTAAAATTT 1500

TGATAAACAT CATTAATTTT GCGTAACTAT CATTAGATTA CAAATCACAA AGTAATTACA 1560

TGTAATACAC ATCTATACAT CACATTTGAA GGGAAATGaA TATAAATGAC TGATAAAAAG 1620

TACACTGCAG CCGATATGGT TATTGATACT TTGAAAAATA ATGGGGTAGA ATATGTTTTT 1680

GGTATTCCGG GTGCAAAGAT TGACTATCTA TTTAATGCTT TAATTGATGA TGGTCCTGAA 1740

CTTATTGTCA CTCGTCATGA ACAAAACGCC GCAATGATGG CGCAAGGTAT TGGAAGATTA 1800

ACAGGCAAAC CGGGTGTAGT ACTTGTTACA AGTGGTCCTG GTGTAAGTAA TTTAACTACT 1860

GGATTATTAA CCGCAACATC TGAAGGGGAT CCTGTATTAG CGTTAGGTGG CCAAGTGAAa 1920

CGnAnATGAT TTATTACGAT TAACGCATCA AAGTATTGAT AATGCTGCGC TATTAAAATA 1980

TTCATCAAAA TATAGTGAAG AAGTACAAGA TCCTGAATCA TTATCAGAAG TTATGACAAA 2040

TGCAATTCGA ATTGCTACTT CAGGAAAAAA TGGCGCAAGT TTTATTAGTA TTCCGCAAGA 2100

CGTTATTTCT TCACCAGTTG AATCTAAAGC TATATCACTT TGCCAAAAAA CAAATTTAGG 2160

AGTACCGAGT GAACAAGATA TTAATGATGT CATTGAAGCG ATTAAAAATG CATCATTTCC 2220

TGTTTTATTA GCTGGTATGA GAAGTTCAAG TGCAGAAGAA ACAAATGCCA TTCGCAAATT 2280

AGTTGAGCGC ACGAATTTAC CAGTTGTAGA AACATTCCAA GGTGCAGGTG TAATTAGTCG 2340

TGAATTAGAA AATCATTTCT TCGGTCGTGT GGGCTTATTC CGCAATCAAG TTGGTGATGA 2400

ATTATTACGT AAAAGTGATT TAGTTGTTAC AATCGGTTAT GATCCAATTG AATACGAAGC 2460

TAGTAACTGG AATAAAGAAT TAGAAACACA AATTATCAAT ATTGACGAGT TCAAGCTGAA 2520

ATTACTAATT ATATGCAACC GAAAAAAGAG TTGATTGGTA ATATTGCTAA AACGATTGAA 2580

CAATTAAGAA CACATATTGA TGAAGAAACT GGTATTAAAG CGACGCATGA AGAAGGAATT 2700

CTACATCCAG TGGAAATTAT TGAATCTATG CAAAAGGTAT TAACTGATGA TACTACTGTA 2760

ACAGTTGATG TTGGAAGTCA CTATATTTGG ATGGCACGTA ATTTCAGAAG TTACAATCCA 2820

AGACATTTAT TATTTAGCAA TGGTATGCAA ACGCTTGGTG TAGCATTACC GTGGGCAATT 2880

TCAGCTGCAC TTGTGCGCCC TAATACGCAA GTTGTGTCCG TTGCTGGCGA TGGTGGCTTT 2940

TTATTTTCAT CACAAGATTT AGAAACGGCC GTACGTAAAA ATTTAAATAT CATCCAGCTT 3000

ATTTGGAATG ATGGAAAATA TAACATGGTT GAATTCCAAG AAGAAATGAA ATATAAACGT 3060

TCGTCAGGTG TAGACTTCGG TCCTGTAGAT TTTGTAAAAT ATGCAGAATC ATTTGGCGCG 3120

AAAGGTTTAC GAGTTACTAA TCAAGAAGAA TTAGAAGCGG CAATTAAAGA GGGCTATGAA 3180

ACAGATGGTC CAGTATTAAT TGATATACCT GTAAATTACA AAGATAATAT CAAACTTTCA 3240

ACAAATATGT TACCTGACGT ATTTAACTAA AATAAAGATA AATGTTAAAG AGGAGTGGGA 3300

GATTTTATGA CTAATGTTTT ATACCAACAT GGTACATTAG GCACATTAAT GGCAGGATTA 3360

TTAAAAGGAA CTGCATCAAT AAATGAATTA TTGCAACATG GTGACTTAGG TATCGCTACA 3420

CTAACAGGTT CAAACGGTGA GGTAATCTTT TTAGATGGAA AAGCTTACCA TGCAAATGAA 3480

CATAAAGAAT TTGTAGAATT AAAAGGTGAC GAGTTAACAC CATATGCAAC TGTAACTAAA 3540

TTTGTAGCAG ATACAAGCTA TGAAACGAAA GATAAATCTT CAGAAGCAGT TTTTGCAGAA 3600

ATTAAGGAAA AGATGTTGAG TGAAAATTTA TTTTCAGCAG TAAAAATTTC AGGCTTATTT 3660

AAAAAAATGC ATGTACGTAT GATGCCGGCT CAAGAACCAC CTTATACACG TTTAATCGAT 3720

TCAGCTAGAA GACAACCTGA ACAAACTGAA ACGTATGTCA AAGGTTCAGT CGTTGGTTTC 3780

TTTACACCAG AATTATTCCA TGGTATCGGA TCAGCAGGAT TTCATGTACA CTTTGCGAAT 3840

GATGATCGTA ACTTTGGTGG ACATGTCTTA GATTTTGAAG TAGAAGATGT TAAAGTAGAA 3900

ATCCAAAATA TAGAAACATT TGAACAGCAT TTTCCAATTC AAGATAAAGA TTTCACTAAA 3960

GCAAATATTG ACTATAAAGA TATTGCAGAC GAAATTAGAG AAGCTGAATA ATGAATCCAG 4020

AAATATAATG ACGGTTTATG AAAATTGACT TCATAATGCG CGATTTAGAA ATGATAGTTT 4080

GTAAATATGA TTAACCATGA CTACAATAGA ACAAATATAT TTATAATTAC GTCTAAGTAA 4140

TAAAATAAAT CCCTTCACTA TTAGCAGTAG TGAGGGGATT TATTAGGTTC CAGATATTTG 4200

AGATTTGCTG TTATGTTTAG ATTATAAATT GTGGTACACA CTCATATAAA ATTTACTATT 4260

GTATAGGCCA ATCTGTTACT ACGAGAAGCA AACAACAATA ATTTACAAGT TCAATAACTA 4320

AAAAGACAAA CGCCAATTTT TCAGCGCTTG CCCTATAAAA CTATTTTCAA ATTATTATTT 4380

TTTCTTTAGA TTCACTACTT TTTTATTACC ATCATTCAAA GTAAGCGTAT AAGTTGCTGT 4500

TTGGGCATTA TTAATTTTTT CTGTTGTAAC ACCACGTTGA GAAGCTAATT CATTTTTTAC 4560

TTTACTGTCA ATTTCTTGAT AAAGAACATT TTTATTTTCT GGGAAGATAA AGTAAGTTCG 4620

ATGTAATGCA GTAATACCAT CTACTGAAAT TGTGTAAGGA ACAGTGTGAT AACCATCCAC 4680

AGTCATTTCT TTATAGCCGT TATTACTATC TGCAGATGCT TCGTGACTCG GTA 4733

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

AATAAATGGT AATTTTATAT CATCAACGGC TACAAATGGG GCAGTTTCAT ATATAAATAA 60

ACACATCTAC TCAACTGnTC TTAATTAATT AATAAATGAT TTACCAGATG ACATATAACA 120

GCCATTATTA GnTTAATTCT AATAGTTTAT TTAAATTTTC TTCGGTTGTC GCCCAACTGG 180

TTGCGAATCT AACAACACGA TGTTGATCAT CGTATTTTTC CCAAACAGCA AATTTAACTT 240

TTTGTTCTAA CTCTGCTATT TTCTCGTTAC TTAAAATAAA AAATTGTTGA TTGGTTGGAG 300

AATCAAAGTA AAGACGATAG CCTTTATTTT TAAACCCGTC TTTCATCTTA TTTGCCATTT 360

CGATAGCATG TCTGCTTATA TTAAAATATA AATTGTCCGT AAATAATTCT AAAAATTGTA 420

TGCCTGTTAA CCGTCCTTTT GCTAAAAGGG CACCGTGGAT GCTTGATTCG AGTGGTAAAT 480

TGTTTCGGTT CATTATTTTT CGTAAAAACA ATGGCTTCCC CGCATAATGC ACCTATCTkC 540

GTACCACCTA TATAAAATAC ATCACAATAT TTAGCGrTGt CTTTAATAGT CATATCTGAT 600

TGGTCACTCA TCAATCCATA CCCTAATCGT GCACCATCCA TAAATAATGG AAGCTGATAT 660

TGCTTACATA CTTTGCATAA CTCTTCCAAT TCTGaTTTAG AGTATAATGT GCCATATTCT 720

GTAGGATGAG AAATATATAC CATTCCTGGG AATACCATAT GGTCCTTTTT AAAATCACTT 780

TTAAATGTCT CCATGTAAGT TTCAACATCT GAAGCACTAA CTTTTCCTTC CTTAGAGGGT 840

ATAGTAATTA CTTTATGTCC ACTATATTCA ATTGCACCGC CCTCATGCAC AGCAACATGA 900

CCAGTGTCTG CTGAAATGAC CCCTTCGTAA CTTTCTAACA TTGAATTAAT AACAACCTGA 960

TTGGTTTGTG TTCCACCTaC TAAAAAACGA ATTGTAGCAT TTGGaCAGTC AATTGTATCT 1020

TTAATCTTTT CAATTGCCTG AGCTGTGAAT TGaTCAAAGC CATATCCCGA AGCTTGTACA 1080

TCGAATGAAA TCACTACATT TCCCCCTAAA ACTAATATCA ACATTTTAAT AAGATAAACC 1200

AATTTCAAAA CTAGTTCGAT ATTTAAAATG TATTATGGAT GGnTAAAGTT TGTATCGCAT 1260

TATCGCGAAG TTGnATAAAT ATAT 1284

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1072 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

ACAGCTTTTG GTAArGGAGA AAwTCAaTAt GAAACAGTAT AArGCGTATT TaATCGATTT 60

AGATGGCACA ATGTATATGG GAACAGATGA GATTGATGGA GCAAnACAAT TCATCGATTA 120

TTTAAATGTA AAAGGCATTC CTCATTTATA CGTAACTAAT AATTCAACAA AAACACCTGA 180

GCAAGTAACT GAAAAATTAC GTGAAATGCA CATTGATGCT AAACCAGAAG AGGTTGTAAC 240

GTCAGCGTTA GCCACTGCTG ATTATATTTC AGAACAATCA CCAGGAGCAT CAGTATATAT 300

GTTAGGTGGG AGTGGTTTAA ATACTGCGTT AACCGAAGCG GGACTTGTCA TTAAAAATGA 360

CGAGCATGTT GATTATGTAG TTATTGGACT TGACGAACAA GTTACATATG AAAAGCTTGC 420

GATTGCAACG TTAGGTGTAA GAAATGGtGC AACATTTATT TCTACAAATC CTGATGTATC 480

AATTCCTAAA GAGCGTGGTT TATTACCTGG TAATGGTGCT ATTACAAGTG TTGTAAGTGT 540

ATCGACAGGT GTATCGCCAC AATTTATTGG TAAACCAGAA CCGATTATTA TGGTTAAAGC 600

ATTAGAAATT TTAGGATTAG ATAAATCCGA AGTTGCTATG GTAGGCGATT TGTACGATAC 660

CGATATTATG TCTGGTATTA ACGTAGGTAT GGATACGATT CATGTACAAA CAGGTGTATC 720

TACGTTAGAA GATGTGCAAA ATAAAAATGT GCCACCAACG TATTCTTTTA AAGATTTAAA 780

TGAAGCAATA GCTGAATTAG AAAAATAGAT ATAGTCATTT TATAAAGTAG GTGAATTGAT 840

TTGGTAAAAA TAGTTGTTTC GAGGAAAATT CCAGATAAAT TTTATCAACA ATTAAGTAAA 900

CTTGGTGACG TTGTTATGTG GCAAAAATCA TTAGTGCCTA TGCCTAAAGA TCAATTTGTG 960

ACaGCcTTCG TGACGCAGAT GCTTGTTTTA TTACATTAAG TGAACAGATC GATGCAGAAA 1020

TTTTAGCGCA ATCACCAAAT TTAAAAgTAA TTGCGAATAT GGCTGTAGGA TA 1072

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3271 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

TAAAAACTTA CTTTAACACC ATTCCTTTTT AACTTTTTTC GTGTTTCnTT TnCTTAAGTC 60
CATCCATATT TTTAATGATG TCATCTGCTG TTTTATCTTT TAAATCTAAC ACTGaGTGAT 120
AmCGAATTTG TAGCACAGGA TCAAATCCTT TATGGAATCC AGTATGTTCA AATCCTAAGT 180
TACTCATTTT ATCAAAGAAC CAATCATTAC CAGCATTACC TGTAATCTCG CCATCATGAT 240
TCAAGTATTG ATATGGTAAA TATGGATCGA TATGTAGGTA TAGACAACGA TGTTTTTTAA 300
CATATTTTGA TAATTCATTA AAGAAAAAGT GTACGAGTTC TTGATTTTCA TAATCAATCA 360
CTGGACCGCG ATTTGAATAA AAATACTTGA ACACTTTCAT AACAGGTACA GCAGTAAGtA 420
AGCAAGCTGC AATGACCTCG TTATTATTGT TTTTTATTCC CACTAAATGT GTTTCATAAC 480
CTTCAGCAAG CTTTAACTCA TAGTGGCCAA CAGTTTGCGT GaAATGACTG TATGGCATGC 540
TATCTGTAAa GGCACCAAAC TCTTTAGCTG TTAAATTTGT AAACTTCATT ATCATTACTC 600
CTATTTGTCT CTCGTTAATT AATTTCATTT CCGTATTTGc AGTTTTTCTA TTTCCCCTCT 660
GCAAATGgCA AAAATAATAA ATCTAATCTA AATAAGTATA CAATAGTTAA TGTTAAAACT 720
AAAACATAAA CGCTTTAATT GCGTATACTT TTATAGTAAT ATTTAGATTT TTGAATACAA 780
TTTCAAAAAA AGTAATATGA ACGTTTGGGT TTGCTCATAT TACTTTTTTT GAAATTGTAT 840
TCAATTTTAT AATTCACCGT TTTTCACTTT TTCAAACAGT ATTCGCCTAA TTTTTTTAAA 900
TCAAGTAAAC TTAATTATTC AATGTTTGTT GGATAGATTG TAAATATTTA ATGATTTCCT 960
CACGCGTGTT AGATTTAAAT CGCTTAACGA TTTCGCTACC AATGACAATG CCATCTGCAA 1020
CCTCTTTTAT ATCTGCAACA TGTTGTGGTG TTCTTATACC AAATCCTGCG ACAACTGGCA 1080
CATTGGCTAT CGCTTTAATT GACTCAATTT TTCGTTTTAA TTCTGGATGA AACGCACCGT 1140
TTTGCCCTGT TGTCGCATTC ATCGTCACAG TATAAATAAA GCCTTCCGCA TGGGATACGA 1200
TATCTTTTAT ACGTTTGTCA TCAGTAGTCA TCGCAACTAA CGATATGATT TTGACGCCAT 1260
AGTGACTAAA TTGTTGTTTT AAACGCTGCG ATAATTCATA TGGTAAATCA GGAATAATTA 1320
AGCCGTAGAC ACCAGTATCT CGACATTTTT CAAAAAACGC TTGTTCTCCA TAATGACAAA 1380
TAATATTATA ATACGTCATT AATACATAGT TACACTTAAT TTGATCACCA TGTTTTTCTA 1440
ATTGATTGAA AATATAATCT ATCGTGATGC CTTGTTTAAT CGCTTGTTGA CCTGCTTCCA 1500
TGATAACTGG ACCATCAGCA ACCGGATCAG AGAAAGGTAC TCCAATTTCA ATTATATCTG 1560

GTATAAATAA TTTAGTCATT TGCAAGACCT CGCTCTACCA TATATTGTCT AATTGTTTCC 1680

ATATCTTTAT CGCCACGTCC AGAAATAGTT ACTACAATAA TATCTTCTTT CGACATCGTA 1740

GGCGCTAGTC TTTCAACATA ACTCAGTGCA TGTGCACTTT CAATTGCAGG TATAATACCT 1800

TCATGTTTTG TAAAGTTGAT TAAAGCATTC ATTGCTTGTG TATCACTAGC ATTTTCAAAA 1860

GTTACTCTAC CAATGTCGTG GTAATAAGAA TGTTCTGGTC CAATACCAGG ATAATCAAGT 1920

CCTGCTGAAA TAGAATGTGC TAGTTGCACT TGCCCATCTT CATCTTGAAT TAAATACATT 1980

TTAGTACCAT GTAATACGCC AGGTGATCCT TTGCCAATTG CAAGTGCATG TTTATCAGTA 2040

TCATCGCCTT GACCTGCGGC TTCAACACCG TATAATGCAA CATCATCTTT AATAAATGGA 2100

TAAAATGTAC CGATTGCATT TGAGCCACCA CCGATACATG CTACAATTGC ATCCGGAAGT 2160

CGACCTTCTT TCTTCAATAT CTGTGATTTT ATTTCTTTAC CAATCACACT CTGAAAATCT 2220

CTAACAATCG TTGGGAACGG GTCTGGACCT AATGCAGAAC CTAATAAATA ATGTGTATCA 2280

TCTACATGAC TTACCCAATA TTGCAATGCT TTATTAACTG CATCCGATAA AGTCCCTTGA 2340

CCATCTTCAA CTGCCACAAC CTTTGCACCA AGTAATTCCA TTCTAAATAC ATTAAGTTGT 2400

TGTCTTTTAA TATCTTCACT TCCCATAAAG ACAACAAGTT CCATATCAAA TAATGCAGCA 2460

ACCGTAGCAC TAGCTACACC ATGTTGACCC GCACCAGTTT CAGCAACAAG CTTCTTCTTG 2520

CCCATTCTTT TAGCAAGCAA CGCTTGACCT AACGCATTAT TAATTTTATG GGCGCCTGTA 2580

TGATTTAGAT CCTCTCGTTT CAAATATATT TTAGCGCCAC CTAGGCTTTC AGTATATGAT 2640

GCAGCATATG TAAGTGGTGT CGCGCGTCCT ACATACTCTG ATAAATAGTA TTCCAGTTCT 2700

CTTTGAAACT CTGGGTCTGC TTTTGCCTCT TTATAAGCTT TTTTCAACTC AATAATTGCT 2760

GGCATTAATG TTTCTGGAAC ATATTGCCCT CCATATTCAC CAAAGAAACC TAATTCATCT 2820

GCTTCTGTTT GTATTTGTTT ATTCATTGTC TCTATCTCCT TTCACAATAT TTACAATTGC 2880

TGTCATTTTT TCTATATCTT TTCGCCCATT TACTTCTATA CCTGATGCAA GATCATAACC 2940

TTGATGTGAT AATTTAAGTT GATTAACTGT TTGAATATTT TCAGAGTTAA TGCCTCCTGC 3000

TATCAAATAA GGTATGTCTT TTATGTGCTT CAAAATAGTC CAGTCATATG TTTGACCGGT 3060

ACCACCATAC GACACTGAGG GTGTGTCGAT AATAAATAAA TCTACGAACC CTTTATATTT 3120

ATTTATGTTT TGGATTATGT TTTCATCTnG CAGtAAAGCT TTAGTGATTT TAATGCTTGA 3180

ATATkTCTTT TTAATTTCCT GTAtAAAAtC AATAGATTCt GtGTAACTGT ATTGTGkTAA 3240

wTGaCGwATg CtTAAwACgT GTGCCAATGG T 3271

(2) INFORMATION FOR SEQ ID NO: 437:

(A) LENGTH: 1553 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

ATAATGAAAT AATACTGTGT TTTATCTGCG AAATGTAtCA TTTTCTAATc GTTTCACAGT 60

AAAATGAAAA GATAAAGTGT GTTTTTACTT GAATTTTGAC TAAAATTACT CTATATTTAT 120

TAATTGAGCT ATGCTTATTA TTACAATTTG ATTACAAATT TTAAATTTGT TAATTGAATG 180

ATAATATTAA ATAAAGAAAC TTACACAAGC AAATATGAGT TGTAGCCCAA AATACTTGTT 240

AAATCAAAGT TGAAAGCTAC AAATAATGAA AATTATAAAC TTGAATCTGA AAGTAATTAC 300

TATAATTATG ACAATGTTAA CTTTTAAACG CACTTATTAA TTAACTACAT AATGTTAATA 360

TCTAATTTAT TCAAGTACTT TCGCAAGATT TATTATCTAA ATAACGGGGG AAAGAATCAT 420

GAGTtCACAA AAAAgAAAAT TAGTCTTTTT GCGTTCTTCT TATTAACCGT AATAACGATT 480

ACCTTGAAGA CGTATTTTTC TTATTATGTT GATTTTTCTT TAGGTGTTAA AGGTTTAGTA 540

CAAAACTTAA TATTATTGAT GAATCCTTAT AGTTTAGTAG CACTGGTTTT AAGTGTGTTC 600

CTATTCTTTA AAGGCAAAAA AGCATTTTGG TTCATGTTCA TAGGCGGCTT CTTATTGACG 660

TTCCTATTAT ATGCCAATGT TGTGTACTTT AGATTCTTCT CTGATTTTTT AACGTTTAGT 720

ACTTTAAACC AAGTAGGTAA CGTAGAATCT ATGGGTGGTG CGGTTAGTGC ATCATTCAAA 780

TGGTATGACT TTGTTTATTT CATTGATACG TTAGTTTACT TATTCATTTT AATATTTAAA 840

ACAAAATGGT TAGACACAAA AGCATTTAGT AAGAAATTTG TTCCTGTCGT AATGGCGGCT 900

TCAGTAGCAT TATTCTTCTT AAACTTAGCT TTTGCTGAAA CTGACAGACC AGAATTATTA 960

ACACGTACAT TTGACCATAA ATATTTAGTG AAATATTTAG GACCTTATAA CTTTACAGTA 1020

TACGaTGGTG TTAAAACTAT CGAAAATAAT CAACAAAAAg CGCTAgCATC TGAAGATGAC 1080

TTAACaAAAG TATTAAAtTA TACGAAAcAA CGTCaAACmG AGCCTAACCC rGAwTATTAT 1140

GGGGTGGcAA rGAAGAAAAA TATTATTArG ATTCATTTAG AAAGTTTCCA AACCTTCTTA 1200

ATTAATAAAA AGGTTAATGG TAAAGAAgTA ACACCGTTTT TAAACAAATT ATCAAGTGGG 1260

AAAGAGCAAT TCACATACTT CCCTAACTTT TtCCATCAAA CAGGTCAAGG TAAAACATCT 1320

GACTCTGAAT TTACAATGGA TAACAGTTTA TACGGTTTAC CGCAAGgTTC TGCCTTTTCA 1380

TtaaaaGGAG ATAATACGTA TCAGTCATTA CCAGCAATTT TAGATCAAAA GCAAGGCTAC 1440

AAATCTGATG TCATGCACGG TGACTATAAA ACATTCTGGA ACAGAGACCA AGTATATAAA 1500

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1419 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

ACAAAATCAA TCAGCAAAAT GATTGGATTA AGACGCAAAT TGAGCGTTCA ATGGAAGGCG 60

AAACAGTTGG CATTAATGAT CAAAATATAG AAATATATAG TGAAcGtTgA GATTTATACC 120

ATACACTCGT ACCTTTAAAT CAAGAATTGC ATAAGTTGCG ACTTAAAACT CAAAACTTAA 180

CCAATGAAAA TTATAATATT AATGATGTGA AAGTTAAAAA GATTATTGAA GATGAACGTC 240

AAAGACTAGC ACGAGAACTT CACGATTCTG TTAGTCAGCA ACTTTTTGCG GCmAGTATGA 300

TGCTATCTGC TATCAAAGAA ACGAAtTAGA ACCACCATTA GACCAACAAA TTCCTATTTT 360

AGAGAAAATG GTTCAAGATT CGCAGTTAGA AATGCGTGCT TTGCTGTTAC ATTTAAGACC 420

GCTTGGTTTA AAAGACAAAT CTTTAGGTGA GGGTATTAAA GATTTAGTTA TTGATTTACA 480

AAAAAAAGTG CCAATGAAAG TTGTGCATGA AATACAAGAT TTTAAAGTGC CTAAAGGTAT 540

TGAAGATCAT TTGTTCAGAA TTACACAGGA AGCAATTTCG AATACATTGC GTCATTCAAA 600

CGGTACAAAA GTGACAGTAG AATTGTTTAA TAAAGACGAT TATTTATTGT TGAGAATTCA 660

AGATAATGGT AAAGGTTTTA ATGTTGATGA AAAATTAGAA CAAAGTTATG GACTTAAAAA 720

TATGCGTGAA AGAGCTTTGG AAATTGGTGC AACGTTCCAT ATTGTATCAT TGCCAGATTC 780

AGGTACACGT ATCGAGGTGA AAGCACCTTT AAATAAGGAG GATTCGTATG ACGATTAAAG 840

TATTGTTTGT GGATGATCAT GAAATGGTAC GTATAGGAAT TTCAAGTTAT CTATCAACGC 900

AAAGTGATAT TGAAGTAGTT GGTGAAGGCG CTTCTGGTAA AGAAGCAATT GCCAAAGCCC 960

ATGAGTTGAA GCCAGATTTA ATTTTAATGG ATTTACTTAT GGATGACATG GATGGTGTAG 1020

AAGCGACGAC TCAGATTAAA AAAGATTTAC CGCAAATTAA AGTATTAATG TTAACTAGTT 1080

TTATTGAAGA TAAAGAGGTA TATCGTGCAT TAGATGCAGG TGTCGATAGT TACATTTTAA 1140

AAACAACAAG TGCAAAAGAT ATCGCCGATG CAGTTCGTAA AacTTCTAGA GGAGAATCTG 1200

TTTTTGAACC GGAAGTTTTA GTGAAAATGC GTAACCGTAT GAAAAAGCGC GCAGAGTTAT 1260

ATGAAATGCT TACAGAACGA GAAATGGAAA TATTATTATT GATTGCGAAA GGTTACTCAA 1320

ATCAAGAAAT TGCTAGTGCA TCGCATATTA CTATTAAAAC GGTTAAGACA CATGTGAGTA 1380

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 608 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

ATGTnGGCGG ACGTAAAGGA CATGTTTATA CTGATGATCG AGCATTAGAT ATTGATATCG 60

TTCCGCCTGC TCAAGCAGAT GGTAAAGCTA CTAACCCCGA ACAATTATTT GCAGCAGGTT 120

ATGCATCTTG CTTCAACGGT GCTTTCGACC TAATTTTAAA GCAAAACAAA GTGCGTGATG 180

CTCATCCAGA AGTAACACTA ACAGTGAGAC TAGAAGATGA TTCAGACTCA GAAAGTCCTA 240

AATTAAGTGT TTCAATTGAT GCGACAATTA AAAATGTTAT ATCTCAAGAA GAAGCTGAAA 300

AATATTTACA AATGGCTCAT GAATTTTGTC CATATTCAAA AGCGACTCAA GGAAATATTA 360

ATGTCGATTT AAATGTAAAT GTTGTAGATT AGCATTAACT TAAAGAGATT ATTCAACGTT 420

ATTAATAAAA TTCACATAAA ATTCAAATTt stCrAcCAAA AATTTTTGGT TGGyTATTTT 480

TTCTATTCGT GATTGAAATT TCTGGCAATA TTTAACTGAA AATGATTGTA CCTTAGTCAT 540

CATAAATGTG ACCGGTTCCA ATACTGGCTT GACTTCTTCG CATACCGTCT ACAAATAAAA 600

GTCCAGTG 608

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 682 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

CCTTTCAAtT TCTCCCAAgA TTTACGCATG TCTGACCAAA TGTCAATACA ATACCTGAAT 60

AATGATTTCT GGAGTAATTG CGAAAAATAT TTAAAAGTTG CTATAGATCA ATTTTCAAAT 120

TATAGTATCT CATCTCAAGT TTCTAACTAT CATTTCACAG TATTACTTGG AGATCGCCAA 180

AAACCACTTA TGTATCTAAA TAAAAATCGC GGTGGTGATG GTGGCATACC AGGTTATATT 240

ATGATTTATT TAGTGCCGAG TACAAGTACA ATTAATTCTA TGAAAAGCTT AATTGCACAT 300

GAAGTAAATC ATAATATGCG CTATCAATAT ATTGATTGGG ATGGCGGAAG TTTGATTGAA 360

ATTGGACCGT GGGTAACAAA TACTAATTGA AGTCGTGATA ACGTAAAAAT TAAAAATACT 480

ATTTATAATC ATTTACATTT AAAGCATATA TTTGAATCGA tGCCTTATCT CTATGGTGAT 540

GATATTAATA AACTTCAAGG TAGGCCTATC GTTGGCTTAT CTCATGCTGC CGGGTATGCA 600

TGTGGCTATC ACTTGGTAAA ATACTTTTTA CAAAAAACAA ACATACCTAT TGAAGTTGCT 660

ACAACACTTC CAGCACAAAA AA 682

(2) INFORMATION FOR SEQ ID NO: 441:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2574 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

ATCTTCTTTT AACATGACAA ATTGCAACAA AATATTAATG ACGCCAAAAG ACATTTTTTC 60

ACGTTCAATT AATTCTTCAA CCATTGTCTT TTGCGATATA GTTGGTTCTG ATTCAGACCA 120

AGAAGCTAAC ATATCAATTG GACTCGTTTG TTCAAGTAAC TCAAACCATT CATCACTTTG 180

TGGCTTTGGA TTCACTTCTG AAGATTTGCC CGCCGAAGAT GATGTAGCAG GAGATTTCAC 240

CTGTAATTTA GGCATTTGAT TTTCGTGTTC CATTAAGTAA TACGAGCGTG CTTGTTTACG 300

CATTTCTTCA AAGGATAACT GTTGTCCACT TGTAATTGAA TTTAAAATAA CATGCTTCAT 360

GCCATCTGCT GTTAAACCAT ATAAAGTCGC GAGTTGTGTA ATTAAACGCT TTGCATCTTT 420

GGTAACAATG TCTTGACTAA TAAAATGTTT ACCTAACATT TGTCTCAACA TTTCAAAGTC 480

AAAAGATTCA TTTGATAAAT CGATACCTTG GTACGGTTCA TTAATCGGaA TATCACTTGT 540

ATCGATATCT ATTTTTGTAG ACGGCACTTT AAAAACATCA GTAAATTGTC TTGTTACCTG 600

TTTAAATTCA CTCAAATCAA TTTGTTGATA CTCAAAGTAT TTCTTCAACT CATGAAATCG 660

ACGATGCTCG ACTTCACTAT ATAAAAAGAT TGACAACATT GGATCATTAA AAAATAAATG 720

TGCTGAAGGG GtTGaATTAA TTGGTAAACA AATTGTGTTT CTTGTTCATC ATGTTTGACA 780

AACGCCTTTA ACAATCCAAT CGCTTCAAGT AAGTCCATTT GTTGTCTAAA CTCTAGTAAA 840

TTAATTTTAA GTTCATTCAT AAAAATATAA TGAGAAAGAA TCAATGTTTC ATTATGACTT 900

TCTTTAACGA ATTGAGTCAT AAAATGATAT AAACCCACTG CTTGCGTTCC AATTAGCGGT 960

GTATACAGTC GATTCAATAC CTCTAAATGA TTCGTATTTA AATCAAAGTG TTGCATAACT 1020

TTGAATTGAT CCTTTGGTCT TAAGCCGAAT TCGAAGGCTT GTCGTCCCaT TTAAGCnATC 1080

AAATTCTTTA TAGACTGATG CAAATCTAAC ATATGAAACT TGATCAACAT GCATTAACAA 1200

GTTCATAACG TGTTCACCTA TATCTCGTGA AGACACTTCC GTATGACCTT CATCTCGTAA 1260

TTGCCATTCA ACCTTGTTAG TTATGTCTTC AAGTTGTTGA TATCTAACTG GTCGTTTCTC 1320

ACAAGAACGC ACAAGTCCAT TAAGTATCTT TTCTCTTGAA AACTGCTCTC TTGTGCCATC 1380

TTTTTTCACA ACTATAAGCT GACTAACTTC GATATGTTCA AATGTAGTGA AACGTGTTCC 1440

ACAATTTTCA CATTCTCTTC GTCTTCGAAT GGCATTTAAT TCATCGGCAT GCCTTGAATC 1500

TACAACTTTA GATTGTGTAG AATTACATTT CGGGCATTTC ATTACATCAC CCTCTTTATT 1560

TTGATTATGC CTAATTATAC TATAAATCTA GAGATGAAAA AAGAATCCCT CAATTTAATT 1620

CATTTAACCA AATAATGAAA CAATAAAAAA CATTATATCG TTACTTATTA AGTAATTTGC 1680

ATGACAATAT TATTGTATTA AAAATAAAAA ACCTAACTCC GAAGTCAGAG TTAGGCTATA 1740

AATTAATTGT ATTAACTTGC ACTTACAGTT TCTTTTGATG TCAAAAGTGC TCCAATTTGC 1800

TCAGCAACAT CTACAACTCT ATTTGAATAA CCCCATTCAT TATCATACCA AGCAATAACT 1860

TTTACTTTAT TCCCTGACAT GACCATTGTT GATTTTGCAT CAATAATAGC TGAATTTGGA 1920

TTAGTATTAA AATCAACAGA CACTAGTGGT TGATGTTCGA CTTCTATGAT ACCTTCTAAA 1980

CCTGCATTTT CAAAAGCTTG GTTTACTTCT TCTGCAGTTA CTTCTTTTTC TAAATCAACA 2040

ACTAAATCAA CGAGCGATAC ATTCTTTGTT GGTACACGTA ATGCCATGCC GTGTAATTTA 2100

CCTTCTAATT CTGGTAATAC TTCTTTTAAA GCTTTCGCCG CACCAGTAGA AGTAGGAATA 2160

ATGCTTTCAT TACATGAACG TGCACGTCTT AAATCTTTAT GTGGATTATC AATATTTTTT 2220

TGGTCATTTG TAATAGCGTG AACAGTAGTC ATTAAACCAT TAACTATTCC AAACTGATTA 2280

TTTAAAACTT TTGCAACTGG ACCAATGCAA TTAGTAGTAC ATGAAGCATT ACTAAAAATG 2340

TCAAATGCTT CTATATCTAA TTGGTTATCA TTTACGCCTT TAACTACCAT TTGAACATGT 2400

CCACCTTTTG nAGGACCAGT TAACAAAAsT TTTtTGGCAC CTGCTTTAAT ATGTGCGATG 2460

GCTTTATCAC CATGaTTAAA TTTACcAGTT GCATCTATAG CAATATCGAT ATCTAATTCT 2520

TTCCATGGCA AGTTTTCAGG ATTGCGATCA GCAACCAATT TAATTTTATG ATCT 2574

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CAAGGTACCG GTTTAGGTTT GTTCATTTGT AAAATGATTA TCGAAGAGCA TGGTGGTTCC 60

ATAGATGTTA AAAGCGAATT AGGGAAAGGC ACAACATTTA TTATTAAACT ACCAAAACCA 120

GAATAAAATT GAATATAGTT ATTTCAGAAC GCATGTTATT GATTAGAGAC TCTAATTTAT 180

AGCATGCGTT TTTTGATTGA TGTGGGGAAT TTTGTATGTG GATTAGAACT TAGGGTTTTT 240

GCGAATATCA ACTATTAAAT ATATTACTAA TTTATACAAA AATATAAAGT TTGATAAAGT 300

TATTTATTTG ATTATAAAAA TAGGGTAAAA TATAGATATA TTGTATTAAT TAAATTATTC 360

GAGGTGTCAT ATGAAAAAAT TCATTGGATC AGTTTTAGCT ACGACATTAA TTTTAGGGGG 420

ATGTTCCACG ATGGAAAATG AATCAAAAAA AGACACAAAA ACAGAAACAA AATCTGTACC 480

AGAAGAAATG GAAGCTTCAA AATATGTAGG CCAAGGCTTC CAACCGCCTG CAGAAAAAAA 540

TGCGATTGAA TTTGCGAAGA AGCATCGTAA AGAATTTGAA AAAGTAGGTG AACAATTCTT 600

TAAAGATAAC TTTGGACTAA AAGTTAAAGC TACAAATGTT GTAGGTAAAG ATGATGGTGT 660

AGAAGTTTAT GTGCATTGTG AAGATCATGG CATTGTATTT AATGCAAGTC TACCTTTGTA 720

CAAAGATGCC ATCCATCAAA AAGGATCAAT GCGCAGTAAT GACAATGGTg ATGATATGAG 780

TATGATGGTG GGTACAGTGC TGAGTGGCTT TGAATATCGA GCGCAAAAAG AAAAGTATGA 840

TAACTTATAT AAATTCTTCA AAGAAAATGA AAAGAAATAT CAATATACAG GCTTTACAAA 900

AGAGGCAATT AACAAGACAC AAAATGTCGG ATATAAAAAT GAATATTTTT ATATTACATA 960

CTCTTCTAGA AGTTTAAAAG AATATCGAAA GTATTATGAA CCACTGATTC GAAAAAATGA 1020

TAAAGAATTT AAAGAAGGAA TGGAACGAGC AAGAAAAGAA GTGAATTACG CTGCAAATAC 1080

AGATGCTGTT GCTACACTTT TTTCTACTAA GAAAAACTTT ACTAAAGACA ATACAGTAGA 1140

TGATGTAATC GAACTAAGTG ATAAATTATA TAATTTAAAA AATAAACCAG ATAAATCTAC 1200

AATCACAATA CAAATAGGGA AACCCACTAT TAATACTAAG AAAGCCTTTT ATGATGATAA 1260

TCGTCCAATA GAATATGGGG TGCACAGTAA AGATGAATAA AATTAATGAT AGGGATTTAA 1320

CAGAATTAAG TAGTTACTGG GTTTATCAAA ATATTGATAT AAAAAAAGAA TTTAAAGTTA 1380

ATGGAAAAAG GTTTAAACAA GTAGACAGTT ATAATGATGA TAAGAATAGT AATTTGAATG 1440

GTGCTGCTGA TATTAAAATA TATGAGTTAT TAGATGATAA AAGTAAACCA ACTGGTCAAC 1500

AGACAATAAT TTATCAAGGA ACATCTAATG AGGCAATTAA TCCAAATAAT CCATTAAAAT 1560

CATCGGGGTT TGGAGATGAT TGGCTCCAAA ATGCTAAATT AATGAATAAT GATAATGAAA 1620

GCACAGATTA TTTAAAGCAA ACAGATCAAT TATCAAATCA ATATAAAATA AAGTTAGAAG 1680

ATGCAGATAG ATTATCAAAT AGTGATTTTT TAAAAAAATA TAGAATGGAA TCAAGTAACT 1740

ATCAAGGAGC GAAACATCCG AATGAAAAAG TTGTTGCTAC TGACTCAGCA ATGATTCCTT 1860

ATGCTGCTTG GCAGAAATTT GCTAGACCAC GCTTTGaTAA TATGATTAGT TTTAATAGTA 1920

CCAACGATTT ATTAACATGG TTACAAGATC CATTCaTCAA AGATATGCCA GGAAAACGCG 1980

TTAACATTAA TGATGGTGTG CCCAGGTTAG ATACTTTAAT AGACAGCCAT GTAGGTTATA 2040

AAAGGAAGTT AAATAGAAAA GATAACACAT ACGATACTGT ACCACTAATC AAAATAAAGT 2100

CGGTAAAAGA TACAGAAATT AAAAATGGAA AAAAAGTAAA AAAGACTATT AACATAACAT 2160

TAGATATGGA TGGGCGAATT CCAATAAATG TTTGGACAGG AGATTCGATT GCACGTTCTG 2220

GAAGAGGAAC TTTAATTAAA CTTAATTTAG AAAATCTTGA TGCGTTGAGT AAACTGATTA 2280

CTGGTGAAAC AAGTGGTATG TTAGCAGAAT GCGTAATCTT TTTAAATGAA AGTTTTAACA 2340

TCTCAGAAAA TGAAAATAAA AATTTTGCAG ATAGAAAGAa ACAATTATCA GAAGGATTTA 2400

AGGATAAGAT TAACTTATTT CAGTTAGAAG AAATGGAAAG AACTTTAATT AGTAAAATAA 2460

ACTCACTTGA AGAAGTTGCA GATGAAACAA TAGAAAGTAT TAGTGCTGTT AAACACTTAT 2520

TACCTGATTT TGCATTGGAT GCATTAAAAG AAAGAATTAA TGAGTTGTTT AAAGGTATAA 2580

AATCTTTTAT AGAAAAAGTG TATGATAGTA TAGATAATGA AATTTTAGAA ATTTTCAAAA 2640

ATATAGATCA CGACTTCAGA GATGGAGTAT CTGAAGAAAT GATGAAACAT TTGAAAGTAG 2700

TGAAACAGAA TATAGACCAA ATAAAAAATC AAAATGATAT TTATGGTAGG CAAATTGCAG 2760

ATATTAGAAG TATTATGAAA CAACAAGATG CAACAATTTT AGATGGAAAT TTTCAAATTA 2820

ATTGTAGCGG CGAAAATATG GTACAGGGTC TAGTTATACC TTCTAATTAT TTAGGAAGAA 2880

AAATGAAAAT ATTAAAAGAC CATATCGATG ATGGTATTAA AAAAATAGCA GACTATGTTC 2940

AAGGTATATA TGATGAATAT GCATCGAAAA TTGTCGATGT AATAAAATAT TTGATTAATA 3000

CAATTCCCAA AATACGTAAG AATTTAAGAC ATGCAATTGA AATGTTAAAT GTAAAAAAGA 3060

AAGAATTTTT GTCCCTGATT CCTAATGTAA CTTGTAATTA TATTAAAACT AAATTAGAAG 3120

AATTAGATAA TACTTTAGGC AAATGGGAGC CTTTTCTTAA TGATTTAAAA GCAGTGTCAC 3180

CAATTTTAGA TAACCATTTA GATGATATTG TTAAGAACAT GAAGCCTTTG ATTGTACAAA 3240

TGAyATwTGA ACCATCACAT TATGaCGATA TGTTTAATTC aAGAAAAGCT TTAACGcCAG 3300

TGTTCTCAAG CGTTTTATAA AGGTTG 3326

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

ACCTATAGCT GGCCCGTCAA GTCCTGAATC ATATGTCGCT ATAAACCCAG TTGCATGCCC 60

AGCAATCTCG GTTTCAATTT CAAAATCATG CTCTTTCAAA CGATCTATTA AAGTTCGAGA 120

CGCAAATATT TCTTCATTAC CAAGTTCAGG ACGTTCATGA ATTCTATGAC TGATTTCGAT 180

ATAACTATAT TTATTTGTTT CTATATAATC GAGAATTTGT TGTTTTTCAC TCATTTTTTA 240

CTATCTCCCT TTTACCCTAC ACTCATTTTA ATCATCCACA ATATTTTGTT CTTTCAAAAT 300

GAATTATTAC TTATTCTATC GGTTTTATCT CATGATGTCA TCTAGTTTTT CTTTATTTAC 360

AAAATTTTCT AATAACTAAA aGCCTTTCAT AAATTTATAA AACAGTTTCA AATTGTAAAA 420

CATAAGCCCT ATTGTTACAA TTTAAGTATT GTTAGAAACA CAACTTACAA CAAACTTAAG 480

TTTTATAATG CAACAAATCA TAAGCGTTTT ATAGTTTTGA GTAGTTAATA GGAGGAAATT 540

CAAAATGACA AAAATGAATG TTGAAAGTTT cAATTTAGAT CaTAcTAAGG TGGTTGCCCC 600

ATTTATTAGA TTAGCGGGAA CGATGGAAGG ATTAAACGGA GATGTCATTC ACAAATACGA 660

CATTCGTTTC AAACAACCAA ACAAAGAACA TATGGATATG cCCGGACTAC ATTCATTAGA 720

ACATTTAATG GCTGAAAATA TTAGAAATCA TAGTGACAAA GTTGTTGATT TAAGTCCTAT 780

GGGTTGCCAA ACTGGTTTCT ATGTATCATT TATTAATCAT GATAATTATG ATGATGTATT 840

AAATATTGTT GAAGCAACTT TAAATGATGT GCTAAATGCT ACTGAAGTGC CTGCTTGTAA 900

TGAAGTACAA TGTGGCTGGG CAGCAAGTCA TTCATTAGAA GGTGCTAAAA CTATCGCTCA 960

AGCATTTCTA GACAAACGAA ACGAATGGCA TGATGTTTTC GGTACAGGAA AATAAATCTT 1020

AGTCAATCAA GTTAATCAGA AAaGCAGTCG AACAATGATT TTACAATCGC CATTGTCCAA 1080

CTGCTTTTTA TTATGCTTCA AAGTCAAAAA ATCGAACAAA TGAAAAAGTA AAATCTTTAA 1140

CATTTGTCCG ATTTATTTGA GAACCACTAT AATTTCTTAA TTAGTCCCAT TAACACGAAC 1200

TGCATAGGTA ACCTTAAATA TAGTTGCCAT GTTGGCAATT GTTTATCTCC TAAAGGTAAC 1260

TTTTTAACTG CCATATAGAT ATTAGCTGGG AATACAGCTA GCAAGAATAG ATTGATTGTA 1320

TTTTTCAAGC ATTGAGATGG TCTTTTAATT AAAAGTGCAA GTCCAAATAA TATCTCAAAG 1380

ATTCCTGTAA CAAGAACCGC TGTTTTTCGA AGTGGCAAAC ATTTCGGTAT GATATTTCTA 1440

AATTGTCGTT CTCGTGTAAA ATGCAATACA CCTATTACAC TAAAACCTAT TCCTAATAAA 1500

TATCTTAGTA TGTTCAATCA GCTTCAACTC CTATTCTGTA ATGATTTTAT GAATTAATGT 1560

AGGCGATACA ACATGaTCAG CAATTGTTAT GCTTGAATCT AATTTTTTAA CAACATCGTC 1620

AATTTTTTTA TTTAAAACAA TACCAACCGC TAAATCAATA TCATCCTCTT TTGTTAAACG 1740

TCCCGCTCCT AACATCATCG AAGCGACACC TATATCGTTA GAGACTAATT CAGTCACATA 1800

ACCTGATTTT TTAGCTTTAT ATTCAATTTG ATATTGAGCT TGTGGCAAAC GCTCTGGATG 1860

GTCAATAACA GTTTCGTCGC CACCTTGGTT TTTAATAAAT GTTTTGAATT TTTCTAATGC 1920

TGCACCTGAA TTAATTGCCT CAATTAGCAA CGCTCTCGCT TCTTCAAGCG TTTCAGCTTT 1980

GTTTGCAAGT ACAACCATTT GAGAACCTAA TGTTAATACA AGTTCTGTTA AATCTTTCGG 2040

ACCTTGTCCT TTCAACGTAT CAATTGCTTC TTGTAACTCA AGCGCATTGC CAATCGCACG 2100

TCCAAGTGGC TGATTCATAT CAGAAATAAT CGCCATCGTA TTACGTCCCA CATTATTACC 2160

AATACGTACC ATTGCGTGCG CTAATGCTTC AGCATCTTCT AATGTTTTCA TAAATGCACC 2220

GCTACCAGTT TTTACATCTA ATACAATTGC ATCTGCACCA GCAGCAATCT TTTTACTCAT 2280

AATTGAAGAG GCAATTAATG GTATTGAATT GACAGTACCA GTAACATCCC TTAAGGCATA 2340

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ATTAACCAAT TTCACAAATG TTGCTTCATC TATTTCAACA TGAAAACCAT CAATTGCTTC 2460

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ACATACTTAT ATATGGTTAC GATGTCCCAT GCTTACATAT TTTTATAAAA TTAGTAATCT 3120

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TTCCTCCTAC CGCTAAAATT CTTTCAGCTA ATTCGTCTAC ATATTGGCTT GCTTCATTAT 5220

AATTGTGTAG CTTTGTGTAA G 5301

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11466 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

GAAGATGAAA GCTATATTGA AGATGATGTT ACTAAAAAGG AAGCTATTTT AAGTATGCAA 60

ATTCCTAAAG GTTTCTCTCA AAAATTAAAA GAGAACCGTT TAAAAGAAAC GATACAGTTA 120

TATGGTAGAG ATGACTTTAT AGGTGGTATT GCTGTAGAAA TTGTTAGTAG TTCATTATAT 180

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TCGCTTACTA AACAAGCACA ACACTCTATT TCAATTAGCT TAATCTTTGC GGTGATTTTA 360

TTTGTTAGCG CTGTTCAAGT AGTACTTCAT TATCGTTTAA ACCAACAAGC AGCATTGCAA 420

CGATTATCAC AATATCATTT AAGCCGTTTC AAACTATATA GTACTTATGT AATGACACAT 480

ACGATTTTGT TATTGTTGGT ACTATTGGCA GTTAGTCTAT ATTTGTCTCA ACCACTCAGC 540

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ATCTTATTCC ATATTCAAAC AATAAGTCAT CGATTATTCA TGACATTTAT ATATGCACTT 660

GCTATGGGTA TCGTATACTT GATTATTTTC ATGTAAAGGA GCGTAACTGA TGATAGAAAT 720

TAATAACCTT TCAAAGCGTT ACCGTAACAA ACAGATTTTC AATCATTTAA CTATGTCCTT 780

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TCGTATGATT GCTGGTATTG AAAAAGCTAA TGATGGAACT ATCAACTATT TCGGCGAAAA 900

ATGGAATCAA AGACaAATAC aAAATCACAT CGGTTATGTG CCACAAGACA TTGCGTTATT 960

TGAACACATG ACAGTGGCTG AAAACATTAA ATTTTTTAAA TCACTTTGTA AAAATCCAAT 1020

TAACGATACA ACTATCAACG AATATTTACA GCAATTAAAC TTTGATGATA CGTCTGCCAA 1080

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AATGCGCACC ACCACCGTGA TATTGTCCAT ATGGTTGTAG TTGTTTACGA CTTGTTAACC 1800

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TGTTGTTACT ATGTGAATAA TAGCTCGCGT CTGGACCTAC ATTTGATTGA TAACCATATT 1980

GATTAATATG CTGTTGGCTT TGACTCGCTG TGTAGTCATT GTTATCTCCT GCTGTTGCTG 2040

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AATAATGCGT ATGTCCTTGA GCATCTACGA ATGTATAGCT ATATTCTTTA TTATCAAACA 2160

TTGCTTGATT CCAGTTACCA TCAGGTGTGT GATGATAATC CCCATTAGAA TCAATTGTAT 2220

AATAAGTACC ATAAGATACG TCTTGTGATT GTGTTGACAT TTGTGTATGT GCTTGTTGGG 2280

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TAwTcT 11466

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

TTACATAGTT AACACTAGTT AATCTATTAG TTAACATTAG TTAATAATTA GTTAATTTCC 60

ATTTGTATTC TCATGTGATA AATTCTAAAA GCATACaATA AATTTAATAT GTAAAAAGAA 120

AGGGAATACA CATGAAAAAT AAATATATCT CGAAGTTGCT AGTTGGGGCA GCAACAATTA 180

CGTTAGCTAC AATGATTTCA AATGGGGAAG CAAAAGCGAG TGAAAACACG CAACAAACTT 240

AAGTATTACA TCTAAAAGGT ATCACAGAAG AACAACGTAA CCAATACATC AAAACATTAC 360

GCGAACACCC AGAACGTGCA CAAGAAGTAT TCTCTGAATC ACTTAAAGAC AGCAAGAnCC 420

CAGACCGACG TGTTGCACAA CAAAACGCTT TTTACAATGT TCTTAAAAAT GATAACTTAA 480

CTGAACAAGA AAAAAATAAT TACATTGCAC AAATTAAAGA AAACCCTGAT AGaAGCCAAC 540

AAGTTTGGGT AGAATCAGTA CAATCTTCTA AAGCTAAAGA ACGTCAAAAT ATTGAAAATG 600

CGGATAAAGC AATTAAAGAT TTCCAAGATA ACAAAGCACC ACACGATAAA TCAGCAGCAT 660

ATGAAGCTAA CTCAAAATTA CnTAAAGATT TACGTGATAA AAACAACCGC TTTGTAGAAA 720

AAGTTTCAAT TGAAAArGCA ATCGTTCGTC ATGATGAGCG TGTGAAATCA GCAAATGATG 780

CAATCTCAAA ATTAAATGAA AAAGATTCAA TTGAAAACAG ACGTTTAGCA CAACGTGAAG 840

TTAACAAAGC ACCTATGGAT GTAAAAGAGC ATTTACAGAA ACAATTAGAC GCATTAGTTG 900

CTCAAAAAGA TGCTGAAAAG AAAGTGGCGC CAAAAGTTGA GGCTCCTCAA ATTCAATCAC 960

CACAAATTGA AAAACCTAAA GTAGAATCAC CAAAAGTTGA AGTCCCTCAA ATTCAATCAC 1020

CAAAAGTTGA GGTTCCTCAA TCTAAATTAT TAGGTTACTA CCAATCATTA AAAGATTCAT 1080

TTAACTATGG TTACAAGTAT TTAACAGATA CTTATAAAAG CTATAAAGAa AAATATGATA 1140

CAGCAAAGTA CTACTATAAT ACGTACTATA AATACCAAGG TGCGATTGAT CAAACAGTAT 1200

TAACAGTACT AGGTAGTGGT TCTAAATCTT ACATCCAACC ATTGAAAGTT GATGATAAAA 1260

ACGGCTACTT AGCTAAATCA TATGCACAAG TAAGAAACTA TGTAACTGAG TCAATCAATA 1320

CTGGTAAAGT ATTATATACT TTCTACCAAA ACCCAACATT AGTAAAAACA GCTATTAAAG 1380

CTCAAGAAAC TGCATCATCA ATCAAAAATA CATTAAGTAA TTTATTATCA TTCTGGAAAT 1440

AATCAATCAA AAATATCTTC TCTAGTTTTA CATCATTTTT TAAATAATTT TCGTAACAAA 1500

CCGTGATTAA AAAGAACCGT TGATTCTCAA TCGAATCTAC GGTTCTTTTT TCATTTTCCA 1560

TCAATTAAAT GCTTCTTCGC TATTTGTCAG CCCACTTTTT TACCTGCAAC TTGTTAAATA 1620

ATCCTTACAT CGTTAACGAA TAGTTCATCA TTTAGTTGAA TCAGCTCAAC TTTATTAACT 1680

TCATATTTTC ACAAACTATT GCGCAATCCA TTCCTTTTCC ACTACAAGCA CCATAATTAA 1740

ACAACAATTC AATAAAATAA GACTTGCAAA GCATAGTTAT GTAGCTATAT AAACGCCTGC 1800

GACCAATAAA TCTTTTAAAC ATAACATAAT GCAAAAACAT CATTTAACAA TGCTAAAAAT 1860

GTCTCTTCAA TACATGTTGA TAGTAATTAA CTTTTAACGA ACAGTTAATT CGAAAACGCT 1920

TACAAATGGA TTATTATATA TATGAACTTA AAATTAAATA GAAAGAAAGT GATTTCTATG 1980

ATTAAAAAAtA AAATATTAAC AGCAACTTTA GCAGTTGGTT TAATAGCCCC TTTAGCCAAT 2040

CmTyCAAArG AcACaGACAT TACTAGCCAA CGATTTAGCT ATnACTCCAA ACCTTCCATT 2160

GGATTTGGTA AAGGnT 2176

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

AAAAGCATGG CTTAAATGAA GTACGCTATA ACAAATTACA AGAACATGCT ATTGTTATGC 60

ATCCGGCACC TGTGAATAGA GGAGTAGAAA TACAAAGCGA TTTAGTAGAA GCTTCAAAAT 120

CAAGAATTTT TAAGCAAATG GAAAATGGCG TTTACTTAAG AATGGCAGTC ATTGATGAAT 180

TATTAAAATA GGTAAGGGGA CGAAAATGAT GAAATTAATT AAAAACGGTA AAGTATTACA 240

AAATGGCGAA TTACAACAAG CAGATATTTT AATTGATGGT AAGGTAATTA AACAAATTGC 300

ACCTGCAATT GAACCAAGCA ATGGTGTTGA CATCATAGAT GCGAAAGGTC ACTTTGTGTC 360

ACCTGGATTT GTCGATGTTC ATGTTCATTT ACGTGAACCT GGTGGTGAAT ATAAAGAGAC 420

AATTGAAACT GGTACTAAAG CTGCTGCTAG AGGCGGATTT ACAACTGTAT GTCCAATGCC 480

TAACACAAGA CCGGTACCAG ATTCTGTAGA ACATTTTGAA GCTTTACAAA AATTAATCGA 540

TGACAATGCT CAAGTACGTG TATTACCTTA TGCTTCAATT ACAACACGTC AATTAGGTAA 600

AGAATTGGTT GATTTCCCAG CACTAGTAAA AGAAGGTGCC TTTGCGTTTA CAGATGACGG 660

TGTAGGAGTA CAAACTGCAA GCATGATGTA TGAAGGCATG ATTGAAGCTG CAAAAGTAAA 720

CAAAGCCATC GTAGCACACT GTGAAGATAA TTCATTAATC TATGGTGGTG CAATGCATGA 780

AGGGAAACGC AGTAAAGAGT TAGGTATACC AGGTATTCCA AACATTTGTG AATCTGTTCA 840

AATCGCAAGA GATGTACTAT TaGCTGAAGC AGCAGGTTGT CATTATCATG TATGTCATGT 900

TTCTACTAAA GAAAGTGTTA GAGTCATTCG TGACGCTAAA CGCGCAGGCA TTCATGTTAC 960

AGCTGAAGTT ACACCACACC ATTTATTGTT AACAGAAGAT GATATTCCTG GTAATAATGC 1020

CATTTATAAA ATGAATCCAC CATTGAGAAG TACTGAAGAT AGAGAGGCTT TGTTAGAAGG 1080

GTTACTAGAC GGTACAATTG ACTGTATCGC AACAGAcCAT GCACCACATG CACGTGATGA 1140

AAAAGCACAA CCAATGGAAA AAGCaCCATT CGGAATTGTT GGTAGTGAAA CAGCATTCCC 1200

ATTATTATAT ACGCATTTTG TAAAAAATGG TGATTGGACA TTACAACAAT TAGTAGATTA 1260

TTATGCAGAT TTAACAATCA TTGATTTAGA TAGTGAACAA GAAATTAAAG GAGAAGATTT 1380

CTTATCAAAA GCAGATAATA CACCATTTAT CGGCTATAAA GTTTATGGAA ATCCGATCTT 1440

AACAATGGTT GAAGGCGAAG TTAAATTTGa GGGGGATAAa TArTATGCAA gCAAACGTTA 1500

TCTAGTGTTA GAAGACGGTC TTTTACGAGG CTACCGTTAG GTCTGATAAC TTACTGA 1557

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1799 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

GCTAGAAATm TTGmATGaCA ATACAACTCT GTTAAAaTGA TGGACGTAGA CAAATATGCG 60

TATTGACGCT TTATTTTAAA AATTaACATG CTTATAACAT GTTTATAGAA GGAGATTAAC 120

CTATGAACTA TCaAGTTCTT TTATATTATA AATATATGAC GATTGATGAC CtGAACAGTT 180

TGCTCAGGAT CACTTAGCCT TTTGTAAAGC ACACCATTTA AAAGGTAGAA TTCTTGTTTC 240

TACAGAAGGT ATTAACGGCA CATTATCTGG TACAAAAGAA GAAACCGAAC AATATATGGC 300

ACATATGCAT GCCGATGAAC GATTCAAAGA TATGGTGTTT AAAATTGATG AAGCTGAAGG 360

ACATGCTTTT AAGAAAATGC ATGTACGTCC TCGAAAAGAA ATCGTTGCTT TAGATTTAGA 420

AGATGACGTC GATCCAAGAC ACACAACTGG CCAATATTTA TCACCTGTAG AATTTAGAAA 480

AGCTCTTGAA GATGATGACA CAGTCATTAT TGATGCACGT AATGATTATG AATTTGATTT 540

AGGTCATTTC CGAGGTGCAA TTCGTCCAAA TATCACACGT TTTAGAGATT TGCCTGACTG 600

GATTAAAGAG AATAAAGCGT TATTTGCAGA TAAAAAAGTG GTTACGTACT GTACTGGTGG 660

CATTCGATGC GAAAAATTTT CTGGATGGCT TTTAAAAGAA GGTTTCGAAG ATGTAGCTCA 720

ACTTCATGGC GGTATTGCTA CATATGGTAA AGATCCTGAA ACAAAAGGTG AATATTGGGA 780

CGGTAAAATG TACGTATTTG ATGACCGTAT CAGTGTTGAT ATCAACCAAG TTGAAAAnAC 840

AATTATTGGT AAGGATTGGT TTGATGGCAA ACCATGTGAA CGTTATATTA ATTGCGCTAA 900

CCCAGAATGT AATAAACAAA TATTAGTTTC TGAAGAAAAC GAAACTAAAT ATTTAGGTGC 960

ATGCTCTTAT GAATGTGCTA AACATGAGCG TAATCGTTAT GTTCAAGCAA ATAATATTAG 1020

TGATAATGAG TGGCAACAAC GTTTAACAAA CTTTGATGAT TTACATCAAC ATGCTTAGTT 1080

TTAATTAAAT ACCTTTCAAA ACACGCTTTG AAAATCCGAT TTATAAAGGT TTTTCAAGGC 1140

TAAATTTTAA TACTGCGGGG TGTCTTAAAA TGCACATTTT AGTAACAGGG TTTGCGCCTT 1260

TTGACAATCA AAATATCAAT CCCTCATGGG AAGCTGTGAC TCAACTAGAA GATATTATTG 1320

GCACACATAC AATCGATAAA TTAAAACTAC CAACCTCTTT TAAGAAAGTA GATAATATTA 1380

TAAATAAAAC GTTGGCATCT AATCATTATG ATGTTGTACT AGCTATAGGA CAAGCTGGTG 1440

GTAGAAATGC CATTACCCCA GAACGTGTCG CCATTAATAT TGATGATGCA CGTATTCCAG 1500

ATAATGATGA TTTTCAACCT ATTGATCAAG CCATTCACTT AGACGGTGCG CCAGCTTATT 1560

TTTCAAATTT ACCaGTTAAA GCAATGACTC AAAGTATTAT TAATCAAGGA CTTCCTGGAG 1620

CACTTTCAAA TAGCGCAGGT ACATTTGTTT GTAATCACAC ACTTTATcAC TTAGGTTATT 1680

TACAAGATAA GCATTACCCT CACCTACGAT TCGGATTTAT TCaTGTGCCA TACATACCAG 1740

AGCAGGTcAT TGGTAAACCC GATACACCAT CTCATGnCCA TTGAGGAAAA GATnAGTTG 1799

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

ACTTGGTTTT TTATTGTTTA TAAATAAAAC TCACTTAATA ATGTTTTCAT AATCTTCTTC 60

GACTACTTAA TTCTTTAAGA TATTCGTGAA AAGAGACATT ACACTAGTTA ATTTTCAAAC 120

AATACAAAAA GCGTCTACCT CCTACATATA ATTGTAGCGG AGATAGACGC TTAATATTTA 180

TTTAAAAATT ATTTTAAACC ACCGAATGTC ATAACATCAC GGGCAATCAT ACTTTCTTCA 240

TCTGTTGGAA TAACGACAAC TTTAACTGGT GAATGAGGAT AGTTAATAAA TCCTTCTTTA 300

CCACGTAGTA AGTTTTCATT TTTCTTAGGA TCCCAGTAAA CACCCATAAA TTCTAAGCCT 360

TCAAGAACTT TCGCACGAAT TTCTACTGAG TTTTCACCGA TACCTGCTGT AAATACGATA 420

ACATCAACAC CATGCATTCT CGCAGCATAT GATCCAATAT ATTTGTGAAT TTTAGAAGCA 480

AATACATCTA AAGCCATTTG TGAACGTGCT TTACCTGATT CAGCTTCTTC TGATAAGTCA 540

CGTAAATCAC TAGATGTACC TGATAATCCT AATAAACCTG ATTCTTTGTT TAAGATTTCC 600

AATACTTGTT CAGCAGTTTT ACCTGTTTTT TCCATAATAA ATGGAATTAA AGCAGGGTCA 660

ATATTACCAG AACGAGTACC CATTGTTACA CCAGCAAGTG GTGTGAAGCC aTTGATGTAT 720

CAATAGATTT ACCGCCATCG ATAGCTGCAA TTGATGCTCC ATTACCAATG TGACATGAAA 780

TATGGCTTGT ACCATGGAAA CCATACTTAC GAATGCCATA ATCTTTATAA TAATGATATG 900

GCAAGCTATA TAGATATGCT TTTTCAGGCA TTGTTTGATG GAATGCTGTA TCAAAAATTG 960

CCACATGAGG GATATTTGGT AATAATTTAC GGAAAGCACG AATACCCAtC AAGTTaGCTG 1020

GGTTGTGaAG CGGTGCTAAT TcGCTTAATT CTTCAATTTC CTTTTCAACC TCATCAGTAA 1080

TAGCTACTGA TTCAGGGAAT TTTTCACCAC CATGTACAAC ACGGTGACCT GTTCCATCGA 1140

TATCGTTAAT ATCATTAATA ATATTGTGCG CTTTAAAAGC ATCCAACATG ATATCAACTG 1200

CCTCAACGTG ATCCTTGATA TCTTGTACTG TTTTAACTTT TTCCCCGTTG ACTTCAATTG 1260

TAAAAATTGA ATCCTTCAAT CCGATTCTTT CTACTAAACC TTTTGTTACT AATTCCTCTT 1320

CAGGCATTCT AATTAATTGA A 1341

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1529 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

TTTTGAAGAT ACTACCGATG AAAATAGACA AAAGATTTTT CAATATTTAT CACCTGAAgA 60

AGTTGCAAAT TTCTTTGATC AATTAGATAT TGATGACGAT GAATATGAGT TGCTATTTGA 120

TAAGATGAAT GCGACATACG CAAGTCACAT ATTAGAAGAA ATGTCATACG ACAATGCAGT 180

AGATATTTTA AATGAGTTGA CTAAACCAAA AGTTGCTAGT CTTTTAACAT TGATGAATAA 240

AGATGACGCG AATGAAATCA AAGCATTACT TCACTATGAT GAGGATACGG CCGGCGGTAT 300

TATGACGACG GAgTATTTAT CACTTAAAGC GCATACGCCT GTTAAAGAAG CATTATTATT 360

GGTCAAAGCG CAaGCACCAG ACGCAGAAAC AATATATGTT ATATTTGTCG TTGATGATGA 420

TGGTAAATTA GTAGGTGTTT TATCGCTAAG AGATTTAATT GTAGCTGAAA ATGATGCTTA 480

TATTGAAGAT ATTATGAATG AACGTGTCAT TAGTGTGAAT GTAGCAGACG ACCAAGAAGA 540

TGTTGCTCAA GTTATGAGAG ACTATGATTT CATGGCTGTA CCTGTTATAG ATTACCAAGA 600

ACATTTGCTT GGTATCATCA CGATTGATGA TATTTTAGAC GTTATGGATG AAGAGGCTAG 660

TGAAGACTAC TCTCGTTTAG CCGGGGTATC AGATATCGAT TCGACTAATG ATTCAATCAT 720

TAAAACAGCA TTAAAACGTT TACCATGGTT GATTATTTTA ACATTTTTAG GAATGATTAC 780

TGCGACAATT TTAGGGAGAT TCGAAAAAAC ATTAGAAAAT GTAGCGCTAC TCGCAGCGTT 840

TCGTAACATT ACGAcAGGGG AAATTAATGA GCAAAGTAAA TTTAGAATTG CATTAAGAGA 960

AGCAGGAAGT GGTGTATTAT CGGGTGTTGT ATGTTCAACA ATATTATTTA CAATTATTGT 1020

TGCAATATAT CATCAGCCAC TTTTAGCATT AATCGTTGCA GGAAGTTTAA CTTGTGCGAT 1080

GACGGTGGGG ACGTTTGTAG GTTCGATGAT TCCATTATTG ATGAATAAAT TAAATATCGA 1140

TCCAGCAGTG GCTAGTGGAC CATTTATTAC AACAATTAAT GATATTATTA GTATGTTGAT 1200

TTATTTTGGT TTAGCTACAT CATTTATGGC TTACTTAATT TAAGGAGGAG TTATGGAGTT 1260

TTTATCTTTA GTTATTGTTG TTTTAGCAGC GTTTTTAACT CCAATAATTG TCAATCGATT 1320

AAATATTAAT TTCTTGCCAG TTGTTGTTGC AGAAATTTTG ATGGGGATTG TGATTGGAAA 1380

TTCATTTCTA AATATAGTAG AAAGGGATTC AATTCTAAAT ATTTTATCAA CGTTAGGCTT 1440

TATCTTTTTA ATGTTTTTAA GTGGTTTAGA AATTGATTTT AAAGCTTTTA AAAAAGATAA 1500

ACGCGCACGT CAAGGACAAA ATGATGATG 1529

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1827 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

TTCTGGAAAC CAAAGTATTG TCATCTTCTA CTAGTAGTAT nGGCATCCAT ATCACCCAAT 60

ATCATTTAGT ATATTTCATA TTTTCTCCTG ATTTTAATCG ACTTTGAAAA TCTTTAATCC 120

GGCAGTCAAC TTCAAAGCCA TGAATCATCA TTTTTTGCAT TGGTGCTTGT ATAAAGTAAT 180

AAATCGGCCA AAATAATCGA GGGATATAAT CGTATAGATG TATATAAACG ACTGCCGACT 240

CTTTGATTAA TCTAAATTCT AACTTCCCTT GATTAACTGT ATATTTTTTC ACTAAACTTC 300

CACTCAATAA AATTAAAGTT ATTATTCCAT CAGCTGTTTC TTCTATTTTA AATACTGCGA 360

GCGGTCGCAC CTTATTCTTA ATATATATCT TAAATTGATC ATGTGATTTT TCTGTTTTCA 420

CAAAAGTTCC TTTAGTGTAA CCCATCCATG CAATAAAATG GTTTACAACG TTCTTTAATG 480

TCCATCCCTT TGGTAAAACT ACCTTCATCG TTGATCTAAC ATCATCATAC TTTGAAACTT 540

GTAATTCTAC ATTAACTAAA GAACGTTTAA AAACTAAATT TGTTGTTTCT ACAGGTGTAC 600

CATATGCACC TAGGCGTTCA ATTGTTTCAT TATCATAACG ACTCCCAGGT ATGTAGATTA 660

CTTTTTTTAC TTGATTGATA GCCGCTGCTC GACCAAAATT ATCTGCTGCG ATTAATGTTA 720

CAGCAATATC TATTTGATTC ATTGCTGCAA CAACCTGTTC GTAATGAAAT ATATCACACT 840

GAATCCAAGT CATTTCAACA TCATCTGTTT kTTTATTGTC TGGATATTTT GATATAGCAA 900

AAAGTTCAGC ATCATTTTCA ATCACTTCAC TTAAATACTT ACCAATATAT CCTGTTCCAC 960

CTGCTAATAA AACTTTAGGT TTCATCTAAA ATACTCCTTT AAACTGTAAC CAAAAAACAT 1020

ATTACTCCAC CTTTTAGTTA CATATATATT ATAATAGTAG CAAATGTTTT AAAATTTCAA 1080

AATACTGGAG GCTTTTTATG GCCCATATTA TACGTAGAGT TAGTATCAAA GATGTAGAAA 1140

ATTTCATTTC AATGTTAGCG AACATATACG ACGAATCTCC GTATATGTTC TACACACCAG 1200

GAGAATATGA TCCTAGCGTC ACATCGGCTA GTAAACAATT AGAAGAATAT ATCACTTCTC 1260

CGCATAAAGT CATCTTCGTT GCTGAAAGTG ATGAACAACT CGTTGGCTTT GCCTTTGTTA 1320

ATACGACACC ATTTCAACGC ATTAAACATG TTGCTAAAAT TGATTTAGGT GTAAAGAAAT 1380

TATATCAACA TCGTGGAATT GGCCAAGCAC TTCTTGATGC CATTATGGCT TGGTGTTTAA 1440

ACAATCAAAT ACACCGAATT GAAGCAAATG TACCACTCAA TAACCAACCT GCCCTCGAGC 1500

TTTTTAAAAG TGCCGATTTT CAAATCGAAG GCGTTTTAAA AGATAAGTTA TTTATCGATG 1560

GTAAATATTA TGATGACTAT ATGATGGCTA AAATTCTTAA TTAAAGCTAT TTTATCATAA 1620

TCTTGTATCA GAATCGTATA ACAACGAATT TAATGGTTAC CTAATACATT ACTCATACTT 1680

ATCAATGTTA TCTAATCTCA AATAAATACG TACACTCTTA TTCATTTATC AAATTTAAAT 1740

TCAAAATAnA ACACCACTAA TGTGTAATTG ATTAACTATC AACTACGATT AGTGGTGCTT 1800

TATATATGTG GTTAGTTTTC CTnACTA 1827

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 616 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

ATATAGATTA ATGTTTGTTA TTTGTACTGT GTTTGCCAGT GACATTTATT ATAAAACATA 60

TGACGTTATT CTATGkTGTA CTCATTtTCT ATATTGTAGG TTTATTAACG ATTAGAAGTA 120

TTATTAAAAA GTTGAAATAT CAGGAAACAT TATTACGAGA CTAAAAAACT TCCATTGGCA 180

TGTATGTTGT AAAGGTGCAT GTAATGTTGA ACGCCAAATG ATACGGCGTT CAGATTACAT 240

TAGCATCTAT ACGTTAACAG CATAACCAAT GGAAGTTTTC TTCGAATCTA TTCTTTTATT 300

AATGCGTCTT TTGAAAAATG GTCATTAAAG GCATCAGATT GCTTAAAGTC TTCGTATGCA 420

TGTCGATCAG CAAATCCGAA ATAAATTTTG TATGTTGTAC CTTTAGCAGG TCTTAACAAA 480

CGATAGCTTT TAAAGCCACC AAAGTTTCTG AAATTATCGT CTACACTAAT CAGTTTCTTT 540

TCAAGTTGAT ATGCATGATC TTCTGTTGAT GGaATGAAgA TTGCACaATA GAAATGaTGT 600

TCACtGAATT CACCAA 616

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 944 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

GCACGAGTGA TTAAACGGTT AATCAATGAA ACATTTGATG CAAATTACAT TGAAGTTATT 60

GAGGGAGGAA TTGAAGAAAC GCAAACGTTA ATTCACTTAC CTTTTGACTA TGTCTTCTTT 120

ACAGGAAGTG nAAATGTAGG CAAAATCGTT TATCAAGCTG CCAGCGAAAA TTTAGTTCCT 180

GTGACATTAG AAATGGGCgG TAAAtCTCCa GTCaTCGtTG ATGAAACAGC GAATATTAAA 240

gTTGCTAGTG AGCGCATTTG TTTTGGGAAA TTCACTAATG CCgGCCaAAC ATGTGTTGCa 300

CCAGATTACA TTTTAGTACA CGAATCTGTA AAAGATGATT TAATCACAGC CCTATCAAAA 360

ACGTTGCGTG AATTTTATGG TCAAAATATA CAACAAAGTC CAGATTATGG CCGCATTGTA 420

AACCTTAAAC ATTATCATCG TCTGACTTCA TTACTTAACA GTGCACAAAT GAATATTGTA 480

TTTGGTGGTC ATAGTGATGA GGATGAACGT TATATAGAAC CAACATTGTT AGATCACGTT 540

ACAAGTGATT CAGCAATTAT GCAAGAAGAA ATTTTTGGTC CTATCTTACC GATTTTAACG 600

TATCAGTCAT TGGATGAAGC AATAGCCTTT ATTCACCAAA GACCAAAACC TTTGAGTTTA 660

TATTTATTTA GCGAAGATGA AAATGCTACA CAACGTGTAA TAAACGAGCT ATCATTTGGC 720

GGCGGCGCTA TTAATGATAC ATTGATGCAC CTAGCGAATC CTAAATTACC ATTTGGTGGT 780

GTTGGTGCCT CAGGTATGGG ACGCTATCAT GGTAAATATT CATTCGACAC TTTTACACAT 840

GAAAAAAGCT ACATTTTCAA ATCnACACGA TTAGAATCAG GTGTCCATTT ACCACCATAT 900

AAAGGTAAAT TTAAATrCAT CAAAGCTTtC tTTAAAnATT AATT 944

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4820 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

TCTCCAGTAG ACCTTGTGTA TGAACAGTTT CTTTCATATG AATGAACATC GTTTTTAAAG 60

TTTGTTTCAA CTCAGCCTTA TCAGGATAAT ATCTAGAGAC AGTCGTCTCT GGCATCTCCA 120

TTGTATGATA TTTAACCTTA TGCAGCGACC CATGATTTTC GTTATAAACA AATGTATGAT 180

TCACTTCATC GAAATCATGA TCTTCTCCTG CAATCCAAAA AACTGGTACT ACTTGTTGCT 240

TATGTGTATC CGTTAATTCC TTAGATAAAG TAATGATTGa AAATATTTTA TGGAATGTAT 300

ACAATGGTCC CCCGAAAAGC CCTGCTTGTT GTCCACCAAT CACAACTTTT GAACCATTAG 360

CTAAATGTTG TATGTTTAAT TCTTGTTCAC TTGAAAGCTT GAAAGCTTTA AATCACTCAT 420

ATATTCACGA ATAACATTCG CTAATGCCGC TTCTCTTCCA TTATTTTCTT TAGACATCCT 480

TTTTTCAAAA CTAGTTTGTT GAGCTGCATC ATATTGAAAT AATCCTGTTA TTACAGGGTC 540

ACTGCTCTTT ATTTTTGGTA TAAACTGATC TTTTTCATTT AAACTAACTA CTTTACAGTC 600

CATGTTTTTT CTCCTTAAGT ACGCGATTAC AAACTATAGT ATAAAGTCTA TACCGGTGAT 660

TGACAATTTT ACGGCTTGAA AATCAATTTA ATCATGGAAA ATTTATAATA TTCATTGTTT 720

TACATTTTCA AATCAATGAA AAACACAAGT GGTTTAATGT ATAATAATAG TAGTAAACAA 780

ATAAGGGGTA GATAAATATG AGTGAAATCA AACGTCTTGA AATTAATTAC AAAACTGACG 840

AATTATTCGA AAACTTTAGA GCGTTTGGCA ACAAAGACTT ATACATGGTC AATGAGTTAA 900

ACGGTCAAAT GATTGATGCA AGTTCAGATT CACCATTTTA TGGCATATTT GTCGaGATCA 960

ATTAGGAGCT AGAATGGCAT TACTAAAAAA AGGTGATGTC GAAGAAATCT ACTTCCCAGA 1020

TTTTGAAGAT TATATATTAT TATGGAAGTT AGAAGTATTA CCAAAATATC AAAACAGAGG 1080

GTACGCTTCA GAATTGATTG ATTTTGCAAA GAGTTTCAAT ATGCCAATTA AAGCCATTGG 1140

CAGAAATGAT TCTAAGGATT TCTTTTTACA TCATGGATTT ACAGATGTGG AAGCTAAAAA 1200

TATAGAGGGA CATGATGTCT TATTGTGGAA ACCATAAGAT AATAATATTC GACACTACGA 1260

GCATGAAAAT GCATCTTTTC GTAGTGTCTT TTTTACAATT ACTTTCTTAA GCTAATATAA 1320

GTaAATCATT TTCAAATTAT TTGTCTTAAC GTACAATATC ATTTAGTTGT TTCCATGrAT 1380

TAATTTCATA ATCAGGTATA ATTCCTGGAT TATGATCAAA TCCTCTAAAa TTAAACCAGC 1440

AAGTAGCTAT ACCcGCATTG ATTCCACCTA GAATGTCAGA TGTTAnAGAA TCTCCaACTA 1500

TAATCGAGTG CTGtCTTTCA TCCTCACCAA TATCATTAAA AACATAATTA AAAAATTCCG 1560

ACGGCGTCTG ATTTAACCTT CTCTTTTGCG TTTCGGTTAC ACCATTAGTA ACAATATATA 1680

AATCATGTCT TTTCGATAAT TCGACAATTG TTTCTAATGT TTGATCAAAG TATTTAACTT 1740

TAGCTTCTGC TAATCCATTT CTAAATAACA CATCTGCACG ATGCCCATCA ACTTCCATTT 1800

GATGATGTTT GAAGTAATTC ACAAATCGTT CTGATAATAC TTCAGACTTC GkTAATTTAT 1860

TTTGkTGAAA AGCTTCCCAA TGTTGGTGaT TGaTTTTTTT AAATGkTAAA AAATCATCCy 1920

TTGTTGCTTT ATGATTAAAA ACATTCGCCA TATAGTGAAn CGCCCATTCT TCTGcATCAT 1980

AAAAATCAAC AATTGTATCA TCAAAGTCTA TCAAAATATT TTTATATCCC AATTTCCCCA 2040

TCTCCTATAT TGTCTATGTA TCTAAATCTT AACAGAGGCT CAAATTTCTG CAAATAAAAT 2100

AAACTGAGTG CATAACATTA AAGTATGCTC ACCCAGTTTA TTTTAAAGAA TATTAGTTAT 2160

TATATTAGAA TCCAAATAAT TTACCTAGTA AACCCACACC GTTAGCAACG ATGTCTACGA 2220

TACTTGTGCC TAATTTCACA CTATCATGTT GTTGTGCAGC TTGCACAGTA TTTGCGATTG 2280

CTTCTGCTAG TCCAGTCATT TAAATCTCTC CCTCACCTTT GAAATAATAC TGATTACTTA 2340

CATAACATAT TGAAATTAGA ATCCGAATAA TTTACCTAAT AAACCTACGC CATTTTCAAC 2400

GATGCTCACA ATGCTTGTGC CTAATTTTGC GCCATCATTA TTAATTGCTG CAGTTACGGT 2460

ATCTTTAATT GCGTTAAATA AACCTTCCAT TGAAAACACT CCTTAAAATT TAAATTTGAA 2520

GATAACAAAA ACGTGCGTAg yTTTTAAATC ACCGAAATGT TATTCGCTTA ACGTTTTGTT 2580

GTTGTTATTT TAAAATAAAT TTGATGCAAT TAGTTTGTTT ATCCGCACAA CATCTTATAA 2640

TGTACTTAAC TGTATTTTAA AGAGAAAAGA AATACAGTTA GGCATTCAAA ACTGTATTTA 2700

ACACAATTAA GTTGCCTGAA TTCGTATTTA AGTCTTATTG AACCTTTTTA GATAAATAGC 2760

TCTATAATAG TGAAAAATAT AAACATTTTT TATTTACAAG GTATTGCTAA TTTAAGTTCA 2820

TTTAGATATA ATAATTCTTG TGTTGTTAAA CGTGTCCTGG TAGCTCAGCT GGATAGAGCA 2880

ATGGCCTTCT AAGCCATCGG TCGGGGGTTC GAATCCCTCC CAGGACGTTT ATAGGTATTT 2940

TTATACGCAT TACCAAACAA AAGAGTTCCG TGATTACGGG GCTCTTTTTG TTTTGAATTT 3000

CAGTAATATA GTATGATGCG TCACCAAAAC GTCCCCCGCA TAAGCCCCGA AAATACAGTA 3060

ATTAAAACAA GCATGCTTAT TCGTTATAGA ATTTTTTGAC ACACAATTGA CACGCGTCTG 3120

ACACTTGTTT ATACATTTTT AATTAAGTAA TTTTGTGCTC AAATTTCATC TATACTGCAC 3180

CTGAACTACA CCAACACTAC ACCAAGATTT TTAACACTCA CCATTTGCAT GCGTAGAGAT 3240

TTTTATTATT ATATTATTCC TATAGATTTT GATACTATTC AAAATTTTAG GGACTTTTCA 3300

GGGGCCCGAA ATCCTATAAT TATAATTATA TACATCTAAA AAAAATAACC ACGTCCATCG 3360

ATACTATTGG CAAATTTATA AAGTAGTTCA GCGTTTTTCA ATGACATATT GTCTAATGAT 3480

CTTTCATTTT TTCTCATTCT GTGTATTGTG CTTTGTGGAA CTCCTGTTTG TTTCGATATA 3540

TGTAAACTGC TCAAATCACT GTCTAATAGT TTTTGAATTT GATTTCTCAT TTTGTACACC 3600

CCCTTGTAAA TCTTCAATCA TCATTTAAAT TAAATAATTA CTTTTCCACA TATTCCAATA 3660

TTTAGGTTGC AAAGCATACC TCAAATATCA TTAATTTTGA GATTTAAATG TCAATTATGT 3720

GTCTATCAAT CCAATATACA TACTCTAATA ACGTAATAGT ACACACTCTT CTTATTAATT 3780

GGCCATAGCT ATCATGATAT AATTAGTGAA GAAAATCACA TAAGAAAGGT TGTAAATCAT 3840

GAGACTTCAA AAAGCACCTC TAGTAACGTC AGGACTAGTC TTAGGATTAT TAGGCCTGGG 3900

TAATCTATTA AAAGACTTAT CTCTTACTTT AAACGCTGTT TGCGGAATCT TTGCTTTCTT 3960

GATTTGGATT CACCTTTTAT GTACTATGAT CAAATATTTT AATAATGTGA AAGAACAATT 4020

AAACAGTCCT CTAGTTTCAT CAGTGTTCAC AACATTTTTC ATGTCTGGCT TTTTAGGTAC 4080

TACTTATTTA AATACATTTT TTAGTAACAT AACTTTTATC AATAGCTTAA TAACGCCTAT 4140

TTGGATTTTA TGCCTTGTGG GAATTATGAC GCATATGATT ATTTTTTCAA TAAAATATTT 4200

AAAAGATTTT TCACTTGAAA ATGTTTATCC TTCGTGGACT GTACTTTTTA TTGGTATTGn 4260

TATCGCAGGA TTGACGGCAC CCGTTAGCGG ATATTTTTTC ATAGGTCAAT TAACAGTAAT 4320

ATATGGCTTT GTAGCTACTT GTATTGTCTT ACCTATAGTT TTCAAGCGAT TAAAAGCATT 4380

TCCATTGCAG ACGTCAATCA AACCGAACAC ATCGACAATT TGTGCACCAT TTTCTTTAGy 4440

CGCTGCAGCA TATGTTATAG CTTTTCCTAA GGCGAATGCT TTTATCGTAA TTATATTTTT 4500

ACTATTAGCT CAAATATTTT ATTTTTATAT CATTATACAA TTGCCTAAAT TACTAAAAGA 4560

ACCTTTTTCG CCCGTATTTT CAGCTTTCAC ATTCCCTTTA GTAATCTCAG CAACTGCTTT 4620

AAAGAACAGT TTGCCTGTAC TTATGTkTCC AGACATTtGG AAAGGkCTTT TGTTTATCGA 4680

AGTGTTATTA GCCACTGTAA TAGTACTTAG AGTCTTTATA GGATATCTTC ACTTCTTTTT 4740

AAAAAAGGAA AAACAAGATA AATTTCTnCG TAATGCGTCT CAGTAACACT ATTACCAAGA 4800

ATTAACACGT ATATTTAATA 4820

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATTTGGATCT TTAATATCAC CAATATTTTT AATATCTTCC GGATTCAATC CATATACTTG 60

TACTGTATCT GAGTATTTAA TTGTGAAATA ATCACCTGAT TTAACTTTGT CATCAACTGT 120

AATTTGTGAT TTTAATGATA AATAATCTTG GGCTGGTACG ATTTTATTGT TTTTATCTGC 180

ATCAACGACA GTtAATGTTG TATTTGATGT GATTAAATCA TTAACATTTT TAGCCTCTGT 240

TGATGATGGC TGTACTGCTG CTATACGCAT TCTTGTATTC AAACGTTTAG GTGCTGTACT 300

TTTTGGCAAA ATGATATCTG CATTATTTTC ATTATTTGAA TTACTATTGT TATCAACAAG 360

AGTTTCATCA TTACTCTTGA TAGCATCACT TTTAACATTT AATGTAGTTG ATTCAGTTTT 420

GGCATCTACC TTTTTGTTTT CCTCATTAGT TGGTTGAACA TTTACCACTG ATTTATTCTC 480

TTGCAAATCA GGTTGTAACG CTTCTTGATT ACTTATAGTT TGTTTAGTGT TTAAATCTTC 540

ATTCGTAGAT TTTGGTGAAG CTTGCTCATC TGATTTGGCA GTTGAAACTT CAACTTTATT 600

TCCAGTGGTA GATTGTACAC TTTCTTTTTC TATTAATTTA TTCCCATTTG AAGTCGTTTC 660

ATTACCTTGa GATGATACCA TTTCTTTTTG ATTATCATTT TTAGTATTGT CTTCTTGATT 720

TAGTTGCTGC ATATCAACTT TATCACTCGA TTGATTATCA CTTGCTGAAG TTGTCGCTcG 780

TTCAATTCTT TATTAGTACT TTCTGCAGCC TTTGCTTCTT GGTTCCCCAG ACCAAAAATT 840

AATGTTGTAC CTACTAAAAT TGATGCTGTT CCCACTGTGT ACTTTCTAAT CGAAAATTTA 900

TTTAATCGAT TGGATACCAT GCCTTTCCTT GTTATTGCCG TTTTATTTTC TCTGTTTAGC 960

ATTAGATTAC TCCTAATTCA TCAAATTTTT AAATAATACA ATTGTTTTAA ATACAAAAAT 1020

GTATATCAAT ATAGTATTAC ATTTTTAGAT AAAGCACAAT ACTTTAATTA TTTTTCTTTA 1080

TCGTAAAACG TTATTTAACA TTTGTGTTTA AATAAAAGTT TTTATGAGTt TTGTAATCTT 1140

TATTTAATCA TCATAAAAAA TAGTATTATT TGCCCTTGAA ATTAATATCT TAGCTTTTCT 1200

AATTCATAGA CAATTACATT TCTGTAACAA ATTAAATTGT ATCTATTCCT TAAAGATTTT 1260

TTGTTTTATA TCTGGGAATT TCTAAACAGA AAAAACCAGG CCACATGGAC CTGGTTAAGT 1320

TAATCATATT ATTTATTTTG TTTTTTACGA CGACCGAATA ACAATAATGA TCCTAATGCC 1380

GCGAATAATC CACCGAATAA TGTGCCATTA TTTGAATTAT TATTTTCACT ACCTGTTTCT 1440

GGTAATGCTT TAGCTGTTTT ATGCTGATCT TTAACCGTAC TCATTGGTTT AGCCGGAGTA 1500

TGTTTACCTG CATCTGAATC TGAATCGCTA TCTGAATCTG AGTCGTTGTC TGAGTCCGAA 1560

TCGCTATCTG AATCTGAGTC GCTGTCTGAA TCTGAATCGC TATCCGAGTC TGAGTCGCTA 1620

TCTGAGTCTG AGTCGCTATC TGAATCTGAA TCGCTGTCTG AGTCTGAATC GCTATCTGAG 1680

TCTGAATCGC TGTCCGAATC TGAGTCGCTA TCTGAATCTG AATCGCTATC TGAATCTGAG 1740

TCTGAATCTG AGTCGCTGTC TGAATCTGAA TCACTGTCTG AGTCTGAGTC GCTGTCTGAG 1860

TCTGAATCGC TGTCAGAATC TGAGTCGCTA TCTGAGTCTG AATCTGAATC ACTGTCTGAG 1920

TCCGAATCGC TATCTGAATC TGAATCGCTA TCTGAGTCTG AGTCGCTATC CGAATCTGAG 1980

TCGCTATCTG AGTCTGAGTC GCTATCCGAG TCTGAATCGC TGTCTGAGTC TGAGTCGCTG 2040

TCTGAATCTG AATCGCTATC TGAGTCTGAG TCGCTGTCTG AATCGCTGTC TGAATCTGAG 2100

TCGCTATCTG AATCTGAGTC GCTATCTGAG TCTGAATCGC TGTCAGAATC TGAGTCGCTA 2160

TCTGATGTTT CTTCTTCGTA GTAGCCATTA TCAAGTGTGA AATCATCATG ATCCGTAATT 2220

GTTACATCAA CTTCGCCACC ATCGGCATCT TTATCATCTT CAGTTGTATT TGTACCTGTT 2280

TGAGTTAAGC CAGCAGGTTT TTCAAAGATA ACTTTGTATT TACCACTATC TAAATTATCA 2340

AAGCGGTATT TACCATTTTC ATCTGTyTCA GTTGTACCAA TTACTTCGCC TTTTTCGTTT 2400

TGCAAAGTAA CTTTAACACC TTTAATTCCT TTTTCAGTCG AATCTTGTTT ACCATCTTTA 2460

TTACTGTCGT ACCAAACATA ATCACCTAAA CTATATTTTG GTGTTTTGTA GAATCCACTA 2520

TCTAATGTCA TGTTGTCAGC GTCTTTAATG ACACCTGTTG TAGTTAGTCC ATCAGAATCT 2580

ACAGCATCAT CTGTACCTAC ATTTGCAGTT GTCGGTGTAT AACCGGCTGG TGTTGAAAAC 2640

TCTACACTAT AAGTTCCATT GCTTAAACCA GTGAACTGAT ATTTACCATT TTCATCTGTT 2700

GTCGTACGAT CTAATTCTTT ACCGTTACTA TCTTTAAGAA TGACATAAAC ACCTTTAATC 2760

CCTTTTTCAT TGGCATCTTG TTTACCATCT TTATTTGTAT CTTCCCATAC ATAGTCACCT 2820

AGATTATATT TCTTTTGGTC GCCATTAGCA GTTGATGAGC CATTCACATT TGAATAACTA 2880

TTTGACCAAC TATATTTAGT TTTGTCAGTG TCTAAAGTAT AATCAATTTT TCCATTATCT 2940

GTTGAACTAT TATCTGGATA AGCAACTTGT TGAATGATGT ATTGTTTATT GCTGCTTGTT 3000

TGGCCTTTCA TTAAATCGAC TGTAGCTGTT TTATTATCAT TACTATAAAT AACATCGAAT 3060

TGATCAGTAA CATCTTTAAG TTTTGAAGTA TCAGGGGTGA AACTATCCAC AAATTGATTT 3120

TGATCTGtCA CTtCGTAAAT TTTGAAGTTT TTTGCATTTG GATTAAATTT ATATCCAGTT 3180

AAATTAGTAA CAAACGTTTG TTTAGTATAT GTATTTTTAG GTTGATTTAC ATATGCAGTC 3240

ATATTACGCG ATAAATCTTC ATTGTTAATA TAGTTTGTAC TTGAAATAAG CGGTTGTGCT 3300

TTTTTATTAC CATAATCGAC AATGATTTCT TCGCTATATG TATCATTACC TAAAGTTACT 3360

TCCATTTTAT AAGCTGTTTT ATCAGTTGTT GCATTTTTAC GTTTCGCAAA TGCAACTTGT 3420

TCAAAGCTAC CTCTAACATT TGTATATTGA TCTACATAGT TCGTAAAAGT ATATGTTGTT 3480

GTGTTTGTTG TACTATCATA AATACCTTTT GCAATAATAT TACCTTGGGC ATTATATAAA 3540

GTAAATGTAT CGCCCTCTTT AACAGAATCA TCGATTGTGT AATTTGCTTT TAATTTTAAA 3660

ACATCACTTG AAGTTGCCCA AAATTCAGTT TTACCAGTAG TCTGATTAAC ATGTCCTTTA 3720

TCAATCGCAA TGTCAATATT TGAAAAATGT ACTTTATCAT TAACATTTGT TCCTTGTTGT 3780

GGAGCTGCAA CAGTATTCAC TGCCATGCGA TTTAAAGTTC TTGGTTTAAT AGTCGTTGTT 3840

TTAGGTGTAG TTGAAACATC TTTTGCTTGT GTTAAATTAC TTTTATCAGT TTCATTACTA 3900

TATGTAGTTG ATGATTTATC ATTTGTTGTT ACATTGCTAG TTTTTGTAGT AGATTGATTA 3960

GCTGTAGCGT TTTGTGGTGA TTGCATGTTA CTACTAGTTT CTTTAACTGT TGCACTATCA 4020

CTCATTGTCA CTTTAGGCTG ATCTGCAGTT GCAGTTTGCG TATTGTCTTT TAGTTGACGA 4080

CTATCAACTT TTTTAGTTGT TTTATTCTCA CTTGGGGCTG TCGTTTCATT TTTTGATTGA 4140

TTTAATTCTC CATTCGTATG TTCTGCCGCT TTAGCTTCAT GACCACTTAA CCCAAAAATC 4200

AATGTTGTCC CTACTAAAAT TGAAGCAGTA CCTACAGAAT ACTTTCTTAT CGAAAATTTG 4260

TTTAATCGAT TTGGTATCAT GCCTTTnCTA TTTGTnGCTG TCTTTTTATA ATTCATTTAA 4320

TAATACTCCT TTAAAATATC AAAATTTGAT AAATATAA 4358

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1060 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

TTGACTTCTT AATTCAGCAT TTTCTGCACT TAATGCTTTG TTCTTTTTAA TAAGTTGCTT 60

TCTTGCATAA ACTTCGGTAT CTATTTTACT ATTACTATAC CTTTGATTTA AAACTAATAT 120

ACCAATTAAT GCTACAATGA TAATGATAAG TACAACATAA AAAGACATTT TTTCACCAAT 180

CCTTTTTGAC TTCTTTAACT TTGTATACAA TAATAATTAA TAAAGATTAA TTGTTATTCA 240

ATTTCCCACA TTTTTATTAG TTGATTTTAG TTCATCATTG TTATAATCAA ATTATAAACT 300

GACAGATATT GATGTTCAAT GAATATGACG TGAAAGATTC GTGAATTCAA GTTTATGTCG 360

AATTTATGTT ATAACGGTCA TTTAAATGAC AGAATTAGGT CACTCATAGT ATTTTGAAGA 420

TTGAATTCAT TAATTTTAAA ATGTATAATG ATATTTGTGA AAGCGCTTGC TTAGGAGGTG 480

TATTTGAGAG TGAATGAAAT GAATGCTAAA GAACAATTAG TGGACAATTT AATGAAAACA 540

TCATCGCAAT TATTTAAATT TCACGGTGAA GTTGCCATGC AGCTTTTCTT AAATGATGAA 600

AAAGTTATTC CGCAATCATA TGCGTTACTA TACATAGATA AGCAAGATCA AGCAATAGCT 720

AAAGAAGATT TATCACTTTC AAAAATTGCA AAAGTTTATG TGCAATATGA TGATACAACA 780

ATAATGAGTA TTTTCGTTTA TGATGTAGTA AACGATGAAT GGATTTTTAG ATTGGATCCG 840

AATATACGTA TACCTAAGAG TAACATATAC TTCCATAGTT TAAATTGGGA TGTGGATATA 900

TTAAACCGGA GtCGTCTAAT GTATGTCTAA TGCaCACCAT CAGaTCATCA TtATCCATTA 960

TAAcGrGCAT AGTGCATAAn yACTwCAtTT TaTTaaATTG AGaGGgGCAC GATAGGTGCA 1020

TCAGGACATA ATATAGGAAG CATCAACGCG TGAnCAGGTC 1060

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

ATAATnACTA AATACnAAAG TTTAACTGTC TTACTAATAA TGACTATGTT ATAATTTTAA 60

AAGTGATATT TTGGGTAATC GCTATATTAT ATAGAGGAAA GTCCATGCTC ACACAGTCTG 120

AGATGATTGT AGTGTTCGTG CTTGATGAAA CAATAAATCA AGGCATTAAT TTGACGGCAA 180

TGAAATATCC TAAGTCTTTC GATATGGATA GAGTAATTTG AAAGTGCCAC AGTGACGTAG 240

CTTTTATAGA AATATAAAAG GTGGAACGCG GTAAACCCCT CGAGTGAGCA ATCCAAATTT 300

GGTAGGAGCA CTTGTTTAAC GGAATTCAAC GTATAAACGA GACACACTTC GCGAAATGAA 360

GTGGTGTAGA CAGATGGTTA TCACCTGAGT ACCAGTGTGA CTAGTGCACG TGATGAGTAC 420

GATGGAACAG AACATGGCTT ATAGAAATAT CACTACTAGT TTAGCTCTCC TAGATGATGG 480

AGAGCTTTTT TCATGAAAAG AACACTTAAA ATTAACGCCy TGTCTTGaTA tAATGACaCT 540

GCcTTGTTTT AAAATAGTAA GCGGATGCgT TAATGTATCA GCGATTAAAT TTGTTGGAAA 600

TGTATAAAAA ACACAAGCTA AGAATAAAAT ACCTGTATAA AAGGAGAATC ATATATGTTT 660

CAATTACTTG CAGTTTGTCC GATGGGATTA GAAGCTGTTG TTGCTAGGGA AATTCAAGAA 720

TTAGGCTATG AAACAAATGT TGAAAATGGT CGTATATTTT TTGAaGGAGA CGCAAGTGCA 780

ATTGTAAAGG CAAATTTATG GTTGCGCACA GCAGACCGAA TCAAAaTTGT TGTTGGACGT 840

TTTAACGCAA CAACGTTTGA CGAATTATTC GAACAAACCA AAGCGCTCCC TTGGGAATCT 900

ATAATTGATA AAGAGGGTAA CTTCCCAGTT CAAGGTAGAA GCGTTAAATC AACACTACAT 960

TATAACGAAA AAGGTTGGTT AAATGAATCA GGTGCCAAAT ACCCTGTTGA AGTTGCCATT 1080

TTAAAAGATA ATGTATTATT GACTATCGAC ACATCAGGTT CTGGTTTGAA CAGACGTGGT 1140

TATAGATTAG CACAAGGTGA AGCACCAATT AAAGAAACGT TGGCAGCAAG TTTAATCCGT 1200

CTTGCCAAAC TGGGAAAGGT GATTACACCT TTnAATTGGT CCCATTTGCG GTTCnGGTTA 1260

CA 1262

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

CCTGGCTGCT TTATCAGCAT CTACTACTTT AAAACCGAAT ACGGATAAGA GTTCTGATAC 60

TGTTGATTTT CCTGAGGCGA TTCCACCTGT TAGACCAATA ACTTTCGGCA TAATTTCACT 120

CTTTCTTTAT TTTTGACATA CTGGACAATA ATGACTATTT CTTGTCGCGA TGATTTTTGT 180

TTCAATTTGA CTTCCACACA CTTTGCATAC CGGCTGCTTA TATACATTAA GATGCAATTG 240

CATCTCACCA GTTTTTCCAT CAGCATGACG ATAATCTGAA ATACTTGTAC CGCCATATTT 300

AATACCTTCT TCTAGTACTT CTCTAACATA ATAAAAAACC ATTTCTTGTT GTTGGTGTGT 360

TAAGTCTTTT ACTTTTTTAT CTGGTAAAAC ACCTGCACGA AACAACGCTT CACATGCGTA 420

AATATTTCCA CAACCTGCGA TTACTTTATG ATCCAAAATC ACTTGTTTGA TTGGTTTATT 480

CTTATTAGAC TGTTGATGAA TTCGATTTAA ATAATACGTC AATGCTTCAT TTGAAAAAGG 540

TTCAGGCGCT ATTTCTAAAA ATGAAGGATA AGATGCTACA GACGCAACAT TTCTAATTTC 600

TCCAAAACGA CGTATATCTG AATAAATTAA CTTTTTGTCA TTTGACAACT CAAAAATAAC 660

ATGCCAATGC TTACGATAAT TAGGTATCAT AATATCTTCA AGTTCATCTA CAATGAAAAA 720

ACCGCCCGCC ATACCTAAAT GACTAATTAA TGTACGTTGT TCTCGTTTAT TATCTAGCTG 780

AAAAACGATA TATTTACTTC TTCGTTCTAC ATTTGTAATG GTATAGCCTT CCGATAAAGT 840

TTTAAAAGTA TCTAATTCAA TTCCTTTTAT AATTGTTTCC TTGCCTTGAG CTTTACCTTC 900

GATTACTTTA TCCGAAAATA TAACGTGTTC AATTTTTTGA TTTATAACGT AGGGTTCAAT 960

TCCTCTTTTT ACATGTTCTA CTTCTGGTAA TTCGGGCATA CCATTAACCT CACTTTATTT 1020

TGCATCATAC CAGGTTGCAC CATAACTTGA GTCTACTTTT AATGGAACAT CTArTTGCAA 1080

TT 1142

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

CCTTTAGTAA ACAATCCTTC TTTAGTTTTA GTACGTTGTT CCAATCCAAA TAATTTGTAT 60

TTCATTGCCT CGCCCGATTG AGTGCCGCTA AAGTTATCAT CTTTCATGTT AGGCGTGTTG 120

GTAAACATGT GTATATCACT GTTTAAACGG TCTTTATAAG CTTCGGTACC TTGTACATCG 180

TATTGCTTAT AAATATAACC ACCATCAACA GAGCCTTCTG TTTCTCTACC TTCGCTATCA 240

GCATAAACAG TCGGTTCTAA AAACAACACG TTAGCTTCCT TTTGTTTTCT AACTTCTACA 300

GGATCTAAAT TTAAATTACC TTTAATAAGT AACATAGCGT CATTTAAATC ACTCATATAG 360

TTAGCAsymy CTGATTCAGC ATTATCATAC AAATCAATTA AAGTGATTAC TTTCTCATAA 420

TCCCCTTTTC TTCTTTCGTT GTTGCTAAAT TCTGTAATAG GCATACGTTC GAAAGAGTGT 480

GATTCAAAAC CGTTTTCACG TGGTGTGAGC TTCAATCCAT TTGTTCTACT GGTAAGATAT 540

CTATAAACAC CGTGTGAAGT GAATAAATCA ACTGTAAACA CTTCATCTTC GTCAGTCTTG 600

TCTATTGGTT TAGTTCTTAA ATATCTAACG CCTGCGATAC TATTACGTTC AATTGTATTG 660

TCGTATATGA CAAAAGTACT CATTGCATCA CTCTTGTATA AACGCGTTTC ATCATCTTGG 720

TTTCTAATCA TTAACTCATA AGCTTTGCCA TAAATTGACA AATCTAATCC TAAAGATCTA 780

TTGTGTGACT CAACATCATT TAAATCATTG AACGCCTCAA TAACTTCTAA TACATCTTTG 840

TCATCATCTT GATATTGAAT TGGATTACCC AAGAAATAGC CGTTGATAAA ATCGCTAATA 900

TAAGATGCGT AATCATGCGC TACACGGTTA TCTGCCATGT ACTCTTCTTT GCGTCGTGTT 960

AACTCAACTA AGTTCTTAGT TTTACCTTCG TAATAATCAC TTAACACTTT CAATCTAGGT 1020

CGTTGGTAAT CCATGTGATG TTCAATGTAT TTACTTACTT CATTAACGTT TTGTAATAAA 1080

TCGGATTCCG TCCCGTCATA TGTGTAAACA ACATTGGCTT CATCATTAAA TAAGTAATTT 1140

ATGTTTCCCC GTAGATCTGT ATCTGTTTCA AATTCGTTTA CTTTTAACAT TTGTTCCCTC 1200

CTATAATCCT AGAGATTTTA TTGTGTCAAC TTTCGAACTG AGATTTGTGC GTTTtCTAAC 1260

CGGTCTGTAG AATCGTTCCA CTGAATAACG CAACGAATCG ATACAATGAT TGTATGTATC 1320

CTCTTCAATA GTCTTGAAAC AACGTTCATC AACAATGATT TCAAATTGCA TTAAGAATTG 1440

TAACCCTTGT ACAACCGAGC CCTTCCCTTT TTTGGTTGGT AAAATCCTTT TAAGCCCTAG 1500

ATTCCTTAAT TCAGCTATAC TTTTTTGTTC TGCACTATCT GCTGTAATTT CTTCTTTAGC 1560

ATAACCAAGT TGCTTTATGA CATTAGCTAT TTCATCATTC AGCATACCTT GTTTAACATA 1620

CTCTTCAATG ATGTATAACT TCTTTTTCTT TACATCTATT TTAGAATGTA TAAAAGCACT 1680

AGGATCATTA ACGTAGCCAA AGTCCAATCC AAAATAAGAA GGTAAATGTC TTAACTCATC 1740

TTTATTTATT AAACGTTTTT CATACTTAGG GAAAACCAAT TTGTCTAGTG TAGCAAATTC 1800

ACCTAACGCA TAAA 1814

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 686 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

AATTnAGATT ATTACCCTCC TTTAAAAATA TTTGTTTCAC AATTTTTTAT TACCTATTTA 60

CTGGTTTCAT GTCTTATGGG GCATTTTACT TGTTGGTATT TGAAAATGTG CAAAATTTAA 120

TCTTATATGT TTCTTGGCTT TTCATGACTA TGCTATTTAT GTTTATGAAT ATGCATTCAA 180

TTATAGATAA AAAAGTACAT ATATTCTTAA AGTCTAATAA ATAGTTACAA ATTTAGTTAG 240

TTTTCAATTG TTAATTAGGG GTGGTAAACA GTGCTTTGTG AATCTAGACA AATTTATAAA 300

AATCCTAAAT ATCGAGTTAT TAGATATAAT AATGAATATT TCATGGTCGA TTTAGTAAGT 360

ACTTGGATTA CTTATTTTTT CCCTATGATT AATTGGTTTT TGCCCAAAAA ATACGCAAAA 420

ATTAGCGAAA ATGAATTTGA AAGGTTAAAT ATAGTCGAGC CTGTTAAAAA TAATGTTTTT 480

TGGCCGGTTG CAGGAAGTTC AGTTCTATTT GGAATTATAT TGAGAAAGTA CGGTAACTTC 540

TTTAATGTTC AGTTTGAAAA ACAACTAGCA ATCACTGTAT TTTTTATCAT GTTAATAGGG 600

ATGTTAATTT TTTATTTTTA TCTAAATAAA AAATTAACAT TAAAAATTTT TAATACCAAC 660

GTGGGTAATA AGAATAGGAG TTGTAT 686

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

ATCTGCAATT ATGGGCACAC CCAAGCTnAT GCAAGTAACT AAAGGAGAAG TACTTTTAGA 60

CGGTGTAAAT ATTTTAGAaT TAGAAGTTGA TGAAAGAGCA AAAGCAGGAT TATTCTTGGC 120

AATGCAATAT CCATCAGAAA TTACAGGTGT TACAAATGCT GATTTCATGC GTTCAGCAAT 180

CAATGCGAAA CGTGAAGAAG GACAAGAAAT CAACTTAATG CAATTTATTA AGAAATTAGA 240

TAAAAACATG GATTTTCTAG ACATAGATAA AGACATGGCA CAACGTTATT TAAATGAAGG 300

TTTCTCAGGT GGAGAGAAGA AACGTAACGA AATCTTACAA TTAATGATGT TAGAACCTAA 360

GTTTGCaATC TTAGATGAAA TCGATTCAGG GTTAGACATC GATGCATTAA AAGTTGTATC 420

TAAAGGTATT AACCAAATGC GTGGGGAAAA CTTTGGTGCA TTAATGATTA CACACTATCA 480

ACGATTATTA AATTACATTA CTCCTGATAA AGTACATGTA ATGTATGCTG GTAAAGTCGT 540

TAAATCTGGT GGTCCAGAAT TAGCAAAACG TCTTGAAGAA GAAGGATATG AATGGGTTAA 600

AGAAGAGTTC GGTTCAGCTG AATAATCTTA TTAATACAGT ATCCATGAGA TGTTCATCTA 660

TATATGATGA AAATGAACAT TTATACGAAA TAGTAAATTT CATCAAGTAG GAGGAAAAAG 720

TTATGACAAC TGATATTTTG rACaTTyCTG AAGAACAACT TGTTGATTAT TCTAAAGCCC 780

ACAATGAACC TTCTTGGATG ACAGAATTAC GTAAAAAAGC TTTGAAATTA ACAGAAACTT 840

TAGAAATGCC AAAACCTGAT AAAACAAAAT TAAGAAAATG GGATTTTGAT TCTTTTAAAC 900

AACACGATGT AAAAGGTGAT GTTTATCAAT CTTTATCACA ATTACCTGAG TCAGTAAGAG 960

AAATTATTGA CGTAGATCAT TCTAAAAACT TAGTAATTCA ACATAATAAT ACGATTGCGT 1020

ACACACAAGT TGATGATAAT GCATCGAAAG ATGGCGTTAT CGTTGAAGGT TTAGCAGACG 1080

CTCTTATGAA CCATAGTGAT TTAGTACAAA AGTACTTTAT GAAAGATGCA GTAACAGTAG 1140

ATGAACATCG TATCACAGCG CTACACACGG CATTAGTTAA TGGTGGCGTA TTTGTTTATG 1200

TTCCTAAAAA TGTAGTTGTA GAACATCCAG TACAATACGT TGTGTTGCAC GACGACGAAA 1260

ATGCAAGCTT TTATAACCAT GTTATCATCG TTACTGAAGA 1300

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GACAGCAAAT TCAAGATACA TTAAATAAAG ATATTGTCAT AAAGCATATT CTTGTTCGAG 60

ATAAATCTAA AAAGAGACCG CTAAATATTA GCCAATATCA TTTAACTGAA GATGTTAATG 120

AAATTTTAAA TGATGATTCA TTAGATATTA TCGTTGAAGT CATGGGAGGA ATTGAACCAA 180

CTGTAGATTG GTTAAGAACA GCACTTAAAA ATAAAAAACA TGTTATTACC GCAAATAAAG 240

ATTTATTAGC AGTACATCTT AAACTTTTAG AAGATTTAGC AGAAGAAAAT GGTGTAGCTT 300

TAAAGTTTGA AGCGAGTGTA GCAGGTGGTA TTCCGATCGT AAATGCCATA AATAATGGTT 360

TGAATGCGAA TAATATTTCA AAATTTATGG GAATTTTAAA TGGTACCTCT AATTTTATTT 420

TATCTAAAAT GACTAAAGAG CAAACGACAT TTGAGGAAGC ACTTGATGAA GCGAAAAGAC 480

TTGGTTTTGC TGAAGCGGAT CCAACTGATG ATGTAGAAGG GGTAGATGCA GCGCGTAAAG 540

TTGTCATTAC ATCATATTTA TCATTTAACC AAGTCATTAA ATTAAACGAC GTTAAACGAA 600

GAGGAATTAG TGGCGTAACT TTAACTGATA TTAATGTAGC CGATCAACTG GGGTATAAAA 660

TTAAATTGAT TGGTAAGGGA ATATATGAAA ATGGCAAAGT TAATGCATCG GTAGAACCAA 720

CGTTAATTGA TAAAAAGCAT CAATTAGCAG CTGTAGAGGA TGAATATAAC GCGATTTATG 780

TTATTGGTGA TGCCGTTGGT GACACGATGT TTTATGGAAA AGGAGCAGGC AGTTTAGCAA 840

CAGGTAGTGC CGTTGTCAGT GATTTATTGA ATGTAGCATT ATTCTTTGAA TCAGATTTAC 900

ACACATTGCC ACCACATTTT GAATTAAAGA CAGATAAAAC ACGGGAAATG ATGGATTCAG 960

ATGCAGAAAT TAATATTAAA GAAAAATCCA ATTTCTTTGT AGTAGTGAAT CATGTCAAAG 1020

GTTCAATTGA AAATTTTGAA AATGAGTTAA AGGCAATATT ACCATTTCAC CGATCATTAA 1080

GAGTTGCAAA TTACGATAAT CAATCATATG CCGCTGTTAT AGTTGGATTG GAATCATCAC 1140

CGGAAGAATT AATCACTAAG CATGGATACG AATTGACAAA GTATACCCAG TAGAAGGAGT 1200

TTAATTATAA TGAGAAGATG GCAAGGATTA GTAGAAGAGT TTAAAGCACA TTTACCAGTA 1260

AATGAAAATA CACCAAAATT AACATTGAAC GAGGGAAATA CACCACTCAT TCATTGTGAA 1320

AATATGTCTA AAATACTAGG CATAGATTTA TATGTGaAGT ATGAAGGTGC CAATCCGACA 1380

GTTCATTTAA AGATCGCGGT ATGGTAATGG CTGTGACAAA AGCAAAAGAG CAAGGTAAGA 1440

AAATTGTAAT ATGCGCTTCG ACTGGAAATA CATCAGCGTC TGCAGCAGCA TATGCAGCGA 1500

GAGCAGGTTT AAAAGCTATC GTCGTAATAC CAGAAGGTAA AATTGCATTA GGTAAATTGT 1560

CGCAAGCAGT AATGTATGGT GCAGAAATCG TTTCTATTGA AGGAAACTTT GATGAAGCTT 1620

TAGAAATTGT AAAAGAAATT GCAAAAAGTG GCGAAATCGA GCTTGTAAAC TCTGTCAATC 1680

CATTTAGAAT CGAAGGACAA AAGACAGGCT CATTTGAAAT TGTACAACAA TTAGACGGTG 1740

AAGGCTTTAA AGAATATCAT GAAGCTAAAG GATCACAATT GCCGAAAATG TTTGGCTTCC 1860

AAGCTGAAGG CGCATCACCA ATTGTTCAAA ATAAAGTCAT TAAAAATCCT GAAACGATTG 1920

CAACTGCTAT TCGAATTGGT AATCCTGCTA GTTGGGATAA GGCGACTAAT GCTCTTAAAG 1980

AATCAAATGG ATTAATAGAT AGTGTTACTG ATGATGAAAT TCTAGAAGCA TATCAGTTAA 2040

TGACAACTAA AGAAGGTGTC TTTAGTGAAC CAGCGAGTAA TGCTTCTATT GCAGGTTTAA 2100

TTAAATTGCA TAGACAAGGT AAATTACCTC AAGGTAAAAA AGTAGTTGCT ATTTTAACTG 2160

GTAATGGATT AAAAGATCCT GATACTGCTA TTTCACTACT AGATAATCCG ATAAAGCCAT 2220

TGCCAAATGA TAAAGATAGC ATTATCGATT ATATTAAAGG AGCTTTATAA CATGTCGAAT 2280

GTTTTGGAGT TAACAATTCC TGCATCAACA GCCAACCTTG GAGTTGGCTT TGATTCTATA 2340

GGTATGGCTT TAGATAAATT TTTGCATCTG TCTGTAAAGG AAACATCAGG GACAAAATGG 2400

GAATATATTT TCCATGATGA TGCATCTAAG CAATTGCCTA CTGACGAAAC AAACTTTATT 2460

TATCATGTAG CACAACAAGT TGCTTCTAAA TATAGTGTTG ACTTGCCTAA TTTATGTATC 2520

GAAATGAGAA GTGATATTCC ATTGGCAAGA GGGTTAGGTT CGTCAGCTTC TGCTTTAGTA 2580

GGAGCTATAT ATATCGCAAA TTATTTTGGT GATATCCAAC TGTCTAAACA TGAGGTATTA 2640

CAATTAGCGA CTGAAATCGA AGGACATCCT GATAATGTTG CGCCGACCAT TTATGGTGGT 2700

TTAATCGCTG GATATTATAA TGATGTCTCG AAAGAAACGT CaGTtGCACA TATCGACATA 2760

CCAGACGTGG ATGTGATTGT AACGATACCA ACTTATGAAC TAAAAACAGA AGCATCAAGA 2820

CGTGCTTTAC CACAAAAATT AACACATAGT GAAGCGGTTA AAAGTAGTGC AATTAGTAAT 2880

ACAATGATTT tGgCATTAGC ACAGCACAAT TATGAATTAG CAGGTAAACT CATGCAACAA 2940

GATGGCTTTC ATGAACCGTA TCGTCAGCAT TTAATTGCTG AATTTGATGA AGTGAAAACA 3000

ATTGCTAGTC AACATAATGC CTATGCAACT GTAATTAGTG GTGCTGGACC AACTATTTTA 3060

ATATTTAGTC GTAAAGAAAA TAGTGGGGAA TTGGTTCGCT CTTTAAATAG TCAGGTAGTA 3120

TCATGCCATT CTGAA 3135

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

AGnTCAATAT TTAGATCAAG CCGTTTTAAG TAATTACGAA CAAGTTTATA TCATTCATGG 120

TAAAGGTACA GGTGCACTTC AAAAAGGTGT ACAACAACAT TTGAAAAAGC ATAAAAGTGT 180

TAGTGACTTT AGAGGTGGTA TGCCAAGCGA AGGTGGATTT GGCGTTACCG TTGCAACACT 240

AAAATAAATT ATAATTTGAT AAATTAAATA GCTGCAGTTA AAATAATGTA AAGCAACAAG 300

AATACATTTC AAACATGTTA TTTGAAATAA GCATAAAAAT TGAGCAAATA GAAATACATG 360

AAGCATGTTA TCTGATATAA TTTGAACATC ATAATAATAA TTAAGGAGGA TTGGCATTTA 420

TGGCAATCGT AAAAGTAACA GATGCAGATT TTGATTCAAA AGTAGAATCT GGTGTACAAC 480

TAGTAGATTT TTGGGCAACA TGGTGTGGTC CATGTAAAAT GATCGCTCCG GTATTAGAAG 540

AATTAGCAGC TGACTATGAA GGTAAAGCTG ACATTTTAAA ATTAGATGTT GATGAAAATC 600

CATCAACTGC AGCTAAATAT GAAGTGATGA GTATTCCAAC ATTAATCGTC TTTAAAGACG 660

GTCAACCAGT TGATAAAGTT GTTGGTTTCC AACCAAAAGA AAACTTAGCT GAAGTTTTAG 720

ATAAACATTT ATAAGTTACA ACCAATGACG ACTGGGGCAT TTCTTTAATG AATTGCTCCA 780

GTTTTTGTTT GTGTTTTTAA TATAAAAAGT TGAATGATAA GTCATCATAT TGTTTACGAC 840

TTGAGAATGG TGGGATTAAT AAATCTATGA ACGTTAAATG ATAATCTAGC ATGCTGATAG 900

ATTTGTAGCA GTTGGTTTGA TAAAACCATG TTCAATATTA CATGATGTGC ATGAAAAGTC 960

ATACTCGAAG ATGTTGATTA TTAACTAGAA TTAGTGGTGA TAAATTTGAA GCACTTTTGT 1020

AGCATCATTC ATTTTAAAAT TAGAAGGGGG GATATTTTTG GAAGACTATA AGCAACGAAT 1080

TAAAAATAAA TTAAATGTCG TACCTATGGA ACCAGGATGC TATTTAATGA AAGATCGTAA 1140

TGATCAAGTG ATATATGTTG GCAAAGCTAA AAAGCTAAGA AATCGATTGC GATCATATTT 1200

TCACGGGTG 1209

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2410 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

AGTTCAACAC GACGAATTTT ACCTGAGTTT GTTTTTGGTA AGTCGTCAAC GAATTCAATC 60

TCTCTCGGAT ATTTATATGG TGCAACTTCA TTTTTAACAA ATTGTTGTAG TTCTTTAACT 120

AACGTATCAT CACCCGCAGT ATGGTCCTGT AAAATAACGA ATGCTTTAAC AATATTTCCT 180

GCATCTTCAA CTTCAAAAGG CCCAATCGTA TAGCCTGAAC TAATAATAAT GTCATCTCGA 300

CGTCCTTCAA ACCAGAAATA ACCATCATCA TCTACATGAG CTAAGTCACC AGTGATGTAG 360

TATTtACCTG TTTGCGCTTT CGCCGTACGT tCTGGCTCTT tATAATACCC TTTGAAAAGT 420

GCTGGCAAAT CAAGTGGTAC TGCAATATTC CCTTTCGTAT TAGCAGGTAC GCTATTCCCC 480

TCATCATCTA CTACAGTGAC CGAACTACCC GGAATGCCTT TACCCATTGA TCCAATCCTC 540

TGTGGTGTAT CTTTTAAAAA GCCTATAAGC AAGGTACTTT CAGTCTGGCC ATATCCATCT 600

CTTACAGTTA AATTAAAGTA TTTCTTGAAT TGTTCAACTA CTTCTCGATT TAGTGGCTCA 660

CCTGCAGAAA CGGCACTATG TAAATGCGTT AAGTCATAAT CATTTAAGTT CTGTAATTTA 720

GCCATCATAC GATATTCTGT CGGTGTACAA CATAAAACAT TAATTTGATA TTTTTGAAGC 780

AATTCTAAGT ATGTTTCAGG ACTGAACCTT CCATTAAATA CAAAAGCAGT TGCACCTGAA 840

CCTAATACAG ATAAGAAAGG ACTCCATACC CATTTTTGCC AACCTGGTGc TGCTGTTGCC 900

CAAACTAAGT CATCTTCATT aATACATaAC CAATGTTTTG GTGCCATTTG TaAATGTGcA 960

AATCCCCaTC CATGACAATG TGTAACGGCT TTAGGATTGC CAGTTGTACC AGATGTATAT 1020

GACAGAATCG CCATATCATC ACGCGTCGTA TCTGCCATTT CTAGTTTGTT ACTTGCGTTT 1080

TCTTTTTCAG CTTCAAGTGA AATCCATCCA TCTTTTTGAC CGGCAATAAC AAATTTAGTT 1140

AACGCATCAT ATTCTTTAAT TTTTTCAAAT TCAACTGTGA ATGGCTCTAG TGCAATAACT 1200

GCATTAATTT CACCATGTGT GATACGGTAT TGTAAATCTT TAGTTCTTAG CATTTCAGAA 1260

CATGGAATGA TTGCAACACC TAATTTTAAA GCAGCAATAT ATAATTCATA CGTCGCAATA 1320

GATCGTGGCA TCATAATGAG TACTTTATCG CCTTTAGATA AACCGTGCGA TGCTAAAACA 1380

TTACCTACTT TATTAGACTG TTCAATGAGC TGTTGGTAAG TGACTGATAT ATCTTCGCCT 1440

TCAGTATTAT GATATAAAAT TGCCTTTTTA TCTGGTATGT GGCTATATTT TTCGATTTCC 1500

GAAATAATGT TATATTTTTC AGGCGCGAAT AGAGCTGACT TTTGCATAAC TAACTTCCTT 1560

TCATACATCC ACTTTTCCTG TGATGAACAT TGTAATTTTA TAAATGAATT ATATACATCA 1620

TACGCCTATC TTTACAGAAT TTTCAATTAA ATAGGGTTAA ATACCAAAGT CCTCGACACT 1680

ACACTTTGAC ATGACGTAGC ATTCAAGGAC TTTCAAATGA TTGAGGGTTG ATATCTCGGG 1740

CTAGACCATA TCAGCTAATT CAATACGAAT ATTGTATGAT AATTCACGAT TAATTATTTT 1800

TACATCTGCA CCTTTCGAAG TGCCACGATG CTTGTGTGTA TGCTTGTACT CAGCTGAATT 1860

TTGCCAATGA TAAAATGCTT GCCTATTTTC CCACAGCGTA ATAATGATAT AGTGTCTACC 1920

AGCTGTTCTA GGTCTTAAAA ACCTTAATGC TTTAAATCCA TCAACGTTTT TTAAATGCTT 1980

ATTTAACACA CATAATGAAT CATTTGATAA ATCATTTATC GCTTCTAGCA CATCGTAATA 2100

TGCAGTGTCA TTATTTTTTT GTATTGTGAG ACAATCATCC AGTTCTTCTA TTACATAACT 2160

TCTATATTCA TCATAAATTT TCATAATAAA TGCCTTCATT TCATTTATAT TTTTGGTCAT 2220

ATTACTkTAT ATCTATTACT AAtkCATTCC CGTATTTATT AATTACAATC ATAGTTTGGC 2280

TyCTTTTTAA AAGATAAGAC TTTGTAAAAA GTATTAATAT TTCATGCAAA TGGGGGACAG 2340

GAGTCGCCCA CTATTTTTGT GTCTTCAATT TCATGATCAT TATTTAACAT TAGTCATGAA 2400

AATAGCCGAC 2410

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 590 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

TTTATTAATT GTAAAAAATT GAGTAAATTA TCTTTACATT CTAAATTAGT CTTAACTACA 60

ACTAGTATCC TAATAATTAT AGGAGCTATT ACATTCTTTT TATTAGAACA GTTTAATACT 120

ATGCAACATA TGGGACTAGT TGAAAAAATC GGAAATTCTT TTTTCCAATC AGTAACAACA 180

CGAACAGCGG GTTTTAACAG TATAGATATA GCAAGCATTA rCAAATCTAC CGCATtAaTG 240

TTAATGCTAC TTATGTTTAT TGGTGGTGCC CCTCTCAGTG CAGCTGGAGG AATTAAAATA 300

ACTACTTTTG CAGTTGCGTT TATTTTTGTA CTAAATTATA kACGTAAAGA AAATAATGTT 360

TCAGTATTCA ATAAAGAAAT ATCTGACAAA CATATAAAAC TATCTATTGT TACCATTAAT 420

ATCTCATTTC TATTTATCAG CATCATTACT TTTATATTAT CGATAATTAA TCCGAACATA 480

TCATTAATCA AGTTATTATT CGAAGTGGTT TCTGCATTCG GAACAGTAGG GTTAAGTATG 540

AACCTTACCA CAGAATATCA TGGTATTACT AAAATAATTA TTATATTCGT 590

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 905 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

TATTCGATTT GAnTCTTTTA AAATTATGTT TAAAAACATG TCTAATGATT CCGCATCATT 120

TTTTGCACCA TCAATAAGCG TTTCAGcAAA CCCCTTAATT GAAGTAATAG GTGTTTTTAA 180

TTCATGTGAA ACATTTGCTA CAAATTCACG TCTTAGATTT TCAAGTTGTT TCAGATTTGT 240

TATATCATGC ATCACaACTA AAATCCCtTG CAAACTTTTT TGAGACCTAG TTAAAATCGG 300

AACGCATGAA ATATCAAAGT ACTTGGCATG GACTTGGTTT ATTGCAACTT CCAATTGTTC 360

ATAAATAGGT TTTTCAACTT TAAAACTTTC TAAAATTAAT TGCTCAATTT CAGTATTAAC 420

ATAGCCGTGA TAGCCTACTT GTTCAATATT ATGCGAGATG TTGAACTGTT CATAATACGC 480

TTTATTTGCA ACAACGATTT TTCCATTTCG ATCTATCATT AAAATAGCAC TTGGAATATT 540

TTCAATCGTT GTTTTTAAAC GGTTGGATTG AATTTTTTGC TCATTATTAA GCTTTTGAAG 600

GCGTCGTGCT AAATCATTGG TAGACACAAA AAGCGCTTTA GTTTCTACAA CATTACTTTC 660

AGGTACACGT ATGTGATAAT AACCATTTGC CAACAATTGT GTTGCATAAG TAACTTCTTG 720

AATGGGACGG ATTAATGTAC GCTTAAAACT ACGGCTTGCA AAATACAGAC AAATGAGTAC 780

AACTAAACAT GTCAAAATAA GATATTTCCA CAACGTCCAA TGCATTTCTG TAATATCGTT 840

ATTGTAACCT TTAATCCATA CATGATAACC GTTAACCTTC TTATtAAAAA TAAAAACGTC 900

CCTTT 905

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1016 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

TTTGGTTAGC CCATAAAAGA AAAAAACAAG TAGTCATTTT TAAACAACAT ATCAAGTCTA 60

CCCAAGAAAT ACGTTTTGAC AAAGCGAAAG TGCTTGAACA CAAAGATGAA ATAGCAAATT 120

TTATTTCTTT CGAACCACAA AGTTTTGAAT TTTATTATTT TACAGAATCG GAATTTTCAG 180

AAGAACAATT AAATGAAGTT TCGCCAATTA GAATTAAATT CAATGTTATA AGACACACAA 240

AAGATTTGaT AAAGCATATG CCGAATATAT TTTTGGcTAG ACTTATTTCA GAAGATAATG 300

ATAAAAAGAC ATATATGTTC TATAAACGCA AAGTATTAAC CGATAACTTT TTAGATAAAT 360

ATATGCAGAA ATTTTCACCG GCAACATACA CAATAATATT TGTAAATGTC TTAATATGGT 420

TATGTATGAT TTTATATTTA AATAATTTTT CGGATGTAAA ATTATTAGAT GTTGGCGGGT 480

ATTTTAGTTT TGAACATATA CTTATGAATA TGCTTTCATT ATTTATTTTT GGTAAAATAG 600

TCGAAGCAAT TATTGGTTCA TGGCGGATGT TAACTGTATA CTTTATTGCA GGGTTGTTTG 660

GAAACTTTGT ATCACTATCA TTTAATACGA CTACAATTTC AGTTGGGGCT AGTGGTGCTA 720

TATTTGGTCT GATTGGATCA ATTTTTGCGA TGATGTATGT TTCAAAAACA TTTAACAAAA 780

AAATGTTAGG ACAGTTATTA ATTGCATTAG TGATATTAGT TGGTGTTTCT CTGTTTATGT 840

CAAATATAAA TATTGTGGCG CATATTGGAG GATTCATTGG TGGTTTATTA ATAACTTTAA 900

TTGGCTATTA CTATAAAGTG AATCGtAATA TTTTTTGGaT TTaCtAATTG GTATGCtTGt 960

tATATTTAwT GCACyTCmAA TTAgAtTTTT ACmATTAAAG AAGATAATAw TTATAA 1016

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 406 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

AACTTTAAAT TTAGACATCT TTAAAACCTC TCTTAAACCA TGCCTATATC TCAAGATGAT 60

ATTTCAAATG AACAATACTA TTGCTTGAGA CCATTAATGA ATGATCATAA ATATTTCTTT 120

CTATAAAATT AGCTTTCCAA TAACTGTGTT GTTGCATAAT ATCATTCACA AGTACACCAT 180

TTTCGGAAGT ATGATTATCT TTATCTATAC TTAAAACAAT TTGTTTAGTT TTAGCATGGC 240

TAAATTGTTG AAGACCCTTA CACGATAAAC GTATAGCGTC TGAATTCTCA TTTAACAATG 300

CGGCTGGgCA AACAAATGAC ACATTGTACT TCATGTTTGA ACtTCGTTAC AATCaTCGTG 360

kCatTTTGat AAATAACAAT CCCTCGTAAT kGATTAAGTA TATTAT 406

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

AGATAATACA CTTGAAGTTG GAATGGTTTG TGACGGTTAT TTAATGCGAA TTGAAAACTT 60

AACACCATCA AATTTCTTCA ACTCAGCAAG TGAAGATACG ATTACTAAAA TTAAATTAAA 120

AGGTACAGCG TTAAAACTAA GAGAAGCCAT CAATTATGAT GAAATGGTTA TTGTAGATAG 240

TATGACGTAG TTCCTAATTA TGCkAAAAGG GATTGATGAA AAACTGAAGG GCTTTTCATC 300

AATCCCTTTT ATTTTAGGGG AATTGAATAG ATAGTTTTAA ACTATACGAA TTATTAATAT 360

TTGAGATTTA ATTGAAATAA GTTTTAAAAA TTGGAGGAGA TAGATTAAGC GAAGTCATTT 420

AAAGGTGAAG TTAAGTGTAT TCACAAAAAn TAGCCACACT CATATGACAT CGGATGAGTG 480

TGGCTTAAGG ATCTATGGGG GGAGGAAnCC ATAGATGTTT ACTTTGATAG GCCAGATTAA 540

ATATCAAAGT ATGCGATTAT TTATAGCTTG ATGCAAAAGT GGTATGCCTA TTAAAAGTTA 600

CTGCACATAG CTTTTAATAT TCCGTTCAAA GGAAAGGGGC ATACAATTGA ACAATCTGTA 660

ATAGTACTTT TAACCAGCTA TGCTAAAAGT CTAGTAGGGA GAACAGTTGT CCAATCACAT 720

AAGAACCTCT AACTTCGTTA GTACGATTAA GAAAAGCTTT TTAGTTAGTA TGTAATACAA 780

TTTATTGACG CGCGTGAATC TCTTTTATAA GAGTGTGTAG GGAATGGCGT TGTATAAATT 840

GTATTAGAAG AACTTCTAAC GCATCTCTGT GGTTAAAAGA GATGAAGGGA ACGACAGTTT 900

aATTAAAACT GCATAAGAAC TTCTAGCTTT TCTCTCTCGT TCAAAGAGAA GCAGcTGTTC 960

GCAGTTTAAT CAAAACCACA TAAAGCTTTT AACTTTACTC TTTGATTTAA AGAGTGATAA 1020

ATGTTTACAG TTTAATTAAA ACTGCATAAG AACTTCTAGC TTTTCTCTTT CGTTCAAgAG 1080

AAGCAGCTGT TCGCAgTTTA ATCAAAACCA CATAAAGCTT TTAACTTTAC TCTTTGATTT 1140

AAAGAGTGAC AAATGTTTAC AGTTTAATTA AAACTGCATA AGAACTTCTA GCTTTTCTCT 1200

TTCGTTCAAA GAGAAGTTCT AATACCACCA TATCGTGCGA TCGGGAACGG TATATATATT 1260

AATAGGAGGG TAATATATAT TTAACGCACG ATATGGGACT ATTAGCCTTC GACTTTGTTA 1320

TGTTGATGTG TGGCCTAAAA TATTGGAGAT ACCAATATTT TAGGTTGCAT CAACATCA 1378

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

TCCCAACCAA TAATCGTGGC AAAAATACGG ATATTGGTAT GGCTTAACAA ATTGCAAATA 60

TCGTTTAATC ATACATCCCC CCTAATCTAT TGCCCTATCC TATTCaTAAG CATAAAAATG 120

AATAGAGGTT GGATACATAA TTTGTAGATG TAAATTCTTC TTACAATTTA CATTTTTAAA 180

TTATATTCTA TTCAATTTAA TCTATGGATA CTGTGTCCCC ACACGACAGC AAAAGTTATC 300

ATACTTCTTT ACATCACTAA GTCAATATAA ATGATTTAAT CAGTATTTAC ACTTTATTTG 360

CTTAATACTG TCTAATTTTT TTGTAACGTT CTTTCCAAAC TTTGATAAAA TCTGGCGCGA 420

ATGGGCCCTT CTTCTGTTCT ATCCATTGTT GAAGAATGTC CACGTTGCGT CTTAAAATAA 480

TATCAATATC ATGCGGATAA TTCATTTGAT TCATATGTTG CTCATATTCA TCTTCATCTA 540

ATAAATGATA CTTTCCGTTT GGATATACTT TAATATCTAA ATCATAGTCT ATATATTTTA 600

ATGCCTCTTC ATCACAAACA AATGGTGATG ACAAATTGCA ATAGTAATAA ATTCCATCTT 660

CTCTAAACAT GCAGATAACA TTaAACCAAT ATTCTGAGTG AAAGTaAACA ATTGCCGGTT 720

CACGTGTTAT CCAAGTTCTT CCGTCACTTT CAGTCACTAA CGTATGATCA TTTCCACCAA 780

TGACAACATG ATCAGTACCC TTTAATATTG TTGTTTCAGA CCAAACGCGA TGAATCTTAC 840

CATCATGTTT ATAACTCTGA ATTTTAATGT TTTCCCCTTC TTTAGGTATG GATTCTCTGA 900

CCATACTCCA CACCACCTTC TGTTAATTTA ACCATTATAA ATTATAGCAT ATTTCAGAAA 960

TAGTATTATA TAAATACATA TTTTTACGAA ATAAGATTTT ACTACTTAAT AATTAAACTC 1020

GGTAATATTG CTAAGTACTA CAACAGAGAT TTACATGTCC CATTTAAAGT ATATAAAATC 1080

ATCACTTTTA TATATCAACA CTTTAACTTT TTGACATTGT TATTCTATGA GATTTAAAGA 1140

TATCATTTAT ACTTTTTAAA ATTAATGTCA CTATGTTTTC CGATAATATT ACCAATCATC 1200

GAATGTTACC CATTTATAAA TTGATAAATs TTTGACATAG GTACAGGGAA TGTATATTGA 1260

TCTCGATCAC TTAAATCAAA CCAAATCATG TCATCTGGTA ATGTTTCAAT GTTAATTGCT 1320

CCTGAAACGG CGTATACTTT AATCTTCCAT GTTAAATGAG TAAATTGATG CTTCAACTCA 1380

AAAATAGGTG TTTCTACTGG TTGAATGTCA TGACCGATTT TTTCAGTCAT TTTACGTCTA 1440

GCATGCTCAC TTTCAAACAT AGGAAATTGC CACATACCAT GCAATAATTT TTCGCTACGC 1500

TTTTGCAACA GATATTGACC TTGATTATTT CTAATTAAAA AGACGGATTG CTCAATTACT 1560

TTTTTACTTA CATTTTTAGA TTTAACAGGT AACTTTTCAA ATGTACCTTT ATCAAATGCC 1620

TCACAGTTTT CTTGAACTGG ACAAAATAAG CATAATGGAT TTTTTGGTGT ACAAATTAAC 1680

GCCCCTAATT CCATCATAGC TTGATTAAAC GTTCCAGCTT CTGTAGTAAC ATACGGTAAT 1740

AATTCTTGTT CGTACGATTT CCTCGTCGAT TGTAATTTAA TATCTCGATA GTCATCATTC 1800

AATCTAGACC ATACTCGAAA AACATTTCCG TCTACAGTTG CTAGTGGTAC ATTATATGCA 1860

ATGCTCATTA CTGCAGCTTG TGTGTATGGG CCAACACCTT TTAACGCTTT AAATTGATCA 1920

GGATCTTTGG GAACTAAGCC TTCATATTTA TCATGAACTT CTTTAATCGC CGTATGAAAA 1980

GCTTGaCTCA AAACTTCCAC AGTTGGAAAT CGTTCAACAA AACGATGATA ATAGTCAATA 2100

ACTGTTTTAA CTTGTGTCTG TTGTAACATG ACCTCACTTA ACCAAATATA GTACGGATTG 2160

GTCGTTTGTC GCCATGGCAT TTCTCTTTGA TTTTCATCAA ACCAGTGTAT CAAATTTTCT 2220

TTAAAACTAG ACTGCTGATA CATTTATAAA ACCCTTTCCT CACCAAAATT AATTGTCTTT 2280

ACTCATAATG TTTTTATTGT ACATTAAAAT CATGGTTAGT ATGTAAGTTA ATTTAGTTAT 2340

TTGCGAAATT GGATTATAAT AGTATATATA ATATTATGAA ATGAGTGAAC TGATATGGAC 2400

ACTGCAACAC ATATCGCAAT TGGGGTGGGC CTTACAGCAC TTGCAACTCA AGATCCAGCA 2460

ATGGCTTCTA CGTTTGGTGC AACAGCTACA ACCCTTATCG TTGGTTCATT AATTCCTGAT 2520

GGGGATACTG TTCTTAAATT AAAGGACAAT GCAACATATA TTTCGCATCA TAGAGGTATC 2580

ACGCATTCCA TCCCTTTCAC AATACTATGG CCAATTTTAA TTACATTTTT AATATTCACG 2640

TTCTTTAGTG GAACCAACCC ATTTCATGTA TGGATGTGGG CTCAGCTCGC AGTATTTTTA 2700

CATGTCTTTG TAGATATATT CAATTCTTAT GGTACACAAG CGCTTAGACC TATCACAAAC 2760

AAATGGATTC AATTAAGTGT GATTAACACA TTTGACCCTA TTATTTTCAC AGTTCTTTGT 2820

ATTGGTATTG TATTATGGGT TATAGGCTTG CATCCATTTG CAGTCTTCTT TCCTATAATC 2880

GCTTTACTAA TCATTTATTA CATGATTCGT TTTAAAATGA GAGCCGTAAT TAAGCAACAA 2940

GCTTTAAAAG CAATTCAACA AGAGCATCAC CCTGTTAAAG TATTTGTTGC GCCAACAATA 3000

AAATTTATGG AATGGCGTGT CGCGATACAA ACTGATGCAC ATGACTATGT TGGAAAAGCA 3060

TATGGTAGGA ATGTGGTGTT TAGTGATAAA GTGGAACGTC AAACATTATC AACAGACTCC 3120

ATTTTATGGA AAGTCAAAGG TAATAAAGAT ATACGTACTT TTTTAAACTT TTCATCAATC 3180

TATCGTTGGC AAACAACAAC GTTAGCAGAT GGTTCTACTG AAATTCGTTT GATTGATTTG 3240

CGTTATTTAA AAAATGATCA TTATTCATTT GTGGCAATTG CACATGTAAC AAACGATAAT 3300

GTCATAGACC ACTCTTATAT TGGCTGGGTA TTTACAGAAG ATAAGTTACA ACGTAAACTG 3360

TATGCTAAAT AATTTCAAGT TATTATTCAC TAAAGTTAAT CTATAAAAAA TGAACAACCG 3420

GGCAGAATGA AAATCAAAAC GATTTTTACT CTGTCCGGTT TTTTAATGTA AAACTATGAA 3480

TGCTTTTACA AAATCTAAAA TTTATATTGT TGCTAACAAA CTACCTTTAA TGACTCGAAA 3540

TATCAAAATC AGTATAGGAA AACAATATCT AGATGATATT CTAATTGTTT CTGATTCTCA 3600

CAGATTAATT TACACAACAG GTCAGCTAAA CATCATGAAG AAGTATCCGC CTCGTCTGTA 3660

CTATCATTTG AAACATCCTG TTGATTATCa GTTTGTGTCA CTTTAGATGT TTTATTaTAA 3720

ATTGCGTGTG TCGTATACCT TGCTAATACG AAATTTACTG CAGCTATTAA ACATAAGAAT 3780

TGTGCTATAC CATTAACAAT GTAATACATT GGATTTAGCA TTAGGATGTG ATTGATAAAT 3900

ACATGATTTG GATTTGGTAT GAAAATAATT GGTAACAATA AGAAACACAA TACACAAACC 3960

CCATAAAATA TGATATTTAT TTTTTCAGwT AACAGTCGAA TAAGACCAAA AGTAACGGAT 4020

ATTAATCCTA CAAAAATAGT TGCCATCACA ATAAAATAGA ATAGCGCTAT ATATGATGTT 4080

TCGAAGTTTA CTGGTTTAAC CAATGCACTA ATCATCGTCA AAATGACTAG CATAATAAAA 4140

CTTAAAATAG ACATAATAAC TACTGGCGTC G 4171

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9821 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

TGGTTGAAGT AGCAGTTAAT TCAAAATCTG CAACAGTTTC AGCAGAATaG GGGCTTTCAA 60

AATAAtCAAA GGAGAATAAT TTATGACTAA AACTTTAAAG GTTTATAAAG GAGACGACGT 120

CGTAGCTTCT GAACAAGGTG AAGGCAAAGT GTCAGTAACT TTATCTAATT TAGAAGCGGA 180

TACAACTTAT CCAAAAGGTA CTTACCAAGT GGCATGGGAA GAAAATGGTA AAGAATCTAG 240

TAAAGTTGAT GTACCTCAAT TCAAAACCAA TCCAATTCTA GTCTCAGGCG TATCATTTAC 300

ACCAGAAACT AAATCAATTA TGGTAAATAC CGATGACAAT GTTGAGCCAA ACATTGCACC 360

AAGCACAGCA ACGAATAAAA TATTGAAATA TACAAGTGAA CATCCAGAAT TTGTTACTGT 420

AGATGAAAAT ACAGGAGCAA TTCACGGTGT AGCTGAAGGT ACTTCAGTAA TCACTGCTAC 480

GTCTACTGAT GGAAGCGATA AGTCAGGACA AATTTCAGTG ACAGTAACAA ACGGATAGGG 540

ATTTAAGGCG CAGTATATCT GCGTCTTTTT TATTTGAATA AAAGGAGCTA ATACAATGAT 600

TAAATTTGAA ATTAAAGATC GTAAAACAGG AAAAACAGAG AGCTATACAA AAGAAGATGT 660

AACAATGGGC GAACAGAAAA ATGCTATGAG TATTTAGAAT TAGTAAATCA AGAGAATAAA 720

AAAGAAGCAC CTAACGCAAC AAAAATGAGA CAAAAAGAGC GACAGTTATT AGTAGATTTA 780

TTTAAAGATG AAGGATTGAC TGAAGAAGAT GTTCTGAACA AGATGAGTAC TAAAACTTAT 840

ACAAAAGCCT TACAAGATAT ATTTCGAGAA ATCAATGGTG AAGATGAAGA AGATTCAGAA 900

ACTGAACCAG AAGAGATGGG AAAGACAGAA GAACAATCTC AATAAAAGAC ATTTTATCGA 960

ACATTAAGAA AATACAACGT TTCTGTATGG AGCAGTATGG GTGGACATTA ACTGAAGTCA 1020

AAGAAAAACA AAGTGAACAA AAAGTCATTA CAGGTACGGA TTTAAGAAAA CTTTTTGGAA 1140

GCTAGAAAGG AGGTTAATAT GAATGAAAAA GTAGAAGGCA TGACCTTGGA GCTGAAATTA 1200

GACCATTTAG GTGTCCAAGA AGGCATGAAA GGTTTAAAGC GACAATTAGG TGTTGTTAAT 1260

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CAGGCGAGAA TTAAGGGGTT AAATGATAGG CTTAAAGTTC AAAAAAAGAT GTATTCTCAA 1380

GTAGAAGATG AGCTTAAACA AGTTAACGCT AATTACCAAA AAGCTAAATC CAGTGTAAAA 1440

GATGTTGAGA AAGCATATTT AAAGTTAGTA GAAGCCAATA AAAAAGAAAA ATTAGCTCTT 1500

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TATAAACGTA CAAATCAACG TAAACAAGAT GCGTATCAAA AACTTAAACA GTTGAGAGAT 1620

GCAGAACAAA AGCTTaAGAA TAGTAACCAA GCTACTACTG CACAACTAAA AAGAGCAAGT 1680

GACGCrtACA GAAGCAGTCC GCTAAGCATA AAGCACTTGT TGAACAATAT AAACAAGAAG 1740

GCAATCAAGT TCAAAAACTA AAAGTGCAAA ATGACAATCT TTCAAAATCA AATGATAAAA 1800

TTGAAAGTTC TTACGCTAAA ACTAATACTA AATTAAAGCA AACAGAAAAA GAATTTAATG 1860

ATTTAAACAA TACTATTAAG AATCATAGCG CTAATGTCGC AAAAGCTGAA ACAGCTGTTA 1920

ATAAAGAAAA AGCTGCTTTA AATAATTTGG AGCGTTCAAT AGATAAAGCT TCATCCGAAA 1980

TGAAGACTTT TAACAAAGAA CAAATGATAG CTCAAAGTCA TTTCGGTAAA CTTGCAAGTC 2040

AAGCGGATGT CATGTCAAAG AAATTTAGTT CTATTGGAGA CAAAATGACT TCCCTGGGAC 2100

GTACAATGAC GATGGGCGTA TCTACACCGA TTACTTTAGG TTTAGGTGCA GCATTAAAAA 2160

CGAGTGCAGA CTTTGAAGGG CAAATGTCTC GAGTTGGAGC GATTGCACAA GCAAGCAGTA 2220

AAGACTTAAA AAGCATGTCT AATCAAGCGG TTGACTTAGG AGCTAAAACA AGTAAAAGTG 2280

CTAACGaAGT TGCTAAAGGT ATGGAAGAAT TGGCAGCTTT AGGCTTTAAT GCCAAACAAA 2340

CAATGGAGGC TATGCCAGGT GTTATCAGCG CAgcAGaAGC AAGTGGTGCA GAAATGGCTA 2400

CAACTGCAAC TGTAATGGCT TCAGCGATTA ACTCTTTCGG TTTAAAAGCA TCTGATGCAA 2460

ATCATGTTGC TGATTTACTT GCGAGATCAG CAAATGATAG TGCTGCAGAT ATTCAATATA 2520

TGGGAGATGC ATTAAAATAT GCAGGTACTC CAGCAAAAGC ATTAGGAGTT TCAATAGAGG 2580

ACACTTCTGC AGCAATTGAA GTTTTATCTA ACTCAGGTTT AGAGGGGTCT CAAGCAGGTA 2640

CTGCATTAAG AGCTTCGTTT ATTAGGCTAG CTAATCCAAG TAAAAGTACA GCTAAGGAAA 2700

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TACGTGCAGT TGGGAGCGCG GCTAAAGGCT ATGCATCATT AAATAGACGC ATTGCTGAAA 3240

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TGAAAGTAGG AGTCAACAAG TTTAAAGGAT TTATGCAAAC CATGGGCACA GCTTCTAAAA 3840

AAGCATCTGA TACTGTAAAA GTGTTGGGGA AAGGTGTTTC AAAAGAAACA GAAAAAGCTT 3900

TAGAAAAATA CGTACACTAT TCTGAAGAGA ACAACAGAAT CATGGAAAAA GTACGTTTAA 3960

ACTCGGGTCA AATAACAGAA GACAAAGCAA AAAAACTTTT GAAAATTGAA GCGGATTTAT 4020

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AGCAAGAGCG TATTTTAGTA AGAATGCAAA GAAACAGAAA TGCTTATTCA ATAGACGAAG 4380

CGAGCAAAGC AATTAAAGAA GCAGAAAAAG CAAGAAAAGC AAGAAAAAAA GAAGTGGATA 4440

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CTAAAAAAGA TGCTGTAGTA GACGTTGTTA AAAAGCAAAA TAAAGATATT GATAAAGAAA 4620

GTTGGTGGTC TAACTTTAGA GAAGACCAAA AGAAGAAAAG TGATAAATAC GCTAAAGAAC 4740

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ATGATTGGAT TAGAGATATT GGTAAAGACA TGGGAAGAGC TGCGGCTGAT TTAGGTAAAA 5460

ATGTTGCTAA TAAAGCTATT GGCGGTTTGA ATAGCATGAT TGGCGGTATT AATAAAATAT 5520

CTAAAGCCAT TACTGATAAA AATCTCATCA AGCCAATACC TACATTGTCT ACTGGTACTT 5580

TAGCAGGAAA GGGTGTAGCT ACCGATAATT CAGGAGCATT AACGCAACCG ACATTTGCTG 5640

TATTAAATGA TAGAGGTTCT GGAAACGCCC CAGGTGGTGG AGTTCAAGAA ATAATTCACA 5700

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GAGATAGTGT AATAAATGCC AATGACACTC TGAAGTTACA GCGGATGGGT GTTTTGCCAA 5820

AATTCCATGG TGGTACGAAA AAGAAAAAAT GGATGGAACA AGTTACTGAA AATCTTGGTA 5880

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CAGAAGAAAT GGTTGAAGCG GCAGGCGATA AAATCAAAGA TGGTGCATCT TGGTTAGGCG 6000

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ACGTCGTGCA GCAAAACGAA TGGGTGTTAA TGTTACTTCG GCTGACGTAG GAAATATCAT 6720

TAGCTTGATT CAACACGAAT CAGGAGGAAA TGCAGGTATA ACTCAATCTA GTTCGCTTAG 6780

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GTTACATCTA ATTTAAAAGA TGGTTCTTCA ACTGAAATTG AAGTAAGTTT AAATGTTTAT 7740

AAAGGGTATT CTGAATCAGT TAATTGGACC GATAGCGAGT TCTTATTCGA CTCTAATTGG 7800

ATGTTTGAAA ATGGAATTCC TCTTGATTTC ACACCTAAAT ATACTCATAC ATCAAATCAA 7860

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TTTCCTTTTA TTTATAGGTA GGTGATTTAA TGGATTATCA TGATCATTTA TCAGTAATGG 8220

ATTATGAACT GAATGAAGCT AGGTACATCA CCTTTACAGT TTATAGAACT ACTCATAATA 8340

GTTTTGTTTT TGATTTATTG ATTTGTGAAA ACTTCATAAT TTATCATGGT GAAAAATACA 8400

CAATTAAGCA GACAGCGCCA AAGGTTGAAG GTGATAAAGT TTTTATTGAA GTTACGGCAT 8460

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TCTATCAAAG AAGCGAAAAA GTAATAAGGT ATCAATATAA TACTGATACT GTGTCTGCTA 8820

CTGTCAGTAC GTTGGAATTA AGAACAGCTA TAAAAGTTTT TGGGAAAAAG TACACAGCCG 8880

AGGAAAAGAA AAATTATAAT CCTATTAGAA CAACTGACAT TAAATATTCA AATGGTTTTA 8940

TAAAAGAAGG TACTTATCGT ACCGCAACAA TTGGGTCTAA AGCTACTATT AACTTTGATT 9000

GCAAGTATGG TAATGAAACA GTTAGATTTA CAATAAAaAA GGGCTCTCaA GGTGGAATAT 9060

ATAAGTTGAT TTTAGACGGC AAGCaAATTA AGCaAATTTC TTGTTTTGCT AAGTCGGTTC 9120

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TATTTTTrGG AGArGrCCCC AAAAATAGAA TTGATATATC TTCAAATAAA AAAGCTAAGC 9240

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ATGAAAAAAT AGAGCCAAGA GATAGCGTAT TCTTTGTTCA TGAATTAATG GGATATAACA 9540

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GTACTTTGAA TTCTCCTTTC GAGACAATGG ATATAGGGAG TGTATTAATA TAATGGCAAC 9780

AGAAGAAGTT AAAATCAAAG CGCTACTTGA AAACGATAAA C 9821

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1017 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

TTATTGTTTT CCAAATGGTC TTCTCGGTTA TTTAACCATC GGTTTCAATC CTACGTGCTT 60

CACTTTCTAT CtATTAATTC AaTTTCAGCT TGACCACCCG CTGTATAAAG GGTCAAAGTT 120

GCTAATCGAT AGCGTCTCAT TATAGGACCA ACATCGATAT CAATATTTTG AATACGAAAA 180

TATGGTATTA CCTTTTCATC CAAAAATAAA ATGCCGTTTC GTACACGCAA ATGGTGTTTT 240

TCAAATGCAT ATCTGCAGTG CTTATATCGA TAGACTGGCG CTATAACAAG CGTGAAAACA 300

GCAACAAGTA ATATTATAAT CACACTACTA ACAATGGATA AATGGTTATC TAAAATCTCC 360

CAAAATAGCC AGTTCAAAAT ATTAAATGCG ATTAAAAGTA CAAGCGCTAT GGGTATCCAA 420

AACAGCACAG CACTTAACCT CATCACTTTT TTAGCGTGTG GTGACATAAA ATTATAATCC 480

CTCATCATTT TCACCTCTTA AATACCATGA TTTCAATTTA TTTGCATCTT CACTTCTTGC 540

GTATTTTAAG TTAATCGATT GGGCTCCCAC ACCTTTAGCA ACAATAAAGC TAAAATTATT 600

TAAATTGTTG CGTTTAAGTA ATGTATGTTG CCAAGTGTCA AATCCTATAA TGTGATGCGC 660

TTTAAAATAA TAAATATTTC GTTTCAATAG CTCGAAATTC TGGATAGTAA TTTGTTCTTC 720

TGTCATTTTA AAACCCGCAT GTTTGACATA AAGATATCCT TTGATCACAA ATAAACCAAT 780

AATGACTATT GTTATAATCG TAAATAACAA TAATAATTGA TTCCAAAAAT AACAGCCTAT 840

ACCTGCCATA GCTATGACAA TAATACTAGG TATTAAAAAG TGTCTGTGGA AACCTGACAA 900

AGGCATACCT TCATTAACTT GTTGATAAGA TAAATCTGGT ACTAAATTCT GGATAATTTG 960

ATATGCTTTG TCTCGTTTAA TAAACGGCaA TATCGGCACA CTACCTGAAT CATTGTC 1017

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6806 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

TAGGATTGAT TAATCCTTTC TTCAAAATGA TGAATGTGTA ATGTTAAATA TATAATTTCA 60

GACTCACTGA TATTAACATC AAATTGTTTT TGTATCATAG TTAAAATTTT ATATGCTGTG 120

TTATAGCAAA TCGGATAGTG ATTTTTAATC ATAGACACAA AATCATCTTG TGCATGTATA 180

TATTCTTTTC TTCTTAATCG GCGAATTAAA AATTGTACGT GCCTTATAAA ACGTTGGTAT 240

TTAATAACAT TATTnGATCA AGGTCATCTC ATGCATAGAT AAATCTTCTG TATTaGATGC 360

AATATGTAAT GCAATAAATC CTATCTCATC TTCAGGaAAA TGTaCATCTA ATGCTGCATT 420

TAACTGATCA ATCACCTGTT TAGCAATATG ATATGCATCA CTATATAACT GCATAGTTTC 480

CATAACAAAT GGATTGCTAA TAACTTGATT TTGTTTTAAG CGTTTATAAG CAAATATAAT 540

ATGATCCGTT AATGAAACTA CAAGTTGTTT TGAATCAACA TTCATCGCAG TATTAGAAAT 600

AAAATTCAAC GAATCAATAA TTACTTGTAA TACATTATCA TCAGCGATTT CAACTAAACT 660

TTTATAATGT GCTTTTTGTT GCTCACTTTC TAATTTATAA ATTTTCTCTA TTGTAATAGT 720

TTGGTCGTTT AACGCCATTC CCTCTTTTTT GTTAAAACCA ATACCTTTAC CGATTAAAAT 780

AACTTCTTGA TCATTATTAG TACATACTAC GACATTGTTG TTCAATGTTT TAGTAACAAT 840

ATATTCTCCC ATTATCATCA CCTATTTTTC TATTATTAAG ATTATATATC GGAAATGTCT 900

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CTAAAACGTA CTATTAAATT GTGCAAAGCT AAAACAAATT TATATTCATC TATCCAACAA 1140

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TACAAATTTA AAACCCTGAG ATTTTCGCTT TAATTTGAAA ACCTCAGGGT TTATTTGATT 1320

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CGCCCCAAGC ACTAATTCCA AATAAGTTAA TTTCTAAGTT TTCAGGTTTA AAGACAGGGT 1440

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GTCCTATAAT GGAAATAATG TTTACAATTG CCATTAAGCC CATAAATAAG TCTGCCGTAT 1560

TCCATACTGT TTCTGTTTTT ACAACTGCAC CGACAAAGAC AAGTACTACA ACAAGACATC 1620

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CGTTATCACC AAATTTCAGT CCTGAATATA GTAAAATCAT GATTGCAGTT GCTGTACAAA 1860

CCAACATTGT ATCAAAGAAC ACACCTAATG ATTGGATTAA ACCTTGCTTA ACAGGGTGTG 1920

GTACGGCAGC AGTTGCCGCT GCATTCGGCG CAGAACCCAT ACCAGCTTCG TTAGAGAATA 1980

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TAATACCTGT GATTACTGGA CTAATATTAT ATTGCGTATT TAACGACTCC GCAATTGTAT 2280

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TACCTAGCCA TTTTTGATTT AAACCTTTAG TAATATAGTA AGCTGGACCA CCACGGAATC 2400

CACCATCTTT ATCATGTACT TTATAAACCT GAGCCAAAGT CGCTTCTATA AATGCACTCG 2460

CTGCACCTAT AAATGCAATA ACCCACATCC AAAATACTGC ACCTGGACCG CCTAAAACAA 2520

TCGCAGTCGC AACACCAGCA ATATTACCAG TACCAACTCT CGAACCAGCA CTAATCGCAA 2580

ATGCTTGGAA TGGCGAAATA CCCTTCTTAC CATCTTCTAA AGTTTCTGGA CGTTCTACTA 2640

AAGCTCTAAA CATTTCAGGT AACATTCGTA ATTGAACGAA TTTAGAACTA ATCGTAAAGA 2700

AGAATCCAGC TGTCAATAAT AGACCAATTA AATATTGAGA CCATATTAAA TCGGTACCAA 2760

CATGGACAAA TTCTTTAAAC CATCCAGGTA TTAAACTATC GAAATCTTTC AAAATAAACC 2820

CCTCGCATCC TCTACATGAA TCATGTACCT TCTATAAAAT TAGACCGAAT TGAACCTTCA 2880

GTAAATATAG AGATACATCA TCATTTCTTA TACAATACAA GAGATTTATA TTAGTTTGGT 2940

CAAAGTATAT CGCTAATTTA ACGATAAGTA CTTGGTCAGC ATTTAATATA AATCCCTTGA 3000

ATTTAGTCAA AATTTAACAT TACTGTATTT TATCATTTAA TTTCGTGATT GCATATAGTT 3060

TTTAGCTAAT ATACATGTCT ATTACTTCAC CAAAATCATC TGTATCTACA ATGAATGAGC 3120

CATTTGTATA TTGTTCAGAT TTATGAATAT CATTAATTAA ACCATGTTCT TCATTTGATT 3180

TTGAATATAA TGTATATTGA CTATGTTCAC CTGTCACTAC ATGTGCAGCT ACAATACGAT 3240

GTGGATTTTT CTTTAATTCT TTTAATAAAG TTATTCCaCG TTGTGCTCTT TTAGCAACTT 3300

GTAAGATTTT AAAACTAATA CGTTTTAACG AGCCGCGTTG TGTGGCCATC AATATAGTAT 3360

CATTTTCAGA AACACCTTCT GTCATAACAA CGAAATCTTC AGCTTTAAGA TTTATTGATT 3420

TAACACCAGC TGCCCTTAAT CCGGTATCTG ATAGTTCACT TGTATTATAC GTTAATGACA 3480

TACCTTTATT AGTAATGACG GTAATTAATT GATCTTTTTC AAAGCGCATA ACACTAATCA 3540

AATCATCATT TTCTTTAACT TTAGTAGCAA TTAAAGGTTT ATTAAAACGC GTTGTTTTAA 3600

ATAGAGGCAC TGTACTTTTC TTAATCATGC CATTTTGAGT CGCAAAAACA TAAAATGCAT 3660

CTGTATTAAA GTCCTTTTCA TTAAAGACAT TAATAACCAC TTCATCTTCT TCGATAGGAA 3720

CTATTTGTGA TACATGTTGT CCCAATTCTT TCCAACGAAT ATCTGCTAAT TTATGAACCG 3780

GTATAAATAG ATAACGACCT TTATTTGTAA ATACTAGTAC GGTATCTTGC GTATTTACTT 3840

TAAAGCTACG AATAGAAGTA CGTTTAATAT ATCCATGACG TGTCATACTT AAAATAACTy 3960

CTTCACTAGG CACCATAACT TCTTTGTCAA TTTTAATTTC TTCAATTTCT GCTTCAATTA 4020

AAGACAGTCG TTCAGATTTG AATTTCTTTT TAATTTCATT CAATTCTTCT TTTATGACAT 4080

TCAATAATGC ATCATGGTTA TCAAGAATAT GACGTAATTG TTTGATTAAT GCTTCAAGTT 4140

CTTTATGTTC ACCTTCAAGC GCAACTATGT CAGTATTTGT TAAACGATAT AACTGTAACA 4200

TTACAATTGC TTCAGCCTGT TCTTCTGTGA ACTCGTATAC TTCGATAAGG TTTTCTTTAG 4260

CGTCACGCTT GTTTTTAGAG CwACGAATCA ATTCGATTAC TTTATCTAAA ATTGACAACG 4320

CTTTAATCAA ACCTTCAACG ATATGCATAC GTTTTTCTGC ATTATCTAAT TCAAACTTCG 4380

TTCTATTTGC AACAACCTCA ATTTGGTGAT TCAAATAACT ATCTATAATT TGACGAATAC 4440

CCATCAATTT TGGACGACCA TCACTAATAG CGACCATGTT GAAATTATAT GAAATCTGTA 4500

AATCAGAGTT TTTATAAAGA TAATTTTTGA TTGATTCACT GTTCACATCT TTTTTCAATT 4560

CAATTGCTAT TCGTAAACCA GTTCTATCAG TTTCATCACG TACTTCAACG ATACCATCGA 4620

CTTTTTTGTC AGCACGTAAT TCATCGATAC GTTTTACTAA GCTACTTTTG TTCACTTCAT 4680

ATGGAATTTC AGTAATAATT AACTGTTTAC GTCCATTGCG TAAAGTTTCT TCTTCAACTT 4740

TAGAACGAAC TATAATTCTA CCTTTACCTG ATTCATAAGC TTTTTTAATA CCATCAATAC 4800

CTTGAATAAT ACCACCAGTT GGAAAATCAG GACCTTTAAT ATATTTCATT AATTGATTGA 4860

CTGTAATATC CGGATTATCA ATATATTTAA GTGTTGCTTG AATCACTTCA GCTAAATTAT 4920

GTGGTGGTAT ATCTGTCGCG TAACCTGCAG ATATACCTGT AGAACCATTC ACTAGTAAGT 4980

TAGGAAATCT TGATGGCAAT ACCATTGGTT CGAGTGTCGT ATCATCATAG TTTGGAATGA 5040

AAGAAACTGT CTCTTTATTA ATATCACGTA ATAACTCTTC AGCTAGTAAG CTTAACTTAG 5100

CTTCAGTGTA ACGCATTGCC GCTGGCGGAT CATTATCGAT ACTACCATTA TTACCATGCA 5160

TTTCTATTAA GACATGTCGT AACTTCCAGT CTTGACTTAA ACGGACCATT GCTTCGTACA 5220

CTGAGGAGTC TCCATGTGGA TGATATTGAC CAATAACATC ACCGACTGTT TTCGCACTTT 5280

TACGGAAATT TTTATCGTGT GTATTACCAC TTGAATACAT TGCATATAAA ATACGACGTT 5340

GTACTGGTTT TAAACCATCA CGAACATCTG GCAATGCACG CTCTTGAATA ATATATTTAC 5400

TATATCTTCC AAAGCGATCA CCTAAAACAT CTTCAAGTGA TAAATCTTGA ATTATTTCAC 5460

TCACTAGATT TCCTCCTCAT CAAATTGATC ATTTTCAAGC ACTTGTACTT CAGAATTATC 5520

TAAAATACTT TGGTCCTCTT GCATACCAAA CTCAACATGC TTTTCAATCC ATTCACGTCT 5580

AGGTTGTACT TTGTCACCCA TTAATGTTGT TACACGTTTA GATGAACGCA CTTCATCTTC 5640

AGGGTTCATT TCACCCAAAC CTTTGTAACG TTGTAACGTG AaGCCTTTAC CAAGTTCTTT 5760

TTGCAATTTA TTAAGCTCTT CGTCTGTCCA AGCGTATTCA ACTCGCTTTG TTTTGCCTTT 5820

ACCTTTTTCC AATTTATAAA GTGGAGGTAA AGCAATAAAT ACACGACCTG CTTGAACAAG 5880

CGGTTTCATA TATTTGAAGA AGAATGTTAA CAATAGCACT TGAATATGCG CACCATCAGT 5940

ATCAGCATCA GTCATAATAA TTACACGATT ATAATTACTA TCTTCAATTT TAAAGTCAGT 6000

ACCAACGCCT GCCCCGATTG TGTGGATAAT TGTATTAATT TCTTCATTTT TAAAAATATC 6060

TTCTAGACGT GCTTTCTCTG TATTAATTAC CTTACCACGT AATGGTAATA TCGCTTGGAA 6120

TTTGCGGTCT CGTcCAAGTT TTGCTGAACC TCCCGCAGAA TCACCTTCGA CTAAATACAA 6180

TTCATTTTTT TCAGTGTTTT TACTTTGTGC AGGTGTTAAT TTACCAGATA GCAAAGTGTC 6240

TTTACGCTTG TTTTTCTTAC CTGAACGAGC ATCTTCACGA GCTTTACGTG CAGCTTCCCT 6300

TGCTTGTTGT GCTTTAATCG CTTTTTTCAC AAGTGATTTA GACAATTGTC CTTTTTCTTC 6360

TAAATAGAAT GGCAATTTGT CTGCAACAAC TGAATCAACA GCACTTCTAG CTTCAGAAGT 6420

ACCCAATTTA GATTTCGTTT GTCCTTCAAA TTGCAATAAT TCTTCTGGAA TACGAACAGA 6480

CACAACAGCT GTTAAACCTT CACGAATATC ATTACCATCT AAGTTTTTAT CTTTTGTTTT 6540

AAGTTCATTA ATACGACGTG CATAATCATT AAATACACGT GTCATTGCTG TTTTAAAACC 6600

AACTTCATGT GTACCACCAT CTTTAGTACG TACATTATTT ACAAAACTTA AAATACTTTC 6660

TGAATATTGA TCATTATATT GGAAAGCTAC GTCTACCTCT ATACCATTTG CTTCACCTGA 6720

AAATGTAGCC ACGTCATGCA AAACTTCTTT TCCTTCATTG ACATAACTAA CAAACTCTTT 6780

GATTCCTTCT TATAATGGTA TGTCTT 6806

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1716 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

GGGGCAnAAA TTCCAATACA CTCATTACCA AATATATACA CCACTTCCTG CTACAAGTnn 60

TTTTACTTGA TCTTGGTCTT TTCCGCAGAA AGAGCATTTC CAAATTTTCT TCATCTTCCA 120

TTGAATTTAA ACATTCTTTT TACACCCCTA TTCGTTAAAG ACTATACTAG ATTGGATGTT 180

ACAATGCAAC ATATTAACAT ACAAACTTTT TGCTTAAAGA ATAGTAGCAG ATACATAAGC 240

CCtTCAACGA ACTTTGCGTT ATCTCTTAAT AAATCGATAA CTTTTTGGAT ACGAACATCA 360

TTTTTAATGA TATCAGTATT ACCTAAAGTA TTTTTGATAT CTTCAACTGA GATATTAAAT 420

TGTTTACTCA TTTTTTCTAA TTCTTTATCG ATATCTTCAT CAGTAGCTTC GATTTTTTCA 480

GCTTCAGCGA TCGCAGTTAA AGTTAAGTTA GTTTTAACAC GTTGTTCTGC ATCGTCTTTC 540

ATTTGCTCTC TTAATTGAGT TTCATCTTGA CCTGAGATTT GGAAGTACGT TTGTAAATCT 600

AAACCTTGTT GTTGAATTCT TTGTGCAAAT TCAGACACCA TACGATCTAA TTCAGTATTA 660

ACCATTGCTT CAGGAATATC GATTGTTGTA TTATCAGTAG CTTTTGTAAT CGCTTCTTCT 720

TTTTCAACAT TTTCAGCATC TGTAGCTTTT TGTTCAGCTA AACGTTTACG TAAGTTTTCT 780

TTGTACTCGT CTACTGTATT TGCTTCTGCA TCTAATTCAT TAGCAATTTC ATCTGTTAAT 840

TCTGGGACTT CTTTAAATTT AATTTCGTTA ACTTTTGTTT TGAAAGTTGC TTCTTTACCG 900

GCTAATTCTT CAGCATGGTA TTCTTCTGGG AATGTTACGA CAACATCTTT TTCTTCGTCA 960

ACTTTCATAC CTTCTAATTG CTCTTCGAAA CCAGGTATGA ATGAACCTGA ACCGATTTCT 1020

AAATCGTAAC CTTCAGCTTG TCCACCTTCG AATTCTTCtC CGTCAACTGA ACCACTAAAG 1080

TCGATGTTAA CTGTGTCGCC ATTTTCAACA ACACCATCTT CTTTAACGAC CATTTCAGCT 1140

AAATGTCCTA AGCTGTGGTC AATCGCTTCT TGTAACTCAT CATCAGATAA TTCAGTTTCT 1200

TGTTTTTCAA TTTCAAGACC TTTATAGTCT CCTAATTTAA CTTCTGGCTC AACTGTAACT 1260

GTTGCTTCAA AAATGAAATC TTTACCTTTT TCAATTTGAG TAACACTTAC TTCtGGTTGT 1320

GCAACTGGTT TAATATCAGT TTCGTCAATT GCTTCACCAT AAGCATCTGG TAATAAAATG 1380

TCGATAGCAT CTTGATATAA TGCTTCTACA CCAAAGCGTT GTTCAAAAAT TGGACGTGGC 1440

ACTTTACCTT TACGGAATCC AGGTACGTTA ATTTGTTTAA CCACTTTTTT GAATGCTTGA 1500

TCTAACGCTT TGTTTACTTT TTCTGCAGGA ACAGTAACAG TTAATAAACC TTCGTTACCT 1560

TCCTTTTTTT CCCAAGTTGC TGTCATGTAT ATATACCTCC ATGATTAACT AATTTATTTT 1620

TTCAACTTCC CTATTATATC ATACGTCTAT TCCCTATACA AACATTGAAA TCACAACGTT 1680

TATATATTTG TAAATCAACT TTTTTCGTCA AAACTA 1716

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 795 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TGACCAAGTA CGTTTCGAAG TTGCCATTAA AGCATTAAAC CCATCATTGA AAGCATTCGC 60

ACCTGTACGT GAGTGGGCAT GGAGTCGTGA AGAAGAAATC GATTATGCAA TTAAACATAA 120

TATCCCTGTA TCAATCAACC ATGATTCACC TTATTCTATC GATCAAAATC TATGGGGCAG 180

AGCGAATGAA TGTGGTATTT TAGAAGATCC TTATGCTGCG CCACCAGAGG ATGCGTTCGA 240

TCTAACAAAT GCTTTAGAAG AAACACCAGA TACTGCTGAT GrAATCATTT TAACGTTTGA 300

TAAAGGCATC CCAGTTCAAA TTGATGGCAA AACATATGAA TTAGACGATT TAATTTTAAC 360

GTTGAATGCA TTAGCTGGTA AGCATGGTAT CGGAAGAATT GACCATGTAG AAAATAGACT 420

TGTAGGTATC AAATCAAGAG AAATTTATGA GGCACCTGCT GCAGAAGTTA TTTTAAAAGC 480

GCATAAAGCA TTAGAAACGA TTACGTTAAC GAAAGATGTC GCACACTTTA AACCAATCAT 540

TGAGAAGCAA TTTGCTGAAC AACTATACAA TGGACTTTGG TTCTCACCTT TAACTGATAG 600

CTTGAAATTA TTTATTGATA GTACTCAGCA ATACGTAAGT GGTGATGTCA GAATTAAATT 660

ATTCAAAGGT AATGCCATCG TGAATGGTAG AAAATCACCT TACACATTAT ATGATGAAAA 720

ATTAGCAACT TATACAAAAG AAGATGCATT TnATCAAGAC GCTGCTGTTG GCTTTATCGA 780

TATCTATGGT TTACC 795

(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 887 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

CGATTGAAAG AAGACGGTTC AGTTGAAAAG TTTCCAAAGC CAGTAATTAG CCAACAACCA 60

GAAGGATATA CGAGTCATTT TAGAGATCCT AAAGTTTTTA AATATGATGr GaAATATTAT 120

GCAATCaTTG GTGCmCaAAA TAATGATCaG CaAGGTCGAT TATTACTTTA TAATACTGAA 180

GATATAATTA ATTGGCATTA TTTAGGTGAA ATAAATACAG AGTTGGATGA TTTTGGATAT 240

ATGTGGGAAT GCCCAGATTA CTTTAATGTA GATAATCAAG ATGTCATACT TATTTGTCCA 300

CAAGGTATTG AACCAAAAGG CGATCAGTTC AAAAATATTT ATCAAAGTGG TTATATACTT 360

GGAAAGTTTG ATATTGAAAA GTTAACATAT GAACATGAAA ATTTTGTCGA GCTTGATAAT 420

GGTTTTGATT TCTATGCACC TCAAACATTT TTAGATGAAA AAGGCCGACG AGTACTAATT 480

GGATGGATGG GGTTACCGGA AATCGAATAT CCTACTGATA ATGAAGGATG GGCCCATTGC 540

GCGTTGGAAA AATTACGTCA CAATAAAGAG ACAGCATTtA GGctACGCAA ATAAATTTAC 660

TCGAAAATTA CATCCGTATG AAGGTAAACA GTATGAATTA ATCATAGATA TTTTGGATAA 720

TGATGCTACC GAAGTGTACT TTGAATTACG TACATCTAAG ACTTCTTCAA CATTAATTGC 780

TTATAACAAG CGTGAAAATA AAATAACATT AGATCGCAGC GACAGTGGTT TATTGCCGAC 840

AAATGTTGAA gGTACGACGC GTAGTACGAT ATTAGACACG CCATTAA 887

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

TTGGAAnCAA AAAACCATTG GTAAACCGTG TTnAACCGGA TTTCCGATGG ACCTTTTAAA 60

ACnACCAAAT AGAAAGCTTT GATAAAAGGT AATTATGGTA CTGATAACAA ACAAGTTCAA 120

AAACATCATG ATTTAGTACG TATGCTTTTG ATGGATCAAG ATGGTTTTTT AACTGAAAAT 180

AATAAAGTTG ATCATTTCAT TGATGGAAAT GATTTATATG ATCAAGTTTT AAAAGATATT 240

AAAAATGCAA AAGAtATATC CATTTAGAGT ACwATACTTT CGCTTwAGAT GGTTwAGGTA 300

AAAGAATTTT ACATGCTTTA GAAGAAAAAT TGAAACAAGG TCTAGAAGTA AAAATATTAT 360

ATGATGATGT TGGATCTAAA AATGTTAAGA TGGCAAATTT TGATCATTTT AAATCGTTAG 420

GTGGAGAAGT TGAAGCATTT TTTGCTTCAA AATTACCGTT ATTGAATTTC AGAATGAATA 480

ATAGAAATCA TAGAAAAATC ATCGTAATCG ATGGTCAACT AGGTTATGTC GGAGGATTTA 540

ACATTGGTGA TGAATATCTm GGATTAGGAA AATTAGGATA TTGGAGAGAT ACGCATTTAC 600

GTATACAAGG GGATGCGGTT GATGCACTGC AGTTGCGATT TATTTTAGAC TGGAATTCGC 660

AAGCGCACCG TCCACAATTT GAATATGATG TTAAGTATTT CCCTAAAAAG AACGGACCAT 720

TGGGCAATTC ACCAATTCAA ATAGCTGCAA GTGGCCCGGC TAGTGACTGG CATCAAATTG 780

AATACGGTTA TACAAAAATG ATTATGAGTG CAAAGAAATC TGTATATTTA CAATCACCAT 840

ATTTCATTCC GGATAATTCA TATATaAATG CCATTAAAAT TGCTGCTAAA TCAGGTGTAG 900

ATGTACATTT AATGATTCCA TGTAAGCCAG ATCATCCATT AGTATATTGG GCGACATTTT 960

CAAATGCCTC TGACTTATTA TCAAGTGGTG TTAAAATTTA TACGTATGAA AATGGATTTA 1020

TACATTCTAA AATGTGCTTA ATTGATGATG AAATCGTATC AGTGGGCACA GCAAATATGG 1080

CTAAAGATTT AAGGGTGGCT TATGAACATG ATATTACAAA ATC 1183

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

GGTTATATGT TTGGTATTAC TCATTATATT GATTGGAGGT TGTGTCATTA TGACAAAAAC 60

AAATGGTCGA AACGCTCAAA TTAAAGAAAA TTTCAACAAA ACATTAAGTG TATATCTAAC 120

CAAGAATCTC GATGATTTTT ACGATAAGGA AGGTTTTCGA GATCAAGAAT TTGATAAAAG 180

AGATAAAGGG ACTTGGATTA TTTATTCTGA AATGGTTATC GAACCAAAAG GGAAnAATAT 240

GGAATCGAGA GGAATGGTGC TCTATATCAa TCGCAATACT AGAACmACGA AGGGTAATTT 300

TATTGTCACC GAAATAACTG AAGATAGTAA AGGATATTCA CGTAGTAAAG AAAAAAAATA 360

TCCTGTCAAG ATGGAAAATA ATCGAATTAT TCCAACAAAG CCTATACCGG ATGACAAGTT 420

AAAAAAAGAG ATTGAAAACT TTAAGTTCTT TGTACAATAT GGAAATTTTA AAGATTTTAA 480

AGATTATAAA AATGGTGATA TTTCATATAA TCCTAATGTG CCAAGTTATT CTGCAAAGTA 540

TCAATTGAAT AATGATGACT ATAATGTTCA ACAGTTAAGA AAACGATATC ATATTCCAAC 600

CAAACAAGCG CCCGAATTAA AATTGAAAGG ATCCGGCAAT TTAAAAGGCT CATCCGTAGG 660

ATCTAAGGAT CTAGAATTTA CGTTTGTAGA AAATCAAGAA GAGAATATCT ATTTTTCAGA 720

TTCGGTCGAA TTTACACCTA GCGAGGATGA TAAATCATGA GTCAAACGGA ATATCAAATA 780

AAATCTGGCA ATATAAAAGG TAACTCTGAA GAAACAAGTA CAGTATCTAA TATAAGTTAT 840

GAAATAGAAA ACGCAAATAA CAGTGGTTTA AAACAAAATA AAATTGATAA ACAAATTAAA 900

AAGTTACAAG AAAAAAATAA ATTCCCTAAA AATCTTTCAT ATCTTAAAAG TTATACGGAC 960

CCCAAAACAG GCACGACTAC AAGCGCCTTT TTAAATAAAG ACACTGGCAA AGTTACTTTA 1020

GGTATGACAG GTACTAATGT ACACAAAGAC GCAATATTAA AACAAACATT TGGTGTTCCT 1080

TCTTATCAAG GATATATAGA CGTGAGTGAA ACgCTaAAAG ATATTGGGGC CGATGTCAAT 1140

ATTGGCCTTC ATTCCGTCAC AGATAAAGAT CCACATTATA AAAATACCCA AGACTTTATC 1200

AAAAATATCA AAAAAGACTA TGATATTGAT ATTATTACCG GACATTCGCT GGGCGGTAGA 1260

GATGCGATGA TTTTAGGTAT GAGTAATGAT ATTAAACATA TCGTTGTGTA TAATCCAGCT 1320

ATTGAAAAGT ACGATGGTCA CATTGTAAGA TTTGTGTCTG ATGAAGACGA ATTAGATGCA 1440

GGTGTCCGCA ATCATTTATA TGAAACTGCT GGAGAAAAAA TAGTACTTAA AAATGGAGAA 1500

GGCCATGCAA TGAGTGGTAT TTTAATGAGC AGAACACAGG CTATAATCTT AGCTGAATTA 1560

AACAAAGTTA AAGGCTACCA AGACGAAAAT AATAAAGCAT TAAAATCCGT TCGTAAACAA 1620

ACGAGGCATA GATTACATAA AGTAGAGACG TTAAGAGCGA ATTGGATTCA AACAACGGGT 1680

GGATCACTCT CTTCCTCCCw ACAACAATTA TTAGAAGCTT TAACAGCACT AACCATTGCC 1740

GAAGGCTTAA ATCAATTAGT GAATGAAGAA AGCCAACATT TGAAAAAATG TATCACGCGA 1800

TGGCACATAA ATTTGGAGAC AACTGGAAAA AAGCGCAAGA AGTTGGAAAT GAAATTGGTG 1860

AAAAATTAAC CTCTGAAGAG GTTATAGATG rATTAAGAAA AGGTGGCGCG TATGAAAGTa 1920

AACTTGAAAC AGATCCCAAA AGAAAAATTG ATGATAAGAT AAAGAAATTA AATGATGTTT 1980

ATAAAAATTG TAATGGCTAT ATCGCAAAAA TTAAACAGAG TATCGAAGCA ATTGTTTCTA 2040

ATGACCAAAT GTTAGCGAGC CAGATTGATG GGATGATGTA ATGTTTACTA CGTATAAnAA 2100

TATTAATGAA CTTGAAAATG CCTATGATGA AGAAAGAAAA CAATTGAATG ATGCATTCAA 2160

TCAAATTGAT GAATTAAGAC ATCAAACACG CAAGAmATGT GAACAAATGT ATGATCATTT 2220

CTTATATCTC AAACATAAAA TGAATTmyms TGAAGACGCT ATGATCAGGA TGACACGTAT 2280

TATAGAATCT TTCGATAGAG AAACGAATCA ACGTATCCGA CATCACGAAA TG 2332

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 865 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

TTTACTACCC AGTATCTCTT TTTATAAATT ATATAGCCAC CACATATGGT GGAAAGTCTT 60

TTTAATTAGA ATTTTGTTTT TTCAGTTAAG AAAGCTTCTA ACTCTGAGAT TGGCATACGA 120

ACTTGTTCCA TTGAATCTCT GTCACGTACT GTAACTTGAT TATCTTCTAA TGAATCAAAG 180

TCGAATGTtA CACAATAAGG TGTaCCGATT TCATCTTGAC GACGGTATCT TTTACCGATA 240

GATTGTGATT CATCGAAATC GATTGAGAAT TTAGAACTTA ATTGCTCAAA AATCTTAATC 300

GtTCGCCAGA TAATTTCTTA CTTAAAGGTA AAATCGCTGC TTTATATGGT GCTAATGCAG 360

GATGGAAGTG TAAAACTGTA CGTGCATCTT TACTACCTTC AACGCCTTCT TCATCATATG 420

GAATATATTT TTCGTTCGTT TCTGGATCAT GGTATCTGAA ATCTTCACCA GAGTGTTCAG 540

CATGTTTACG TAAGTCGAAG TCTGTACGAC TTGCGATACC CCATAACTCA CCCCAACCAA 600

ATGGGAATTT ATATTCAATA TCAGTTGTTG CATTTGAGTA ATGAGATAAT TCATCTTCAT 660

CATGATCACG TAAACGCATA TTTTCACTGC TCATATTTAA GCTTGTTAAC CAGTCACTTG 720

CAAAAGTTTT CCAATAATTT TGCCATTCGA TTTCTTCTCC AGGTTTACAG AAGAATTCAA 780

GTTCCATTTG TTcAAATTCT CTTGTTCTGa AAATGaAGTT ACCTGGAGTG aTTTCaTTAC 840

GGaATGaTTT ACCAATTTGG ACCGG 865

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1444 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

TAATGAGTAA ATAAGTACCA GATAAAATCA TGAATATCAT CCAACATGCG GTTAACTCTA 60

CTAAATAATT AATAATAGTA TTTTCAGTAA ACAAAGAACT ATGTATACTT CGCATCACAT 120

TAGAATACGT ATGTTTCGCA TTTTGATCTG CAACAAATTG ATTGTTATGA TCTAGAAAGA 180

CGTAACGTTG ATTTCCTGCC ATATCACTCA GTGTAATTCG TTTGTTATAT GGTTCATCAA 240

GTATGCTAAC TTTACTTACA AAGAATCCTT CATATTGTTG TTCAACTTGA TGTACTGCAT 300

CATTTAATGT TTGATGCGTT TTTACATCAC TGTCACCAAA AAACTCATTC TTATAAATAT 360

TATTTTCAAC TTCTGGAAAG AACAAGTAAC CAATGCCCGA AATGGTTAAA GTGATTAACA 420

GTGGAGCAAT AAATATTGCT GCATAGAAAT GTAATCTTTG TAATGGATTA AATGTATTTT 480

TCATATTTCC CTCCCAATTG GCTATTATAC GGTGTCAATT CTGTGATGTG TGTGAACAAA 540

CTGTGACAAT ATTTATTTTC TAGAAAAATT TAACGATGAT TTGTGATTTT TAGAAAAATG 600

AACTTTTAAG TTGGAATGTT TGAAGAAAAT TGATTATTCG TATGTTTTAT CAAGCAGCTA 660

TGATAAAATT TAAACATAAT ACAATGCGAG CCATTTAACG ATCTATGTTT AAATGGACAT 720

CGATATTGTA TGAATTCGTT GTAACAAGCA AGCATTTCTA TGTGAACGAA CCAAAGGGGA 780

AAGTAACATG ATTAATAAAG AACAATTAGA TCTTTTATAT AAATTAAAAA AAGAAGTTGA 840

AAAGTCGCGA AATGAAGCAC TTTTACATAC AATTAACCAA GTAATTAAGA AAGTATATTT 900

GCAGCAATAT ACATGTTCGT TCGTTGGACA TTTTTCTGCA GGTAAATCGA CACTGATAAA 960

TATTGTGTCA GTTTCAGACA ATCACGATAT TATTGCTAAT TTGCCGAATC AAACGTATGC 1080

CAAATTATCT AATTATGATG AAGTAAGGGA AATGAATCGC CAAAATGTCG ACGTTGAATC 1140

TGTAGAAATT AATTTTCAAT CAGCTAAATT TGAAAATGGG TTTACGTTGC AAGATACACC 1200

AGGTGTTGAT TCAAATGTTG CATCACATCA GTCAATAACA GAACAATATA TGTATACAAG 1260

TAATATGATA TTTTATACGG TTGACTATAA CCACGTTCAA TCTGAACTTA ACTTTAAGTT 1320

TATGAAGCAT ATAAATGATG TTGGaATACC TGTTGTGTTT ATCATTAATC AAATTGACAG 1380

CATCCAAGAC GATGGAATTG TCATTCTCTA CGTnTTAAAT CTCGAGTTGG AAAAATCAAT 1440

TGGC 1444

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

GCAGCAGCTT ATCGTGAGTT ATCATTATTA TTACGTAGAC CTCCAGGTCG TGAAkCATAC 60

CCAGGTGACG TATTCTACTT ACATAGTAGA tTATTAGAAA GAGCAGCAAA ATTAAACGAT 120

GACTTAGGTG GCGGTTCAAT TACTGCATTA CCAATTATCG AAACACAAGC TGGTGATATT 180

TCAGCTTATG TACCAACAAA CGTTATTTCA ATTACAGATG GACAAATCTT CTTACAATCT 240

GATTTATTCT TCTCAGGTGT AAGACCAGCG ATTAATGCCG GACAATCTGT ATCTCGTGTT 300

GGTGGATCTG CACAAATTAA AGCAATGAAG AAAGTTGCTG GTACGTTACG TCTTGACTTA 360

GCGTCATACA GAGAACTTGA ATCATTTGCA CAATTCGGTT CAGACCTTGA TGAATTTACT 420

GCAAGTAAAT TAGAACGTGG TAAACGTACT GTTGAAGTCT TAAAACAAGA TCAAAACAAA 480

CCATTACCAG TCGAACACCA AGTGTTGATT ATTTATGCAT TAACAAAAGG ATATTTAGAT 540

GATATTCCAG TTGTAGATAT CACACGTTTT GAAGACGAGT TAAACCACTG GGCAGAATCA 600

AATGCTACTG AACTGTTAAA TGAAATCAGA GAAACTGGTG GCTTACCAGA TGCTGAGAAG 660

TTTGACACAG CAATTAACGA ATTCAAAAAA AGCTTTAGCA AATCTGAATA ATAAACAAGT 720

TTAGTATAAG GTGGTGAGAT AGTGGCTTCT CTTAAAGAAA TAGATACTCG AATAAAATCA 780

ACCAAAAAAA TGAAGCAGAT TACGAAAGCG ATGAACATGG TATCAAGTTC AAAACTTCGT 840

AGAGCTGAAA AAAATACAAA ACAATTCACA CCATATATGG ATAAAATGCA AGATGCAATT 900

ACTAGAAGTG GATATTTAGT TATCACGAGT GATAAAGGTT TAGCAGGTGC ATATAGTGCA 1020

AACGTGCTTA AAAAATTGAT TACTGATATT GAAGCGAAAC ATCAAGATAG TAGCGAATAC 1080

AGTATTGTAG TTTTAGGGCA ACAAGGTGTT GATTTCCTAA AAAATAGAGG TTATGACATT 1140

GAGTATTCTC AAGTAGACGT ACCTGATCAA CCTTCTTTCA AATCTGTTCA AGCACTAGCT 1200

AACCATGCTA TAGACTTATA CAGTGAAGAA GAAATTGATG AATTAAATAT ATACTATAGT 1260

CATTATGTCA GCGTTCTTGA AAACAAGCCT ACATCTAGAC AAGTATTACC ATTATCTCAA 1320

GAGGATTCTA GTAAGGGGCA TGGTCATTTG TCTTCTTATG AATTTGAGCC AGATAAAGAA 1380

TCTATCTTAA GTGTAATCTT GCCTCAATAT GTTGAGAGTT TGATTTACGG AACAATATTA 1440

GACGCAAAAG CAAGTGAGCA TGCAACACGT ATGACTGCGA TGAAAAATGC CACTGATAAT 1500

GCAACTGAAC TTATTGATGA CTTATCATTA GAATATAACA GAGCGAGACA AGCAGAAATT 1560

ACGCAACAAA TTACTGAAAT TGTTGGTGGT TCCGCAGCGC TTGAATAATA TTTAAAGGAG 1620

GAAAATAGCA TGGGAATTGG CCGTGTAACT CAAGTTATGG GTCCTGTAAT TGATGTTCGA 1680

TTTGAACATA ACGAAgTTCC TAAAATTAAT AACGCCTTGG TTATTGATGT GCCTAAAGAA 1740

GAAGGTACAA TACAACTAAC ATTAGAAGTT GCGCTGCAAT TAGGTGACGA CGTTGTTCGT 1800

ACAATTGCGA TGGATTCAAC TGATGGTGTC CAAAGAGGCA TGGATGTAAA AGATACAGGC 1860

AAAGAAATTA GTGTACCTGT TGGTGACGAA ACATTAGGTC GTGTATTTAA TGTACTAGGT 1920

GAAACAATTG ACCTTAAAGA AGAAATTAGT GATTCTGTTC GCCGCGATCC TATCCATCGT 1980

CAAGCACCAG CATTCGATGA ACTTTCAACA GAAGTTCAAA TTTTAGAAAC AGGTATTAAA 2040

GTAGTAGATT TACTAGCACC TTATATTAAA GGTGGTAAAA TCGGATTGTT CGGTGGTGCC 2100

GGTGTAGGTA AAACAGTATT AATCCAAGAA TTAATTAACA ACATCGCTCA AGAGCACGGT 2160

GGTATTTCTG TATTCGCCGG TGTAGGTGAA CGTACTCGTG AAGGTAACGA TTTATACTTC 2220

GAAATGAGTG ACAGTGGTGT AATTAAGAAA ACAGCCATGG TATTCGGGCA AATGAATGAG 2280

CCACCTGGTG CACGTATGCG TGTTGCATTA TCTGGTTTAA CAATGGCTGA ATATTTCCGT 2340

GACGAACAAG GTCAAGACGT ATTATTATTC ATCGATAACA TTTTCAGATT TACACAAGCT 2400

GGTTCTGAGG TATCTGCATT ATTAGGTCGT ATGCCTTCTG CAGTAGGTTA CCAACCAACA 2460

CTTGCTACTG AAATGGGACA ATTACAAGAA CGTATTACGT CTACAACAAA AGGATCAGTT 2520

ACTTCTATTC AAGCGGTATT CGTACCTGCC GATGACTATA CTGACCCAGC GCCTGCGACA 2580

GCGTTTGCCC ATTTAGATGC AACTACAAAC TTAGAACGTA AATTAACTGA AATGGGTATT 2640

TATCCAGCCG TGGATCCATT AGCGTCTACA TCAAGAGCAT TGGAACCATC AATTGTAGGT 2700

CAAGATATCA TTGCTATCTT AGGTATGGAC GAATTATCTG ATGAAGATAA ACAAACAGTT 2820

GAACGCGCAC GTAGAATTCA ATTCTTCTTA TCTCAAAACT TCCACGTAGC GGAACAATTT 2880

ACTGGTCAAA AAGGTTCTTA TGTACCTGTT AAGACAACAG TTGCAAACTT TAAAGATATC 2940

TTAGATGGTA AATATGACCA TATTCCAGAA GATGCATTCC GTTTAGTTGG TAGCATGGAT 3000

GATGTTATTG CAAAAGCTAA AGATATGGGT GTTGAAGTAT AACAATTAGG AGGAATGGAT 3060

AATGAATACA TTAAACCTAG ATATTGTCAC TCCTAATGGT TCTGTTTACA ATCGTGATAA 3120

TGTTGAACTC GTTGTTATGC AAACAACAGC TGGTGAGATA GGTGTCATGA GTGGACATAT 3180

TCCAACTGTA GCTGCTTTAA AAACAGGCTT TGTAAAAGTG AAATTTCACG ATGGAACTGA 3240

ATATATTGCT GTAAGCGATG GCTTTGTTGA AGTTAGAAAA GATAAAGTTT CAATCATTGT 3300

TCAGACTGCA GAAACTGCAA GAGAAATTGA TGTTGAAAGA GCTAAATTAG CCAAAGCAAG 3360

AGCAGAGTCT CACTTGGAAA ATGATGACGA CAATACTGAT ATTCATAGAG CCGAAAGAGC 3420

TTTAGAGAGA GCAAATAACC GTTTGCGTGT GGCTGAATTA AAATAGTAAA TAAAGGGTCG 3480

AAGATGTGAT TTCATATCTT CGACCCTTTT TTGAATTATA TTGATTTAAA GATACAAAAC 3540

ATGAGAGGGG GGAAGGAATT GATAAAGAAC CATTAAAGAT TTATGATGTA GTGGTTCTTT 3600

ATCATTAAAC ACAGCTAATG TGTATTTAAA AATAGGaayA CATgAGTAAA ACTCATGTAT 3660

AAGAAATACT AATTTCTAAA GAAAAAGTAT TTCTTTATGT TGGGGCCCCG TCAACTACTG 3720

CCAAATACAA CACTATAGAG TCTAGACATT GATTTATGTC CGACTCCCAA GAATAGTTTT 3780

ACTTTTTTAC AATCACTAAT AGATTGCTAA AATCAAAATT TCCTTCACCA CTATCTACAG 3840

TCGACATTTC ATTTTTTGAA ATTATCTACA TTTTTTCATA CCAAGATATT TTATAGTTAT 3900

GATATTTATG TAAAAAGAAT TATATAGTAA GTTAGCTTAA ACTTTACTAA AAACGGGTAT 3960

TAAACTTTGT ATCATTATTT AAATTTTTCA TGTACAATGT AATACAGTAA TCTTATGAGG 4020

TGATAAAATG GATTATATCG GACAATATGC AGTTATCCAT TTAGTGTTAC ATGTTGTATG 4080

TATTTGTATT GCCTATTGGG CTTTACAATC AATTAGATTA GATCAATTTT TTAAAAAAGG 4140

ATACGCCACT CAATTACAAG TGTGTATGAT ATTTGTTGCT ATTTTATTAG GCACTGCAGT 4200

AAGCAATTTT ATTGTAGATT TGTTACAATA CTCGACGCAG GTAAAATATT TAATAAAATA 4260

AGTCTAACTC TATGATTTGT AATCAAAACT AGATATAATT AAATAATGAC TTAAAATAAT 4320

TTTAAAATAG GGAAATGTAA AGTAATAGGA GTTCTAAGTG GAGGATTTAC GATGGATAAA 4380

ATAGTAATCA AAGGTGGAAA TAAATTAACG GGTGAAGTTA AAGTAGAAGG TGCTAAAAAT 4440

GCAGTATTAC CAATATTGAC AGCATCTTTA TTAGCTTCTG ATAAACCGAG CAAATTAGTT 4500

GACGTTACAT ACAAAAAGGA CGAAAATGCT GTTGTCGTTG ATGCAACAAA GACTCTAAAT 4620

GAAGAGGCAC CATATGAATA TGTTAGTAAA ATGCGTGCAA GTATTTTAGT TATGGGmCCT 4680

CTTTTAGCAA GACTAGGACA TGCTATTGTT GCATTGCCTG GTGGTTGTGC AATTGGAAGT 4740

AGACCGATTG AGCAACACAT TAAAGGTTTT GAAGCTTTAG GCGCAGAAAT TCATCTTGAA 4800

AATGGTAATA TTTATGCTAA TGCTAAAGAT GGATTAAAAG GTACATCAAT TCATTTAGAT 4860

TTTCCAAGTG TAGGAGCAAC ACAAAATATT ATTATGGCAG CATCATTAGC TAAGGGTAAG 4920

ACTTTAATTG AAAATGCAGC TAAAGAACCT GAAATTGTCG ATTTAGCAAA CTACATTAAT 4980

GAAATGGGTG GTAGAATTAC TGGTGCTGGT ACAGACACAA TTACAATCAA TGGTGTAGAA 5040

TCATTACATG GTGTAGAACA TGCTATCATT CCAGATAGAA TTGAAGCAGG CACATTACTA 5100

ATCGCTGGTG CTATAACGCG TGGTGATATT TTTGTACGTG GTGCAATCAA AGAACATATG 5160

GCGAGTTTAG TCTATAAACT AGAAGAAATG GGCGTTGAAT TGGACTATCA AGAAGATGGT 5220

ATTCGTGTAC GTGCTGAAGG GGAATTACAA CCTGTAGACA TCAAAACTCT ACCACATCCT 5280

GGATTCCCGA CTGATATGCA ATCACAAATG ATGGCATTGT TATTAACGGC AAATGGTCAT 5340

AAAGTCGTAA CCGAAACTGT TTTTGAAAAC CGTTTTATGC ATGTTGCAGA GTTCAAACGT 5400

ATGAATGCTA ATATCAATGT AGAAGGTCGT aGTGCTAAAC TTGAAGGTAA AAGTCAATTG 5460

CAAGGTGCAC AAGTTAAAGC GACTGATTTA AGaGCAGCAG CCGCCTTAAT TTTAGCTGGA 5520

TTAGTTGCTG ATGGTAAnAC AAGCGTTACT GAATTAACGC ACCTAGATAG AGGCTATGTT 5580

GACTTACACG GTAAATTGAA GCAATTAGGT GCAGACATTG AACGTATTAA CGATTAATTC 5640

AGTAAATTAA TATAATGGAG GATTTCAACC ATGGAAACAA TTTTTGATTA TAACCAAATT 5700

AAACAAATTA TACCTCACAG ACAGCCATTT TTATTAATTG ATAAAGTAGT TGAATATGAA 5760

GAAGGTCAAC GTTGTGTGGC TATTAAACAA GTATCAGGAA ACGAACCATT CTTTCAAGGG 5820

CATTTTCCTG AGTATGcGGT AATGCCAGGC GTATTAATTA CTGAAGCGTT AcTCAAACAG 5880

GTGCGGTAGC TATTTTAAAT AGTGAAGAAA ATAAAGGTAA AATCGCTTTA TTTGCTGGTA 5940

TTGATAAATG TCGTTTTAAA CGTCAAGTAG TACCTGGTGA TACTTTAACG TTGGAAGTAG 6000

AAATCACTAA AATTAAAGGA CCAATAGGTA AAGGTAATGC TAAAGCTACT GTCGATGGTC 6060

AACTTGCTTG TAGTTGTGAA CTTACATTTG CAATTCAAGA TGTAAAATAA AACAAAAAAA 6120

ACATTCAAAG ATTTAATGTG TTGGCATAAT CTTTGAATGT TTTTTATTTT ACTCTTCTAA 6180

TTTTTCATCC TTTAACTTTG GTTTAGACTG CaTCATTCGA TTAAATGATT TTTTTAATTC 6240

TTCACCAGAT AATCCATCAT CAATAAGTTG GTTCTAATAA ACTTTCAGCA TACTGTTGGA 6300

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

AGTTGCTACA CCAGACATGA TGGGTGAAGT TGGTAAATTA GGTCGTGTAT TAGGACCAAA 60
AGGTTTAATG CCAAACCCTA AAACTGGAAC TGTAACAATG GATGTTAAAA AAGCTGTTGA 120
AGAAATCAAA GCTGGTAAAG TAGAATATCG TGCTGAAAAA GCTGGTATCG TACATGCATC 180
AATTGGTAAA GTTTCATTTA CTGATGAACA ATTAATtGAA AACyTCaATA CyTTACAAGA 240
TGTATTAGCT AAAGCTAAAC CATCATCTGC TAAAGGTACA TACTTCAAAT CTGTTGCTGT 300
AACTACAACA ATGGGTCCTG GAGTTAAAAT TGATACTGCA AGTTTCAAAT AATAAATGAT 360
ATAAACAATT ACAGGCTGAA AGAAATATCT TTCAGTCTGT AAAAATATAT TGACAATAAG 420
TAATTTCCAA GTTATATTAC TTATTGTGAT TATTTTACCT AAGACAGTAG GAGTTATTTA 480
TAACTTAAAA TTTATCCTGC CGAGGCTAAA ATTGACTTGA ACGTGATGAT CTATGATCTT 540
TCAAGCACTT TTTGCCGTGG GTAGAAAGTG CTTTTTTTAT TAATTTTAAA AAAAGCACCA 600
AAAATTTAAA TGGAGGTGTC TGAATGTCTG CTATCATTGA AGCTAAAAAA CAACTAGTTG 660
ATGAAATTGC TGAGGTACTA TCAAATTCAG TTTCAACAGT AATCGTTGAC TACCGTGGAT 720
TAACAGTAGC TGAAGTTACT GACTTACGTT CACAATTACG TGAAGCTGGT GTTGAGTATA 780
AAGTATACAA AAACACTATG GTACGTCGTG CAGCTGAAAA AGCTGGTATC GAAGGCTTAG 840
ATGAATTCTT AACAGGTCCT ACTGCTATTG CAACTTCAAG TGAAGATGCT GTAGCTGCAG 900
CGAAAGTAAT TTCTGGATTT GCTAAAGATC ATGAAGCATT AGAAATTAAA TCAGGCGTTA 960
TGGAAGGCAA TGTTATTACA GCAGAAGAAG TTAAAACTGT TGGTTCATTA CCTTCACACG 1020
ATGGTCTTGT ATCTATGCTT TTATCAGTAT TACAAGCTCC TGTACGCAAC TTCGCTTATG 1080
CGGTTAAAGC TATTGGAGAA CAAAAAGAAG AAAACGCTGA ATAATTTTTA GCGTAAAAAA 1140
ATTAAAAATA ATGGAGGAAT TATAAAATGG CTAATCATGA ACAAATCATT GAAGCGATTA 1200
AAGAAATGTC AGTATTAGAA TTAAACGACT TAGTAAAAGC AATTGAAGAA GAATTTGGTG 1260
TAcTGcAGCT GCTCCAGTAG CAGTAGCAGG TGCAGCTGGT GGCGCTGACG CTGCAGCAGA 1320
AAAAACTGAA TTTGACGTTG AGTTAACTTC AGCTGGTTCA TCTAAAATCA AAGTTGTTAA 1380

TCCTAAAGTA ATCAAAGAAG CTTTACCTAA AGAAGAAGCT GAAAAACTTA AAGAACAATT 1500

AGAAGAAGTT GGAGCTACTG TAGAATTAAA ATAATTCAAG TATCTTAAAC TTAATAATCA 1560

AAGTTTTATA GCAAGTATTG CTATAATATA ATGATTCTTT GAGAAGTTAA AACCCCGTTA 1620

TTTTGATAAC GGGgTtTTAT TCaTTTAAAG ACTGAGTGAA ATGTTATAAT TATAATGACG 1680

AGTTACAAAG TGAAGATGAG GTGGGAATAA TGAGTCA 1717

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

GTAAATCTGT TACTCGAAAT GTAACGATTA AAGAAAAGGG CTCATCTCAA ACATATATTT 60

TGTTAGGCTA TCCAACAAAA GCACAGAAGA ATAGTCATAG CAAATATAGT GGAGTCTTTA 120

TATATAAAGA CTTGAAATCA ATCGAAGATA CAAATAATGC TATTACGATT ATCACCATAA 180

TTACGGCTGT TATTTTCTTA ACAATTACAA CAGTCTTTGC GTTTTTCTTA TCGTCAAGAA 240

TTACAAAACC TTTAAGACGT TTAAGAGACC AAGCTACACG TGTATCTGAA GGGGATTACT 300

CTTATAAACC TTCTGTCACA ACGAAAGATG AAATTGGTCA ATTATCGCAG GCATTTAATC 360

AGATGAGTAC AGAAATCGAA GAGCATGTCG ACGCATTATC CACATCTAAA AATATTAGAG 420

ACAGCTTAAT TAACTCTATG GTAGAAGGTG TCCTAGGTAT TAATGAGAGT CGACaAATTA 480

TCTTATCTAA TAAGATGGCG AATGATATTA TGGACAATAT TGATGAAGAT GCTAAAGCTT 540

TCTTATTAAG ACAAATAGAA GATACTTTTA AATCAAAACA AACTGAAATG CGCGATTTAG 600

AAaTGAATGC ACGATTCTTT GTTGTGACCA CAAGCTATAT CGACAAGATT GAACAGGGAG 660

GTAaAAGTGG TGTTGTTGTG ACAGTTCGTG ATATGACTAA TGAGCACAAT CTAGATCAAA 720

TGAAGAAAGA TTTCATTGCT AATGTATCAC ATGAATTACG TACACCGATA TCATTACTTC 780

AAGGTTATAC TGAATCAATT GTAGATGGTA TTGTTACAGA ACCGGATGAA ATAAAAGAAT 840

CGCTTGCCAT TGTCCTTGAT GAATCGAAAC GTTTAAATCG TTTAGTTAAT GAATTGTTAA 900

AtGTCGCACG CATGGATGCT GAAGGGTTAT CCGTAAATAA AGAAGTTCAG CCTATTGCAG 960

CGTTACTAGA TAAGATGAAA ATTAAGTATC GCCAACAAGC TGATGATTTA GGTCTAAATA 1020

TGACTTTTAA TTAyTGTAAG AAGCGTGTTT GGAGTTATGA TAwGGATCGC ATGGACCAAG 1080

TTACTTGTGA TGAAAATGAA AGCGAAGATA TTTTATACAT TAAAGATACA GGTACAGGCA 1200

TTGCACCAGA ACATTTACmA CAAGTATTTg ATCGTTTTTA TAAAGTTGAT GCAGCGnAnA 1260

ACCCCGnGGT AACCAnGTA 1279

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

GAGCTGTTGT TACTTTGATG CCTGCAGCTT TATTACGGCT GACTTGGTAA TGATAAGTTT 60

CAGCATATTG CTCAATATAT GCTATATCAT ATTGAATGGT ACGAGGTGAT ACACCAAGTT 120

GATTAGCAAT GGTATTGATT GGAATAAACG TTTGCTCATG AATTAAAAGA TACAAAATTT 180

CGATTTGTCT ATAACTTAAC AACGTAATAT CCTCCTATTT GTAATTGTAA GCGATTTCTT 240

AAAAACGTAG ATATGCAATC TCTTTCATAT TTTAATCCGA AAAATTGCAT ATCAAAATGT 300

TTATGGCGCA AGATTTTATA GGAACTTTTA AAATAAATTA rATATTCATG TTGACAATTT 360

AAAAATGTCG CAGTATATTT AGTTAGACAT CTAACGAAAT GGTGGTGCAA TAAATGGAAT 420

TCACTTATTC GTATTTATTT AGAATGATTA GTCATGAGAT GAAACAAAAG GCTGATCAAA 480

AGTTAGAGCA ATTTGATATT ACAAATGAGC AAGGTCATAC GTTAGGTTAT CTTTATGCAC 540

ATCAACAAGA TGGACTGACA CAAAATGATa TTGcTAAAGC ATTACAACGA ACAGGTCCAA 600

CTGTCAGTAA TTTATTAAGG AACCTTGAAC GTAAAAAGCT GATCTATCGC TATGTCGATG 660

CACAAGATAC GAGAAGAAAG AATATAGGGC TGACTACCTC TGGGATTAAA CTCGTAGAAG 720

CATTCACTTC GATATTTGAT GAAATGGAAC AAACACTCGT ATCGCAGTTA TCTGAAGAAG 780

AAAATGAACA AATGAAAGCA AACTTAACTA AAATGTTATC TAGTTTACAA TAAATGATAA 840

GTGTGACTGG TAGAAATCAG TCACTTTGTC TTTAATATTA TAGTTAGATA TCTAATTGTT 900

AGTAAGCTAA TTATTGGAAA AGACAAGGAG TATTGAACAA TGAAAGACGA ACAATTATAT 960

TATTTTGAGA AATCGCCAGT ATTTAAAGCG ATGATGCATT TCTCATTGCC AATGATGATA 1020

GGGACTTTAT TAAGCGTTAT TTATGGCATA TTAAATATTT ACTTTATAGG ATTtTyAGAm 1080

GAyAGCCACA TGATTTCTGC tAatCTCTCT AACACTGCCA GTATTTGCTA TCTTAATGGG 1140

GTTA 1144

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

ACAACCAATT TTACTAAACA TGGTrrTCAT gCATTTTCAA TATTTAGATG TCGACCGCAT 60

AATCGAAGAA TCGCCGACAA TAGTACTTAT CGATGAGTTA GCACATACGA ATATTTCTAG 120

AGATCGTCAT GAGAAACGAT ATATGGATAT TGAAGAAATT TTAAATCATG GTATCGATGT 180

TCATACCACT TTGaACATTC aaCATATTGA AAGTTTAAGT AGTCAAATTG AACTGATGAC 240

CGGTGTACAT GTTAAAGAAC GTGTACCCGA CTATTTCATA ATGAGCGCCG ATGTATTAGA 300

AGTCGTAGAT ATCTCACCTG AACAATTAAT TAAACGCTTA AAAGCTGGCA AGGTATATaA 360

AAAGGATAGG CTAGATGTAG CATTTAGTAA TTTCTTTACG TATGCCCACC TAAGCGAAtG 420

CGTACATTGA CGTTAAGAAC AGTTGCCGAC TTGATGAGTG ATAAAGAAAA AGTCCGACAC 480

AACCATAAAA CGTCACTCAA ACCTCATATT GCTGTGGCAA TTAGTGGGAG CATTTATAAT 540

GAAGCAGTAA TTAAAGAGGC ATTCCATATT GCTCAAAAAG AACATGCGAa GTTCACTGCT 600

ATTTATATAG ATGTATTCGA AAAAAACAGG CAATATAAAG ATAGTCAAAA GCAAGTGCAT 660

CAACATCTCA TGCTTGCAAA ATCATTAGGA GCAAAAGTAA AAGTAGTTTA TAGCCAAACC 720

GTTGCATTAG GATTAGACGA ATGGTGTAAA AATCAAGATG TAACCAAATT AATTATCGGA 780

CAACATATTA GAAATAAGTG GCGAGACTTT TTCAATACAC CTTTAATTGA CCATTTAATG 840

TCCTTTGAAC ATAGCTATAA AATCGAAATC GTTCCAATCA AACAAATACC TGTTGAATTG 900

AAAATGAACA AATCACCCTA TCGTCCTAAA GGCAAACGTT TCGCCATAGA TATGTTAAAA 960

ATGATTTTGA TTCAAATAAT TTGTGTAATG ATGGGACTGT GGATTTATCA ACTTGATAAG 1020

CATGAGTCTA GTACGATTAT TTTAATGATT TTTCTCATCG GCATCATTTT ATTATCCATT 1080

TGGACGCGGT CCTTCATCAT TGGCTTTTaG CAGCAATTAt TAACGTATTT GTgTkTAATT 1140

ATkTTTTtAC GGAACCTA 1158

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

ATCATATGGT CGATTTAACA GATCCAACGT ACTGCtAAAT AATTACATGA CGTTTAAACA 60

TAGCATTGAT TATAACTATT TCTAAGTCTT CGCATTATTT GCGATGATGT GGGAATAGTT 120

ATTTTTATTT AAAAATATAA AAAAATAGAT GCAGCAAAAT TTTAAAGCAT TTTATTTTGA 180

ACATATTAAA AGGGAGCGTA TCATAATGGA ATGTAATGTT TATATCGTAT GCATTACGGA 240

TAAATAATAT ATAAATCATT CTTGAGGAGT GAAAGAATAA TGAGAGACTA CACAAAGCAA 300

TACATTAATG GCGAATGGGT AGAAAGTAAT AGTAATGAAA CGATAGAAGT TATAAATCCA 360

GCAACCGAAG AAGTAATCGG GAAAGTTGCT AAAGGTAATA AAGCTGATGT TGATAAAGCC 420

GTCGAGGCGG CAGACGATGT TTATTTAGAG TTCCGTCATA CATCTGTGAA AGAAAGACAA 480

GCGTTATTAG ATAAAATTGT AAAAGAmTAT GAAAACAGAA AAGACGATAT TGTACAAGCT 540

ATTACGGATG AATTAGGTGC TCCTTTATCA TTATCTGAGC GTGTCCATTA TCAAATGGGA 600

CTAAACCATT TTGTTGCAGC GAGAGACGCA TTAGATAACT ACGAATTTGA AGAACGCCGC 660

GGAGATGATT TAGTTGTTAA AGAAGCAATC GGTGTATCTG GATTAATTAC ACCGTGGAAC 720

TTCCCTACAA ACCAAACATC ATTAAAATTA GCAGCAGCAT TTGCGGCTGG TAGTCCAGTT 780

GTACTTAAAC CATCTGAAGA AACACCATTT GCAGCTGTTA TTTTAGCTGA GATTTTTGAT 840

AAAGTCGGTG TTCCTAAAGG TGTATTTAAC CTTGTTAATG GTGATGGTGC TGGTGTTGGG 900

AATCCTTTAT CTGAACATCC TAAAGTACGC ATGATGTCAT TTACAGGATC AGGCCCTACT 960

GGTTCTAAAA TTATGGAAAA AGCCGCTAAA GATTTTAAAA AGGTATCATT AGAGCTTGGT 1020

GGCAAATCAC CATATATCGT CCTAGATGAC GTAGATATTA AAGAAGCGGc TAAAGCAACa 1080

aCAGGCAAAG TTGTTAATAA TACTGGTCAA GTATGTACAG CTGGTACACG TGTTTTAGTG 1140

CCTAACAAAA TTAAAGATGC ATTCTTAGCT GAATTAAAAG AACAATTTAG CCAAGTGCGT 1200

GTCGGTAATC CAAGAGAAGA TGGTACACAA GTAGGCCCTA TCATTAGTAA AAAACAATTT 1260

GATCAAGTAC AAAATTATAT TAATAAAGGT ATTGAAGAAG GTGCTGAATT ATTTTATGGT 1320

GGTCCTGGTA AACCAGAAGG ACTTGAAAAA GGATACTTTG CACGTCCGAC AATTTTTATT 1380

AATGTAGATA ATCAAATGAC GATAGCACAA GAwGAAATTT TTGGGCCAGT AATGTCAGTT 1440

ATCACTTATA ACGATTTAGA TGAAGCGATT CAAATTGCAA ATGATACAAA ATATGGTTTG 1500

GCAGGATATG TTATTGGTAA GGACAAAGAA ACATTGCATA AAGTAGCTCG TTCTATTGAA 1560

GCAGGTACAG TAGAAATAAA CGAAGCAGGT AGAAAGCCAG ATTTACCATT TGGTGGCTAT 1620

AAACAATCTG GTTTAGGTCG TGAATGGGGC GATTATGGTA TTGAAGAGTT CTTAGAAGTG 1680

AGTGCACATG ACTAATTAAG TTTTGTGTAC TGTTTTAATT TTGCAATTTT TATAAATAGA 1800

TTTTGTAATT AAAATAAAAA TTTGCTATAG TTATTCATGT ATTTAAAAGG TTGGGGATTA 1860

GCATAATGGG ATTGTGCTAG CACAGTTATT TATGCATTGT CATGCCTATC TATTACTTAC 1920

TAACTAAAAA ATAATGAAAT GGGTGTAAAC TATATGCCTG AAAGAGAACG TACATCTCCT 1980

CAGTATGAAT CATTCCACGA ATTGTACAAG AACTATACTA CCAAGGAACT CACTCAnAAA 2040

GCTAAAACTC TTAAGTTGAC GAACTATAGT AAATTAAATn AAAAAGAACT TGTTCTAGCT 2100

ATTATGGAAG CACAAATGGA nAAAGATGGT AACTATTATA TGGAAGGTAT CTTAGATGAT 2160

ATACAACCAG ATGGTTATGG TTTTTTAAGA ACAGTGAACT ATTCTAAAGG GGAAAAAGAT 2220

ATTT 2224

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1690 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

ACATTACnTT GAATCGAAAG TTTCATAAAC GACTTGAATG CCAGTTTCTT TTTCAAATTT 60

CTTAATTAAC TCTGGATCAA TATATTCGCC CCAATTGTAT ACGTAAATTT TTTGATTTGT 120

ATGCACTTGT TCTTTAGATT TAAACCAATG ACTTAAAGTA AGACAAAGCA TACCCACAAC 180

TAATGCACCT ATAATGAGTT GTAAAAATCG TTTCATTATT TTACACCTCG CTTGATTAGT 240

TTTTTCTTAT TTATCACGTA TTGAATCAAA TAATATCCTA GTATTCCTAA TACAATAACA 300

GCAAACAATA ATGTTGAAAT CGCATTAATT TCCATACTAA TTCCTTTTCT CGCCATAGCA 360

TAAACTTCAA CTGATAACAC ACTAAAGCCA TTACCAGTAA CGAAGAAACT TACTGTGAAA 420

TCGTCTAGTG AATAAGTTAA AGCCATAAAG AATCCTCCTA TAATAGAAGG TAAAATATTA 480

GGAATAATAA TGTTGCTTAA TAATTGTGGT TCAGTCGCTC CTAAATCTCT TGCAGCATTT 540

AACATATTAT TATTCATyTC ATACAGTTGT GGTAAGACGA TAATCACAAC TATAGGTATG 600

CAAAATGCAA TATGAGATAT TAGAACTGTC CaAAAkCCTA AACCAAGACC AGTAAAATGG 660

CCAATCGTTG TAAACATAAT TAAGAATGAT GCACCTATGA CAACGTCGGA TGATACCATC 720

AAGACATTAT TCAATGTTAG TAAAGTTACT TTAAACTTTT TATTTCTTAA ATAATAAATA 780

GCAATGGCAC CAAATGTACC AATAACTGTA GAAATTGAGG CTGCTAAAAG TGCTACAGCT 840

AATGTAAAAT GTTCAAAGTG AATCATATTA CCAGCCGAAT TGAATGAATA GAACATTAAA 960

AAGAATATTG GGATGTATAA AATCGCTAAA AGTATCCCGA TATACAGCTT TCCATACCAT 1020

TTCATATGAT TCACCCTCTC CCATTAGATG ATTTTGTAAT GATTAAAATG AATGCCATAA 1080

ATACAATTAA GAATATAGCT ATAGTTGATC CCATACCATA ATTTTGAATT GTTAAAAATT 1140

GTTCCTCTAT TGCCGTACCT ATATTTATGA CTTTATTACC TGCAATTAAT CTTGTAATCA 1200

TAAATAATGA AAGTGATGGA ATAAAGGTTA CTTGAATCCC AGTCATAACA CCTTCTTTTG 1260

TTAACGGCAT GATTACTTTT CTAAAAGTAT AGAAAGGACT GGCACCTAAA TCACTTGAGG 1320

CCTGCAATAA ATTATTAGGA ATTGCTTTCA TGCTATTAAA TATAGGTAAA ATCATAAATG 1380

GTATATAAAT GTAACTTGCC ACTACTAAAA ACGCACCAGT TGTAAATAAC AAATTGAATG 1440

ATGGTAAATT AAATAAGTGG AAAATTGATT AATCACGCCA TCATGACTTA ATAAACCTAT 1500

AAAAGCATAT GTCTTTAACA ATAAATTTAT CCATGTTGGA ATAATCATTA TCATTAATAA 1560

GATATTTTGA AATTTCGAAC GAGTAATATA ATAGGCAGnT GGATAACTGA TAGTCAAGGT 1620

AATAATTGTT ATTGAAGCGG CATATAAAAT TGAATATGCA AACATTTTCA AATATTTTGT 1680

AGTAAAAATT 1690

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

ACGAAAAGAA ATATTATGAT GAACAAAAAG AAAGAATAAC GATTTATATG AAGTACAATG 60

TGAAAGGTTA TAAAAATATA AGCTTCGCTA ATTTTAAAGA AAACCCAATG GATGGTTATT 120

CTATTAGTGG TTATATAAAT AAtGaTAAAA AGTTATCATT TACAGCTGGT ATAAGATCTG 180

TTGATGATTT TCAATTTGAT ACCGATATTT CTTATACAGA TGAATTGGGT AGAAAATTTA 240

ATAAAAATCC TAAGTCAGTT TCTGAAATAA AAAAAGAGCA AAATACGTCC AATAAATAAT 300

TGTTCATATT GTGATGAAAC AAAAATATAA GTCATTAGAT GAGTTTAACT ATGTTATAAA 360

TATTTGTAGT ATCTATAAAA ATCTCGACAC TATTAAAATG ATAAAGTGCC GAGGTTTTCT 420

TACTTATTTA GTTAATTCAA AGTTTATGCC AGATTCATAA GAATTTGTGA CACTTTTAAT 480

AGTGTAcCAT TGATTATTAC AATTTATCAA ATGGTCCTTT AGAAGGTATA AATAACAAAA 540

TATTATTATG TTCAAAACTT TACGCTCCAA AAAGTAAAAA GGAAGTTAAG CAATGTTTAG 660

TTGCTTAaCT TCGGaTATTG AACGCATCAG TCCAATTTGA CATAGAGCCT TTTTTAGTTC 720

TTGATGTTTC TCTTTAAAAC CTTGCATATT TTACAAAAAG AAAAATTAGC AGTATAATTA 780

AGACAACGAA AATAAGTATT TACTTATACA CCAATCCCCT CACTATTTGC GGTAGTGAGG 840

GGATTTTTAT TGGTGCGGCT ATATGTCACC TATTTTGTAT TGCGTCTACT TAGCCAATAA 900

GAAAAAAACG CAATGGCACA GCCACTGATG ACTGGTGCTA TGATGTGAAC GaAAATAAGC 960

ATCACCTTAT ACACCTCCTC TCTGCGTCTA AATTGACGsC TGAGaGrTAG GcGACTCTAC 1020

TATTATATCA TCGGCAAATA TACAAGCACA GTCACTTGCT TCTGATAAGT TATATGATTC 1080

TAGCTGATAG ATTGAATCGT CTACACTTAA TTGGACAAAT TCTATGAGAA TAGATATTGT 1140

TAATTTAAGA AAGTAGGCGA TTTTATTATG ACAAGAGAAA GAAGATCATT TAGTTCAGAG 1200

TTTAAGTTAC AAATGGTTAG ATTATATAAA AATGGTAAGC CTAGGAATGA AATTATACGC 1260

GAGTATGATT TCACACCTTC GACGTTTGTA AATGGCGGTT ATAAAATGTA GGAAAATGGA 1320

TAAAGCAACA TCAAAACACG GGTACATTCA ATCACCAAGA TAACTTATCG GATGAAGAAA 1380

AAGAGCTGAT TAAATTACGC AAAGAAGTTC AACATTTAAA AATGGAGAAC GATATTTTAA 1440

AGCAAGTAGC GCTGATTATG GGGCAAAAAT AGAAGTCATT CAAAAGAATG CACATCAATA 1500

TTCAGTATCA GCAATGTGTA AAGTCCTGAT AATACTAAGA AGTACCTATT ATGATTCTAT 1560

AAAAAGAAAA GATAATAAAA TCACTAAAGA TGATTCAAAC ATAGAACATG CCGTCATAAA 1620

TATTTTTAAT TCTAATAGAA AAGTCTTTGG TACAAGACGA ATTAAAAATC ATTTAAATGA 1680

CAAGGGTCTC ACTGTATCTG GACAAAAGAT AGGTCGATCA TGAAAAAATC TAGTTTCTGT 1740

TTATACGAAA TCTAAATACA AAAATCATCT AAAAGAAACT AATGAAAAAC GAATTAAAAA 1800

TCTTTATTAT TAGCTGCTGG TGTATTATTT GTTAGTCCAA TTTCATTATC TTATAATTCA 1860

GATGTAGCTC ATGCTGAAGA TAAGTTAGAC CATTCTCAAG CAAAGGTAAT ATATTTGAGT 1920

AACCAAAATT TATTTGATGA ACTTGAGAAA AAAGGTTATA AACTGGAAGA TATATTTACA 1980

AAAGAAGAAA TAAAAAAATA TAAAGCTGAA GACCAATTGA GAGCGGGTAA AACTCAATAT 2040

GTAGAAACAG GTAAAGATAC TGCAACATTA TATCTTTCTT CTGCATATAC AAAAACAATA 2100

GCTGCTTTAG GT 2112

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

GTAGGCACAC ATCTGCCATA TAAACATTCT TTTATACTAG TGTTCTCATA TAGTGTAGAG 60

TTATAGTCTC CTTCTTGAAT CTCGAATAAT TCAATCAACC TATCAACCTT AGTCTCTTCC 120

GTTACTTCTT TTTCAATATC AACTATGAAG GGGATATCAA TTGGAATAAA ACTTGACGTC 180

GAACACTTAT TTGTATTTGG ATGAAAACGA ACGAATCCAT CACTAAATCC TGTTGAAAAA 240

AATATTTTTC CTTGTGATAG ATCCGGATTT TCTCGCGCCC ATTTAATTAA TTCATCTAAT 300

CTCATTTCTT TTTTAACTTT GATTTTCATT GTTATATCTC CTCTTGAACA GTAAATTTAT 360

CGTTAAtTGA TACGTATCCA GTCACATTAC ATAAGATGCT ATCAACATCA AAAGTCACAC 420

AACAGTTGCG TTCAACATCA TTTGAATAGA ATCT 454

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

TTGTCAGAAT TAGAATGCTT TTGAGTTACT TCATAATACT CATCAGTTTT TTGTGTATCC 60

TTTTGACTTT TATTTATTTC TTTCCACTTA CCAGTATGAC TTTCTTTTTT TACAGTTATT 120

TTCGGTTTGT TTAAAAAATG ATAACCGATG TTCTTTTTGG TATCTGTGGA CTCTAAAAAG 180

ACTGAATTGT TTTCCTGATT ATCAGAATTG GTTGTTTGTT TATCGTCTGT ATATAACGTA 240

TACCCATTCG CTTTGCGATT TTCAATCGTT GTAACTGGAT TCTTTGATGA ATCAGTACTT 300

TTAATGCCAG TTCCTAAGAA GACAATTTTA TCGTTTAATA TGAAATATGA TTTTTTGGCA 360

GTTAAAGTTT TGTCCTGATT TTCAAAATCC ATTCCGATAC TAGCATGTTG GTCATCAACT 420

TTTGTTCCGC CAACAAAAGT TTTACTCGAC TTTTTATCAT CCGTATCTTT TAATATTTCA 480

TTGTCTAAAG TTGTTGTACC TGATAAACGT TTCATATCGG CTGTCACCCA GAAGTTATCA 540

TGATAGTGTT TGACATCGCT GTTATATAAA TAAGACATTC CAGCACCAGT GTGCCAACCT 600

TTTAAATTCT CTCCGTTGAT ACTTTCATAG CGTGCTACGT TTTTCGACGT CATACTTAAA 660

CCAAATGCAA AGTCTAAGTC TTTGTTATGA TAGGTGACAC GATCCATGTC ATTATATATT 720

TTAAGTTGTT GTGTTAATCC GTTTTTAGAA ATACTGTTAT CTGTCATTAA AGACTTCATT 780

ACTGAAGATT TGACAATCTT TTTATACTTA GCTTTTGTTG AATCATCCAT GGCATCACTT 900

AATCTCAACA ATGATTTCAT TACTGTTGCA GATGCTGAGT GACTGGTTTC ATTTTCACGA 960

CTGATAGCTC TACCTCGTGA TAAATCCATC ATTTCACCTT TATAAATGAG TGGCATAAAT 1020

CCGTCGTCAA TCCATGACTT TAAGGTTGTA TCATTTTGGG TTTTATCATT AAAAGGTGTT 1080

TCTTTTATCA TCGGCATCAT TTGAGAAATC CCCTCTAAGA GTACAACGCC ATAAGCACCA 1140

GTGTATGGAA CGTCTTGATG ATCAATGTAA GAGCCATCTT TATAAAATCC ATTACGTTCT 1200

TTACCAGTGG CAGAATCTTG AACGTAAGTG AAGACTTTAT TAAATGAATC TATAGACTTT 1260

TTCATCATAT CTTTATCTTC TTCGATAATA CATTCTAAAA GTTTCACCTT AGAAATGTCT 1320

ACTAnATTTC CGCCTTTAGC AAGTTCAGnT TTTCCTACAC AAGATAATAT TT 1372

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

ACAACAATAT AGTAAAGCGT CGTTAATTAA ACAATGGGAC CAATTTGTTC GTCTTATATA 60

AATGTACTTT aCCTTTATTT TTACAAAAAT AGCATTTTCC TATGTCATTT AACTAAACAT 120

GTAAGTTCGT ATGAACGAGG TTTGTTAAAT AGATGATTCT AGGAAAATGC TTTTTTCTTT 180

TGACTTAGTT TAAAATATTT TGCCACTTTG TACTGATAGT AGTTGCATTG TACTGTTGTG 240

CAGATTCTAT GCTATTAATT GAAAACTGTT GCAATTTTTG AGTATTATTT AGTAATTGGT 300

CGACCTTTTC AACCATTTGA TTGATGTCAC CTTGAGGTAC TAAATAGCCA TTAAATCCAT 360

CTTGaATCAG TTCTGaTGGA CCATAATCTA CATCATAACT GATCACTGGT GTACCTACTG 420

AAAgCGACTC TAAAATTGCT AAGCCAAAAC CTTCCATTTT ACTTGTCGAT AACATCAGTT 480

CTGCTTTAGC AATCTCTTCA TTAATATGCG TCTTAAAACC ATGAAATTTA ACATGTTCCA 540

GATATnATGA TAATCTTCTA CAAG 564

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

TATCCACCCC ACGAnAGCCC CGGAAACTTA TTGTGTTACA AGATATATAA GCAGAAACGA 60

ACAACAGTTA ACAAAATAAA TGAAATTAAA CGTTTTAAAA ATGAAACAAA TGAAATCATC 120

TATTAGGTTA TGAAACTGTT TATAGCTTGA ATAGAAGCAT TTATTTTTTA GGAGGACAAT 180

TATTATGCGT CAAACATTTA TGGCAAATGA ATCAAACATT GAGCGCAAAT GGTATGTTAT 240

CGATGCTGAA GGCCAAACAT TAGGTCGTTT ATCATCAGAA GTAGCATCTA TCTTACGCGG 300

TAAAAATAAA GTAACTTACA CACCACACGT TGATACTGGT GATTATGTAA TCGTTATTAA 360

TGCATCAAAA ATCGAATTTA CTGGTAACAA AGAAACTGAC AAAGTTTACT ACCGTCACTC 420

AAATCACCCA GGTGGTATCA AATCAATCAC TGCTGGTGAA TTAAGAAGAA CTAACCCAGA 480

ACGTTTAATT GAAAACTCAA TTAAAGGTAT GTTACCAAGC ACTCGTTTAG GCGAAAAACA 540

AGGTAAAAAA TTATTTGTAT ATGGTGGCGC TGAACATCCA CACGCTGCAC AACAACCAGA 600

AAACTACGAA TTACGTGGTT AATTAGAAGG AGGAAATGAC TTTGGCACAA GTTGAATATA 660

GAGGCACAGG CCGTCGTAAA AACTCwGtAG CACGTGTACG TTTaGTACCa GGTGAAGGTA 720

ACATCACAGT TAATAACCGT GACGTACGCG AATACTTACC ATTCGAATCA TTAATTTTAG 780

ACTTAAACCA ACCATTTGAT GTAACTGAAa CTAAAGGTAa CTATGATGTT TTAGTTAACG 840

TTCATGGTGG TGnTTCACTG GACAAGCTCA AGCTATCCGT CACGGAATCG CTCGTGCATT 900

ATTAGAAGCA GATCCTGAAT ACAGAGGTTC TTTAAAACGC GCTGGATTAC TTACTCGTGA 960

CCCACGTATG AAAGAACATA AAAAACCAGG TCTTAAAGCA GCTCGTCGTT CACCTCAATT 1020

CTCAAAACGT TAATTGTCGG ACGATATATA CAAAACACCT CGATATTATG TCGAGGTGTT 1080

TTTTTGGCGT TTTTGCGGCG AATATGGAAT GTGTAGAATA TAAATGAATT TTTACCTTCC 1140

CACCATAAAA GATGAAGAAC CATGAATGTG GAGAACAATA AATAGTTGGA TATTCTGTTA 1200

TTTTTTTGGA AGTGGAAGTG GATTTGGAAT ACTTTACTCn AAACGATTAA AAGGTTTAAA 1260

AAAACAACAA AnAGAAA 1277

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 673 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

TTATTGACAT TGTTTTTATC CAAAATTCAT TGTTAAGACA TTTTCTTTAT GAAATAATAA 120

TnATATTGAA GTATATTTTT ATTATTATTA AAAATAAATA AGGGGATACT TATGAGCACA 180

AATCAAACAT TTTTAATATT TGTTATAGCA ATTATTCTAC TTACATCTGT AATAGGAATT 240

GTTGGACGAT ACATGAGTCG TCAACGTCTA TTAAAATCTA TGGAAACATT ATGGCAAACG 300

ATTTCTCCAT TAGAAGCTTT TATCAGACCG AACTCACATT TCGACTATGA GTATAAGCTC 360

TACAAGGAAA AATTTGAATC ACATTCATTA GTTGATGATA AAACTTGGTC CGACTTAAAT 420

ATGAATGCAA TCTTTCATAA GATGAATTAT AATTTAACAG CTATTGGTGA AATGAAGCTA 480

TATGCCTGTT TACGTGGAAT GCTTTCAATT ACGAACAAAT CATTACTTAG TTTATTTAAT 540

GATAATGCTG AATTTAGAAA AAACGTAACA TATCATTTAG CTTTGATTGG tAAAACTGTT 600

aTCCAACATT TCCAGACCAA ATCACACCGG kAAACGTCCA AATATATTGn TCTATGCCCG 660

GTTTACCAGT ATC 673

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

AAAAAAAGTT AATGCTGACG GTGTATTAAC TTTTGATATT CTAGAAAATA AATATACTTA 60

TGAAGTTATT AACGCTATAG GGAAAAGATG GATTGTTAGT CATGTCGAAG GTGAAAACGA 120

CAAGAAAGAA TATGTAATAA CTGTCATTGA TAGGAAATCA GAAGGCGACA GACAACTGGT 180

TGAATGTACT GCTAGAGAGA TTCCCATAGA CAAGTTAATG ATTGATAGAA TTTATGTTAA 240

TGTAACAGGA TCTTTTACAG TAGAAAGATA TTTTAACATT GTGTTTCAAG GTACTGGAAT 300

GCTTTTTGAA GTCGAGGGCA AAGTTAAATC TTCAAAGTTT GAAAATGGTG GTGAAGGCGA 360

TACAAGGTTA GAAATGTTTA AAAAGGGATT AGAACATTTC GGTTTAGAAT ATAAAATAAC 420

GTATGACAAA AAGAAAGACA GATATAAGTT TGTATTGACG CCTTTTGCAA ATCAAAAAGC 480

GTCTTATTTT ATTTCTGACG AAtCAACGCC AACGCTATAA AACTCGAGGA AGATGCAAGT 540

GATTTCGCCA CCTTCATTAG AGGATATGGT AATTATTCAG GAGAaGAAAC ATTCGAACAC 600

GCTGGGCTCG TAATGGAAGC TAGAAGTGCA TTAGCTGAAA TATACGGCGA CATCCACGCA 660

GAACCATTTA AAGATGGTAA AGTGACTGAC CAAGAAACTA TGGATAAAGA ATTACAATCG 720

TATCCAGAAG CAGACCCACA ACCCGGAGAC ATAGTACAAA TAAAATCTAC CAAACTAGGT 840

TTGAATGATT TAGTCCGTAT AGTACAAGTT AAAACGATTA GGGGTATAAA CAATGTAATT 900

GTTAAGCAAG ATGTAACGCT TGGTGAGTTT AATCGAGAAC AACGATATAT GAAAAAAGTT 960

AATACTGCAG CTAACTATGT TTCTGGATTA AATGATGTTA ACCTTTCTAA TCCTAGTAAA 1020

GCGGCAGAAA ACTTGAAGTC TAAAGTAGCG TCAATAGCTA AATCAACACT CGATTTGATG 1080

AGTAGAACTG ATTTGATTGA AGATAAACAA CAGAAGGTAA GCTCTAAAAC TGTGACTACA 1140

TCTGACGGCA CTATCGTTCA TGATTTTATa GATaAATCmA ACATTAAaGA TGTAAAAmCG 1200

aTTGGAACGa TTGGCGATtC TGTAGCTAGA GGATCACATG 1240

(2) INFORMATION FOR SEQ ID NO: 494:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

ACGGTGGATT TAGCCTAGAA GATTTAACGC ATCAAGGTAa ATTaTCAGCA TTTAGCTTTA 60

ATGATCAAaC AGGTCAAGCA ACATTGATTA CTAATGAAGA TGAAAACTTC GTAAAAGATG 120

AGCAACGTGC TGGCGTAGAT GCAAATTATT ACGCTAAACA AACATATGAT TATTACAAAG 180

ACACATTTGG TCGTGAATCA TATGaCAACC AAGGTAGTCC AATTGTTTCA TTAACGCATG 240

TTAATAACTA CGGTGGTCAA GATAACAGAA ATAATGCCGC ATGGATCGGT GACAAAATGA 300

TCTATGGTGA TGGTGATGGT CGCACATTCA CAAGTTTATC GGGTGCAAAT GACGTAGTAG 360

CACACGAATT aACACACGGT GTGACACAAG AGACAGCGAA CTTAGAATAT AAGGACCAGT 420

CAGGCGCTCT AAATGAAAGC TTTTCAGATG TTTTTGGATA CTTTGTAGAT GACGAGGATT 480

TCTTAATGGG TGAAGATGTC TACACACCTG GAAAAGAGGG AGACGCTTTA CGCAGCATGT 540

CAAACCCAGA ACAATTTGGT CAACCAGCTC ATATGAAAGA CTATGTATTC ACTGAAAAAG 600

ATAATGGTGG CGTACATACG AATTCTGGAA TTCCAAATAA AGCAGCTTAT AACGTGATTC 660

AAGCAATAGG GAAATCTAAA TCAGAACAAA TTTACTACCG AGCATTAACG GAATACTTAA 720

CAAGTAATTC AAACTTCAAA GATTGTAAAG ATGCATTATA CCAAGCGGCT AAAGATTTAT 780

ATGACgAGCA AACAGCTGAA CAGGTGTATG AAGCATGGAA TGAAGTAGGC GTGGAGTAAA 840

AATATATAAA CaAGAAGAAG TAATGTTAAA CACTTATAAA TAATTAAATT TTAAATACAG 900

ATTAGATGAG AGGAGTGTGA GGGTTGTCTG CCGAAAGACT ACTCGGCAGT CTAAAATCAT 1020

TACAAGTAGT AGATATGTGA TAATTAAATG CTGACTTAGA ATACAAAATT CATTTTAAAA 1080

GTTGTCACAA AAAATTTACA TGTATTTTTA TTATCTTTTG CAAAACAAAG TGTTAAATTA 1140

TAAATGAaAC ATGCATGAAT TTATTTTTTA ATACAAGAAA CGTAACTACC AAAGGAGTTT 1200

ACAATATGAA GAAAAGTAAA CGATTAGAAA TTGTTTCTAC AATAGTTAAA AAGCATAAGA 1260

TTTATAAAAA AGAACAAATc ATTTCATATA TTGAAGAATA TTTTGGTGTA A 1311

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1761 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

TGCACTTTCT AAAAATACTT GCTTTACTTG TTCCAATTCC TTGTCAGACA TTGATTCGGC 60

TAATTTATTC ATTATTGCCT CAAATACGTT AATTATGTCA TCCATTTCAG TACTATAAAA 120

ATCAAACCAT TTTGCCGTAT CTTTTTCTCT ATTAAGCTTA TGATCACTTT GAGAGCGCTT 180

AGCTAATTCT GCATAAATAT ATGGACAAGG TGCCATTGCA GCAATTGTAT AAATAGCATT 240

TTCACGACTA TGCGCTTGGA AATACATATG TTTTATGTAA TGGTCGCCAC TTGGAGGCCA 300

AACTTTTGTT TTAATGATTT CTTCGTATGA TTCACCAACA ATTTGCGCTA AAATATCATG 360

CGCAAGTACT TCACCTTCAA CCATAAATTC TATTTGCTCT ACTAAAAATT TTACGTCATT 420

CATGCTATTC ATTTTTGGAA TTAACAAAGC ATATAAGTTT GTAAATTCTT TTAAATACGC 480

AGCATCAGCT TTTAAGTAAT GGCGTAATGC GTCAGcTCCT ATATCTCCGG ATAACATCTT 540

CTGAATAAAG TCATCCTCAT AAATATCATT AATGATTGGC TTTGCAGCTT GGTACAATTT 600

TTGTGAAAAT TCCATTGTAA AAAATCCTCC CTAAATAAAA AAACTACTTC CAACATGAAA 660

GTAGTTTGAT GGCAATGTTG CTATACTAGC CCCATCACTT CAATAACTAC TTTCCTACGT 720

TGGTACTAAC CAAATCAGGT CATAAGGGTC TGAACAATTC ATCTCAGCCA TATCATTAGG 780

CTCCCCTAGT AGTTCCTTAG TATTCAATTG CAAATTAATC TTAGCAAACG GTTTCAACAT 840

TTTCAATTAT TGTTGCTCAG TTGTATTATT ATCTTTAAAT AATAATTCTA TAATGACATA 900

TATTTGCGAA ATAAAAAAAC CGGAACATAT CGAGAATTCC CCGATATATT CCAATCTAAA 960

AGTTACTTAT ATAACTATTA ATTAGCTATG CATAAATGGC TTATGCAGTA ACCCAATGTC 1020

TTGCTGGTGA TACACCTTTA TATTTAGCAG GTGCTACTGA ATCCCAAGTT GATTGTAAGA 1140

ATTGATACTT ACCAGCTGCA CCTGgATGTT GGrTTTACAG CATGAATATT GCCACCTGaT 1200

TCACGTTGrG CAATTTGTTT TAGATGAGCa TTCACATTTA CTGATGAACC TTCTGATGAT 1260

TTTGATyCAG TTGGTGTTGC AGTAACTTGT GAATTGTTTG ATGTTGATGC TTGTGGTTGT 1320

TGAGTTTGAG CATTTTGTGG TGCTTCAACT TCTTGTGATT GTACTTGATT AGCTTGAACA 1380

GCTGATGGTG CAACATTATT AGTTGCAGGT GCTTGTGCAC TCATGTCTGC TCCATTAGTA 1440

CCTGTTGCAT GGTAATTCCA AGCAAAGTGT GTACCATCTG ATTCAAAGTG ATAAGTAAAC 1500

CCTTCATAGT CAAATGTATA ATTATAAGCC CCAGCTTCAA TTGGTTTTTG ATTTAATGTT 1560

TGATCATTTG ATTGCGCCAT TTGCCTGAAA GATGCTTTAT TTAAGTCCGC TTCACnTGCA 1620

TGGGCTTCGT GGACCTGCAT TTCCTGGCTA CGATTCCTAA ACCTACTGGC nAAnGATGAT 1680

GCGAGTAATG TTTTCTTCAT AATCTTAAAA TCCTCCTACA AGTGAATTTG TGTCTCTAAA 1740

AGTTTTACAG TGGACGACTG T 1761

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 794 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

TCATTTATGA AAAATGTCGG AnAGAnCCaa GaAAmaCAAT TGAgCGTGAA GAAAAAGCAA 60

GACTTAAAGA AGAACAAAAG GCACGTCAAA ATGAACAGCC ACAAATAAAA GATGTGAGTG 120

ATTTTACGGA AGTGCCTCAA GAAAGAGATA TTCCAATTTA TGGGCATACT GAAAATGAAA 180

GTAAAAGCCA GAGTCAACCA AGTCGAAAAA AACGAGTGTT TGATGCAGAG AATAGTTCGA 240

ATAACATCGT AAATCATCAT CAAGCAGATC AGCAAGAACA ATTAACAGAA CAAACTCATA 300

ACAGTGTTGA AAGTGAAAAC ACTATTGAAG AAGCTGGTGA AGTTACGAAT GTATCGTATG 360

TTGTTCCACC GTTAACTTTA CTTAATCAAC CTGCAAAACA AAAAGCAACA TCTAAAGCTG 420

AAGTGCAACG TAAAGGACAA GTACTAGAGA ATACATTAAA AGATTTTGGG GTAAATGCAA 480

AAGTGACACA AATTAAAATT GGTCCTGCAG TAACTCAATA TGAAATTCAA CCAGCTCAAG 540

GGGTTAAAGT GAGTAAAATT GTAAACTTGC ATAATGATAT TGCATTAGCT TTAGCAGCAA 600

AAGATGTTAG AATCGAAGCG CCAATACCTG GTCGTTCTGC AGTAGGTATT GAAGTGCCAA 660

ATAAACTAGA AGTTGGATTA GGaAGAGATA TATCAGGTGA TCCAATTACT GTTCCACTAA 780

ATGAAATGCC ACAC 794

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

AGCCAGTTTT GcATTTCGTC AAATCGCAAT GAATATATTG ATTGCTTGTC AAAATTTGGA 60

AGAAATTTAT TCTTCTTTTT CTTTTCAGCA GTTATCATTC CTAATTGTCC TTTCTTTTTA 120

TCTTAGTGAT AAAGAATCCA TCTGAATTAA AGTCTTGCGG CATGATTTGT AACGTTTTGA 180

CCAACTCTCC AGTTATCGGA TGTTGAAACG GTTCAAATTC GAAGTTTTTA TTATTTTTCA 240

AAAACGTATA AATCACGTTT TCATTTTCTA GTTGCTCAAT TGTACATGTT GAATAGATGA 300

TTTCTCCACC TATTTTTACA TTGTTTTTTA CATTTTCCAA TATTTCAAGC TGTAATTCAA 360

CTAGTGACTC AATATGTTGT TTGCTTTGAG TATACTTAAT CTCCGGCTTA TGTCTCATTA 420

CACCTAATCC GCTACATGGT GCATCAACAA GTATCTTATC GTATGTTTTA TCATAAGGTT 480

TTGTCGCATC ATGTTGAAAA GCTTTAATAT TTGTTAATCG TAATTnTTTT ATATTAAAAT 540

TAATTAAGTC TATTTTGTGA TCATGTATAT CTGAAGCGTC AACTTGCCCT TCTGGCATTA 600

AAACTTCAGC AATGTGACAA GCTTTACCGC CAGGTGCACT ACATGCATCT AATACGTGAT 660

CATGTCGGTC TACATTCATA ATGTGTGCAa CAAACATTGA GCTTTTATCT TGAATTGAAA 720

CGAATCCATC TTTAAATGAA CGAGAATGAA TAATTGGTTG TCCTCCTATA TGGAGACAAT 780

AAGGTAAGTC ATGATCTTTT TCAACGTCAT AACCTTCGTC TTGCAACTTT TCAATAATAT 840

CATCTAATGA TGCTCGCGTC AGGTTGGCAC GCACAGTTGT TGATGTCGTT TCTAAAAATG 900

ACTGTAAAAT TTTTTCAGTT TCTTCGAGAC CATAATGTGT TGCCCAATGA TCTATAATCC 960

ACTTCGGCAT ACTATACTCG ATTGCCATTC TTTTTTTAGG ATCTGCAATT TCATTAAAAT 1020

CAGGTAAGTC ACTACGCATC ATTGTACGTA AAATACCATT TACGACATTA CCATTATGAT 1080

AGCCACCGCG TTCTTTTGCT ATTTCAACTG CTTCATTAAT AATGGCATGA TTTGGAACTT 1140

TATCTAnATA nACATATTGA T 1161

(2) INFORMATION FOR SEQ ID NO: 498:

(A) LENGTH: 1504 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

AGCTCACGTC ATCTTCGGCG GCGCTAAATT AAAATAATCA ATTTCTGAGT TAAACTTTTA 60

TTTACAACAT ACTATTACTA TACATTACAA ATTTTTAAAA TATACATTAC ACTCATTACT 120

CAATGGmAAG CGTATGATTT CmCAGCCCCC CTAGCTTGTA GAAATCATAC TTTCCTTTTT 180

TCAATATATA TACAACTATT AAATCCCATA AGATTGCAGA GCACATAAGT AAATTTTTTT 240

AGAGCTTGAG GTTTGTTTAG CTTAAGCAAC CCATGAGCTC AAACACTTCC TGTTCACATA 300

ACACTACAAA TCGCATTATG TTGCTTAATC TTATGTTTAT ATAAATTACA CACAATAAAT 360

AGAAAGAATG TGAACATCAT GAATAAATTA TTGCTACTCG TTACATTTAT CATTCGTGTG 420

GGTTCAGGTA TTGTTATGTT AATGCAAGGC TACGAAAAAT TAACGGGCGG ATTTACGCTG 480

AAAGGTTTAG TACCAGTCAT CGCTAACAAT ACTGATTCAC CAGAGTGGTA TAAGTGGTTT 540

TTCGCAAATA TAGTTGCACA TACGACGTCA TTATTTGATA TTGTTGTCCC ACTCGGAGAG 600

ATTGCAATTG GATTAGGTTT AATTTTTGGA GTTTTTGCAT ATGCTGCTAG TTTCTTTGGA 660

GCCTTTGTTA TGATAAATTA TATCTTAGCA GATATGATAT TTACGTATCC TCTTCAATTA 720

ACTTTCTTTA TCCTTTTACT AATGAGTCAC TCATTGTTAA AACAGATTTC ACTTAAAGAA 780

ATCATTAATT ACTTTAGAGG TCGTAAGAAC AGAGGTGAAA AAATAGATGA CCCACTTACT 840

GATCGTGGAT GATGAACAAG ACATTGTAGA CATTTGTCAA ACCTATTTTG AATATGAAGG 900

TTACAAAGTA ACAACGACAA CTAGCGGTAA AGAAGCAATT TCTTTACTAT CAAATGATAT 960

TGATATCATG GTACTTGATA TCATGATGCC AGAAGTTAAT GGTTACGACA TTGTCAAAGA 1020

AATGAAAAGG CAAAAATTAG ATATCCCCTT TATCTATTTA ACTGCCAAAA CACAAGAACA 1080

TGATACCATT TACGCCTTAA CTTTAGGTGC AGATGACTAT GTCAAAAAAC CATTTAGTCC 1140

AAGGGAACTC GTTTTACGTA TTAATAATTT ACTTACAAGA ATGAAGAAAT ACCATCATCA 1200

ACCAGTTGAA CAACTGTCGT TTGATGAATT AACACTTATT AACTTAAGTA AAGTtGTGaC 1260

tGTAAaTGGT CACGAaGTCC CTATGCGTAT TAAGGAATTT GAGTTATTGT GGTATTTAGC 1320

TTCTaGAGAA AATGAAGTTA TTTCTAAATC AGAATTACTT GAAAAAGTTT GGGGATATGA 1380

CTATTACGAA GATGCTAATA CCGTGAATGT CCATATACAC CGTATTAGAG AnAAATTAGA 1440

AAAAGAGAGC TTTACAACAT ATACCATCAC AACTGTATGG GGATTAGGAT ATAAATnTGA 1500

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1623 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

ATTGAAAGCG ATAATTCGTA nTAATTGAGT TTGTTGAAAA ATTTAGGGTA ATGTAAAGAT 60

ATAAAAGATA CATAGAyTGG AGAGATATAA AGATGTTGAA TGAGATACAA ATATTAaATA 120

aTGGATACCC GATGCCTTCA GTTGGGTTAG GTGTTTATAA AATCTCTGAC GAAGATATGA 180

CTAAAGTTGT AAATGCTGCA ATTGACGCAG GCTATAGAGC GTTTGATACA GCATACTTTT 240

ATGATAATGA GGCTTCACTA GGACGAGCAT TAAAGGATAA TGGCGTCGAT AGAGAAGATT 300

TGTTTATAAC AACGAAGTTA TGGAATGACT ATCAAGGTTA TGAGAAAACA TTCGAATATT 360

TCAACAAATC GATTGAAAAT TTACAAACTG ATTATCTTGA TTTATTTCTA ATACATTGGC 420

CTTGTGAAGC AGATGGTCTA TTTTTAGAAA CATATAAAGC TATGGAAGAA CTTTACGAGC 480

AAGGTAAGGT AAAAGCAATA GGTGTATGTA ATTTTAATGT TCATCATCTA GAAAAATTAA 540

TGGCTCAATC AAGTATCAAA CCAATGGTGA ATCAAATTGA GGTACATCCA TATTTTAACC 600

AACAAGAATT ACAAGAATTT TGTGATCGTC ACGATATTAA AGTGACTGCA TGGATGCCTT 660

TGATGAGAAA TAGAGGACTA CTAGACGACC CTGTCATTGT TAAAATTGCT GAAAAATATC 720

ATAAAACACC AGCACAAGTT GTATTACGTT GGCATTTAGC ACACAATAGA ATTATTATTC 780

CAAAATCTCA GACACCTAAA CGCATTCAAG AAAATATAGA TATTTTAGAT TTTAATTTAG 840

AATTAACAGA AGTAGCTGAA ATTGATGCTT TAAATAGAAA TGCAAGACAA GGTAAAAATC 900

CAGATGATGT GAAAATTGGG GATTTAAAAT AACTGGATGT TAAATTTTAC GTTTATGAAT 960

GCCTTTTAAT GTGTACATTA AAATAAATGA GTTGGTTTTT ACTATTTGAT AAAACAATAC 1020

TCAGGTACAT TCAAAATCTT TTAAATAAAA AGGATGGACA TAGATGAAAA TTAGAGTCGT 1080

CATTCCTTGT TTTAATGAAG GGGAAGTCAT TACACAAACA CATCAACAAT TAACTGAAAT 1140

ACTTTCACAA GATAGTAGTG TGAAAGGCTA TGATTATAAT ATGCTTTTCA TAGATGATGG 1200

TAGTACGGAT ACCACTATAG ATGAAATGCA ACATCTTGCC ACAATAGATA GGCATGTCAG 1260

CTTTATTTCT TTTAGTAGAA ATTTTGGAAA AGAAGCAGCT ATGATTGCAG GTTACCAGCA 1320

TAGTACTGAA TTTGATGCAG TCATCATGAT AGATTGTGAT TTGCAACATC CACCTGAATA 1380

TAGAAGTGGT GAAAATTTTA GTCGCAAAAC ATTAAGCCAT TTGTATTATA AGTTAGTTAA 1500

TTGCTTTGTA GAAGAAGTAC AATTTGATGA TGGTGTTGGT GATTTTAGAC TTTTAAGCCA 1560

AAGAGCTGTT AAATCCATTG CATCACTTGA AGAATATAAT CGnTTTTCAA AAnGGnTATT 1620

TGA 1623

(2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 605 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

AAAGTnGGTG AAnCTATATA CTTAATCTAT ATTTATATAT TAACCATTAG GGTTAAAAAT 60

TACTCTAGCA TTTATGAATA GATGGGAGTT TATTTTATTA TTATATAGGA GAGATGTTGA 120

ATGACACATC GCGCACTATT AGTTGTTGAC TATTCATATG ACTTTATCGC AGACGACGGC 180

TTACTAACAT GCGGTAAACC TGGACAAAAT ATTGAAGATT TTATTGTTTC TCGTATCAAT 240

GACTTTAATT ATTATCAAGA CCATATATTC TTTTTrrTGG ATTTACATTA TTTACATGAC 300

ATTCATCATC CTGAAAGTAA ATTATTCCCA CCACACAATA TCGTAGATAC AAGTGGTAGA 360

GAATTATACG GTAAAGTAGG TAAATTATAC GAAACAATTA AAGCGCAACC TAATGTACAT 420

TTCATTGATA AAACGCGCTA TGATTCGTTC TTTGGTACCC CGCTTGATAG TTTATTGAGa 480

GAAAGAAGTA TTAATCAAGT CGAAATCGTT GGTGTATGTA CCGATATTTG CGTGTTACAT 540

ACAGCAATTT CTGCATACAA CTTAGGtTAT AAAATTTCAG TACCTGCTGA GGGAGTGGCT 600

CATTT 605

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1739 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

TAGGTTnAAA GCATAGnTTT nTCAAAAAGA CAAATCATTC ATATATTGGA GGATATTTTG 60

GTGTAAGATA TAGTGCAACC ACAATTGCTA AAGACTTGAA GGAACTAAAT ATATATCGTG 120

TGAGAGAAAA GTTTAGACAC TATTGTGAAC ATGAAGTTCT AAGTTCAATC ATCAATGGTT 240

CATACATTAT CGTCAAAACC TCACCTGGTT TCGCCCAAGG CATAAACTAT TTTATCGATC 300

AGCTAAATAT AGAAGAGATA TTAGGTACGG TGAGTGGAAA TGACACTACA TTAATCTTAA 360

CTGCCTCAAA TGATATGGCA GAATACGTAT ATGCAAAATT ATTTAAATAG ACATGTATCA 420

AATGAATAAT AAAAATTTGT TTCGTATCAC GTGTACTCAA GTTAGTTACC AAATATTAAC 480

TTGTGTACGC GTTTTTTTAT GGAAAGAAAG AATTCATAGT CATTCAATTG ACTGTATAAA 540

AAACTTTATA CAACATGTTT TTATGGGTAT TTTTGAATAA AAAATGTATA TTTTGACCCA 600

AAATACCTTT ATTTATGTAT AAAAATCCAT TATTATGTAT TGTATAACAA AAAGATATGA 660

AATTTTCGAC TTTCTTTATG TGAATATAAT CACATGTAAG CGTTTGAAGA TTGTCTATAC 720

TCTAAATGAA TTCAAAGATA AAAGGAGGAA ATAGACATGA CAGATGGTCC AATTAAAGTA 780

AATAGCGAAA TTGGAGCTTT AAAAACTGTG TTACTTAAGC GTCCTGGaAA AGAATTAGAA 840

AATTTAGTAC CTGATTATTT AGATGGATTA CTATTTGATG ATATTCCATA TTTAGAAGTA 900

GCTCAAAAAG AGCATGACCA TTTTGCGCAG GTGCTAAGAG AAGAGGGTGT TGAAGTACTT 960

TACCTTGAGA AGTTAGCAGC TGAAAGTATT GAAAATCCTC AAGTAAGAAG TGAATTTATT 1020

GATGATGTAT TAGCAGAGTC TAAAAAAACA ATATTAGGTC ATGAAGAAGA AATTAAGGCA 1080

TTATTTGCGA CACTTTCTAA TCAAGAACTT GTAGATAAAA TAATGTCAGG GGTACGTAAG 1140

GAAGAAATTA ATCCGAAATG TACACATCTA GTAGAGTATA TGGATGATAA GTATCCATTC 1200

TATTTAGATC CAATGCCAAA CCTTTATTTT ACTAGAGATC CACAAGCCTC AATAGGACAC 1260

GGTATAACAA TCAATCGGAT GTTCTGGAGA GCACGACGAC GAGAATCAAT ATTTATTCAA 1320

TATATTGTAA AGCATCATCC TAGATTTAAA GATGCGAATA TTCCAATCTG GTTAGATCGA 1380

GATTGCCCAT TCAATATTGA AGGCGGCGAT GAACTTGTTT TATCTAAAGA TGTCTTGGCT 1440

ATAGGCGTTT CAGAACGTAC ATCTGCACAA GCTATTGAAA AGTTAGCGCG ACGTATTTTT 1500

GAAAATCCGC AGGCGACGTT TAAAAAAGTA GTAGCAATTG AAATTCCAAC TAGTCGAACT 1560

TTTATGCACT TAGATACAGT ATTTACAATG ATAGATTATG ACAAATTTAC AATGCATTCA 1620

GCCATTTTAA AGGCAGAAGG CaATATGAAT ATATTTATTA TTGAATATGA TGACGTAAAT 1680

AAAGATATTG CCATCAAACA ATCTAGTCnT TTAAAAGATA CTTTAGAAGA CGTACTAGG 1739

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1745 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

CTGTACATAC AGCAATATCG TTAACAAATG AAAACAGTAT TTTAGGATTG TAAACCATGA 60

TAAACCTAAA ATACTGTTAT TTTTATTACT TAAATTTCTT CTTCAATGCC TTTTCAACAT 120

AAGGTGGAAC GAATTCAGAA ATATCTGCTC GATAAGCTGC AACTTCTTTA ACAATACTTG 180

AACTTATAAA TGAATAATTA GTACTAGACA TCATATATAA CGTTTCAATT TCATTGTTCA 240

ACTTTTTATT CATTGAAGTT AAGCGTAATT CATATTCAAA ATCACTGACT GCTCTTAAAC 300

CACGTATGAT TGTTTTAGCT CCTACTTGTT CACAATAATC GACTAGTAAA CCACTAAATT 360

GATGAACCTT GACATTAGGT AAATGTTTAA CAGATTGTTC AATTAAATCC ATACGCTCTT 420

CTAAACTAAA CGTACCTTCT TTTTTACTAT TTTTAAGAAC ACAGACATGA ATTTCATCAA 480

ATCTATCTGT ACTTCTCTCA ATAATGTCTA AATGACCATA AGTAATGGGG TCAAAACTAC 540

CCGGAATGAC CGCTATTGTA TGTTCCATGC TATTCTCCCT TTTCTAATAA CAATGTGTCT 600

GTCAACCCAT AATGGTAACG TTTAATCATA TTAAACGGTT GATAATCtAT TTCTTCATGA 660

TTGCTAAATT CACAAACGAT GATACCATTT TCTTTCAATA AATTAAACTC TGAAATTAGT 720

TTTAAAGCTT TATCAATGAG ACCTTTATTA TAAGGTGGAT CTAaGAAAAT GACATCAAAT 780

TGAATATCAC GTTTTGACAA TGCTTTTAAA GCTCTATCTG CATTATTTTT ATAAACTTCA 840

GATTGTGCCT CTAAATCCAA ATTCGCAAGA TTTGaTTTAA TAACTTTTAC AGCTTTAAAA 900

TTTTGaTCAA CAAAGATTAC CTTATCCATA CCTCGAGAGA GTGcTTCTAT TCCAAGCGCC 960

CCGCTTCCTG CAAATAAATC TAAACCTATA CCTGACACAT CATATAAACT ATTAAAGATA 1020

CCTTCTTTAA CTTTATCCAT AGTTGGTCTC GTATTACGGC CTTCCATACT TTCTAAAGCT 1080

TTACTTTTAT GTTTACCTGC AATGACGCGC ATGTTGTTCA CACTTCCAAT TCATTTAGTT 1140

ATTTAATATA ATTTATTGAG AAAAAGGAGA ATGATAAACC AATGAAACAA ACATTTATTA 1200

CACTTGGTGA AGGTCTAACA GATTTGTTCG AATTCATGAC GATGATTGAA TATAACCATC 1260

AACGTATTGA TAAAATTATC TATTTTCATT CACCACAAGC TGAAAATAAA AAGTCATCTG 1320

TAGCAATCAT TATGAACCCT ACAACTGGCA ATCATTTCCA AGCATTTTAT ATCATGATAA 1380

ACGCTATTAA ATATCCATAT CCAGATTCAA ATAAAAAGTT TCAAATGATA AATGATTGTG 1440

CTGAAAAATT CGACATACCA ATTTTAGGTA TCGATGTACA GCCCCCTCAA GCATTTCATG 1500

ATTTATCGTT ATATTATAAT TATTTAATTA GTGTGTTAAG GCTCCAAAAA TGGATACCAG 1560

aACTTCAATA ATATTAATTA TATATTTCGT GTTTCTCTTT TTCGTAAGTT TTCTTTAAGT 1620

TTTGATCAAC ATCTTGCTCA TTCACATACA TAATTACAAA TTTACGATCT CTATTTGAAT 1740

GAACG 1745

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1035 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

TCGTCTTTAA TCTTGCTGAC TTTAGAAGGC TTACGAGTGC GGTTACCATT TTTTGCATCT 60

TTAACTGATT GAACTAAAGC TtGACGTGTA GATTTATCAG CTAAACTAAT TGCACCACCA 120

ATTACGGCAC CAATTAAAAT ACCAGGAACA AATTTATTTT CCATAAAAAA CTACCCCTCT 180

TTCAAATTTG CATCTTTTAC GATGTAGTCT ATTAAATTAT CACAAGATGA TAATACCATG 240

TCGTATACAC CTTCAAAATT ATTCGTGTAG TATGGATCTG GTACATCACT CTCTTCCATA 300

TTACTAAATT CTAACAGTTT GAACAATTGT CCCTTAAGAT TAGGATTGAT AGATTTAATA 360

TTATCAACGT TACTTTGATC CATAGCCACA ATGTAATCAA AATCATCTGT CGCTTCGAAT 420

AATTCACTAA TCATGCCATC AAATGGAATA TTGTGTTTGT TGAGAATTTT TTGTGTACCT 480

TCATGAGGTG GCTCTCCTAA ATTCCAGCTA CCAGTACCTC TTGAATGTAC TTTAATATCA 540

TGAATATTTC TGTCTTTAAG TCTTTGTCGC ATGATTGCTT CTGCCATTGG AGAACGACAT 600

ATATTGCCAA GACAGACAAA TGCTACATCT ACCATTTTGA TTCCTCCAAA CTATGTAGTT 660

ATATCCCCAT TTTATAGCGA CTTTAAACAA TAAGAAAGCA GATTATATAA AATTCTATTA 720

AAGTTTATTA AATTGTGATA CTTTGATAAC ATAACTATTA TTAGAGGTGA ACATTGTGGC 780

TATGACAAAT GAAGAGAAAG TnTTAGCTAT TAGAGAGAAG TTAAATATTtG TTAATCAAGG 840

ATTATTAGAT CCTGAAAAAT ATAAAAATGC AAATGaAGAA GAATTAACAG ATATATATGA 900

TTTTGkTCaA yCAAGAGaAA GATTGTCGCC AAGTGaAGTG mCAGCTATTG CTGaCGCTTT 960

AGGACAATTG CGACACGAAT AGGAGTGGGA ATTTTGACTA ATTACAAAGA AAAGTTACAA 1020

CAATACGCTG AACTA 1035

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

AnCCTGACAA GATTCTTATA TTCATAGATA TGAGAGCTAA AAATGAAATC AACAAACAnA 60

CAATAAAGTA AACGATAATA GCCCATATAC CATTTTGTAA CCATATTACA AATTGTGTTG 120

TATTATAGCC ATTTCCAGCT AATAATTGCT GGATAAATGC ATTATTGTTT AATGTATTTT 180

CAAGATTAGC AAtCGATGTG TTATTACTGA ATGAAACAAG TGCTATAAAC ATCGTAATGA 240

CAGTAAGCAC TAATAACATC ACCCAACATA ACCAACCTAG AACTTTTTCA GTTAATCTAC 300

TTACTGGACG TTTAATTTGA GTAAATTGTT CTCCAGTCAT TCGTTACAAC TCCTTATAGT 360

ACTTATCCCG TTATTATAAC TAAATATACA GTAAATAACT ACTATTTATG ATTTTATTTT 420

AATGACATTT TGAAATTCAA AAAGTTTTCA TTGTATTCAC TTAAAACTTC AGGTCCTAAA 480

TCTTTATAAA CTTCAAGGCG TTCTTGCTCT TTCTTAGTCG GATAAAAACG ATGGTCGTCT 540

TTAATCTCTT TAGGCAACAA TTGTCGAGCA GCCTTGTTTG GCGTTGCATA GCCTACGAAT 600

TCTGTATTTT GCTTGTTATT TTTAGCATCT AATAAAAAAT TCATAAATTT ATATGCACCC 660

TCTTTATTTT GTGCCGTTTT TGGAATTACC ATATTGTCGA ACCATAAATT CGATCCTTCT 720

TTAGGAATAA CATAATTATA TTTATCCCCT TCTTGCACTA GAGGTGCTGC AACACCACTC 780

CAAACAACCG CTATGTTACC TTCATTTTGT TGAAGCATCA TGGTAATTTC ATCACCTACG 840

ACACCTCTTA CTTGTGGTGC TAGTTTGGTT AAATCTCGCT CTGCTTCTTT TAAATGGTGC 900

GAATTACGGT CATTAAGATT ATACCCAAGT TTATTCAAAC TCATGCCTAT AATCTCTCTA 960

GCACCGTCAA CTAGTAAAAT TTGGTTTTTA AATTTAGGAT TATACAATGA CTTCCAACTA 1020

TCAAATGATT CATTTGGATA CTTTTCTTTA TTATATAAAA TACCTACAGT TCCAAAGAAA 1080

TAAGGTAAAG AATATTTATT GCCTCTATCA AATGACATAT TCATATAATC TGAATCTAAA 1140

TTTTTAATAT TAGGTACCTT ATTATGATCT ATTGGTAACA ATAAATGATC TCTTTTCAAT 1200

TTTTGAACTG nATATTCACT AGGAnAAGCA ACATCATAAT GTGTACCGCC AGTGCGAATT 1260

TTGGnGTCCA nCGCTTCATT TGAA 1284

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5763 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATAATTAACA TCTTTTGCTA TATACCACCA GTTTGATACA TAAAATATCG CAGCAATAAT 60

ATCATGTTTA ACCCTAATGA TATTATCTGA TTTTAATAAT AAGGTTGCTG TCCCTACAAC 120

CATTAATAAA ACTATGACTG CTGGTAATAA ACGTTTTAAA CGACGTATCC AAAAGCTTTT 180

CAATTTAATG ATACCTGTGT CATCATACTC TTTGAGTAAT AAGCTTGTAA TTAAATAACC 240

AGAGATCACA AAAAATGTAT CCACACCTAA AAAGCCACCT GtCAACCATT GCTTATTTAA 300

GTGGTAAATA ATAATTCCTA GAACAGCGaT TGCCCTCAAA CCATCGAGCC CTGGAATATA 360

TCTCATTTTC TTATACTTTG TAAAACCCTT TGTTTTGTTC ATTTTTGCAT TCTTCCCTTT 420

TAAAACTGTT CTTCTTAGAT GCTTAATTAA ATTTAGTTAT GCTGTTTAAA AGAATATTGA 480

AATGCATATG TATATTATTG AATTACGACA TCATCAAAAT CATATTGACT AAAATACTGT 540

TAAATTAAAA AAATTACCAA TGATGATTCT TACTTCGAAA TCCAATTTGT AATGCAACTC 600

GGCAACTTAA AAACTATGAA GTATTATGTA TTGTAATATA ACTGTAATAT AAATTCAATT 660

TATTATAAAA ATTTTCAAGA AAATATTCAA CTAGAAAATG AATTGTGCAC TCTTGGAAGT 720

GCAAGTCACT GTCTTAATTC ATATTTTTTG AAACAAGTTA GATATAAATT TTCAAAATAA 780

AATCAGAAAC TAGAACATAA ATAAGGCTCC CTTCAAAATT TTCATTTTTC AATGTCTACT 840

TTGAAGGGAG CTTATTCACA ATGAATTATA CTCTACAATG TTATATTGAC TGCGGGCCCA 900

AACACAGAGA ATTTCGAAAA GAAATTCTAC AGGCAATGCA AGTTTATGTT AGCTCACACC 960

AAGTGCAATC TTAGCGTAAC GTGACATCAT ATCTTTTGTC CAAGGTGGAC TCCATACGAT 1020

ATTCACTTCA GTATCCTGAA TTTCAGGAAT CTCTGCTAAT ACTGTTTTAA CTTGaTCAAT 1080

AATTTGAGGT CCCATTGGAC ATCCCATTGA TGTTAAAGTC ATATCAACTG TACATACGCC 1140

TTCATCATCA ACATTCACTT TGTATACTAA ACCCAAATTA ACGATATCAA TTCCTAATTC 1200

AGGGTCAATT ACCATTTCTA ATGCACCTAA GATACTATCT TTCAATGCCT CTTCCATCCA 1260

TATCACCTCT TTAATGTCAT ATTATTCATA ATATATCAAA TATCCGACAA AACGCCAATA 1320

AAATGCTATG ATGTATCTAT ATGAACTAAG CAACTTATGA GGAGAGAGAT ATGCAACCAC 1380

ATTTAATATG TCTAGACTTA GACGGAACAT TATTAAACGA TAACAAAGAA ATTTCATCAT 1440

ATACTAAACA AGTATTAAAT GAATTACAAC AACGTGGaCA CCAAATTATG ATTGCGACTG 1500

GCAGACCTTA TCGTGCAAGT CAAATGTATT ATCATGAATT AAATTTAACG ACACCAATTG 1560

TTAATTTTAA TGGCGCTTAC GTACATCACC CTAAAGATAA AAACTTCAAA ACTTGCCATG 1620

AAATTTTAGA TTTAGGCATC GCACAAAACA TTATTCAAGG ATTACAACAA TATCAAGTAT 1680

CGAATATTAT AGCAGAAGTG AAAGATTATG TTTTCATTAA CAATCATGAT CCAAGATTAT 1740

AAGAATCCCC TACCTCAATT TTAATTGAAG CCGAAGAAAG TAAAATACCT GAAATCAAAA 1860

ATATGCTTAC TCATTTTTAT GCCGATCATA TTGAGCATCG ACGCTGGGGC GCACCATTCC 1920

CTGTCATTGA AATTGTAAAA CTTGGTATTA ATAAAGCAAG AGGCATTGAG CAAGTTAGAC 1980

AATTTTTAAA TATTGACCGA AATAATATTA TTGCATTCGG TGATGAAGAT AATGATATTG 2040

AAATGATTGA GTACGCGCGT CACGGTGTTG CTATGGAAAA TGGTTTGCAA GAACTTAAAG 2100

ATGTAGCGAA CAATATTACA TTCAACAATA ATGAAGATGG CATTGGTCGA TATTTGAATG 2160

ATTTCTTTAA TTTAAATATT AGATATTACT GTTAATTTAT AACTAATCAT TTTATAATAT 2220

TTTAAAACAA TAGGAGGTAA GTTACGATGC CCAAAATAGT CGTAGTCGGA GCAGTCGCTG 2280

GCGGTGCAAC ATGTGCCAGC CAAATTCGAC GTTTAGATAA AGAAAGTGAC ATTATTATTT 2340

TTGAAAAAGA TCGTGATATG AGCTTTGCTA ATTGTGCATT GCCTTATGTC ATTGGCGAaG 2400

TTGTTGAAGA TAGAAGATAT GCTTTAGCGT ATACACCTGA AAAATTTTAT GATAGAAAGC 2460

AAATTACAGT AAAAACTTAT CATGAAGTTA TTGCAATCAA TGATGAAAGA CAAACTGTAT 2520

CTGTATTAAA TAGAAAGACA AACGAACAAT TTGAAGAATC TTACGATAAA CTCATTTTAA 2580

GCCCTGGTGC AAGTGCAAAT AGCCTTGGCT TTGAAAGTGA TATTACATTT ACACTTAGAA 2640

ATTTAGAAGA CACTGATGCT ATCGATCAAT TCATCAAAGC AAATCAAGTT GATAAAGTAT 2700

TGGTTGTAGG TGCAGGTTAT GTTTCATTAG AAGTTCTTGA AAATCTTTAT GAACGTGGTT 2760

TACACCCTAC TTTAATTCAT CGATCTGATA AGATAAATAA ATTAATGGAT GCCGACATGA 2820

ATCAACCTAT ACTTGATGAA TTAGATAAGC GGGAGATTCC ATACCGTTTA AATGAGGAAA 2880

TTAATGCTAT CAATGGAAAT GAAATTACAT TTAAATCAGG AAAAGTTGAA CATTACGATA 2940

TGATTATTGA AGGTGTCGGT ACTCACCCCA ATTCAAAATT TATCGAAAGT TCAAATATCA 3000

AACTTGATCG AAAAGGTTTC ATACCGGTAA ACGATAAATT TGAAACAAAT GTTCCAAACA 3060

TTTATGCAAT AGGCGATATT GCAACATCAC ATTATCGACA TGTCGATCTA CCGGCTAGTG 3120

TTCCTTTAGC TTGGGGCGCT CACCGTGCAG CAAGTATTGT TGCCGAACAA ATTGCTGGAA 3180

ATGACACTAT TGAATTCAAA GGCTTCTTAG GCAACAATAT TGTGAAGTTC TTTGATTATA 3240

CATTTGCGAG TGTCGGCGTT AAACCAAACG AACTAAAGCA ATTTGACTAT AAAATGGTAG 3300

AAGTCACTCA AGGTGCACAC GCGAATTATT ACCCAGGAAA TTCCCCTTTA CACTTAAGAG 3360

TATATTATGA CACTTCAAAC CGTCAGATTT TAAGAGCAGC TGCAGTAGGA AAAGAAGGTG 3420

CAGATAAACG TATTGATGTA CTATCGATGG CAATGATGAA CCAGCTAACT GTAGATGAGT 3480

TAACTGAGTT TGAAGTGGCT TATGCACCAC CATATAGCCA CCCTAAAGAT TTAATCAATA 3540

GTTAGAATTA TGTTGGACTG GTACTACTAT CCAGTCCATT TTTTATGTTT AACATTTTTA 3660

GAATCAAAAA AGACATAAGG TCTTGGACTA ATAATTGTCC ATGCCTTATG TCATATACTA 3720

TATGTCTTAT CAATTAGCCA ATACCGAATA ATTTTGATAT AGGsCCTAAC GGTAGAATGA 3780

CACCTAATAC CATTGTGATG ATAATTAATG CAATTGTTAT CCAAAACATT GTGTGACTTT 3840

GTTCATGTCT CTTTCTTTTA GCAATCGACA CTTCCATCAA TCCAACTACT GCAACACCAC 3900

ACAGCATTTT CAATGTAAGC AACATATGAT TTGCCCCGCC ATTCATAAAT GACTGAATTA 3960

ATATCCAAAA TCCTGAAATT AACGTCAACA GCATAAATAA GCGTAAAATC ATGTGCAACG 4020

GTTTGAAAAA TGGTGATCTG CCTTGATTTT TTGAAATGTT TAAGTATGTA GCGATAAATA 4080

AAATAATCGC TAATACCCAA CTTAATATAT GTAAATGTAA CATACTGATT CCCCCCACTT 4140

TAATTATTTA TATTATTAAA TTAAAGCTTC TTGGGATTAA TACCCACTTG CTTGTAATTT 4200

AATCATGATT TGATTATACA CGAATATATA TTCTACCACA CTTCTATATT TGAGAGGAAG 4260

AACATGACAT TTTATTCCTT ATTAGAATAT TGTGAATCTG CTGTAAAATA ATCAACTACT 4320

TCTTAATATC AATATTTCAC TTTCATCTCA AAATGGTAAC ATTATAAATA ATTTATCTTT 4380

AACACCTTTT TAGAAAAGCA AGAAAAAACT AACCAATCTA TATAAAGACT GGTTAGCTTT 4440

TTAAATGATA ATTATTTAGC GATATAAGTT GTCAGCGTTC CAATATTATC AATAGTCACT 4500

TTAACTTCAT CACCTGGTTG TAAAAATTTA GGTGGTTGCA TACCTGCACC AACGCCTGCT 4560

GGTGTACCAG TTGCAATAAT ATCTCCCGGA TGTAGTGCAA CATATTTTGA AATTTCTTCT 4620

ATTAATTCAT CAATTTTAAG AATCATTTCG CCAGTGTTAC CATCTTGTCT AATTTCATTG 4680

TTAACTTTTG TAACAATATT TACATTTTCA GGTAATGGTA GTTCGTCTTT AGTAACGATA 4740

TAAGGACCCA TTGGGCAACC GCCAGTTAAA CTTTTTGATA AAAATGCTTG ATCTTGTTCA 4800

CTTTGTGCTT TGCGATCAGT GATATCGTTA ATAATTGTAT AGCCGTAAAC ATAATCTAAA 4860

GCTAATGCTT TTGGAATCTT TTCACCAGAC TTACCAATAA CAATACCTAA TTCACCTTCA 4920

TAATCTAATT GATCAGTAAT ATCTTTATGA TTTGGAATTG TTGCATTATC TCCTGTTAAA 4980

GATGACGCTG CTTTTGTAAA TACATATAAT TTTTCCACTT CATGATTTAA TTCGTTCGCA 5040

TGATCTTTGT AATTTCTACC AAAAGCAATC ACATTATTCG GAGGTGTTAC TGGTGGTAAA 5100

AATTCAATGT CATTAAATGA AATTTTATAG TCTTCAGCTT TGCCGCTATC TTCTGCTGCT 5160

ACAACTGCTT TACGTACTTG TTCTTGAAAA TCTAAAGTAT GATTTTGTTG TAAACCAGCT 5220

AACAATGTTT TAGGATGGAA ATCTCCTTCT GCAAAGTCAG CAAATACTTG TGTTAAATCC 5280

CATACAGCAT CTTCGCGTTT TACTTTAACG CCATATGAAG TTTTGTCATT ATACTTGAAT 5340

TTCGTTATCA AATAACAAAT AAATAAGTAA GACAATTTTG AAAATGAGTT GTGTTCATTC 5460

TGCTACAAGG ACTTTGCACT TAATCGAAAT TATTTTTTAT TCTTTTGAAA ATCAAAATAC 5520

TATAGTTGCA ATGTACCAAA TTTGAAGAAG TATAAATAAC CTTTAACTTC TTTATTAAGA 5580

ATCGTTTGAA GCGTATTTTG ATAATATTTC ATCTGTATCT TATATTTATT TTTTAATTGT 5640

GTACCAATTT CTTCATCTGT CATCCCACGG CGACGATTAA ATGCATCGGT TTTATAGTCT 5700

ACAAAATAAT GCACACCATC TTTAACAAAG ATTAAGTCAA TCATACCTTG AATAATTGAG 5760

ACG 5763

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 422 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

CCATATGATT TTGTGCAATA ACTCTTTTTC TTTCTTCTTT TCGTAAAAAG TTGTACATCG 60

CTTTTGTGTT TAAGAGACTA TTGTTTTCTT TAGGTTTTTG AACTTCACTC AGTGTATTTC 120

TAGTTGTTAA CACTAAAATT CCAACTGTTG TATCTTTGTA TCTAGCCATA ACTTTATTCA 180

GATGTTTGTC ATTTGTAATA ACTACGACAT AATTAAACAC TTCATAATAA TCATTAATTT 240

GATTATCTAA TCTATCCAGC TTATCTAATT CTGTTTTAAT CTCATAGACA ACGCCTTTGC 300

CGTTTAACAA TATAAAATCA GCaATACTTT TCCCTATGGG CATCTCAGAA AGTGCAGTAG 360

TTGTATTAAT AGAATGTCGT CCTAGAAGGA GTkTATTAAG TATnGTGTTT TTGTAAAAAT 420

AT 422

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

GCTTATGTAT TCTCAAAATA TTTATGTGAT ACGCAAAGGA GACATGGTTA TTCGACCAGC 60

ATTTGATGAT GACGATCAAA GAAACGGTAG TGAAATAATT CGGTTTGACA AAACGCGTAT 120

TTATCTTGGC AAGAAAGCAG AGACAAACCG CATTACTGGC ATTTCTAGTA AACCACCTAT 240

TTTACTAACA CCATTATTTC CAACTTATTT TTTCCCAACA CATTCTGACA GACAAAATGA 300

AAATATTTGG TTAAATATGC ATTATATCGA AAGTATTAAA GAATTAAAAA ATCGTAAATG 360

TAAAGTGACA TTTATTAATA ATGAATCAAT CATTCTTCAT GTTTCATACC ACAGTTTATG 420

GCATCAATAT AACAATTCCA TTTTTTACTA TTACATGGTA GATAAACAAT CTCGCATGAT 480

ATCAAAAAAT CCCGACCAAC CAATAGATTA TAATAAAGCC ACATTGAATG TGTTTGAAGC 540

ATTGACACGC TATTCTTTAT TTGAAGATAA ATAAATTGTT TATTTTTAAA ATATGCGGAA 600

TGTTTTATAA ATATAGTGTA AATGTTCTGC ATATTTTTTT AAGGTATCTA TTGCAAATTA 660

ACTTAATCTT GTTATAATAA TATTTGTGCT TGaTATTCAA ACACATACAA ATTAATCCAC 720

AGTAGCTCAG TGGTAGAGCT ATCGGCTGTT AACCGATCGG TCGTAGGTTC GAGTCCTACC 780

TGTGGAGCCA TTGGAAACGT ACTCAAGTTG GCTGAAGAGG CGCCCCTGCT AAGGtGTAGG 840

TCGCGAAAgG CGCGAGGGTT CGAATCCCTC CGTTTCCGTT ACTTGCTAAA ATGGTATATA 900

CCATTTTAnC TTTTTTGTTT ACTTATATAT AATGAATGAG AATTTCACTG TTCTTTTATA 960

TCAATTTTAA AATTCTAAAA ACCTTTCCTA GATAATCTTC TCTAAGAAAG GTTTTTATAC 1020

TTGTTGAACT TATAATTAAT TTATTACATA GCAATATTTA CCTGTTTTTA ACTATAAAAT 1080

TATCACTACA TGAAATACGA TAATTCGGaT CTCTTAACTT CTCTGCaATT AATGtACTCA 1140

TTGgTTTCAT CGTATGATTC ATGTATAATA GCATTTkTTA AATAATTC 1188

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 840 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

CCCAACTTCG GTTATAAGAT CCCTCAAAGA TGATGAGGTT AATAGGTTCG AGGTGGAAGC 60

ATGGTGACAT GTGGAGCTGA CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT 120

TTGCGAACAA AAtCACTTTT ACTTACTATC TAGTTTTGAA TGTATAAATT ACATTCATAT 180

GTCTGGTGAC TATAGCAAGG AGGTCACACC TGTTCCCATG CCGAACACAG AAGTTAAGCT 240

CCTTAGCGTC GATGGTAGTC GAACTTACGT TCCGCTAGAG TAGAACGTTG CCAGGCATAA 300

TATTAATCCA CAGTAGCTCA GTGGTAGAGC TATCGGCTGT TAACCGATCG GTCGTAGGTT 360

GGCGGTAACA CGGGTTCGAG TCCCGTAGgA GTCATACAAG CAGAAGTGAA ATATCGCTTC 480

TGTTTTTTTA TTACATATTT ATTGTTGAGG AAGGTTGTCC GAGCTGGCCG AAGaGCACGC 540

CTGGaAAGTG TGTAGGCGTC ACAAGCGTCT CAAGGGTTCG AATCCCTTAC CTTCCGTAAA 600

GGcGCTTAAA TTGGTTTTAC CCATTTTAAG CGCTATTTTT ATTTTGGACT CAATCCCTTG 660

ATATATCTGC ATTTGAGCTA TTATCCTCAT TTTTACACTT CTTATTTATT TATATCCATT 720

TAAAATTTTT TAGCCACAAT GTGACTAATT TTTGaTGAAT AATCCTAATT TTAGtCACAA 780

GATTTTGAAG TTTAGTCACA AAACAAATCA TTCAGATTTT TTTCyATAAA TTTAGTTTCA 840

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

TTCTATGAAA CTATCAGCTG TTTCTTTTTC CTTGGTAAAA ATCGTTTTAA CGCCATGATA 60

CATGTATTCT CTTTCAaCAC CCGATTGGTC ATAAGCATCG AAAACACAAA TAATTTCATC 120

TGAAATAACT GCATTATAAT TTGCAATTGC ATCTATTAAT TGCATTCTAG CTTCTTCTAA 180

ATTCTCTTTT GCAATGGCGC TTAGCGTTGG TGATTGTCCT ATCATATTGT ATCCATCAAT 240

GATTAAGTAA CGTTCTTTCA TTATATTTCT CCAACATCAT GTCTTTTTCG AAATACTTCG 300

TACATCATTA AACTTGCTGC AACCGAAGCA TTCAAACTGT TTACATGTCC AACCATTGGA 360

ATCTTAATAT AAAAATCGCA TTTATCACTT ACTAGGCGAC TCATACCCTG TCCTTCGCTA 420

CCAATTACAA TAGCCAATGA CATGTCCGCT TCTAGATTTC TATAATCTGT TGCATTATTA 480

GCTTCAGTGC CAGCTACCCA AAAGCCATTA TCTTTTAGTT CATCGATAGT TTTAGCTAAA 540

TTTGTCACTC GAATAACTGG TACATGTTCA ATTGCACCTG TTGAGGCTTT TGCAACTGTT 600

TGCGTTAGTG TAACTGAACG ACGTTTAGGA ATAATAACAC CATCAACTCC CGTTGCATCG 660

GCTGTTCTTA AAATTGATCC CAAGTTATGT GGGTCTTCTA AGCCGTCTAA TATAAGTACT 720

GTCAATAAAC CTTCTTTTTC TTTTTGCTGT TTTAAAAATT GATCGAAGTC AGCATATTCA 780

TATGGTGCAA TAAGCGCTGC AACACCCTGA TGTGGTGCAT TTGCTAAAAA ATCTAATTTA 840

GATTTTGGTA CAGTTTGAAC AATGATTTTT TGATCTTTTG CATTTTTTAA AATTTCATTA 900

ATTTGTTGCT TTTTAATACC TTCTTGAATC AATATCTTAT TTAyCGGATG CCCAGTAATA 960

TTCGTTTACT ATTGTTATTA TTTTATTTAA TAATGCCTCT AATCGTTCTT CTCTTTTTTC 1080

TAAATAaAGA AAACCTATCA CTGCTTCTAT CkCTGAACTT TTACGATATG TTTGAACATC 1140

AGTGTTTTTA GCTTTAGTAT GACTTTTCGC GTTACGCCCT CGCTTCAAAA TATCCATTTC 1200

TTCGTCTGTA AACCATTCTT GCTCCATTAA ATATTCTAAC GTTTGCGCCT GACTTTTGGC 1260

AGATACATAT TTTTTAGACA TTTGATGTAG TTTATTAGGC TTACTTTTAA GCTTTAAAAC 1320

GATATAGGTA CGTACATATT GATCTAaGAC TGCGTCnCCC ATATATGCTA AGG 1373

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

TCAAGTGCCA ACTACACAAC TGATTTACAT TCTTTAGGTC AATATGTACA AGAAGGCCGT 60

CGCTTCTTAT TCGAAACAGT TGTAAAAGTA AATCATCCTA AATATGATAT TACTATTGAA 120

AAAGATAGTG ATGATCTAGA CGGATTAAAT TATTTAGCTG GTAAAACAAT CGACGAAgTT 180

AACACAAAAG CATTCGAAGG TACATTATTA GCGCATACTG ATGGTGGTGT TCCTAACATG 240

GTAGTGAACA TTCCACAATT AGATGAAGAA ACTTTCGGTT ACGTCGTATA CTTCTTCGAA 300

CTTGCTTGTG CAATGAGTGG ATACCAATTA GGCGTAAATC CATTTAACCA ACCTGGTGTA 360

GAAGCATATA AACAAAACAT GTTCGCATTA tTAGGTAAAC CTGGTTTTGA AGaCTTGAAA 420

AAAGrATTAG rAGAACGTTT ATAAAATACA TTACTTCAAA GATTAGTGAA GTTTGAAAAG 480

ATAGAACTAG ACGTTAACTA TTTAAAGCAT ATTTTCGAGG TTGTCATTAC AAATGTAAAA 540

ATGTAATGAC AACCTCGTTT TTATTTATAT GCAAGAACTA GGTTACTAGC TAaTGTGACA 600

AGATGTTAAG AGAAAATTAA aGATAAAATA ATATCTGCCT TACAATAATA TTGTTATACT 660

ACTAGnGACT GATTTATTAG CATGATTACA TGTTAATGTT TCTTTACTTA GTAATTA 717

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2700 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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AATCTAATTT TTCCTCCTAA TCTCGGATTG GATAGTGGTC AATTTTTCTG GCCCGCCATT      60
TTAGCGTTTG TTCTAACTGG GATTGGTTTA CCATTATTAG GTGTGATTGT AGGTGCACTT     120
GATAAAGAAG GATATATTGG CGCATTAAAT AAAATTTCAC CTAAATTTTC AATATTGTTC     180
TTAATCATCA TTTATTTGAC TATAGGACCA CTTTTTGCAA TACCTAGAAC TGCATCTACA     240
TCTTTTGAAA TGACAATTAC ACCAATTATA CATAGCAATA GTAGTATCGC TTTATTTATA     300
TTTACGATTA TCTACTTCAT AGTCGTTTTG TATATTTGTT TAAATCCATC TAAGTTAATC     360
GATCGTATTG GTTCATTATT AACACCATTA TTATTGATTA CTATTTTAGC GATGATTATT     420
AAAGGATACT TAGACTTTAG CGGTAATAGT GCTGGAAAGG GCAATGAAGC ACTATATCAT     480
TCTAATTTTT CAAGTTTTGC TGAAGGCTTT ACACAAGGCT ATTTAACAAT GGATGCCATT     540
GCAGCAATTG CTTTTTCAAT GATTGTTGTT AATGCAGTAA AACTAACAGG CATTACTAAA     600
ACAAATCAAA TATTCAAACA AACTTTGACT GCTGGTTTAA TTGCAGCCGT AGCTTTAATT     660
TTCATATATA TTTCATTAGG TTATATTGGT AATCATATGC CAGTAAGTGA CATGACGTTA     720
GATCAATTGA AATCCAAAGA TCGAAACATT GGGACATATT TATTAACGAC AATGGCTTCA     780
ACAGGATTTG GTTCATTCGG AAAATATTTA TTGGGCATCA TTGTGGCGCT GGCATGTCTA     840
ACTACAGCAT GCGGGCTTAT TGTTGCAGTT TCTGAATATT TCCATAGAAT CGTACCTAAA     900
GTATCATACA AAGCATTTGT ATTAGTTTTC ATTTTAATGA GTTTTATTAT TGCTAACCAA     960
GGTTTAAATG CTGTTATCTC AATGTCAATT CCGGTATTAA GCATTGTATA CCCAGTAGCA    1020
ATAACTGTTG TATTATTAAT TTTAATTGCC AAATTCATAC CGACAAAACG CATTTCACAA    1080
CAAATTCCAG TTATTATCGT ATTTATATTG TCGATTTTCA GTGTTATTAG TAAGTTAGGT    1140
TGGcTGAAAA TTAACTTTAT AGAATCATTG CCTCTAAGAG CGTATTCTTT AGAGTGGkTC    1200
CCAGTAGCAA TTATTGCAAC GATATTAGGC TATCTAGTCG GCATATTTGT AAAACAAGAT    1260
CCAATTAAAT ATCAACAGGA ATAACGAATA ATATAAAAGA GGTTGGGACA TAAATCCCTA    1320
AAAAAACAGC AGTAAGATAA TTTTCAATTA GAAAATATCT TACTGCTGTT CTCTATTTAT    1380
ACAATACTTC GTATTGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG    1440
ACTGGCACTG CTCCCTCAGG AGTCTCGCCA TTAATACTAC GTATTAACGT GTAATTTTAC    1500
TTTGAAATAC TTTAAAAAAA TAAGACACTT TGCCCAACTT GCACATAAAT GTAAAATTCA    1560
ATAAAATAAA TTTTCTGTGT TGGATCCCTT CGTATAATTT AATAAATACT ACTAAACTAA    1620
ATTAACGAGG TGCCTTATGT ATAAAAATTA TAACATGACC CAACTTACAC TACCAATAGA    1680
AACTTCTGTT AGAATTCCTC AAAATGATAA TACGCGATAT GTTAATGAAA TTGTTGAAAC    1740
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AAGATATGCA TACCGTAATG ATAGATATAG TTTTAAACGT GACTTCAAGC TATATGAATG 1860

TGATGACTGT TCATCATGTT CTTTGAGACA TCAATGCATG AAGCCAAATT CGAAATCCAA 1920

TAAGAAAATT ATGAAGAATT ATAATTGGGA ATACTTTAAA GyCCAAATTA ATCAAAAGCT 1980

TTCTGAACCA GAAACGAAAA AAATCTATAG TCAAAGAAAA ATTGATGTAG AGCCTGTTTT 2040

TGGATTTATG AAGGCTATTT TGGGTTTCAC TCGAATGTCA GTTCGAGGAA TAAATAAAGT 2100

TAAACGAGAG CTAGGTTTTG TATTAATGGC ACTTAATATA AGGAAAATAG CAGCTCAACG 2160

AGCTGTACAT TATAAAATAC ATATCAAAAA AGCTGATTTC TATCAAATAA TTAATAGAAA 2220

TCAGCTTTTT TACATTGCCT AAGAATTTAA TGTCCCAAGC CCTTTTTATC GAATAACTTA 2280

TTGTAAACCT TGTCTTTCTT GGTTATTGTT TTCGTTATTT TTTTCGTGTT TTTGTTTCCA 2340

CTCTTTTTGA GTCATTACAT CGTCAACTTG CATGTTAACT TCAACTACAT CTAAACCAGT 2400

AATATATTTA ACTTGTTCTT TAACTAATTC AGTTACTTTA CGGAAGATTT TTGGTGCTGA 2460

TTCACCATAT TCTAAGATTA CTTTTAAGTC TACAGCAGCT TGTTTTTCAC CAACTTCAAC 2520

AGATACACCT TGAGTAACAT TGTTGCCACT TGAGAATGCA TTAGTGAATG TATCAGTTAA 2580

GCCACCTTTC ATATCTAAGA TACCTTTAAC TTCACGTGCA GCGATACCAG CAATTTTTTC 2640

AACAACTTCA TCAGAGAATG TTAATTTGnT TTTGAATTGA GGCTCCTGAT TTnGTTCnTG 2700

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

ATCAAATACA ATAATTAAAA TAaTGGCTAA TACaCCTAaA ATaATAATcG AGTTaGAGTA 60

GCCTAAGCGA yCACCcTAAC aGTArACATT CTAGGCATAT ATTTaTCTTT AGACATTGAA 120

GCCGCTAACA TCGGAAAAGC TGTAAATCCA GTGTTGGCTG CTAATACCAA AATCATCACG 180

GTCGTTGCCT GTACAAAATA GAAGGCAGCA TTATCACCAA ATATTTGCAT AGCTAATTGT 240

GATAAAACTG TCGTTTCCGT TTGTGGcAAA ATTCCATAAA CATATGCTAA ACCAACGATA 300

CCAACTAATA AAAACGCTAA AATTGAACCC ATAGCAATTA ACGTTTTCAC AGCATTTTTA 360

GCACTTGGCT CTCTAAAATT GGTTACCGCA TTTGAAATAG CTTCAACACC CGTTAACGAT 420

GAAGCCCCTG ATGAAAATGC TTTTAATAsC AAGAATAATG TTACTCCAGG AACCGCAGTT 480

AATATTAATA TCACTAACCC TATAATGAAA AGATATACTG GATAGGATAA TACGGTGGCA 600

GATTCAGTTA AACCACGTAA ATTTAATATT AAAATAAAAA GTACAAGTAw ACATGCAATC 660

AGTrCkTTAT GCCCATATAA ACTTGGGAAT GCAGCAACAA ATGCATCAGC ACCAGATGAT 720

ATmCTAACAG CGACAGTCAG TATGTAATCG ACTAATAATG AGCCTCCTGC AAGCAATCCC 780

CATTTTTCTC CTAAATTGGT CTTGGACACC ATATACGCGC CGCCACCTTT AGGATATGCA 840

TAAATAATTT GCCTATAAGA CATAATTAAA GCAGCTAATA AGATCAGAAC AGCACCTGCA 900

ATCGGTAAAG TATACCAAGT TGCAACTGCA CCCACTACTG ATAGTGTAAT CAGTATTTGT 960

TCGGGACCGT AAGCCACTGA AGATAATGCA TCCGACGAAA GAATCGCTAA CCCTTTAAAC 1020

TTCGATATCT TTTCGTCTTT TAGTTCTCTG TTTTTTTTAG GTTGCCCTAT AATAAGtCTT 1080

TTAAATTGAT kGAcATAAtC TCCTATTCCT TTTTATAGTT TTnGATGGAA ATCAC 1135

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

TTATGGTAAA ACTTTAACAC AAGCATTACA TAAATCGCAA TCATTTATGT GGCAAAAACG 60

TTGAATTTAA GCCATTTCTA TTCATTTTAC GTAATTATTA GCCGTATATG TGTAATAATA 120

CACATTTTAT TCAGATTTTT TATCGCGCTC CATTAAATCT TTTACGCATT CTTTTACTGA 180

GATATTTTCA AATAATACTC TATATAATGC ATTTGTAATT GGCATATCCA CATTTTTTTC 240

TTTAGCTAAA TGATAAACTG ATTTAGTTGT ATAAATACCT TCAACAACCA TATTCATTTC 300

AGATAATGCT TGATCCATTG ATTCACCTTG TCCAAGTTTA TATCCTAATG TGAAATTCCG 360

AGAATGTGTT GATGTGCAAG TAACGATTAA GTCACCGATA CCACCTAAAC CTAGAAATGT 420

CATAGGATCG GCACCTAACT TTTCACCTAA TCTACTAATT TCCGCTAAGC CACGAGTCAT 480

TAATGCAGCT TTTGCATTAT CACCGTAGCC AATTCCAGCT ACGATACCAC TTGCTACTGC 540

GATGATATTT TTCAATGCAC CACCAAGTTC AACACCAATC AAGTCATCAT TCGTGTACAC 600

ACGCAAATAA TCATTCATAA ATAAATCTTG CGTTAATTTA CTTACACTTT TATCTTTTGA 660

TGAAGCAGCA ACTGTAGTTG GTTGCTTGAC TACAACTTCT TCCGCATGAC TTGGCCCTGA 720

CAACACGCCA ATACCTGCAT TATATTCAGG TGAAATAGAA TCTTCAATCA TTTCTGACAC 780

CAGCTTATCA TTAATTTGAG AAGCAACTTC TCGCATTGCT TTAGTAGGTA AAGCCATTAA 900

GTAAATATCT GCAAATTG 918

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

CAATACTCGG TATTATAGAT AGTCCTACTA CATTTATATG GGTTTGTATC ATTACATTAA 60

TTGCACATCA ACTTGAAGGT AATATCATTA CACCAAATGT AATGGGTAAA TCTTTAAGTA 120

TCCATCCTTT AACAATTATC GTTGTTATTT TAGCAGCAGG AGATTTAGGT GGCTTTACAT 180

TAGTTCTGAT TGCAGTGCCA TTATATGCTG TACTTAAAAC GGTTGTTAGT AATATTTTCA 240

AATACCGCCA ACGCATTATT GATAAAGCAA ACAGTAATGT TAAGGACTAA TTCTGTGGAT 300

GTCTTTTAAG AATATAAGAT ACTATCGCAT CAAAAGTTGA AACTACAGCT TTTGAGGCGA 360

TTTTTTTGTG CATAAAAAAT CAGTCmAATG AAATATCAAA TAATTTTCCA TCAGTCCGAT 420

TATTATAAAA GCAAAAAAGC TTTGCTCACA TATATAATAA CGTGAACAAA GCTGTTGAAT 480

GATATTATTT AATTGCGTGG AATCCGCTAT CTACATGAAT ATTTTCACCT GTAACGCCAC 540

TTGATAAATC ACTTAATAAG TAAGCCGCAG TTTTACCTAC TTCTACT 587

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 812 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

GGTTCATTCC AAAAAAGTAC GCGATAATTA GCGAAGAAGA ATTTGAAAAT TTAAATGTTG 60

TTAAACCAAA TAAAAATAAT GTTTTCTGGT CAGTTATAGG AAGTTCGGTT TTGTTTGGAG 120

TTACTTTAAG GAAATACATA CATGTTTTTG ATGTTCAATT AGATAAGCTA GTTGTAATGA 180

TATTGTGTGC TCTCGCTTTA ATTTGTGTTA TAGTTTTTTA TTTTAACTTA AATAGAAAGC 240

TTAAGTTAAA AGTGTTTGAT ACAAATATTG AAAAAnATAA GAGAGTTATA TAAAwAcCAA 300

TTTCATTAAT TGCCCTTATG ACAATCGAAC CTCAAAATAT AATAATATTT ATTTATTGGA 420

TTATGATGAC AATGCTTTTC TTTTTGTTAA ATATGACTTC GATAGGTAAT GAAAAAGTTC 480

GCGTTATAAT GAAAAATAAT TGATTACATT TAAAATATTC TAAATGTTGT CGACACAATC 540

CTTTTAAGAC GCTAGTAGAA TTTAAATGAC TTCTAATGTA TATGAAAGTG TATCAATATA 600

AAACCAATTG AAAAGAAGTG GAGACATTGC TTTGTGAAAC TGAAAATATT AATAAGAATC 660

CCAAATATAG AATTATCAAA TACAAAGATG AATATTTGAT GATTGATTTA GTAAGTACAT 720

GGTTAGCACT CTTTTTCCCA ATGATTAATT GGCTGATTCC AAAAAAGTAC GTCAAAATCA 780

GCGAAAAAGA TTTTGAAACT TTAAACATTG TG 812

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 526 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

GTTCTATTAT TTCTTCCAAT GGTAATGGAT TTTCGTAAAA TGATTGATAT AAGTTGATAA 60

TCTCAATAAC TTTTAATTGA TCTGGAAACA TCGTTTTTTG GAACATTATA CTGCGATTTT 120

CACTTTGTAA TAACTTGTCT TTATCAAATA TCTCACCAGA ATTAGCATTA ACATTACCAA 180

TTAATATATC AATTAACGTT GACTTTCCAG CACCATTTTT TCCAATTAAA GCGATACATT 240

TACCTTGTTC AATATCGAAC GAAATATTTT TTAGAACACA TCTTTTATTA AATGACTTGT 300

TGATATTAGA TATTTGAATC AATTTAATCA CCTCTATTTT TTTCTTAATT TAATATTAGT 360

AAATTTATTA GATTTAAAAT AGAACACTTT GTCATAGATT TGAAATGACA AATGTCATTA 420

TTAGATkTAC ATAATATATT TATCGTtATT TTAATTTTGG GCAAAATAAA AAGAGCCTCT 480

ATAATCGrGc TCCTTACAAA TAaATTATAA AAttGGCGAA cTAAAT 526

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4544 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

GGAACACCTA AAGAAAGAAA TGATGCATTA AACACAGAGG CTGATATCTA TGTAACCAAT 120

AAAGAAAATA CTAAATGGTT ATGCGATCAA TATAAAAAAG AATGGCCATT TGATATGGTT 180

GTAATTGATG AACTGTCTAC ATTTAAAAGT CCTAAGAGTC AAAGGTTTAA ATCTATTAAA 240

AAGAAATTAC CACTCATTAA TAGATTTATA GGATTAACAG GAACACCTAG CCCAAATAGT 300

TTACAGGATT TATGGGCTCA AGTTTATTTG ATAGACAGAG GCGAAAGACT TGAGTCTTCA 360

TTCAGTCGTT ATCGAGAAAG GTACTTTAAA CCAACACATC AAGTTAGCGA ACATGTTTTT 420

AACTGGGAGC TAAGAGACGG ATCTGAAGAA AAGATATATG AACGAATAGA AGATATATGT 480

TTAAGCATGA AAGCGAAAGA TTATCTAGAT ATGCCTGACA GAGTTGATAC TAAACAAACA 540

GTAGTCTTAT CTGAAAAAGA AAGAAAAGTA TATGCAGAAT TAGAAAAAAA CTATATTTTA 600

GAATCGGAAG AAGAAGGAAC AGTTGTAGCT CAGAATGGGG CATCATTAAG TCAAAAACTA 660

CTTCAACTAT CTAACGGTGC AGTTTATACA GATGATGAAG ATGTAAGACT TATACATGAT 720

AAGAAGTTAG ATAAGTTAGA GGAAATTATA GAGGAGTCTC AAGGCCAACC AATATTATTG 780

TTTTATAACT TCaAACATGA TAAAGAAAGA ATACTTCaAA GGTTTAAGGa AGCAACCACA 840

TTaGAGGATT CAAACTATAA AGAACGTTGG AATAGTGGAG ACATTAAGCT GCTTATAGCA 900

CATCCAGCAA GTGCAGGGCA TGGATTAAAC TTACAACAAG GTGGGCACAT TATTGTTTGG 960

TTTGGACTTA CATGGTCATT GGAATTATAC CAACAAGCAA ATGCAAGATT ATATAGACAA 1020

GGACAAAATC ATACGACTAT TATTCATCAC ATTATGACCG ATAACACAAT AGATCAAAGA 1080

GTATATAAAG CTTTACAAAA TAAAGAACTA ACGCAAGAAG AATTGATGAA AGCTATTAAA 1140

GCAAGAATAG CTAAGCATAA GTAATGGAGG TATAAGATGG GAAAGGCATC ATACGATATT 1200

AAGCCAGGTA CATTTAAATA TATTGAGTCA GAGATATATA ACCTACAAGA GAACAAGAAA 1260

GAGATAAATA GATTGAGAAT GGAGATACTT AACCCAACGA AAGAGCTAGA CACTAACATT 1320

GTGTATGGAC CGTTGCAAAA AGGTGAACCA GTTAGAACAA CTGAACTAAT GGCAACAAGG 1380

TTATTGACTA ATAAGATGTT ACGAAACCTA GAAGAAATGG TCGAAGCAGT TGAAAGTGAA 1440

TACTTAAAGT TACCTGAAGA TCATAAGAAA GTAATTAGGC TAAAGTATTG GAATAGAGAT 1500

AAGAAGCTAA AGATAGAGCA AATAGGAGAT GCATGTCACA TGCATCGTAA TACAGTTACT 1560

ACTATACGAA AGAACTTTGT TAAAGCGGTA cGwtATCATG CAGGTATCAA ATAACATTGT 1620

GCAAAGATTG TGCAAAAGGC CTACAAATCT GTAGTAATAT GATAGTATCG GAAAGATGTA 1680

TAAAGTTATC TAAAAGTTAT ACGACACAAG TACACGAGGC ACATCGCTAT GCGtGTGTCT 1740

TTTGTTATGC AATCAAAGAG GTGTAAGAGA TGACCAAGCA TAATAACATT TATAAGCATG 1800

AGATAGCATT AGATAGGGAT AATCATCTTT GTCAAATGTG TTTACGTGAA GACATAGTAA 1920

CAGATGCAAA CATAGTGCAT CATATTATTT ATGTTGATGA AGATTTTAAT AAAGCTTTAG 1980

ACTTAGATAA TTTGATGTCA GTTTGTTATA GCTGTCATAA CAAAATTCAT GCAAATGATA 2040

ATGACAAAAG TAATCTTAAG AAAATTAGAG TATTAAAAAT TTAAATAAAA AAATAATTTA 2100

TTTTTATAGC CCCCTACCCA TCGGCTTAAA ATGTTTTTTC GACGGGTACC GGCGGGGGCC 2160

CTTCGCTTGC AACGCGGATA AACTTTTATG AAAGGGGGTC TTTATATGAA ATTAACAAAA 2220

AAACAGCTGA AAGAATATAT AGAGGATTAT AAAAAATCTG ATGACATATT AATTAATTTG 2280

TATATAGAAA CGTATGAATT TTATTGTCGG TTAAGAGATG AACTTAAAAA TAGTGATTTG 2340

ATGATAGAGC ATACAAACAA GGCTGGTGCG AGCAATATTG TTAAGAATCC ATTAAGCATA 2400

GAACTGACAA AAACAGTTCA AACACTAAAT AACTTACTCA AGTCTATGGG TTTAACTGCA 2460

GCACAAAGAA AAaAGATAGT TCAAGAAGAA GGTGGATTCG GTGACTATTA AAGTTTTAAA 2520

TGAACCTTCA CCAAAACTAT TAACAACATG GTATGCAGAG CAAGTCACTC AAGGGAAAAT 2580

AAAAACAAGC AAATATGTTA AAAAAGAATG TGAGAGACAC CTTAGATATC TAGAAAATGG 2640

AGGTAAATGG GTATTTGATG AAGAATTAGC GCACCGTCCT ATTCGATTCA TAGAAAAGTT 2700

TTGTAAACCT TCCAAAGGAT CTAAACGTCA ACTTGTATTA CAACCATGGC AACATTTTAT 2760

TATTGGCAGT TTGTTTGGTT GGGTTCATAA AGAAACAAAA CTGCGCAGGT TTAmAGAAGC 2820

TTTGATATTT ATGGGGCGAA AAAATGGTAA AACAACTACT ATATCTGGTG TTGCTAACTA 2880

TGCTGTTTCT CAAGATGGAG AAAACGGCGC TGAAATCCAT CTTTTAGCAA ACGTAATGAA 2940

ACAAGCTAGG ATTCTATTTG ATGAATCTAA GGCGATGATT AAAGCTAGCC CAAAGCTTAG 3000

AGAAAATTTT AGACCTTTGA GAGATGAAAT TCATTACGAT GCAACTATAT CTAAAATTAT 3060

GCCACAGGCT TCAGACAGTG ATAAGTTGGA TGGTTTAAAT ACACATATGG GCATTTTTGA 3120

TGAAATTCAT GAATTTAAAG ATTATAAATT GATTTCAGTT ATAAAAAACT CAAGAGCGGC 3180

AAGGTTACAA CCCCTTCTTA TCTACATTAC GACAGCAGGG TACCAACTAG ATGGACCACT 3240

TGTTAATATG GTAGAAGCGG GAAGAGACAC CTTAGATCGA ATCATCGAAG ATGAAAGAAC 3300

TTTTTACTAT TTAGCTTCTC TCGATGATGA CGATGATATA AATGATTCGT CGAATTGGAT 3360

TAAAGCAAAT CCTAACCTAG GTGTTTCTAT CGATTTAGCT GAAATGAAAG AAGAGTGGGA 3420

AAAGGCTAAG AGAACACCAG ATGAACGTGG AGATTTTATA ACCAAAAGGT TTAACATCTT 3480

TGCTAATAAT GATGAGATGA GTTTTATTGA TTATCCAACA CTTCAAAAAA ATAATGACAT 3540

TATTTCCTTA GATGAGTTGG AAGGTAGACC ATGTACTATA GGTTATGATT TATCAGAAAC 3600

AACACATTCT TGGATTCCTA AGCATAAAGT TGAATATTCT AACGAAAAGA TACCCTATAT 3720

AGAATGGGAA GAAGACGGAT TACTAACAAT ACAAGATAAT CCTTATATAG ACTACCAAGA 3780

TGTTTTAAAT TGGATAATAA AGATGAATGA GCATTATGTT GTCGAAAAAA TCACTTATGA 3840

TAGGGCGAAT GCTTTTAAAT TAAATCAAGA GTTAAAGAAT TATGGCTTTG AAACAGAAGA 3900

AAcwAGACAA GGGGCTTTGA CCTTGAGCCC TGCaTTGAAG GATCTAAAAG AAATGTTTTT 3960

AGATGGGAAA ATAATATTTA ATAATAATCC TTTAATGAAA TGGTATATCA ATAATGTTCA 4020

GCTGAAACTA GACAGAAATG GGAACTGGCT GCCATCTAAA CAAAGCAGAT ATCGTAAAAT 4080

AGATGGTTTT GCAGCATTTT TAAACACATA TACAGATATT ATGAATAAAG TTGTTTCTGA 4140

CAAGGGTGAA GGAAACATAG mATTTATTAG TATTArAGAT ATAATGCGTT AAGGAGGTGA 4200

ATGTTATCGC AAAAGAGAAT ATTGTCACAC GCATAAAGAA AAAATTGATA GACAATTGGA 4260

TTGaTCAGTC AGCTTCTAAG CTTTATGACT TTAGCCCATG GAAAAATAAA TCTTTTTGGG 4320

GTGTAATCAA TAATACGCTT GAAACTAATG AAACGATATT TTCAGCTATT ACnAAGTTAT 4380

CTAATTCGAT GGCTAGTTTG CCCTTGAAAA TGTATGAAGA TTATAAAGTA GTTAATACAG 4440

AAGTATCTGA TTnACTTACA GTGTCACCGA ATAATTCTCT GAGCAGTTTT GATTTTATTA 4500

ATCAAATTGA AACAATCAGA AATGAAAAAG GTAATGCATA TGTG 4544

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 881 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

CATGGCAGAA TATTGAAGCT GTAAAAAAAG GACATGTAAT TTCATATAAA GCAGAAGATT 60

ATTGGTTCAC AGATCCTATT ACATTAGAAC ATTTGAGAAG TAAATTAAAA AAAGAAATTT 120

TAAATAAAAA ATAATAGAAA TAAGTTGTAA AAATTTTCTT ATGCATTGGT ACTAATGTTT 180

TTAAGGAGTG ATTAAATGAA GCAACTGGTT GGAATTCCCG AATCAATGTT AATTCCTTTG 240

ATAGCTCGAG CAAAAGAGTA CGAAAACGAA AAACCAATAA TAAAAGACGC ACTATCAAAA 300

AAAATATTTG ATGGTTTAGA TGATATGTAC AAAAATGTTA CATGTGATGA CATGTCTCAA 360

ATTGGAATTA GTATACGTAC TGTGATAATA GATTGTGTTA CTAAGAGGCT TATCAAGGAT 420

AATAAAGATT TAATCGTGGT CAATATAGGT TGTGGCTTAG ATACAAGGTT TCAAAGATTT 480

ACATTTTTTA AAGAAAGTAA TAGTTATAAG ATGATATCTA AATCTATGCT AGATTACAGT 600

TGGATTGATG ATGTCAAAAA TTATAAATTT TTTAATAGTA AGTCAGATAT ATTGTTTATT 660

ATTGAAGGTG TATTGaTGTA TTTTGATGAG AGTGTAATGA CTCAATTATT GGACACTATT 720

ATCAAAAAGA TGGGAGATCA TAATTTGACA TTTGCGATTg AATTTTGCTC aAAAACAATT 780

GCGAATAATA CmAAGAGACA TCAATCGGTA TCCAAGTTAT CCTCACCACC TGTTTTTAAA 840

TATGGGTACC ATGATTTAnA AAAATTGGAT GAnATTTACC C 881

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

TGAATaaAAA TATATTAATA GATAAACACA AATGTGTCcA AATACCCCTA GAGGTATTTG 60

ACnAGTTCCA TCCAACTGTT TAAAATACCC CTACAGGTAT TTTTAGGGAG GTTATTATGA 120

AACAATACGG AGAAAaGTTT ATCGATGAAT TTAGTAAAGC AGAATTGGAA AAACTAGCCA 180

AGCAAGGGCA ATTAATTGAC GTTAGAACAG AAGAGGAGTA TGCATTAGGA CATATCAATG 240

GTTCCATACT TCATCCTGTT GATGAGATTG AGTCATTCAA TAAAGAAAAA AATAAAACCT 300

ATTATGTAAT CTGTAGAAGT GGTAACAGAA GTGCTAATGC TAGTAAATAT TTAGCTAAAC 360

AAGGTTATAA CGTTATAAAT CTTGATGGTG GTTATAAAGC TTATGAAGAA GAAAACGATA 420

GTTATGATAC ACAAGAAGAA TATAAAAGTA TAGAAATTAA AGCAGATCGT AAACAATTTA 480

ACTATCGTGG TCTTCAATGT CCAGGGCCAA TTGTAAAAAT TAGTCAAGAA ATGAAGAATA 540

TTGAAGTAGG TGACCAAATT GAAGTCAAAG TCACAGACCC TGGATTCCCT AGTGACATTA 600

AAAGTTGGGT GAAACAAACA AGGCATACTT TAGTTAAGCT TGATGAAAAT AACAATGGAA 660

TTAATGCGAT TATTCAAAAA GAAAAAGCAA AAGATTTAGA TATAAATTAT TCTGCTAAAG 720

GTACTACAAT TGTATTATTT AGTGGAGAAT TAGACAAAGC TGTAGCAGCG TTGATTATTG 780

CAAATGGTGC TAGAGCTGCT GGAAAAGATG TAACTATCTT CTTTACTTTT TGGGGGCTTA 840

ATGCATTAAA AAAAGTGCAA ACAGTTAATG TTAAAAAGCA AGGTATTGCA AAAATGTTTG 900

ATTTAATGTT GCCCAAAAAG AATATACGAA TGCCTCTTTC CAAAATGAAT ATGTTTGGTT 960

TAGGAAATAT GATGATGCGC TACGTAATGA AAAAGAAAAA TGTTGATTCA TTACCAACAC 1020

TCATGGGTAT TCAGAAAGAA GAACTTAGAG ATGAAGTTGA GTACGGTGGT GTAGGCACTT 1140

ATATTGGTGC TACTGAAAAT GCGAATCATA ATTTATTTAT CTAATTAAAT CTATTAATAA 1200

AAGGAGTTGT TATCATGTTT TTTAAACAGT TTTACGATAA TCATTTATCT CAAGCATCAT 1260

ATTTAGTGGG TTGTCAACGT ACAGGAGAGG CAATAATAAT AGACCCTGTT CGTGATTTAT 1320

CGAAATATAT AGAAGTTGCA GATTCTGAAG GTTTAACAAT TACACAAGCT ACAGAAACAC 1380

ATATTCATGC TGATTTTGCT TCAGGAATTC GTGATGTGGC TAAACGCTTA AATGCAAATA 1440

TATATGTGTC TGGCGAAGGT GAAGATGCAT TAGGGTATAA AAATATGCCA TCAAAAACAC 1500

AATTTGTTAA ACATGGAGAT ATCATTCAAG TAGGCAATGT TAAATTAGAA GTTCTGCATA 1560

CTCCAGGACA CACGCCTGAA AGTATTAGCT TTTTACTCAC TGATTTAGGT GGTGGTTCAA 1620

GTGTTCCGAT GGGATTATTT AGTGGTGACT TTATTTTTGT TGGTGATATA GGTAGACCTG 1680

ATTTAtTAGA AAAATCTGTT CaAATAAAgG GTTCTACAGA AATTAGCGCG AAACAAATGT 1740

ATGAGTCCGT TCAAAATATT AAAAATTTAC CAGACTATGT TCAAATCTGG CCGGGTCATG 1800

GTGCTGGAAG CCCTTGTGGT AAAGCATTAG GTGCCATACC TATATCTACA ATAGGTTATG 1860

AGAAAATTAA TAACTGGGCA TTTAATGAAA TTGATGAGAC TAAATTTATT GAATCATTAA 1920

CATCAAATCA ACCAGCACCA CCGCATCATT TTGCACAAAT GAAACAAGTT AATCAGTTTG 1980

GTATGAATTT ATATCAATCA TATGATGTTT ATCCTAGTTT AGATAATAAG AGAGTAGCAT 2040

TTGATCTTCG TAGCAAAGAG GCCTTTCACG GTGGCCACAC AAAAGGAACA ATCAATATAC 2100

CATACAACAA AAACTTTATT AATCAAATTG GTTGGTACTT AGATTTTGAA AAAGATATAG 2160

ATGTAATTGG AGATAAATCT ACTGTTGAGA AAGCGAAACA CACTTTACAA TTAATTGGGT 2220

TTGATAAGGT AGCAGGCTAT CGTTTGCCAA AATCAGGCAT TTCAACCCAG TCCGTTCATA 2280

GCGCTGATAT GACAGGTAAA GAAGAACATG TATTAGACGT ACGTAATGAT GAAGAGTGGA 2340

ATAATGGACA CTTAGATCAA GCAGTTAATA TTCCGCATGG TAAATTATTA AATGAAAATA 2400

TTCCTTTTAA TAAAGAGGAT AAAATATATG TACATTGTCA GTCAGGTGTT AGAAGTTCAA 2460

TTGCAGTGGG TATATTGGAA AGCAAAGGTT TTGAAAATGT GGTGAATATT AGAGAAGGCT 2520

ATCAAGATTT TCCAGAATCA TTAAAATAAT TTAAGGATGT GGAAAAAATG AATAAGCATT 2580

ATCAAATTGT TATTATTGGT GGCGGTACAG CAGGTGTTAC CGTAGCATCA AGACTATTAA 2640

GAAAAAATCA AAACTTAAAA GAGAAAATAG CAATTATAGA TCCAGCAGAC CATCATTACT 2700

ATCAACCATT ATGGACGTTG GTTGGTGCAG GGGTATCTAG TTTGAAAAGT TCTCGTAAAG 2760

ATATGGAAAG TGTTATACCT GAAGGTGCTA ACTGGATAAA ACAGGCTGTT TCAAGTTTTC 2820

TAGTAGCTCC AGGATTACAG ATTAATTGGT CTTCAATTAA AGGACTAAAA GAAAATATAG 2940

GTAAAAATGG TGTTTGCTCT AACTATTCAC CTGACTATGT TAACgAAACT TGGAACCAAA 3000

TTTCTAATTT TAAACAAGGA AATGCCATTT TTACGCATCC AAACACTCCT ATAAAGTGTG 3060

GAGGTGCgCC TATGAAAATT ATGTATTTAG CTGAAGATTA TTTTAGGAAA CATAAAATCC 3120

GT 3122

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3982 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

ATAnAGATAT AnATnAATAT ATTGAGGTCA AACGATGATA ATTAAAATTT TAACAATTCT 60

ATTACTACTT TGTATATTGA GCTATTTGGT TACAAATAGA AAGAAGCCTT TTCTGTTCTT 120

AAAGACACTC TTTATGGGTG TGGTATTTAT CTTTATAGGA TATATTTCAC TGGCAATATC 180

TGCCGTAATT ATTTATGGTA TTATTCAATT TATCACAATT GATTTTGGTA GTTTTTTCTT 240

AATGGGTATT ATATTGATCT TGATTTCAAG TATATTCCAA TTATTTATAG TTAGATTACT 300

TTTTAGAAAA AAGAATGTCG ATTTGACAGA GGTTGTCGTT TTAsAsCATT TAATTCAATG 360

GTTCTTAGTT TACTTTGCGA TCTATCAAGC AGTAAATGAA AAAATGGACA TTAATGATAT 420

TAATATCGAC AATTTCCAAT CTGTCTTTTT TGACGTGTCT AATTTGAATT TAGTAATTCT 480

ACCAACGTTA ATCATTAGCT GGGTCACAAT ATTTAACTAT AGAATGAGAA GTTACAAATA 540

AAATCTATGA GATTATACCT TCAGACACCA ACATTCAAAT GGTGTCTTTT TTGTTGTGTG 600

GTTTTATTTT TGAAATTCGA AAAAGTAGAG GCATGAATTT TTTGACTAGT GTATAAGTGC 660

TGATGAGTCA CAAGATAGAT AGCTATATTT TGTCTATATT ATAAAGTGTT TATAGTTAAT 720

TAATAATTAG TTAATTTCAA AAGTTGTATA AATAGGATAA CTTAATAAAT GTAAGATAAT 780

AATTTGGAGG ATAATTAACA TGAAAAATAA ATTGATAGCA AAATCTTTAT TAACATTAGC 840

GGCAATAGGT ATTACTACAA CTACAATTGC GTCAACAGCA GATGCGAGCG AAGGATACGG 900

TCCAAGAGAA AAGAAACCAG TGAGTATTAA TCACAATATC GTAGAGTACA ATGATGGTAC 960

TTTTAAATAT CAATCTAGAC CAAAATTTAA CTCAACACCT AAATATATTA AATTCAAACA 1020

TGACTATAAT ATTTTAGAAT TTAACGATGG TACATTCGAA TATGGTGCAC GTCCACAATT 1080

TCAAAATCTT GTGAGAGAAT TTGAAAAAAC ACATACTGTC AGTGCACACA GAAAAGCACA 1200

AAAGGCAGTC AACTTAGTTT CGTTTGAATA CAAAGTGAAG AAAATGGTCT TACAAGAGCG 1260

AATTGATAAT GTATTAAAAC AAGGATTAGT TAAATAAAAC TTCAATCGTT GCTGTTATCT 1320

GGAAATAATT AATTAAATGT TATGTTAATT TTTGTTAATG AAAAAAGTAA TCTATTTAAT 1380

GACAGGTTAA TGTAATTGTC CTGAAATTGA CTATATACTC AGTAAGTATC AATTTTAAGG 1440

AGAGCTTATA ATGAAATTTA AAAAATATAT ATTAACAGGa ACATTAGCAT TACTTTTATC 1500

ATCAACTGGG ATAGCAACTA TAGAAGGGAA TAAAGCAGAT GCAAGTAGTC TGGACAAATA 1560

TTTAACTGAa aGTCAGTTTC ATGATAAACG CATAGCAGAA GAATTAAGAA CTTTACTTAA 1620

CAAATCGAAT GTATATGCAT TAGCTGCAGG AAGCTTAAAT CCATATTATA AACGTACGAT 1680

TATGATGAAT GAATATAGAG CTAAAGCGGC ACTTAAGAAA AATGATTTCG TATCAATGGC 1740

TGATGCTAAA GTTGCATTAG AAAAAATATA CAAAGAAATT GATGAAATTA TAAATAGATA 1800

ATAAATAAAA CAGGTTGAGA CAAAAAATGG TCTTAACCTG TTTTCAATTT GCATATGTGA 1860

TAAATTCTAT ATCAAAATGC TTATGTATAA TGAATGACAT TTAAAAGTAG GGGAGACAAA 1920

TATAAATACA ATAGTTCCTA GGATTACTCT CAAAATAACT ATATCAATTA TTTACTTTGC 1980

TCTCCTATTT TTTAAAATAT GTACATGTTT AAACAATCAA AAGTGTACAA TATTAAATTA 2040

TCATTTCCAG TTCTAGTGCT ATATTGGTAG TAGTTGACTA AATGAAAATA AGCTTATAAC 2100

AAGTTTTTTC AATACTCGTG GGGCCACAAC AGAGAGAAAT AGGATCACCA ATTCCAACAG 2160

ACAATGCAAG TTGGCGGGGC CCCAACATAG AGAAATTGGA TCACCAATTT CAACAGACAA 2220

TGCAAGTTGG GGTGGGGCCC AACACAGAAG CTGGCGAAAA GTCAGCATAC AAAAATGTGC 2280

AAGTTGGCGG GGCCACAACA GAGAGAAATA GGATCACCAA TTCCAACAAA CAATGCAAGT 2340

TGGCGGGGGC CCCAACATAG AAGCTGGCGA AAAGTCAGCT TACAAAAATG TGCAAGTTGG 2400

CGGGGCCCCA ACATAGAGAA ATTGGAACCC CAATTTCTAC AGACAATGCA AGTTGGGGTA 2460

GGACATCGAT AAAGAAATAC TTTTTCTTTA GCAATTAGTA TTTCTTATGC ATGAGCTTTA 2520

CTCATGTATT CATTTTTTAA GTACaCATTA GCTACAGCTA ATGATAAAGA ACCACTACAT 2580

AATAAATCAT TAGTGGTTCT TTATCATTTC TATCTCACTC TTTTACTGGA AGAAAAAGTT 2640

TACGTTTGTA GAACATGCCA CAATACCAAA AATAATTAAG AAAAATAAGA CGATAAGCAT 2700

GATGACACTT TTCAAACAAC CTCTATCAGT TTCTTTCGAT TTTCTTTGTT GAACCTTTTT 2760

ATAATCTTCA AGTAGTTTTG CGGCTTTTTT ATTTATATGT TTATTCATGA TGTTGACTCC 2820

TTATAATATA TGTTTAATTC ATTAAAATAG TTGAAAACAT GACTTGAAAT AAAGATATAA 2880

AATTTGATGA TGATATTTGC TTTTTATTTT CCAAATGGAA TTTACTTAAA CTGATGCATT 3000

AAAATATTAA TGAAGCACTA GAATACATAA ATGAATAGTa ATGGTGcACA GTATAGAATA 3060

ATTAAGGCTA TATTAAGTAT AAATATCGTT AACTGTAAGC TATCTTTAGT TTTAATATAA 3120

ACTATTAGGA TAATCGACGT AAGAAGAATC ATATATATTA ATGATGAAGA AGTCCATACA 3180

AAATCCGCAT CATTTGTTGT TAATAATGGG ACTATAATTA ATCCGAAATT AATCATGCAT 3240

GCTATATATA CTATAATGTT ATACACAATG TTAATTTTTG TTCACCACCT TATACTTCTA 3300

TTTTAAAAAC TTCTTTATAA TGATATATTG TTTAATGTTG AAATAATTAG ATTATCTAAT 3360

TTTCATTTGC TTTACATGTA AAAGGCTATA TATAGTATGC TCTTTATGAT TCTAAATGCT 3420

TTTTAATATT TAATGCTCAT CAACATTTGG ATTTTGAATA TTCAATTCAA AAACTTTATT 3480

AGCTACGTCA ATTGTAAAAT CAGAACCATA GTTGACATGA GCTACTTTTA ATTTTCCATC 3540

TAAATAATAG ATTGCGATTG CAACATCGTA AAATTCGTCA ATGACAAATA AACTCTTTTC 3600

GTTTGTTACA ACCTCATGCT CTCCTGAGTA TACAACGTTA ATTTCCCAAT CATTAAAAAC 3660

CATTTGTTAA CCTCCTTGAA CATTTAAATT GATTCAACTT AAGTTTAACT TATTCATACA 3720

ACTTCGTACA ATATCTAGAT GAACATTAAT TGTATTTCTA GAAATCTTTT TCAATTATAT 3780

GTACTAATTA TACTTTTAAA TTTCTTATTT CAGTATAGTT TTAAAACGAT TTTAAAATAA 3840

TTCTGCAAAT ATATTAACAC ATAATGTGTT CAAAAAGTTT TGAACAATTT CAAAACTTTT 3900

ATATAAAGGG nTTGACAACA TGGATTCAAA TnTCTTATTT TAAAAATTAC CTCATATAGT 3960

GTCATGTTAG CCAATTTTTA AG 3982

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

AGCTTGGaTG ATTTAATaTG GtCCtTTCCC AaCcTTAGAT AATGAAAGAT tTGATAATCC 60

TGAATATAAA GAAGCTATGA AAAAATATcA ACAGAGATTT ATGGCTGmAG ATGAGGCTTT 120

GAAGAAATTT TTTAGTGAAG AGAAAAAAAT aAAAAATGGA AATACTGATA ATTTAGATTA 180

TCTAGGATTA TCTCATGAAA GATATGAAAG TGTATTTAAT ACTTTGAAAA AACAAAGTGA 240

GGAGTTCTTA AAAGAAATTG AAGATATAAA AAAAGATAAC CCTGAATTGA AAGACTTTAA 300

GTTAGGTAAA ACATTTTATC AAAACTATAG AGATGATGTT GAAAGTTTAT ATAGTAAGTT 420

AGATTTAATT ATGGGATATA AAGATGAAGA AAGAGCAAAT AAAAAAGCAG TTAACAAAAG 480

GATGTTAGAA AATAAAAAAG AAGACTTAGA AACCATAATT GATGAATTTT TTAGTGATAT 540

AGATAAAACA AGACCTAATA ATATTCCTGT TTTAGAAGAT GAAAAACAAG AAGAGAAAAA 600

TCATAAAAAT ATGGCTCAAT TAAAATCTGA CACTGAAGCA GCAAAAAGTG ATGAATCAAA 660

AAGAAGCAAG AGAAGTAAAA GAAGTTTAAA TACTCAAAAT CACAAACCTG CATCTCAAGA 720

AGTTTCTGAA CAACAAAAAG CTGAATATGA TAAAAGAGCA GAAGAAAGAA AAGCGAGATT 780

TTTGGATAAT CAAAAAATTA AGAAAACACC TGTAGTGTCA TTAGAATATG ATTTTGAGCA 840

TAAACAACGT ATTGACAACG AAAACGACAA GAAACTTGTG GTTTCTGCAC CAACAAAGAA 900

ACCAACATCA CCGACTACAT ATACTGAAAC AACGACACAG GTACCAATGC CTACAGTTGA 960

GCGTCAAACT CAGCAACAAA TTATTTATAA TGCACCAAAA CAATTGGCTG GATTAAATGG 1020

TGAAAGTCAT GATTTCACAA CAACGCATCA ATCACCAACA ACTTCAAATC ACACGCATAA 1080

TAATGTTGTT GAATTTGAAG AAACGTCTGC TTTACCTGGT AGAAAATCAG GATCACTGGT 1140

TGGTATAAGT CAAATTGATT CTTCTCATCT AACTGAACGT GAGAAGCGTG TAATTAAGCG 1200

TGAACACGTT AGAGAAGCTC AAAAGTTAGT TGATAATTAT AAAGATACAC ATAGTTATAA 1260

AGACCGAATA AATGCACAAC AAAAAGTAAA TACTTTAAGT GAAGGTCATC AAAAACGTTT 1320

TAATAAACAA ATCAATAAAG TATATAATGG GCA 1353

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1987 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

GTCTGAGTCA GGTGCTGTTT GGTTAGATGC TGAAAAAACA AGTCCTTATG AATTTTATCA 60

ATTCTGGATT AATCAATCAG ACGAAGATGT AATTAAATTC TTnAAATACT TTACTTTCTT 120

AGGAAAAGAA GAAATTGATC GCTTAGAACA ATCTAAAAAT GAAGCACCGC ATTTACGTGA 180

AGCTCAAAAA ACATTAGCTG AAGAAGTAAC TAAATTTATT CATGGTGAAG ATGCATTAAA 240

TGATGCAATC CGTATTTCAC AAGCATTATT TAGTGGTGAT TTAAAATCAT TATCAGCGAA 300

AGAATTAAAA GATGGATTTA AAGATGTGCC TCAAGTGACA TTATCAAATG ACACAACAAA 360

TGTTAACAAT GGTGCGATTT ATATTAATGG TGAGAGACAA CAAGATGTTA ATTATGCTTT 480

AGCACCAGAA GATAAAATTG ATGGCGAATT TACGATTATT CGTCGCGGTA AGAAAAAATA 540

CTTCATGGTT AACTATCAAT AAATATAATT GCATAGCTAA ATAAATTAGA GCCTACTCAT 600

ATTCATTCCT AAGAATGTAA TGAGTAGGCT CTTAATGTAC TTTTCTGTCT GTAAATTATC 660

TAAAGAAATC TCTATCGCCT TGGCCAGGTG ATTGACGTTC TGATCGGCTT TGACGTTTTG 720

GTTGTTCTTT TTGTTGTTTT AATTTCACTT TAACTTCTTT TGTTTTACCA TCACGGATAA 780

CGGTAACAGT GACTGATTCA CCAGGTTTTT TATTTTCATA TAAATAGCTT CTTAAATCAA 840

CATCATCTTT AATTTTCTTG CCATCAATTT CTGTAATAAT ATCACCTTTT TTAAGATCAA 900

TATCACTATC AGCTTTGGCG ACATAAATAC CGTCTTCTCT ATCAGTATGA AGTTGCTCGC 960

GCTCTTCTTC AGGAATATCT TTCAAATTAA TTAAACCAAT ACCAATCGAA GGGCGGTCAA 1020

TTTTACCATG TTTTACAAGT TGTTCAATTG TTACTTTAAC TTCATTACTT GGAATAGCAA 1080

ACCCGATACC TTCAACTTGT GTCGCAGCAA TTTTCATTGA GTTAATACCA ACTAAATTAC 1140

CATTAATATC TACTAATGCG CCACCTGAGT TACCTGGGTT AATAGCAGCA TCTGTTTGAA 1200

GAACGCTAAC TTTTGTATTG CCACCAGTTG TCTCAGCGTC AATCGTACGT TCGCTTGCTG 1260

AAATGATACC AGATGTTACA GAGTTAGCAA ATTGTAATCC TAATGGGTTA CCCATTGCGA 1320

ATACGCTATC GCCAGTTTGT ACTTTTGAAG AGTTGGCAAA TTGAATCGCT TTAATACCTT 1380

TTGTATTTTC AATTTTAAGT ACAGCAATAT CAGTTACTGc ATCTTTACCA ACTAATTTCG 1440

CTTTAACTTG TTTTTTATTA TGTAATTGGa CTCTAATTTC ATTTGCGCCA TCAATAACAT 1500

GATTGTTTGT AACGATATAA GCTGAATTGT TGTTTATTTG aTAGATAACA CCTGAACCTA 1560

CTCCAGCTTC AGATGGTTTA GATGATTTGC CyTTTAATAA GTCGTCTACA CTTGATGCTT 1620

TTtGCATGTk AATAACTCCA ACAATTGTAG GGGAGACAGA TTTTATCATT TCATGAACGG 1680

TACCGAATTT CTTGCTTTGA CCGTCTAATT GATTGCCACC TTTATTATTT GTTGTCTGAA 1740

CAGTTGAACC ATCTTTATTT AAAATTGTAC TATTTAATAC TTTGCCTATA CCAAGTACTA 1800

GAAGTGCACC AATAATTCCA GCAATCAATG CAACGATGAC TGTnTTAAAC CATGGAAATT 1860

TAGGTCTTCT GTATCTAGGT GTTTGGCTAT GGTTTGTTGT AGAATGATCT GTATGATTAA 1920

AATCTGACAT ACTTAACCTC CATTATATGA TTTATATATG CTTTAATTAT GTCTTTTnTT 1980

TATAATT 1987

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1351 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

TTAGAAGTCA AATCATTAnT GGCGTCnTAT CGAGTATACT ATTAACTTCA ACTATTTTAG 60

CAATTGCATA TATTTTAATG TGGTTTAACG GCCATATGAC aCTAACTTTG ACCTTAACGA 120

CAATAATTAC AAGCTGTTTA ACCTTATTAA TATGTAGTAT TTTTATTAAT CCACTTATAC 180

AAAAAATTAA GCAGTTTAAT ATAAAAACTA AGCAATTTGC TAACGGAAAT TACGCAAGCA 240

ATGATAAAAC GTTTAATTCA CCAAAAGAAA TTTATGAATT AAATCAATCT TTTAATAAAA 300

TGGCTTCTGA AATTACGCAA CAAATGAATC AAATTAAATC CGAACAACAA GAAAAAACAG 360

AACTGATTCA AAACTTAGCC CATGATTTAA AAACACCTTT AGCAAGCATT ATTTCATATT 420

CTGAAGGACT ACGTGATGGT ATAATCACTA AGGATCATGA GATTAAAGAG TCATACGACA 480

TATTAATTAA ACAAGCAAAC AGATTATCAA CATTATTTGA TGATATGACT CATATTATCA 540

CTTTAAATAC AGGTAAAACA TATCCCCCAG AATTAATACA ACTAGACCAA TTACTTGTAT 600

CAATATTGCA ACCATATGAG CAACGTATCA AACATGAAAA CCGCACATTA GAAGTGAATT 660

TCTGTAACGA AATTGATGCA TTTTATCAAT ATCGAACGCC ACTTGAGCGT ATTTTAACAA 720

ACTTACTTGA TAATGCGCTA AAATTTTCAA ATGTTGGTAG TCGCATTGAT ATTAATATTA 780

GTGAAAACGA AGATCAAGAT ACTATCGACA TTGCTATTAG CGATGAAGGT ATTGGCATTA 840

TACCAGAACT ACAAGAACGT ATATTCGAAC GTACATTCAG AGTAGAAAAC TCTCGTAATA 900

CAAAAACGGG TGGTTCTGGA TTAGGCTTAT ATATAGCTAA TGAACTCGCG CAACAAAATA 960

ACGCAAAAAT CAGTGTAAGC AGTGATATAG ATGTAGGAAC TACGATGACT GTAACATTAC 1020

ACAAATTAGA CATTACGTCA TAATCCGATT TATTTATAAA ATAAAATGCA AAGACTAAAA 1080

AGAAGCTCCC ATTAATGAGG GCTTCTTTTT TTGTTTATTT AGAATAAACT TTATGGGTAT 1140

CCTTCTCATC ATTTTCAAGA CTTGAAAGAT TTGTAGCTTG AATAATATAT TTAGGACGTG 1200

CCTTAACTTC ATAATATATC CTGCCAATAT ATTCACCTAC AACACCAATT GAAATTAACT 1260

GTATGCCGCC TAATAATAAA ATAGCTGCAA TCGTTGAAAA ATATCCCGGA ATATTAACAC 1320

CAGATATCAT AATATTGATG GAATAAATAG A 1351

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

TTGTTGTCAG TTTAACGCAA CGTGTTACCG ACTTTTCAAG TACACAAcAA TATATATGTC 60

TATTCCATTT TTAGCCCcTG CCATTTTCAT CATTGGTGGT ATTATGTTGT TTATTTCAAC 120

ATTTAATAGC TTAGATGAAA CTGCTGAAAA TAATAACAAA ATAAAGAAAC TAATGATTAA 180

AGGACTTATC ATTATTAACA TTTCATTTAT CGTTATGATG GTTTTAACAC CATATTGGTA 240

CTTGTATTTA ATCGTCTATC TTATTTTCTT GTTGTTTTTA TTGTGGCAAA AGGTTTATAA 300

ATTTTAATAC CAAAACTATT AAACACTTCT GATATTCTTA GTTCAAAATA TCAGAAGTGT 360

TTTATAGTGT TATCTAGTTC AGATAAATAT TTCCTTACTT AAAAAAACGC CCTCCTCTTA 420

TTTTGACCCC nAT 433

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1845 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

CCCCCACTAT GATATGCTTG GCCTATTGCG TCAATCCCCT TATATTTCGG CAATAGAGAT 60

GGATGTATAT TCAATATTTT ACCTTCAAAT GAAGCTAATA AGTCTGGACC AATTAGACGC 120

ATGTAGCCAG CTAGAATAAT CCACTCTACC TTATCTTCAT TTAATAATGT TACTAAATGT 180

TGTTCATACG CTGCTTTTGA ATCAAATTGT TTTGGTTCAT TAATATAAAC AGGAATATCG 240

TGCTTTTTTG CTCTATCTAT ACAAAACGCA TTTTGATGAT CCGTATATAG CGCCGTAACT 300

TCAATATTTT CAAGTTTTCC TGATTCAACA TGCTCAACTA TATTTkCAAA GTTACTTCCT 360

GAACCTGATG CAAAAATCGC AATTTTAACC ATTGTTATAC CCCCAACAAT TCAATTGCAG 420

TTGACTCATT TTTCACAATA TGACCAATTT GATAGGCTTC CACATTTTGT TCTGCTAAAA 480

TCTTCAAAGC GCGTGATACA TCTTTTTCAT CAACGATAAC CGTATAGCCA ATACCCATAT 540

TAAAAATGTT ATACATTTCA TTTGTGTCTA TATTGCCTTG TTGTTGTAAC CAATCAAATA 600

TTTTTGGTGT TGGAAATGAT GTAGTATCAA TTCTAGCAGC ATATCCGGCT GGCAATGCAC 660

GTGGAATATT TTCATAAAAA CCTCCACCAG TAATATGATT CATTGCCTTA ATAGAAACTT 720

CTTTTTTCAA AGCAAGTACA GGTTTGACAT ATAATTTAGT TGGTTCTAAA AAGACATCGA 780

GCACTAAACT GTATCCATTT GAATGAATGC CACTTGACGC AAGCCCTATA ACAACTTGTC 900

CCTCTTTCAC TTCTGAACCA TCTACATAGT CATCCTTTTC AACTGCTCCA ACAGCAAATC 960

CAGCTACATC ATATTCGCCT TCGTGATACA TTTCACCCAT TTCAGCAGTC TCTCCACCGA 1020

TAAGTGCAGT ATTCGTTTCA ACACATGCAT CACTAATACC TTTAACAATT TGTTCAATAA 1080

CTTCAGGAAC AACTTTGTTT GTAGCAATGT AATCTAAAAA ATATAATGGT TCTGCACCTG 1140

TCGTTAAAAT ATCATTAACA CACATTGCGA CTGCATCGAT ACCTATCGAA TCATGTTTAC 1200

CATAGTCGAT AGCTAGTTTT AATTTCGTAC CTACTCCGTC TGTTCCAGAA ACTAAAACTG 1260

GCGCTGtCAT ATTTAATTGT GATAAATCAA ATGTAGCACC GAATCCACCT AAACCACCGA 1320

TAACTTCTTT ACGCATCGTA CGtTTAACaw GaCtAGaCaT TCtTTCtACA GCTTCATAAC 1380

CAGCATGAAT ATTTACACCA GATTGTTCAT ATGCTTTAGA CATTTAAATT TCCCTCGCTA 1440

TCAAAAAAGT GTTTGTTTTT AGAAATATAT TGCTTTTGTC GATGACTTAA ATGCGCTTTA 1500

TAATTTGCTT CATAATCATA TAACCCTGCA GGATAATCTC CAGTGAAACT TTCTACACAT 1560

AAGCCACTAT ATGGCGCGTC ATAATCTAAA CCAATTGATT CAATTAACCC ATCTACAGAT 1620

AGATATGCTA ATGAATCAGC GCCAATATAA TCTTTAATTT CTTCAGGTGA TTTGCTTGCA 1680

GAAATTAATT CTGCCGTAGT TGAAACATCG ATTCCGTAAA AACTTGGAAA CATAAATTCC 1740

GGTGATGCTA TACGCACATG CACTTkATTT GCACCAGAAT CkTTTAACAT TTTCACAATG 1800

CGTCGAATTG TCGTACCGCG nACAATGGAA TCATCAACAA GACTG 1845

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

TCATAAATnG TAAATGTTAA TCGTCATATA ATATTAATTT ACAACACCAT TTTGGTTATT 60

TGAAGCTTGT GGCGCTTGTT GTGTGCCACC TTGATTTTGA TTTGAGTTTT GATCTGTAGC 120

AGGTTGTTGT TGATTGCTGG AmtCACTGTT ATTAGTTGAm TCACTGTTCT CGTTAGATGT 180

CTTATCTTTA TCTGTCGTAT CATTTTGTTC TTTTCTCAAT AAACTATTAT CTAAAGGCGT 240

TAATGGTATT AATGAACCAT AATGATTAAT GACACGTTGA TCTAAGAAAT CATTTTTATC 300

ATTAATAGGT GATAATTCTA AGTCTTTACG AAGTAAGTTT GCATATTTTT GAATGCTTTC 360

AGTTTTAATT TCAACATCAT TTGTTaAGTA CATTTTTGCT AAAGCTTTAA TTTCAGAGTT 480

AGTTAAATTA TGCTTTGCAT TTTTACCTAC AATTTGAATC ACGTTATCAA GTTTATCAAT 540

AGAATCAACT TCCTGTGCTT TTTGGAATAA AATCTTAATT AATTCCATTT GACGTTGTCC 600

ACGTTTTAAG TCTGAATCAT GATGTCTAGT TCTAGCAACT GCTAAAGCCT CATCACCATT 660

TAATTTTTGG TACCCTTTTT TAATTTTAAT CTTACCAGTA TCATCTGTGT TAGGTTCATT 720

TAAGTCGTAT GGCACATCAT AGTATATGCC ACCAAGCTCA TTTACAGCCT CGACAAATGC 780

TTTCATATTG ACTCTCACAT AATAATCAAC AGGTACATTC ATGGTAGCTT CTACCGAATC 840

CATTGCGGCA ATTGGACCAC CATATGCATG TGCATGGGTA ATCTTATCGT AATAGCCAAC 900

TTTAGGAATG TAGCTGATAG TATCACGTGG AATACTAAGC ATTCTAATTT GATGTTTTGA 960

TTGATTAAAA GTAGTTAAAA TCATAGCGTC TGATCTAGAG TGTTCAGCAT CCTGTCCTTT 1020

TTTTCTTCTT CCATCGTTAT CATCGATACC TAAGAAAAGA ATAGAGATAG GTTGTTCTTC 1080

GGGATGACTT TATTATCTCT TAAGTTGGAT TGACGTTAGC ATTTTTGCTG TCTTGAGAAG 1140

A 1141

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1565 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

GCACCATTAG CATTGGGCnC ACTGATTGGA GTAnCAGTTG TTGAAAATTC GGCGCCAACA 60

AGTAAACmGG CmCaGGCaGC mATamCCCCa TATTATAcTT ATAATGGTTA TATTGGTAAT 120

AATGCTAATT TTATTCTGGA TAAGAATTTT ATTAACGCGA TTAAGTATGA TAATGTGAAA 180

TTCAATGGTA TTAAATTAGC TAAAACGAAT ACGATAAAAA AAGTAGAGAA ATATGATCAA 240

ACTTTTAAAG GTGTTTCTGC AAAAGGAAAC GAAGCAAGTC AATTGCAATT TGTAGTTAAA 300

AATAATATTT CATTAAAAGA TATCCAAAAA GCTTATGGCA AGGACTTGAA AAAAGAAAAT 360

GGTAAAACAA AGGAAGCTGA TAGCGGTATT TTTTACTATC AAAATGCTAA AAAGACATTA 420

GGCATCTGGT TTGTCGTTGA TCATAATAGA GTTGTCGAAG TAACAGTTGG ACATACACCA 480

TACAAAACAA GTAAATAAAA TAATGGCATA TTAAGGCTAG AGTGTGAGGA GTGATACCGC 540

ATTCTAGTCT TTTTTATTAA ATAATAACGA TTATTGCGTC TTACATAGTT GTTTGAAATT 600

GATTAAGTAT ATAGAGCACT ATTTTGTATT TGTTAATATT TTCACAAAAA TAAAGCCTTG 720

ATAAATTTTA AAATATAATT AAGCTCAATT TTTAAAATTT TATTTAGCTA CAGATAACAT 780

TTTTAAAAAA GAAAAGAATC AATAAATAAA ATCAACGAAC AAAAAGTATA GAAATAAATA 840

GAAATAATCA TTTACTTTTC TGAAAAATTA AATTAATATT TTATTTATAA GCTGTTTTTA 900

AGATTTCAGG AGGAATGAAA TGTGaGGAAA TTTTCAAGAT ATGCATTTAC AAGTATGGCA 960

GCATTAACCT TGTTGAGCAC TTTATCACCA GCAGCATTAG CGATTGATTC AAAAAATAAA 1020

CCAGCTAATT CTGATATTAA ATTTGAGGTG ACTCAAAAGA GTGATGCGGT CAAAGCATTA 1080

AAAGAATTGC CTAAATCCGA AAATGTAAAA AATATTTATC AAGATTACGC TGTTACTGAT 1140

GTAAAAACTG ATAAAAAAGG ATTTACGCAT TATACATTGC AACCGAGTGT TGATGGTGTT 1200

CATGCACCTG aCAAAGAAGT GAAAGTACAC GCAGACAAAT CAGGAAAAGT CGTTTTAATC 1260

AATGGGGATA CTGATGCGAA GAAAGTAAAG CCAACGAATA AAGTGACATT AAGTAAAGAT 1320

GACGCAGCCG ACAAAGCATT TAAAGCAGTT AAGATTGATA AGAATAAAGC GAAAAATCTT 1380

aAAGATAAAG TCATTAAAGA rAACAAAGTT GAAATCGATG GTGACAGTAA TAAATACGTT 1440

TATAATGTTG AGTTAATTAC AGTGACACCA GAAATTTCAC ATTGGAAAGT TAAAATTGAT 1500

GCTCAAACTG GCGAAATTTT AGAAAAAATG AACTTAGTTA AAGAAGCTGC AGAAACTGGT 1560

AAAGG 1565

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2870 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

GGATAGGTAA ATCCATTCAA AATTGGTTGT ACTCATTTTA AATCATATTT TTTAATATAG 60

AAACACATAA TTAAAGGAGT GATGATATTA ATGAATAAAC TTCGAGACAC TACTTTTCTA 120

TCATATTTAT TTACTATCAT ATTGTGGGGA TCTGCATTTC CAATGATAAA GATTGCGTTA 180

AATGATTTTA GTGCAGAATC ATTGTCGGCA TTTCGTTTAA TTTTAGCAAC AATAATTCTC 240

TTGCCGTTCG TAATTATAAA GAAATTGCCT ACCCCTGAAC TAAGAGATAT CCCTGTTATT 300

TTTATTTTAG GATTTTGTGG ATTTGTGATA TATCACACAG CTTTAAATTT TGGTGAAaCT 360

TTGATTAGTG CAGGTATAtC TGGrATTCyA GTCTCTACAA CGCCTATTTT TTCTAGTGCT 420

GCATTTATAG GAATATCCAT TATTTCAATA AGTAAAGATG ATTACACAAC TATTAATGTA 540

TTAGGTGTTT TTATTATTTT ACTTGCATCT TTTAGTGAAA GTTTGTATTT TACTTTCCAG 600

AAAAAATACA TAGAAAAATA CGGCTTCATC GCTTTCACAC TATaTACAAT AATGGCAAGC 660

TCACCATTTA TGCTTATTTT TATTCCTGAA ATCATCAACG ATATACACGG CGCCACTTTT 720

ACATCAATAG TATCGGTACT TTATTTAGCT ATATTCCCTA CTATAATTCC ATACGTTTTG 780

CTTGCTTATA TTGTGAAGTC AGTTGGTGTC TCTGATGCAA CAATGTCTCT TTATTTAACA 840

CCTATCGTTT CTTTATTATT ATCTTATCTG TTATTAGACG AGCTACCAAC AACCCTTGCT 900

ATTATAGGCG GAATTATCAC TCTACTAGGC GTTAGTTTAA GTAACTTCTT TCAAAATACA 960

TAATTATTCC AAGTCCCGCA CCTCAGAATC CAAAAACATT CGAGTGATAA AATTTTAAAA 1020

ATCAAAAATA TAAAAATGAT CTAATTTCGT CAAATTTACC AATATAAATA CTAATATTTG 1080

CAATTCACAA AGGGGTATAG TCTGAGTGTA TTCTAATACG AAAGGACTTG GTGGATATGT 1140

ATTACAGTTA TGGAAATTAT GAAGCATTTG CGCGCCCTAA AAAACCTGAA AATGTAGAAA 1200

ACAAATCCGC TTACTTAATC GGATCTGGTC TAGCTTCACT TGCTGCAGCT TGTTTTTTAA 1260

TAAGGGATGG TCAAATGGAA GGTTCGAAGA TTCATATTTT AGAAGAGTTA CCTAAAGCAG 1320

GTGGTAGTCT TGATGGTGAA AATATGCCTT TAAAAGGCTA TGTTGTCCGC GGTGGTCGTG 1380

AAATGGAGAA CCACTTTGAA TGTTTGTGGG ACTTATTCAG ATCTATCCCT TCATTAGAAA 1440

TCGATAACGC GTCTGTATTA GATGAGTTCT ATTGGCTAAA CAAAGAAGAC CCTAACTATT 1500

CTCGCTGTCG TGTTATTGAG AAACAGGGTC AACGTTTAGT CACAGACGGA GACTTCACTT 1560

TGACTAAAAC GGCGATTAAA GAAATTTTAG ATTTATGCTT AACGAATGAA GAAGATTTAG 1620

ATGATGTCAA AATAACAGAT GTATTTTCCG ATGACTTCTT TAATTCAAAC TTTTGGATTT 1680

ACTGGAAAAC GATGTTTGCA TTTGAACCGT GGCATTCTGC AATGGAAATG CGTCGCTATC 1740

TAATGCGATT CGTTCATCAT ATTAGTGGTC TCGCAGACTT TTCAGCTTTA AAATTCACTA 1800

AATATAATCA ATATGAATCT TTAGTATTAC CTATGGTTGA ATATTTAAAA TCGCATGGGG 1860

TTCAATTTGA ATACGATGTA AAAGTCGAAG ATATTAAAAT AGATGTTACG ACAAGTCAAA 1920

AAATTGCCCG AGAAATATTA ATTGACCGTA ATGGTAATGC AGAATCTATT AAACTGACTA 1980

TAAACGATCT TGTCTTTGTG ACAAACGGTA GTATTACAGA AAGCTCTACT TATGGTGATA 2040

ATGATACACC AGCGCCACCA ACTGACGAAT TAGGTGGTAG TTGGACACTA TGGAAAAATT 2100

TAGCGCGACA AAGTCCTGAA TTTGGTAATC CTGATAAGTT TTGCCAAAAT ATTCCTAAAA 2160

AAAGTTGGTT TGTTTCAGCA ACTTCTACAA CAAACAATAA AGAGATTATC GATACAATAG 2220

TCAATGATTC TGCATGGCAA ATGAGTTTTA CAATCAATCG TCAGCAACAG TTTAAAGACC 2340

AACCTGAAAA TGAAATATCT ACATGGATTT ATGCCTTATA TTCAGATGTA AACGGCGATT 2400

ATATTAAAAA GCCAATTACA GAATGTAGTG GTAATGAAAT ATGCCAAGAA TGGCTGTATC 2460

ACTTAGGTGT ATCAACTGAC AAAATTGAAG ACTTAGCAAA ACATGCATCT AATACGATTC 2520

CTGTTTATAT GCCATATATC ACATCTTATT TCATGACGCG TGCTATCGGC GACAGACCTT 2580

TAGTCGTCCC GCATCAATCT CAGAACTTAG CATTTATTGG TAACTTTGCA GAAACAGAGC 2640

GAGACACTGT ATTTACAACA GAATATTCGG TTCGTACTGC CATGGAAGCT GTTTATCAAT 2700

TACTAAATAT AGATCGTGGT ATTCCAGAAG TCATCAATAG TCCATTTGAT CTTCGCGTCT 2760

TAATGGATGC CATATACGAA CTGAATGACC ACCAAGATTT GCGTGAGATT ACTAAAGATT 2820

CGAAAATGCA AAAACTCGCA TTAGCAGGAT TCCTTAAAAA GATAAAAGGT 2870

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

CnGTTTAGCT GCAAAAAGTA AATAACGACA CTGTATTTGG AATTTTGCAA TTAGAAACAC 60

TTTTGGGTGA CATTAACTCA ATTTTCAGCG AGATTGAAAG CGAATACAAA ATGTCTAGAG 120

AAGAAATTTT AATTTTACTA ACTTTATGGC AAAAAGGTTC TATGACGCTT AAAGAAATGG 180

ACAGATTTGT TGAAGTTAAA CCGTATAAGC GTACGAGAAC GTATAATAAT TTAGTTGAAT 240

TAGAATGGAT TTACAAAGAG CGTCCTGTTG ACGATGAAAG AACAGTTATT ATTCATTTCA 300

ATGAAAAGTT ACAACAAGAG AAAGTAGAGT TGTTGAATTT CATCAGTGAT GCGATTGCAA 360

GTAGAGCAAC AGCAATGCAA AATAGTTTAA ACGCAATTAT TGCTGTGTAA GTTTAATAGC 420

ATAAAAAGAG GTTTTCATTA AGTTGAAAAC CTCTTTTTGT TGTTGGCATT AATTTTTCAA 480

ATGTTGACTA CTCAATCCTA AATTATAAAT AGTATAGCGC aCAAaTGCTT AAGAAATTTT 540

TTCTATGGCA CAAATGAATG GAGCATGATT ACGTTGGTTT AAAAATTGAT ATTGCAAAAC 600

TTGCGCATGC TTTTGATCCA AAGTACTCAA GTAATCAAGC AATGCATGCT TCTCAATTTG 660

TCCTTCGCTA TGACCATGAT ATATAACAAG TACAATAATA CCTTCAATTG ACATTAATGA 720

TAGCAATGAA TTAATAGCTT GGATTGTCGT GTCAGGCTTT GTCACGATAG ATTTATCACC 780

TATATGATGT TCAATATTTT CATGTCCATC TTTTATTAAA GAAACATGAT TGAAATCCTT 900

AACTTTATCA CGTGTATTTT CCAAAGCTAA ATCTTGAATG TCGAAACCAT AAACATGTCC 960

TTCTGGTACT TGTTCGGCTA AAAATAAAGT GTCATTGCCG TTACCGCAAG TTGCGTCTAC 1020

AACAATACTT TCTGGTGTTA TATGTTGTTT AATAAGTGTT TTTGAAAAAG GGAGTATACG 1080

TTCTAATTTC ATTGCTTCAC CTTAGACTTG TAACGCAAGC CTTGATAAGA ATTTCTACGT 1140

GCTAATTCAG CATCGATGCC ATTTAATACT TCCCATTTAT TAACACTCCA CATTGGACCT 1200

ACCATGATAT CTATTGGACC ATCACCGGTA ATTCGGTGAA CGATCATTTC AGGGGGAATC 1260

ACTTCTAATT GGTCCACAAC TAGGTTTGTG TACTCTTCTT GAGTCATAAA AGTTAATAAA 1320

CCTTTATCGT ATTGTTTTAC CATCGGTGTA CCTTTTAACA AATGAAGTAA ATGAATTTTA 1380

ATACCTTGTA CATCCATTTG TGCAcTTCTT TGGCAGTAGC CATCATCATG TCATAGTCTT 1440

CGCCAGGTAA GCCATTAATG ATGTGTGTAC ATACATTGAT ATTATGCTTA CGTAATTTTG 1500

CCACACCATC ATAATAAGTT TTCATATCAT GGGCACGATT GATTAAATCA GATGTTGACT 1560

GATGGATTGT TTGTAGTCCT AATTCAACCC ATAAGTATGT TCGTTGATTC AAATCTGCTA 1620

AATATTCGAC AACATCGTCT GGTAGACAGT CAGGACGCGT ACCAATAGAT AATCCCACAA 1680

CACCCGGTTC TTTAAGTACA GGTTCGAATT TTTCTTTTAA TACTTCAACC GGTGCATGTG 1740

TATTTGTAAA TGCCTGAAAA TAAGCAATAT ATTTTCCTTC GTGCCATTTC TCATGCATCT 1800

TTTCTTTAAT TTCTTTAAAT TGTACTGCGA TTGAATCTGC ACGATTACCT GCAAAGTCTC 1860

CGCTACCTGC AGCAGAACAA AATGTACATC CACCATGTGC TACAGTGCCA TCGCGGTTAG 1920

GACAGTCAAA CCCGCCATCC AATGCAACTT TAAATATTTT TTGTCCAAAT TTATTTTTTA 1980

AATGGTAATT CCATGTGTGA TAACGTTTGT TTTCAAAAGC GTATTGGAAA TGATTGCCCA 2040

TATGTCATTT TCCTTTCTAT AAAAAAAGAG TTCTAAGTAC AGATTTTAAC ATATTTTAAT 2100

GTTATAGTGT TTATTATAGT TTGACAAAAA AGAGAGAGGA ACTATGAAAT ATGAATATAC 2160

CTAAATCAGT CTGGTGGCTA GTAATTGGCA TGGCGTTAAA TATTACTGGT TCCAGTTTTT 2220

TGTGGCCTTT AAATACAATT TATATGAAAC AAGAACTTGG AAAAAGTTTA ACTGTTGCTG 2280

GTTTAGTGCT AATGATAAAT TCATTTGGCA TGGTTATTGG AAACTTATTA GGTGGTTCAC 2340

TATTTGATAA ATTAGGTGGA TACAAGACGA TTTTAATTGG AACTTTCACT TGTCTTTGTA 2400

GTACAACGCT ACTTAATTTC TTTCACGGGT GGCCTTGGTA TGCTGTATGG CTTGTAATGT 2460

TAGGGTTTGG TGGCGGAATG ATTATTCCTG CGATATACGC TATGGCTGGA GCAGTGTGGC 2520

CAAATGGCGG AAGACAAACG TTTAATGCGA TATACTTAGC GCAAAATATT GGTGTGGCTG 2580

ATCTTATTAT GTATGTTGTG TTTGCGCTTG TCGCGGTAAC GCAATTTAAT ATTGAAATTA 2700

ATGCGAAAGT TAAATATCCA ACTCATTTAG ATATTACTGG TAAAAAGAAT AAAGCAAGAT 2760

TTATTTCATT AGTACTAATT TGTGCAATGT TTGCAATTTG TTGGGTTGCA TATATTCAAT 2820

GGGAGTCTAC AATCGCTTCA TTTACACAAT CTATTAATAT TTCAATGGCA CAATATAGTG 2880

TTTTATGGAC AATTAACGGA ATAATGATTT TAGTAGCACA ACCATTAATT AAACCGATTC 2940

TCTATCTGTT AAAAGGAAAC TTAAAGAAGC AAATGTTTGT CGGCATCATC ATTTTTATGT 3000

TGTCGTTCTT TGTCACGAGT TTTGCCGAAA ACTTTACAAT ATTTGyTGTC GGTATGATTA 3060

TTTTAACTTT TGGAGaATGT TTGTATGGCC AGCAGTTCCA ACTAT 3105

(2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5532 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

TAATGATTAA ACCAGATGCA GTACAAAGAA ATCTAATTGG TGAAGTAATT TCAAGAATTG 60

AAAGAAAAGG ACTAAAACTT GTCGGTGGTA AATTAATGCA AGTACCAATG GAACTTGCTG 120

AAACACATTA TGGTGAACAC CAAGGTAAAC CATTTTATAA TGATTTAATT TCATTTATTA 180

CATCAGCACC AGTGTTCGCA ATGGTAGTTG AAGGTGAAGA TGCAGTTAAT GTATCTAGAC 240

ATATTATTGG CAGCACCAAT CCTTCAGAAG CTTCACCAGG ATCAATTAGA GGTGATTTAG 300

GTTTAACTGT TGGTAGAAAT ATCATTCACG GTTCAGATTC ATTAGAGTCT GCTGAACGTG 360

AAATTAATCT ATGGTTTAAT GAAAATGAAA TTACTAGCTA TGCTTCACCA CGTGATGCAT 420

GGTTATATGA ATAAAATATA AACTGTAAAC CTTTACGATT TATTTATAAA GGTAGAAAGG 480

GTTTTGTTAT GTGGTTAGTC ATTATGaTTA TACATAACAA GGCCCGTTTT TTATGTTGTA 540

GTAAATTACT TGAAAAATTT TATAGTTTTT kGGTAAcACG TAtTaAAAaG AGAGGAATAT 600

TCTTTATCAA ATGAAACTAA ACAGAGAGAA GGGGTTGTTA AAATGAAgAA TATTATTTCG 660

ATTATTTkGG GGATTTTAAT GTTCTTAAAA TTAATGGAAT TACTATATGG TGCTATATTT 720

TTAGATAAAC CACTTAATCC TATAACAAAA ATTATTTTTA TACTGACTCT CATTTATATT 780

TTTTATGTAT TAGTAAAAGA ATTGATTATA TTTTTGaAGT CAAAGTATAA CAAAAGCGCT 840

TAACATATGT ATATTTTAAT ATCATAATTT TTTTAAACGG ACTGATTAAC TTTATTAATA 900

GATACGATTA TATTAAAACG GCTAATCATT TTTAATTAAT GATTATATGA TGCAACTGTT 1020

TAGAAATTCA TGATACTTTT CTACAGACGA ATATATTATA ATTAATTTTA GTTCGTTTAA 1080

TATTAAGATA ATTCTGACAT TTAAAATGAG ATGTCATCCA TTTTCTTAAT TGAGCTTGAA 1140

AACAAACATT TATGAATGCA CAATGAATAT GATAAGATTA ACAACATATT ATAATGTTAT 1200

CGTGGAAGTA TGAAAGGAGC GAGTGTGTAT GAGATACCTA ACATCAGGAG AATCACATGG 1260

ACCTCAATTA ACAGTTATTG TTGAAGGTGT ACCTGCAAAT ATAGAAATTA AGGTTGAGGA 1320

TATTAATAAA GAAATGTTTA AGCGTCAAGG CGGTTACGGA CGTGGACGTC GTATGCAAAT 1380

TGAGAAAGAT ACAGTAGAAA TAGTATCAGG CGTTAGAAAT GGTTATACAT TAGGTAGTCC 1440

AATTACTATG GTTGTAACCA ATGATGACTT TACGCATTGG AGAAAAATTA TGGGAGCAGC 1500

TCCAATAAGT GAAGAAGAAC GTGAAAATAT GAAACGTACT ATTACAAAAC CAAGACCTGG 1560

TCATGCAGAT TTGGTTGGAG GTATGAAATA TAATCATCGT GATTTACGAA ATGTGCTAGA 1620

GCGATCATCT GCTAGAGAAA CAGCAGCTCG AGTTGCAGTC GGTGCCTTAT GTAAAGTGTT 1680

ATTACAACAG TTAGATATCG ATATATACAG TCGTGTTGTT GAAATAGGTG GAATTAAAGA 1740

TAAAGATTTT TATGATTCAG AAACATTTAA AGCAAATCTT GATCGTAATG ATGTTCGTGT 1800

AATTGATGAC AGTATCGCAC AAGCAATGCG AGATAAAATT GACGAaGCTA AAAATGAAGG 1860

AGATTCAATT GGCGGTGTCG TTCAAGTTGT AGTTGAAAAT ATGCCTGTTG GTGTAGGTAG 1920

TTATGTGCAT TATGATCGTA AGTTAGATGG TAAGATTGCA CAAGGTGTTG TCAGCATAAA 1980

TGCTTTTAAA GGTGTAAGCT TTGGTGAAGG ATTTAAAGCA GCTGAAAAGC CAGGTAGTGA 2040

GATTCAAGAT GAAATTCTAT ATAATAGTGA AATTGGTTAT TATCGTGGAT CTAATCACTT 2100

AGGTGGTTTA GAAGGCGGTA TGTCAAATGG AATGCCAATT ATCGTTAATG GTGTAATGAA 2160

ACCAATTCCA ACGTTATATA AACCATTAAA TTCAGTAGAC ATTAATACTA AAGAAGACTT 2220

TAAAGCAACA ATTGAACGTT CTGATAGTTG TGCTGTTCCT GCAGCAAGTA TCGTCTGCGA 2280

ACATGTCGTA GCATTTGAAA TAGCAAAAGC ATTATTGGAA GAATTCCAAT CAAATCATAT 2340

TGAGCAACTT AAACAACAAA TTATTGAGCG CAGACAATTA AATATTGAGT TTTAACAACA 2400

AGAACAATTG AGGTGTAATC ATGAAATTAC AAACAACATA CCCTTCAAAT AATTATCCAA 2460

TATATGTTGA ACACGGTGCA ATTGACCATA TTAGCACGTA TATTGATCAG TTTGATCAAA 2520

GTTTTATATT AATTGACGAG CATGTAAATC AATATTTTGC TGATAAATTT GATGATATTT 2580

TATCATATGA AAATGTACAT AAAGTTATTA TTCCAGCTGG TGAAAAGACG AAAACATTTG 2640

AGCAATATCA AGAAACATTA GAGTATATTT TATCCCATCA TGTAACTCGT AATACAGCAA 2700

ACGAGGCGTG CACTTTATAC AAGTGCCAAC GACTATACTA GCGCATGATT CTAGTGTTGG 2820

CGGTAAAGTG GGTATTAACT CAAAGCAAGG TAAAAACCTT ATCGGTGCAT TTTATCGTCC 2880

AACTGCTGTG ATTTATGATT TAGTCTTTTT AAAGACGTTA CCATTTGAGC AAATATTAAG 2940

TGGCTATGCA GAAGTTTATA AGCATGCGTT ATTGAATGGT GAATCAGCGA CGCAAGATAT 3000

CGAACAGCAC TTTAAAGATA GAGAGATATT ACAGTCATTA AATGGTATGG ATAAATATAT 3060

TGCTAAAGGT ATTGAAACGA AGCTGGATAT TGTTATTGCA GATGAAAAAG AACAAGGTGT 3120

ACGTAAATTT TTAAATTTAG GTCATACATT TGGTCATGCT GTTGAATACT ATCATAAAAT 3180

ACCTCATGGT CATGCAGTGA TGGTTGGCAT TATCTATCAA TTTATAGTTG CGAATGCTTT 3240

GTTTGATTCT AAGCATGATA TTAATCATTA TATTCAATAT TTAATACAAC TCGGCTATCC 3300

TTTAGACATG ATAACTGACT TGGATTTTGA AACGTTATAC CAATATATGC TAAGTGATAA 3360

AAAGAATGAT AAGCAAGGTG TACAAATGGT CTTGATTAGA CAATTTGGAG ATATCGTTGT 3420

ACAACATGTT GATCAACTAA CATTACAACA TGCATGTGAA CAATTAAAAA CATATTTTAA 3480

GTAGGTGAAT GAAATGGTAA ATGAACAAAT CATTGATATT TCAGGTCCGT TAAAGGGCGA 3540

AATAGAAGTG CCGGGCGATA AGTCAATGAC ACACCGTGCA ATCATGTTGG CGTCGCTAGC 3600

TGAAGGTGTA TCTACTATAT ATAAGCCACT ACTTGGCGAA GATTGTCGTC GTACGATGGA 3660

CATTTTCCGA CTGTTAGGTG TAGAAATCAA AGAAGATGAT GAAAAATTAG TTGTGACTTC 3720

CCCAGGATAT CAATCTTTTA ACACGCCACA TCAAGTATTG TATACAGGTA ATTCTGGTAC 3780

GACAACACGA TTATTGGCAG GTTTGTTAAG TGGTTTAGGT ATTGAAAGTG TTTTGTCTGG 3840

CGATGTTTCA ATTGGTAAAA GGCCAATGGA TCGTGTCTTG AGACCATTGA AACTTATGGA 3900

TGCGAATATT GAAGGTATTG AAGATAATTA TACACCATTA ATTATTAAGC CATCTGTCAT 3960

AAAAGGTATA AATTATCAAA TGGAAGTTGC AAGTGCACAA GTAAAAAGTG CCATTTTATT 4020

TGCAAGTTTG TTTTCTAAGG AACCGACCAT CATTAAAGAA TTAGATGTAA GTCGAAATCA 4080

TACTGAGACG ATGTTCAAAC ATTTTAATAT TCCAATTGAA GCAGAAGGGT TATCAATTAA 4140

TACAACCCCT GAAGCAATTC GATACATTAA ACCTGCAGAT TTTCATGTTC CTGGCGATAT 4200

TTCATCTGCA GCGTTCTTTA TTGTTGCAGC ACTTATCACA CCAGGAAGTG ATGTAACAAT 4260

TCATAATGTT GGAATCAATC CAACACGTTC AGGTATTATT GATATTGTTG AAAAAATGGG 4320

CGGTAATATC CAACTTTTCA ATCAAACAAC TGGTGCTGAA CCTACTGCTT CTATTCGTAT 4380

TCAATACACA CCAATGCTTC AACCAATAAC AATCGAAGGA GAATTAGTTC CAAAAGCAAT 4440

TGATGAACTG CCTGTAATAG CATTACTTTG TACACAAGCA GTTGGCACGA GTACAATTAA 4500

AAACTTGTTA GGGTTTGAAT TACAACCAAC TAATGATGGA TTGATTATTC ATCCGTCAGA 4620

ATTTAAAACA AATGCAACAG TTGATAGTTT AACTGATCAT CGAATAGGAA TGATGCTTGC 4680

AGTTGCTTCT CTACTTTCAA GCGAGCCTGT CAAAATCAAA CAATTTGATG CTGTAAATGT 4740

ATCATTTCCA GGATTTTTAC CAAAACTAAA GCTTTTAGAA AATGAGGGAT AATATAAAAT 4800

GGAAGATATC TATAAATTAA TAGACGATAT CAATCTACAA AAACTAGAAA ATTTAGACTC 4860

TCGTGTTAAT GAAGCAATAA CTACTGACAA CGATGACGCA TTATTTATTC TAGGAGAGAC 4920

ACTTTACAAT TTTGGATTAA TGCCaCAAGG TTTGGAAGTA TTCCGCGTGT TATATCACAA 4980

ATATCCAGAC GAAAGTGAAT TGCTGATTTA TTTTATTGAA GGTTTAATGT CTGAAAATCA 5040

AACTGACGAA GCGTTAGAAT ATTTAAGTTA TGTTGAACCA TCACCTGAAA AGTTGATGTT 5100

AGAAGCAGAT TTATATCAAC AAATTAATAT GATGGAAGTT GCTATTGATA AATTACAAGA 5160

AGCACTTGAA CTAGAGCCAA ATGATCCAAT AATCCATTTT GCATTGGCTG AAATGTTATA 5220

TTATGATGGT CAATATTTAC GTGCTACCTC TGAATACGAA ACCGTTTTAG AAACTGGTGA 5280

ATATCAAGTT AATGGTGTAA ACTTATTCTC TCGTATGGCA GATTGTAGTT TACAAAGTGG 5340

kAACTATAGT GATkCcGATt CgCTTATACG ATGrAATTAA TGAAGATGAA ATGACTTCAG 5400

AAGATTATCT CAAAAGAGCC ATTTCTnACG ATAAAAATGA CATCACTCAA GAAGCAATTA 5460

AAATAATGAC TACATTACTT TCTAAAGATC CTGATTATAT TCAAgGCTAC TTGTATTTAC 5520

aATCaTTATA TG 5532

(2) INFORMATION FOR SEQ ID NO: 531:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 942 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

AATTGGGTTA TACTATAGGT AAATTTAAGG AGGTAAGAAA ATGGATAAAA AAGAATTAGC 60

GAAATTTATA GGCAATAAAA TCAGATACTA TAGAACCaAA TTGaACTTAA CTCAAGATCa 120

ACTTGGAGAA AAACTCmACa CTAAAAArGC TACTATTTCA AATTATGAGA CAGGGTACAG 180

AACTCCTAAA CAAGATGATT TGTTTGAAAT TGCTCATATT TTAAATATCA GTATCGATGA 240

TTTGTTTCCT ACAAGAAATA ATAAAAAAAA CGACATCACT TCCATATACA ACAAACTCAC 300

ACCTCCCCGC CAAGAAAACG TACTTAACTA CGCAAATGAG CAATTAGATG AACAGAATAA 360

AACTGGTGCT GGCATAGGAG AAGAATTATA TGATGACATA TTGCATGAAG AAGTATTTTT 480

TAAAGAAGAC GAAACGCCAT CAAATGCTGA TTTTTGTATT TTAGTTAATG GTGATTCAAT 540

GGAACCTATG TTAAAACAAG GAACATACGC TTTTATTAAG AAAGAAGATT CTATTAAAGA 600

TGGTACAATT GCACTCGTTG TATTAGATGG AGTAAGTCTT ATCAAGCGTG TAGATATATG 660

CGAAGACTAT ATTAATTTGG TATCTCTAAA TCCGAAGTAT GATGATATCA AAGTCGCTTC 720

GTTTAGTAAT ATTAAAGTAA TGGGCAAAGT TGTATTGTGA TTAATAGCGC CTATATGGCA 780

CTTTAATATA AAAGACGTCT ATTTCAGCAG TGTTTAAAAG GAGTTTATAA TGAAAATAAC 840

TAATTGCAAA ATAAAAAAAG AAACTATAGT ATATGAAGTT TTAACTAGTG GTAATCAACC 900

ATTCACTTAT GAGTTACCTA AAGATTTATC GTCACATAAT GC 942

(2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 417 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

TGGnAAATGC AAACCAAAAT ATGaTCCTCG TGcAAGTTGA AGCGGGACGT TATGAAGAAT 60

GGGTAAAGAA TGGTTATTTT AAACCGTCAG AAGATAAATC AAAAGAAACA TATACAATTG 120

TTATCCCGCC ACCAAATGTA ACTGGTAAAT TACATTTAGG ACATGCATGG GATACGACTT 180

TACAAGATAT CATTACACGT ATGAAACGTA TGCAAGGATA CGATACGTTA TACTTACCAG 240

GTATGGATCA TGCTGGTATT GCGACACAGG CAAAGGTAGA AGCTAAATTA AATGAACAAG 300

GAATAACTAG ATATGATCTT GGTCGTGAAA AGTTTTTAGA ACAGGCATGG GATTGGAAAG 360

AAGAGTATGC GTCATTTATT CGTGCGCAAT GGGCTAAATT AGGTCTAGGT TTAGATT 417

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 733 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

GATCCTGAAC CCGCATTTGT TTCCACTAAA ACAGTATGCC CACTTTCTAC TAAAGCGTGC 60

ATTTTCATAC CATCCACCTC CATAATCATC TTAACGCGAA CATTTTGAAA GCGCAATCAA 180

AAATCCACAA AATTGTAAAG GTTATTACAC TGACTTTTCC GAAAATTGTG GTAAAATATA 240

ATTAAGAAAG AACAAGGAGG CACTTACTAT GATTACTTAC AAAAATATTT TAATCGCAGT 300

TGACGGTTCA CATGAAGCGG AATGGGCATT TAACAGAGCA GTTGGTGTTG CTAAACGTAA 360

CGATGCGAAG TTAACAATTG TGAATGTAAT TGATTCAAGA ACGTATTCTT CTTATGAAGT 420

TTATGATGCT CAATTTACTG AAAAATCTAA GCATTTTGCA GAAGAATTAT TAAATGGTTA 480

TAAAGAAGTA GCTACTAACG CTGGTGTTAA AGATGTAGAA ACGCGTCTAG AGTTTGGyTC 540

TCyTAAATCT ATCATTCCTA AAAAGCTTGC ACATGAAATT AATGCAGACT TGATTATGAG 600

TGGTACATCA GGCTTAAATG CCGTGGAAAg ATTTATTGTT GGTTCTGTAT CAGAATCTAT 660

CGTTCGTCAT GCGCCATGTG ACGTGTTAGT TGTTCGTACT GAAGAGTTAC CAGCAGACTT 720

CCAACCACAA GTT 733

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6060 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

TGATGATCCT GAAGCGCTAT TGGATAATTA CAACACTGAA GATGTTGATG CACACAATTA 60

CAATAATATA AATCATGTTA TTTTTGCCTG CGATGCGGGT ATGGGTTCTA GTGCAATGGG 120

TGCArGCATG TTACGTAATA AATTTAAAAA GGCGGGCATT AATGATATTA CAGTTACAAA 180

TACTGCGATT AATCAATTGC CAAAAGATGC TCAATTAGTT ATCACTCAGA AAAAACTAAC 240

TGATCGTGCT ATTAAACAAA CACCAAATGC CATCCATATT TCAGTGGATA ATTTCCTTAA 300

TTCACCAAGA TATGAAGAAC TTTTAAATAA TCTAAAAAAA GATGATCAAG CATAATAATT 360

AAATAAATTA AAAAATGGAG GATACCGCCA TGTTATTGAG TACACGTGAA AAAGAAATGA 420

TAGCCCtAtT GATTAAGTAC CACGGtCAAt ATATCACTAT ACACGACATT GCTCAGCAAC 480

TTGCGGTGTC CTCTCGTACT ATTCACCGTG AATTAAAAGG TGTTGAAGCA TATTTAACTT 540

CATTTTCATT AACTTTAGAA CGCGCAAACA AAAAAGGGcT ACGCATTGCT GGCACAGATT 600

CTGATTTAAA CGATTTGAAG CAATCGATTG CACAACATCA AACCATTGAC TTATCTGTTG 660

AAGAGCAGAA AGTAATTATT ATATACGCTT TGATACAAGC CAAGGAGCCA GTTAAACAAT 720

TAGAGCTTGA TTTAAATAAG TACCAACTAT CTTTATCTCG AAAGCGTGGC GAAGGCATTT 840

ACTTGGTAGG TACTGAATCA AAGAAACGTG AATTTTTAAG TCAATTAATG GTGAATAACT 900

TAAATAGTAC TAGCGTTTAT TCAGTAATTG AAAATCATTT TGTCTTTCAT TCATTAAATC 960

AAATCCACAA AGACTTTGTT GACTTAGAGC GCATTTTTAA TGTTGAAAGA CtATTaATGG 1020

ACTACCTAAG TGCCTTACCC TACCAACTTA CCGAATCAAG TTATTTAACT TTAACTGTCC 1080

ATATCGTGCT CTCCATTTCA CGTATAAAAA ATGGAGAGtA TGTCGCATTA AACGATGATA 1140

TTTATGATTC TGTACAAAAC ACATTTGAAC ACAAAGTaGc AAGCGAACTT GCTGATAAAC 1200

TTGGTCAAAT ATATGACGTC ACGTTTAATC AGGCAGAAAT TGCTTTCATT ACTATCCATT 1260

TACGTGGAGC TAAACGAAAA AATCTTAATG ATACATCATT AAATAATCGT TGTGAAGAAA 1320

ACAAAATTAA AGCGTTTGTT AACAAAGTAG AAATGATTTC CGGTATGACA TTTGCAGATT 1380

TGGATACTTT AGTAGATGGA CTGACGCTAC ACCTTAATCC TGCAATCAAT CGTTTGCAAG 1440

CTAATATCGA GACCTATAAT CCGTTAACAG ACATGATTAA GTTCAAATAT CCAAGACTAT 1500

TTGAAAATGT AAGATTAGCT TTAAATGATT GTTGGCCTGA TTTGATTTTT CCAGAGAGTG 1560

AAATTGCTTT TATAGTtTTA CACTTTGGTG GCTCGATTAA AAACCAAGGT AATCGATTTT 1620

TAAACATATT AGTCGTTTGC AGCAGTGGTA TGGGAACTAG TCGTCTATTA TCAACTCGTC 1680

TAGAGCAAGT TTTTAGTGAG ATTGAGCGTA TTACACAAGC ATCAGTCAGC GATTTGAAGT 1740

CACTAGATTT AAGTCAATAT GATGGCATTA TTTCTACTGT GAATTTAGAC ATCGACTCCC 1800

CCTATTTAAC GGTAAACCCA TTATTACCAG ATAGTGATAT CAGTTATGTC GCACAGTTTT 1860

TAAATACAAA GTCTACGTTC CAAGAGACGC ATGATAAATC ATCAAACATG ATTGATAAGG 1920

ATGATGTTCA TGTTGAAACG AAAGATGTTG ATGGCAACAC ATCTTTTGAA AATGAACAAA 1980

CTTCATACTT AACTTCAGTT TTCGAAAAAC ATTTAAGTGA CGAAAAATCA GAACAATTAT 2040

TGCATCATAT GCGTTCGGGT TTAACTTTGC TTGATTCAGT GAAAATAGTT AGTACCGAAG 2100

TTAAACAGTG GCAAACATAT ATCGCAGATT ATCTATATCA ATGCGATGTA ATAAACGATC 2160

CAACGTCATT CGCTGAACTA CTAGAGCAAC GATTGATTGA CAATCCAGGA TGGATATTAA 2220

GTCCATATCC TGTTGCAATA CCACACCTAA GAGACAATAT GATTAAACAC CCTATGATTC 2280

TAATCACAGT TTTAGAAGAA CCGTTAACAT TGCCTAGTAT TCAAAATGAC AATCAAACAA 2340

TTAAATATAT GATTTCCATG TTTATTTCTG ACAATGATTT TATGGCATCA CTGGTAAGTG 2400

ACTTGTCCGA ATTTTTAAGT TTGAAATTAG AATCTATTGA TACTTTTATG GAAAATCCAC 2460

AGGAACTTGA AACATTATTA AGAAACAAAT TTTTAGAACG AATTAAAAAA CAATTTATTT 2520

TAACAGCCAA AATGAAGCAA TTGAAAAAGC AGGTAAAGCC TTAGTTGATA GTGGTGCTGT 2640

AACAGATGCT TATATTCAAG CAATGAAAGA TCGTGAGCAA GTCGTATCAA CATTTATGGG 2700

AAATGGCTTA GCAATTCCTC ATGGCACAGA TGAAGCTAAA ACAAATGTGA TTCACTCAGG 2760

TTTAACATTA TTACAAATCC CTGAAGGCGT TGACTGGGAT GGCGAAGTAG TTAAAGTTGT 2820

CGTGGGAATT GCTGGTAAAG ATGGCGAACA TTTAGACTTG TTATCTAAAA TTGCAATTAC 2880

ATTTAGCGAA GAAGAAAATG TGGATCGTAT CGTTCAAGCA AAATCTGCAG AAGAAATTAA 2940

ACAAGTATTC GAGGAGGCAG ATGCATAATG AAAGCAGTTC ACTTTGGTGC TGGTAACATA 3000

GGTCGTGGTT TCATTGGTTA TATTCTgCAG ACAACAATGT TAAAGTAACA TTTGCAGACG 3060

TCAATGAAGA AATCATTAAT GCTTTAGCTC ATGATCATCA ATACGATGTT ATTTTAGCTG 3120

ATGAGTCTAA AACAACGACG CGCGTGAAtA ATGtTGATGC AATTAATTCA ATGCAACCTT 3180

CTGAAGCGTT GAAACAAGCA ATTCTAGAAG CTGATATTAT TACAACAGCT GTTGGTGTTA 3240

ACATACTACC TATTATTGCT AAATCTTTTG CGCCTTTCTT AAAAGAAAAA ACAAACCATG 3300

TTAATATTGT TGCTTGTGAG AATGCTATTA TGGCAACTGA TACATTGAAA AAAGCAGTAC 3360

TTGATATTAC TGGCCCTCTT GGTAACnaTA TTCATTTTGC TAACTCAGCA GTTGATAGAA 3420

TTGTACCATT ACAAAAGAAT GAAAATATAT TAGACGTTAT GGTTGAGCCA TTTTACGAAT 3480

GGGTTGTTGA AAAAGATGCA TGGTATGGTC CAGAACTAAA CCATATTAAA TATGTTGATG 3540

ATTTAACACC ATATATTGAG CGTAAATTAT TAACTGTGAA TACAGGACAT GCATATTTAG 3600

CGTATgCTGG tAAATTTGCA GGTAAAGCTA CAGTTTTAGA TGCAGTTGAA GATAGTTCAA 3660

TTGAAGCTGG CTTACGCCGT GTTTTAGCTG AAACTAGTCA ATATATTACT AATGAATTTG 3720

ATTTTACTGA AGCGGAACAA GCTGGTTATG TTGAAAAAAT AATAGATCGT TTCAACAATT 3780

CTTATTTATC TGATGAAGTA ACACGTGTCG GACGAGGTAC ATTACGTAAA ATTGGCCCTA 3840

AAGATAGAAT TATAAAACCA TTAACATATC TTTATAATAA AGATTTAGAA CGCACTGGTT 3900

TATTAAATAC AGCTGCATTG TTATTGAAGT ATGATGATAC AGCAGACCAA GAAACTGTTG 3960

AGAAAAATAA TTACATTAAA GAACACGGTT TAAAAGCGTT TTTAAGTGAA TATGCTAAAG 4020

TTGACGATGG CTTAGCCGAT GAAATAATTG AAGCGTACAA TTCACTTTCA TAATTTATTG 4080

AGCTTTGTTT GAAACAAGAA GTTTCCAACG TTATTCGTTA ACAATCAGTA ATAATGTAGT 4140

AGTTCCCTTG AATTAACAAT ATTAAATTTC TGAACATAAA AAATACTCCC TTCAACATAG 4200

ACACTTAACT TGTGTTATGT ATGAAAGGAG TATTTTTGCG TTAATAATTT GTTTTATTTT 4260

CGAGCCACAG CCACCTATTC AATGGCTATT GGTCATTACT AAAACAAATT CATATTAACT 4320

TTGAATAAAT TTTATTCTTC AGTTTGTTGG TCTTTCTTAG TGAATCTTCT AATTAAGAAT 4440

GCCATACCTG CACCTAGAGC TAATTCAGCA TATGGTAAAT CGTCATTATG TGACATACCA 4500

GTATCTGGTA AAGTTTTAGC TTGTTGTTTA GCTTTATTAA CTTTTCCTTG TTGAGCTGAT 4560

TTTGTCTTAG CTTGGTGGTC GTCAGTGTTA GTTACATTAA GCATATCTTG ATTAGCACTA 4620

TTGCTTCCAT TTGAAACTGT AGCTGGAGAT GCATTGGCAC CGTCGTTTTG CGTAgyTTTA 4680

TTGTTTGCAG CTGAACCAAC TGATTTTTGC GTATCATTAG TATCTGCTGT TGCCGTATCA 4740

TCTTTTTGGC TAACATTAGT TGAAGTCATT TTTTCTTTTG CTTCAGAAGA TGCAGATGTT 4800

GATGGTTTAT TCGAAACTTC AGTATCAGCT TTGCTTGGCG ATTTATCTGC TTCGTTAGAT 4860

GCAACGTTAG TTTCAGACTT AAGTTGTCCT GCATCAGTTT GATTTGTCGT ACTTTCTTCT 4920

TTATCTTTTG ATGTATTAGA AGGTACATTT GGTTCTGTTA TGTCTGCTGA AGGCAATGTT 4980

TCAGTTGTtG ATTCAACCAT ACTTTGATTT GTTGAATCAC TACCATCTTT TTCTGCCTTA 5040

GCTTTATTTT CAGATTTTGG TTGTGCAACC TTGTCATTAG TTGATTGAGA TTCAGCACTA 5100

TTATTTACTT CAGCATTTTG TTTTGAATCA TTTACAGATG CATTATCTTT GCTATCAGCA 5160

GATGATGCTG CTTCTGTGCT CGCAGTTGTT GGAGCCGTTG CTGTTGATCC TGTTGGTGCA 5220

TTCTCGTTTG TTGCTGTAGT TGTACTATTG TTATTTGTTG TGCTTTCTGC TGGCGTTGCA 5280

TTATCAGTTT CTGTTACAGG TTTATCAGTT GTGCCGTTAT TAGTTGATTC TACTTCTGGT 5340

TTACTAGTTA CATCGTTATC CATTGTCGGA CTGTTTGTTG ATGCATCTAC ACTAGAATTG 5400

TTATTAGCTT GCGGTTTATC ATTTGCATCA TCAGTTGCTG ATGTTGCTGT TGTTTCACCT 5460

GTTGCCGCAT CACTATTATT TGGTGTTGTC GGAGAAGCGT CTGCTTTGCC ATTAGCTGTC 5520

GTCTCAGATA CGTTAGGTTG TCCAGTATTT TCTGGTGTTG CATTAGCATT TGAATTTGCT 5580

GTTGCATCAT TATTATCTAT ACCATTATTA GTATCATTAG CATCTGGATC ATTCTGAGGC 5640

ACAATCGCTT CAATTGCAGG TATCGTTACA TTTTGTAATT CAGCAACTTC TGCATTTGTT 5700

TGTGTTTTAT CTAATTTATC AGCAAATCTG TCAAAATATC TACCTAAATC CGTACGTGCA 5760

ATTTCTTTCG CCGATGCATC TGCATCTGCA TTTTTAATTA TTTCTATTTG CTTGTTAACC 5820

ACTTCTCTGA TTGCTTCCAA AGCATTTTTC TTAACTTCAG GATTAATACG TTGTGCTTTA 5880

AGTTGTTCAA GCGCACTATT TTTGACAGTA GCGATTTCTG CATTTGTAGT TTGATCAGAA 5940

ATATCTTCAG TTGCTTTTGA TAAAATGTCT TCTAAAGCAT TCGTAAACGC TTCTTTTTCT 6000

TCAGTTGTAG CATCAGCGTT GACATTTACA CCTGCTTCAA TCTGGTCTAG TGCAGTTTCT 6060

(2) INFORMATION FOR SEQ ID NO: 535:

(A) LENGTH: 977 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

AACAAAGCCT TCCAATTATC TGCGTCGGTA GAACAAGTAT TAGCAACTTT ATCACCTACG 60

CTAAACAGTC CTTACGATTT ATACGGCACG ACAAAAATGC TAGATATTAC ATTCGATTCA 120

TTTGAACATG ATGGTACAAC GTACCCTGTC GACTATGCTA CGTTTGAAAA TGATTATGAA 180

GATAATAAAG ATCCTGAGTT TAGACGTAAA AGTTTCAAAT CGTTTAGCGA TGGGATTCGA 240

AAATATCAGC ATACTACCGC GGCTACATAT AATATGCAAG TACAACAAGA AAAAATTGAA 300

GCTGATTTAC GTGGATTTGA ATCAGTCATC GATTATTTAT TACATAGTCA AGAAGTAACG 360

CGTGATATGT TTGACCGTCA AATCGATATG ATTATGCGTG ACTTGGCACC AGTTATGCAG 420

AAATATGCTA AACTTTTACA ACGTATTCAC GGATTAGATA ACATGCGTTT TGAAGACTTG 480

AAGATTTCTG TAGACCCTGA TTATGAACCA GAGATTTCAA TTGAAGACTC AAAAAATTAT 540

ATTTTCGGTG CGTTAAGTGT TTTAGGTGAT GACTATACAA ACATGTTACG TGAAGCATAC 600

GATCAGCGAT GGaTTGATTT TGCACAAAAT AAAGGTAAAG ATACAGGCGC ATTTTGTGCA 660

AGTCCATACT TTACACATTC ATATGTGTTT ATTTCTTGGA CTGGTAAAAT GGCTGAAGCA 720

TTTGTCTTAG CACATGAATT AGGTCATGCA GGTCATTTTA CATTAGCTCA AAAACATCAA 780

CCATATCTTG AATCAGAAGC ATCAATGTAC TTTGTTGAAG CCCCTTCTAC AATGAATGAA 840

ATGTTGATGG CCAATTATTT ATTTAACACA AGTGATAATC CAAGATTTAA GCGTtGGGTT 900

ATTGGCTCAA TTTTATCTAG AACATATTAT CATAATATGG tACCCmTTTA TTAGAAGCnG 960

CTTATCCACG GGGAGTG 977

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

AGACAGTGAT yGaATTTCAT TTACAGTACA CAAATCATCG AAAAATTGGT AACATTCTTC 60

TCTATTTTCT AACGTTAgwA TTgCATCAAA CAATTCATCT AACGCTGCAC CTCGTAATTT 120

AATCTATTAA AGTGTAGCGa TTTATATTTT ATTAAATCTG AATCGTTACT TTATTTAATT 240

TTATGCTAAT CCAGCGCGTT CGAAAATAGT GTCAACTTGa TTCAAATGAT GTTTAGGATC 300

GAAACATTCA TCCAATTCTT CTTTTGTTAA AACACTTGTA ATAGACTCAT CTTGTTCGAT 360

TAATTCACGG AACGGTGTTT TCGTTTCCCA AGATATCATC GCTTTTGGTT GTACTTTGTC 420

GTATGCTTCT TCACGAACCA TACCTTTATT AATTAATGCT AATAAGACAC GTTGTGAGAA 480

AATCAGACCA AATGTTTTAT CTATGTTATT ACGCATATTA TCTTCAAATA CAGTTAAACG 540

GTCCACAATA TTTGTGAACG ATTCAATGCA TAATCTAGTG CtATTGTAAC ATCTGGTAAC 600

ATAATACGCT CAGCAGAAGA ATGAGAAATA TsTCTTTCAT GCCATAATGG CACATTCTCA 660

TAAGCTGTAG TAATATAACC ACGAATGACT CTTGAAATAC CTGTGATATT TTCAGAACCA 720

ATTGGATTTC GTTTATGAGG CATTGCAGAT GAACCTTTTT GGCCTTTTGC AAATGCTTCT 780

TCAACTTCTC TCGTTTCGGT TTTTTGAAGG TTACGTATTT CAACGGCAAA TTTTTCTAGT 840

GATGTCGCGA TTAATGCTAA TGTCGCAATA TAGTATGCAT GTCGATCGCG TTGCAATGTT 900

TGCGTTGATA CAGGCGCTGT GCCAATACCT AAATGTTTAC ACACATAACT TTCTATTTCA 960

GGAGGAATGT TAGCAAAAGT ACCTACTGCA CCACTCATTT TCCCTACTTC AATTTCTTCT 1020

CTTACTTGTT TGAAACGTTG TAAGTTACGT TGCATTTCCG TGTACCACAA TGCCATTTTG 1080

ACACCAAATG TAGTTGGTTC TGCATGCACT CCATGTGTAC GTCCCATCAT CAATGTATAT 1140

TTATAATTTT TTGCTTTTTC AGCTAAAACG TCGATAAATC TTTCTAAATC TTTTTCAATA 1200

ATGTCATTTG CTTGTTTAAT AACGAAACTT AAAGCTGTAT CTACAACATC AGTAGAAGTT 1260

AAACCATAAT GTACcACTTA CGTTCTTCAC CTAGCGTTTC AGAAACTTGT CTAGTAAAGG 1320

CTACAACATC ATGGCGCGTT TCTTGTTCAA TTTCTTGTGC ACGTTCGACA TTTACCTTTG 1380

CGTTTTGACG AATTTTTTGT ACGTCAGCTT TCGGTATATG TCCTAATTCA CTCCATGCTT 1440

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 784 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

GATAAATCTA TnCAGTTTCC GTCCAAATAT CtGCaCCTAA AGCTTTTAaG TGTTCTACAA 60

TATCTgTATA ACCTCTATAA ATATGTTTAA CATTGTAAAT TGTAGTTACA CCCTCAGCAA 120

CATGTAATGT TGATGGTTTT ATCGTTGCTG TGCCTTCGTC AACTTCAATA TTTGCACCCA 240

TGCGCTTTAA TTCTTCAACA TGTTTAAAAC GCTCCGGATA AATCGTATCA GTTACAAATG 300

AAGGACCATT TGCCATAAAT AATAATGGTG TAATAGGCTG TTGCAAATCA GTAGCAAAAC 360

CTGGATATAC TAGTGTTTTA ATATCAACAA ATTGATATGG CGCATTATTA TTGATGCGAA 420

TTCTTTCGTC TCTTACATCA ACATTCACAC CTAATTCACT AAATTTAGCA GTTAATGTTT 480

CTACATGTTT CGGAACAATA TTATTTAATA TAACATTTTC TCCACATGCT GCAGCGATAC 540

ACATATATGT GCCTGCTTCA ATTCTATCAG GTATAACTTG ATACTCAGAA CCATGTAATT 600

CTTTGACGCC ATTGATTTTA ATTGTTGATG TACCCGCTCC CTTAATATTA GCTCCCATAC 660

TTGTTAAGAA GTTAGCAACA TCAACTACTT CCGGTTCTTT AGCAGCATTT TCAATTACAG 720

TTTGTCCTGT TGCATAAACT GCAGCTAGCA TAATGtnAAT TGTTGCACCT ACGCnAACCA 780

TATC 784

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3733 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

CAATCTCCAC CAATGACACG TCGTCATTCG TGACCTCATA CCArACAAAA AACAGTCTCG 60

CAATCAAGAC TGTTTTCCAC TCAATATATT CATCCATTAG CGTAATAGAT TATTTGACTT 120

CTGTAGCTAC AAAGaTTTTA CGTTTTTCCC AAACGCCTGT cTTTTCATTG TAATCATCAC 180

AAGTAATTAA TGTTAATTGT TTATCTTTAC CTTTTTGTTC ATCTAGAAcT CCTACATCTG 240

TAGGCTTAAC ATCTCTTATA CTTGTCATTT TATACTTACG TGTTTCATTA CCAACTTTAA 300

AGTACACCAT ACTACCTTTT TTGGCTGCTT TAAGATTTGT AAATTGATAG TTCGGACGGT 360

CAATGAAAGT GTGTCCTGCA ATTGAAATAT TTTGATCATC TAGTGATTCA TTTTCTTCTG 420

CAAAGCTTAC ACCTCTATTT AATTGTTCAG GTGTTGCTGG TCCTGGATAT ACTGGTTCTT 480

TAATATCAGC ATCTGGAATT TCAATATAGC CTGCCACTTT CGATTTATCT TTCGGAATTT 540

GAGGTTTAGC TTGCTGCTTT TTATCTTTAC TCGCCTGTTC TTTTACATTT TTATCATATT 600

GTTCAATCTT TTCATCTTTA TCTTTATCGT GAAGATAATT ATCGATATGT GGTTTAGCAA 660

ACAAATATGC TGCCACTAGG aTAAGTACCA CACCAGCGAT TGTCATTAAT CGATTTGTCC 720

AGTATACCAT TAATTTCAAA ATGACTCATA GCAATTCATT TTATACTATA AAATTTACAT 840

GTATACTTTT ACGTTAGATT TCATTACACA TATTTGCATT CAAATAACGA AACGCTTTTA 900

ATAATTACTA AGGGGGAATT GATATGATTA GATACGCTAA AAAAGAGGAT TTAAACGCTA 960

TATTAGCGAT ATACAATGAT GCCATTATCA ATACTACAGC TGTTTATACT TATGAACCAC 1020

AAACCATAGA CGAACGTGTC GCATGGTTTG AAACGAAACA ACGTAAGCAT GAGCCTATCT 1080

TTGTATTTGA GGAAAATGGA AGTGTCTTAG GGTTTGCGAC GTTCGGTTCA TTTAGACCTT 1140

GGCCAGCATA CCTATATACA ATCGAACATT CTATTTATGT CGATGCTTCA GCTAGAGGAA 1200

AAGGTATTGC TAGTCAATTA CTACACCATT TAATTGTGGA AGCAAAAGCT AAAGGTTATC 1260

GTGCGCTAGT TGCAGGCATT GATGCTTCCA ACAAAGCGAG TATTCAGTTG CATCAAAAGT 1320

TTGCTTTTAA GCATGCCGGC ACACTGACCA ATGTAGGTTT TAAATTTAAT AGATGGTTAG 1380

ATTTAGCATT TTACGAATTA GATTTACAAG ACTAGTAATG TTTGAATCAC ATAATATAAA 1440

CAAGACAACC ATGTTAATTC CCTTAACATA ACAAGCCAAC ATATAAAATT TTAAACTTCT 1500

CAGGGGAGTG GGACAGAAAT GATAAAGAGC CACTAATGAT TTATTATGTA GTGGTTCTTA 1560

CACATTAGCC ACAGCTAATG TGTAcTTAAA AATAGGAATA CATGAGTAAA ACTCATGCAT 1620

AAGAAATACT AATTTCTATA GAAAAAGTAT TTCTTTATCG TCGTCCCACC CCAACTCGCA 1680

CATTATTGTA AGCTGACTTT TCGTCAgCTT cTGTGTTGGG GCCCAAAAAG CTTGTTACAA 1740

GCGCATTTTC GTTCAGTCAA CTACTGCCAA TATAACTTTG TAGAGCATAT TACATTGATT 1800

TACATTGTCC CTTTTATTTA TTCTTTTCAA ATACTATCCC CATAGCTTTG ATTTAACGCT 1860

TTTTCTCAAT AACAAAACGA ATATAGTAGA ACATGAAAAC GATAATCATG CTGAGCGATA 1920

AAGATTTAAA TAATAGATTG ACCCACGTTC CCTCAGTCGT ATATCCATAT GTAATCGTTG 1980

TGTTAATGAT GAATGCTATA AAGATGATTG ATAGTCTTAG CATATCATCA CTCCTTTTAA 2040

GTTATTTTAG ATATACGGGG GCGCTTTTGC AATCACTATT TTGATTAGTA TGCATTTTCC 2100

ATAAATCTTT CAACTTCTTC AGAGATAATT AAGAAGCATC TATCTGGTAC TAATGATCCA 2160

GACAGATGCT TCTTTTTTAT CAATATTTTA TTGTTATCTC ATTAATTATT TTTAACCATA 2220

TCTTCAGCTG TGCCAAAGAT TTTACGTTTA ATTGCTTCGC CAGTTGGTGT GCCTGCTAGT 2280

CCACCCAATC CAGTTTCACG TAATGATGCA GGAAGGTTAC GACCAACCTT ATCCATTGCT 2340

TCAATAACTT CATCAACAGG GATTCTACTT TCAATACCTG CTAATGCTAA ATCTGCTGAA 2400

ATTAAAGCGT TACCCGAACC AATTGCATTT CTCATAACAC AAGGAATTTC AACAAGTCCG 2460

GCTACTGGAT CACAAACTAA ACCTAATAAA TTACTTATCG CTAATGCCAT AGCGTGCCCG 2520

GAACCAACTT CAGnTTGGCA GCCACCTGTT GCACCAGCTA CACTTGCATT GTTTGCTACG 2640

ACACGCCCAA ACAATGCTGA AGTGAATAAG AAATCAATCA TTTGCTCTTC TGTTAAATCA 2700

TGTGTTTTTT CTAATTTAAA AAGTGCACCG GGAATGGTAC CCGAGGAACC AGCTGTTGGC 2760

GTtGCACAAA TAATACCCAT CGCAGCATTG ACTTCATTTG TTGCAATGGC AcCtTTGcTG 2820

CGTCAATCAT TTCATATCCA GACAAAGCAT GATGTGTTTC ATTATAATCA CGTAGTTTAG 2880

CAGCATCATG ACCAGTGTAG CCCGTTACAC TTTCAACCCC ATCACCTGTC GTCCCTTTGA 2940

TTACTGCGTC TCGCATGACA TCTAAATTTT GTTTCATTTG CGCTCGCACT TCATCACGTG 3000

ATTTACCGCT TAATTCCATT TCTTCTTTAA CCATGATATC CGCAAATGAC ATATTATTTT 3060

CTACGGCATA ATCTATAGTC TCTCTAATTG AATCAAACAT GTTTATTCCC CCTCTAATTT 3120

ATATAGGAAA CGTTTACGTC ACTGTATTTC TCTTTAATTG TATTTAATGT TGATTCTGAG 3180

ATTGCTTTAT TTAATGGTAT TACAACCAAG CATTTATCTT CATCTATCTT AATAAATTCA 3240

TCTTTACAGT CTAATTTCAT ATCGTTGATA TCATTGATGA AATGATTTAC TTGTGCTTTA 3300

GTCATATTTC CGTCAACAAC TAAAATTGGT AATCCATGAT TTAAATCTAC TTCTAGTCCA 3360

TTTATATGAA TACCTTTAAT TTTAATTGTA CCACCACCGA TTGAAATACC GATAATTTCA 3420

ATGTAGCGAC CATCATTACG AGATGATTTG ATATAAGCAC AGTTTGGATG TTGACCAATA 3480

CTATCGCCTT CTTCTTCGAT GATATCTATT TTAATACCAT CATCAGCTGC AATTTCTAAT 3540

GAAGATTTAA TTCGGTTATC AAATGTTGAA TATCCCATTG CTCCACCCAC AATAGCGACA 3600

TCTGTACCAT GTCCTTGGTG TGTTTGAGCA AATGATTCAT AATAATGTAT TTCAATATTT 3660

TTATATCTCC CAATATTGCG CGTGCTGAAT TCCCCTTTAC TGCACCAGCC GTATGAGAAC 3720

TTGAAGGGCC CAT 3733

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 525 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

TGGCTGTCTT CTCTATGAGT GTAGTAAGTA AGTTAACGGA TTTAACGCCA AGGCAAATAC 60

GTTACTATGA AACACATGAA CTCATCAAAC CTGAAAGAAC AGAAGGTCAA AAACGTCTGT 120

TCTCACTCAA TGATTTGGAA AGATTACTAG AAATTAAATC ATTATTAGAA AAAGGATTTA 180

AAGAGATAAG AAAAAAGATG ATTGTAGATG CCACGCAAAA GCCTATTGGA GArACTTTGC 300

CAATAAATCG TGGTGATTTA TCCCGATTTA TTAAATAAAA TTTGGAGGAT TTTAAAATGC 360

CAAAACGTAC TTTCACTAAA GACGACATTC GTAAATTTGC AGAaGAGGAA AaTGTAaGaT 420

ATTTAAGATT ACAATTCACT GATATTTTAG GAACAATTAA AAATGTTGAA GTGCCTGTAA 480

GCCAATTAGA AAAAGTACTT GATAACGAAA TGATGTTTGA CGGTA 525

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1408 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

TTGATTTGCT ACAAAGTATC TnCTCATTTC TGTATCCTGA AAAATCTTTA GTGTAATAAT 60

GTTGTTCAGT TTTAATATTT TCAGTCATAG TTGACTACCT CCGTATATTT TGATTTAATT 120

AAGTTGTATA TTTTGATGAA CACTTATTGT TACTTGTTGG CGCAAGTAGC AGTTTTTTCA 180

TTCTTCATAA AAGTATTCCT TATAGAATAT GAATGTTGCG ATACTTGCGA ATCCTGCAAT 240

TGaCCATGCT GtAGTGAAGT ATAGAAACGG CATAAGTACA ATCGCTAAGA CTGTGAAGCA 300

TAGTACTGCT ACTAGGTAGC TTTTATAAAT GTTACTCATT TTCTTTTTTC AACTCCTCCA 360

TTATTCTCTG GTCTGATAAG TCGTGATAAG GGAATTTTTT CCtAGCTAAT TGGACTGGTA 420

TTCTGCCTCG TATCGCAATG TATCCTTCAT CTTCAAGCTC TTTATTCAGT TCTCTTATTA 480

TTTGTCCTGC TTTGGATTTA GAAACAGATA AAATTACCgC AAGTTCTTTA GCTTGCAAAC 540

TATTTTTCAT CATATCTTTT CCTCCTTTAA AATAACTGTT GATTCTCTGG GTTATCTGCT 600

TCGTAATTAT CTGCAATAAT ACTTTTAGCG AAAAAGTCCA AACTGACCTT ATATAGGTTG 660

TTCATAGATT TCTTTACGTT AACCCCTTCC TCAAGTACAT AAGGCACCCT AAAATCATTT 720

ATAAACAGTC CGTTTTCGTC TAAAGTAACG GTTGGTAATT CAGGTTTGTT CCGTCTATAA 780

ACTTCTCCTA GTGTAGGTTT TTGCTTTTCA GCTTGTTTAG TGAAGTCGGA AAATGCCTTA 840

AGTAGTTTTA TTCCTGAATC AGGATCACTG TGTCGCTCAA TCGTTTCTGC TGTAGACTCT 900

TTACTAAAAT CATTTCTATT GATTACAGGC TTTCTCGTAT TTCGTTCAAT CTTCCAAACC 960

TTCCACGTCA CAACTGCCAT TGTGGTGAGG AGGGTTGTTT TGTATAGTGC GTTCATTTGT 1020

AATTCCTCCT ATTAAGTTGT TTGTTCAATT GTGTGTGTTA TTCTTCTTCG TCTAAATCAA 1080

CGACTTCGTA AGTGTGCTCA ATCTCGCCTG cATATGTCAC AGTAAGAGTA TCTTTGTGTG 1200

TGTATGTTTG ACTTTTGTTy TCTtTAACTG CATAAAGTGT TAATACTATA TTGTTTAGCT 1260

TTyCTTTTTG TTCTGGTGTC ATTTACGCTC CCCCTAmATT AGCyTCATAA CCGAATTCAG 1320

TCATGATTTC ATGTATTTTC AATCTGCCTT TTTGTGTCCA TCTAGTTTGT AAAACTGTGT 1380

CTTCTCTGCC ATCAGAACGC ACAATTGT 1408

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

GTTCGTCAAT GATTTTTATC CGATGCTATG AGCATTaTCA AATACAAAAT GCTCTCTTAA 60

AAGCAGTTAT TGACTGAAAA TCTACTTCTA AGAGAGCACT TTATTTAATT ACTTAAGAAA 120

TCTTGAAATT TCAATATACG ATGTTTATGA TAAGTCGCTT ATTTCATCTT TAGGCTTGTT 180

ATTAGTAAGT AGTTTAATAC CACTGATTAA CCATAAAGCA AATGTAATTA TGTTACCACT 240

TATTACAGCT CCAATAATCA ACAATATACC ACTCATTTTT TTGTTTTTAG ATGCTTTAAA 300

CATACCGATT GCACCTAAAA TAATTGAAAT GATTCCAAAT ATGAATAGGG ATAAGAATAA 360

TACAGTGAAA ATTGCTGCTG CTGTTTCTGc ATCAACTGGG nCAACCTCAC CATTAACTGT 420

TGTTGGACAC AT 432

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

ATAATCATGA AGTnGCTAAA nCGCCAAATA ATGATGGTTC TGGACATGTT GTGTTAAATA 60

AATTCCTTTC AAATGAAGAG AATCAAAGCC ATAGTAATCG ACTCACTGAT AAATTACArG 120

GAAGCGATAA AATTAATCAT GCTATGATTG AAAAATTAGC TAAAAGTAAT GCCTCAACGC 180

AACATTACAC ATATCATAAA CTGAATACGT TACAATCTTT AGATCAACGT ATTGCAAATA 240

GTATAAAAAG TCAACGAAAT ATTATTTTGG AAGAACTTGC ACGTACTGAT GATAAAAAGT 360

ATGCTACACA AAGCATTTTA GAAAGTATAT TTAATAAAGA CGAGGCAGTT AAAATTCTAA 420

AAGATATACG TGTTGATGGT AAAACAGATC AACAAATTGC AGATCAAATT ACTCGTCATA 480

TTGATCAATT ATCTCTGACA ACGAGTGATG ATTTATTAAC GTCATTGATT GATCAATCAC 540

AAGATAAGTC GCTATTGATT TCTCAAATTT TACAAACGAA ATTAGGAAAA GCTGAAGCAG 600

ATAAATTGGC TAAAGATTGG ACGAATAAAG GATTATCAAA TCGCCAAATC GTTGACCAAT 660

TGAAGAAACA TTTTGCATCA ACTGGCGACA CGTCTTCAGA TGATATATTA AAAGCAATTT 720

TGAATAATGC CAAAGATAAA AAACAAGCAA TTGAAACGAT TTTAGCAACA CGTATAGAAA 780

GACAAAAGGC AAAATTACTG GCAGATTTAA TTACTAAAAT AGrAACAGAT CAAAATAAAA 840

TTTTTAATTT AGTTAAATCG GCATTGAATG GTAAAGCGGA TGATTTATTG AATTTACAAA 900

AGAGACTCAA TCAAACGAAA AAAGATATAG ATTATATTTT ATCACCAATA GTAAATCGTC 960

CAAGTTTACT AGATCGATTG AATAAAAATG GGAAAACGAC AGATTTAAAT AAGTTAGCAA 1020

ATTTAATGAA TCAAGGATCA GATTTATTAG ACAGTATTCC AGATATACCC ACACCAAAGC 1080

CAGAAAaCGt TAACACTTGG TAAAGGTAAT GGATTGTTAA GTGGATTATT AAATGCTGAT 1140

GGTAATGTAT CTTTGCCTAA AGCGGGGGAA ACGATAAAAG AACATTGGTT GCCGATATCT 1200

GTAATTGTTG GTGCAATGGG TGTACTAATG ATTTGGTTAT CACGACGCAA TAAGTTGAAA 1260

AATAAAGCAT AATTATATTG GGGGAAGAGC ATCTATATAT TTTTTTAAGT ATATAAGACG 1320

TCTTATTTCC CCTTAATTTA TTGTGAAGTA TATGCAAAAT GCAATGAATA GATTGTCCAT 1380

CATTTTAACG TTATAATGAA TTTAACGACT TAGAACTACA CAAGTAAAGG AGAATGAAGA 1440

TGTCTCGAAA AACGGCGCTA TTAGTTTTGG ATATGCAAGA AGGTATAGCG AGTAGTGTAC 1500

CTAGAATAAA AAATATTATT AAAGCGAATC AGAGAGCAAT TGAAGCAGCA AGACAACATC 1560

GAATACCAGT CATTTTCATA CGTTTAGTGT TAGATAAGCA TTTTAATGAT GTCTCCTCGA 1620

GTAATAAAGT GTTTTCAACA ATTAAAGCTC AAGGATATGC GATTACTGAA GCAGATGCAT 1680

CTACACGAAT ACTTGAAGAT TTAGCACCAC TAGAAGATGA GCCGATTATT TCTAAGCGAC 1740

GCTTTAGCGC ATTTACAGGT AGTTACTTGG AAGTTTATTT ACGTGCAAAT GATATTAATC 1800

ATTTAGTATT AACGGGTGTC TCTACAAGTG GAGCTGTATT GAGCACGGCA TTAGAAAGTG 1860

TAGATAAAGA CTATTATATT ACTGTTTTAG AAGATGCTGT TGGTGATAGA TCAGATGATA 1920

AACATGACTT TATTATTGAA CAAATTTTAT CACGCTCATG TGACATTGAA TCCGTAGAGT 1980

CATGGAAAAG TAGTTTATAG TTAATATAAC GTCAATTAAA GCTCGGCAGT AATGTTTGAG 2040

GAGGAACATT TGAACATAAA ATAATATATT TATATAAAAC GACCgAGGCG TTCGAACTGA 2160

ATGtCCTCGG GTTTAATTGA ATAGAAATCG GACTTATGAA CGAAATATGT TTAAGTCGAA 2220

CTCCTTGTTT ATACTTATAA ATTTTACGGG TTTAATATAA TACTTATTTA CCTGTAATAT 2280

ATGCATAATT nCTTCAGTCG GTCAGCCTGT CGTTGCATAG TTCCTATGCA GCAAATGCAT 2340

ATCCTAATCC TTTAACATTG GCATTnCTGC AAATGAACGC ATAGAATCCA TTCACTGTTA 2400

ACTTTTTnCA ACAAATGTCT nACATG 2426

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1874 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

GAGTTGGGGA ATGTGCTCAA AATATGCGGA CTTTATGCAT TyCGGAATTG sCCaATTGCA 60

GCTTTAAGCT ATGGTCAAAA AAAGAGGGTC ACTATAGCAT CTGTTTTAGT CTTAAATCCG 120

GAAATAATCA TATTGGATGA ACCGACTGCT GGTCAAGATT TCTATCATTA TAATGAGATA 180

ATGTCATTTT TAATTGAACT AAACAGACAG GGGAAGACGA TTATTATGAT TACGCATGAT 240

ATGCATTTAT TGTCTGAGTA TAGTTCAAGA ACAGTTGTAT TATCAAAAGG TCAAGTCGTT 300

GCTGATACCA CGCCAgTATT GGTTTTAAAT GATAAAAAAA TCTGTGAGAT TGCATCATTG 360

AGACAAACAT CGCTATTTGA AATGGCCGAA TATATAGGGA TTAGCGAGCC ACAGAAATTA 420

GTACAATTAT TTATTAACCA TGATAGGAAG GTGAGACGcC AATGAATCAA TATAATACTA 480

TAGGTTTTCA CCCGGGAAAT AGTCGTATTC ATCAATTAAA TGCGACTGTT AAACTTTTAT 540

TCTTATTAGT TGTTTCTATT TCTGCAATGG TGACTTATGA CACAAGATAT TTAATTTTAA 600

TTAGTGCTTC ATCTATTTTA TTGGTCAAAT ATGCTCATAT TGAATGGAAA CAAGTTCGCT 660

TTGTTGTTAA ATTCATTCTG TTTTTCACAA TAtTAAATAT TATTGCCGTG TACATATTTG 720

ACCCTGAATA TGGTGTGAAG ATTTATAATC AGCGTACAGA GTTAGTCAAT GGTATTGGTC 780

GATTTACGCT AACATCACAG GAATTATTCT ATCTTTTTAA TCTAATATTA AAATATATTA 840

GTACAGTTCC TTTAGCGTTA ATATTTTTAT TCACAACGAA TCCGAGTCAT TTTGCTGCAA 900

GTTTAAATCA GCTAGGTGTG AATTATAAAA TCAGTTACGC AGTCTCACTA GCATTAAGGT 960

ATATTCCAGA TATTCAAGAA ACATATTttA ATATTTCACA AGCGCAACAA GCAAGAGGAT 1020

TACCTTTAAT ATTTTCTAGT ATCGAAAGAA TTGACACTAT TAGTACTGCT ATGGAGTTAA 1140

GACAATTCGG ACAGTATAAA AGGAGAACCT GGTACGTCAA AAAACAATTA AAAAAAGATG 1200

ATTATGTTGT TTTGTGTTTG ACGTTAATAC TTCTGATGTT AGTAGTTACA TTATTCTTTT 1260

TAAATAATAG TCGATATTTC AACCCGTGGC ATTAGTATTC ATATAAATAG TCTTTAAATA 1320

GAAATAGGAG GGAGACATTT AATGATAAAT ACTGAAAGAT TAAATTTAAT GATTCCAAGT 1380

TCCTCGCATT TAATTGAACT TTATAATATT TGTAGTCATC CACAAGCAAA TATATACACT 1440

CCCAAAGGTT TACATAATTC CAAATTAGAC ACACAACGGT GGATTGAAAA ATGGCGAAAC 1500

CATTGGCAAC AATATCAATT TGGTTACTTT GTATTGGTAA AAAAAATAGA TTGTAGTGTT 1560

ATTGGTATTT GTGGATATGA ATATCGACAA TTAAAGCAAG AaACAGTATT AAATTTATTT 1620

TATAAATTAC ATCCAAGTTT TGAAGGACAA GGGTACGCAT GTGAGGCTAT TACAGCAATC 1680

ACAAATTTTG TGAATTATAT CGATCAAGAA ACAGTAAAAG TTATCAGGAC AAATAAGTGT 1740

AACCAACGTT CAATAAATTT AGCAGAAAGG CTTAAATTCA AGCGAGACGA TACTATGGAC 1800

GACATTATCA ATCAAGGAGA TATTGTGTTT TAAnAATAAA ATACTATGAC ATTATCTAAA 1860

AAATAAAATT AAAA 1874

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

TCAACATTTC TAACACCAAT GTGAAAATGA TCTATGTGAT TTGCAATGGC TTGATTTGTA 60

ATATGTGTGC CTAAATGACC TGTAGCACCT GTTAACATAA TATTCATTCA CTTCATCTCC 120

TAATCTTTAT ATACATAACA TAATACTTAT TTGATGGTTT TCAAAACATT TGATTTTATA 180

AAAAATTCTA ATCTGTATTT ATTGTCGACG TGTATAGTAA ATACGTAAAT ATTATTAATG 240

TTGAAAATGC CGTAATGACG CGTTTTAGTT GATGTGTATC ACTAATATCA TTGAAAATTT 300

TAATCaGGTA CTACGACAAT ATGATGTCTG TTTTGTGTCT GAAAGTTTTA CAGTTTTTAA 360

AATAAAAATG GTATAAAGTG TGATTTGTAT AAAAAAGAGT CTCGACGGAT AAGAATTGAT 420

TAATAACAGT TAGCATTTTA TTAATTACCT TAACAATGAT TCAAGTTTAG TTAAATGAGG 480

TTTAATTTGA AAGGGGATAG CGCCTCAATA TAATGTAGGT AGATTGTTCA TATTACGTAA 540

AAGCAAGTTT AGCATTGGGA ATGTTAGCAA CAGGTGTAAT TACaTCGAAT GTACAATCAG 660

TACAAGCGAA aGCAGrAGTT AAaCAACAAa GTGAaTCAGA GTTAAAACAC TATTATAATA 720

AmCCAATTTT AGAGCGTAAA AATGTGACTG GATTTAAATA TACTGATGAG GGTAAACACT 780

ATTTAGAAGT CACAGTAGGG CAACAGCATT CTCGAATCAC TTTACTTGGA TCTGATAAAG 840

ATAAATTTAA AGACGGAGAA AACTCAAATA TAGATGTGTT TATCCTTAGA GAAGGTGACA 900

GTAGACAAGC AACAAATTAC TCAATTGGTG GCGTTACAAA ATCAAATAGT GTGCAGTATA 960

TTGATTATAT CAATACGCCA ATTTTAGAAA TCAAGAAAGA TAATGAAGAT GTACTTAAAG 1020

ATTTTTACTA CATTTCAAAA GAAGACATCT CATTAAAAGA ACTTGATTAT AGATTAAGAG 1080

AACGTGCGAT TAAACAACAC GGCTTGTATT CAAATGGTCT TAAACAAGGT CAAATTACAA 1140

TTACAATGAA TGATGGCACA ACACATACAA TCGATTTAAG TCAAAAACTT GAAAAAGAAC 1200

GTATGGGTGA GTCAATCGAC GGCACTAAGA TTAATAAAAT TCTAGTAGAA ATGAAATAAT 1260

ACTTTCTAAC AACAAAGCGC TATGTTGAAT AGTGCTTGTT ATGGAAATAT ATGGAAGTTA 1320

AGCGACGTAC TGTTGCTTAG CTTCTTTTTT TGAGGGGAAA AGTTACAAAA CTCACACAAA 1380

CAGTCGCACC ACGCATTATC TTTTGCTTAA ATAGCTTAAT CATATTTTAT GAATAGTTAA 1440

AAACAGGTTA ATGTGAATAT CCGAATACAG CTCCTATAAT ATGGGTGTAT GATTCAAATT 1500

ACGTAATAAA ACAATCTAAT TATAATAGAT TGGAGCATAC AACTATGAAA ATGAAAAATA 1560

TTGCAAAAAT AAGTTTGTTA TTAGGAATAT TAGCAACAGG TGTAAACACT ACAACGGAAA 1620

AACCAGTTCA TGCCGAAAAG AAACCTATTG TAATAAGTGa AAATAGCAAA AAATTAAAAG 1680

CTTATTATAA TCAACCTAGT ATTGAATATA AAAATGTGAC AGGTTATATC AGTTTCATTC 1740

AACCAAGTAT TAAATTTATG AATATCATAG ATGGTAATTC TGTTAATAAT ATTGCTTTAA 1800

TTGGCAAAGA TAAGCAACAT TATCATACGG GTGTACATCG TAATCTTAAT ATATTTTACG 1860

TTAATGAGGA TAAGAGATTT GAAGGTGCAA AGTACTCTAT TGGGGGTATC ACGAGTGCAA 1920

ACGrTaAAGC TGTCGACCTA ATAGCAGAAG CAAGAGTTAT TAAAGAAGAT CATACTGGTG 1980

AATATGATTA TGACTTTTTC CCATTTAAAA TAGATAAAGA AGCGATGTCA TTGAAAGAGA 2040

TTGATTTTAA ATTAAGAAAA TACCTTATTG ATAATTATGG TCTTTACGGT GAAATGAGTA 2100

CAGGAAAAAT TACAGTCAAA AAGAAATACT ATGGAAAGTA TACATTTGAA TTGGATAAAA 2160

AGTTACAAGA AGACCGTATG TCCGATGTTA TCAATGTCAC AGATATTGAT AGAATTGAAA 2220

TCAAAGTTAT AAAAGCATAA CACATATACT TGATGACGAA ATAAGTTGAA ATTGAAATAG 2280

AGAGGTTAAG TGACGATCAA ACGTTGCTTA ACTTCTTTTT AATGCTTAAA AATTATTTCA 2340

TTAATAATAC TTCAATAATT GTTAAAAGGG GTTTAATGTG ATTATCTTAG AACGCCATCT 2460

ATAATGATGT TGTATGATTC AAATTACGTA AAAAGACAAT CGAATATAAT ATAGATTGGA 2520

GCATACAATT ATGAAAATGA GAACAATTGC TAAAACCAGT TTAGCACTAG GGCTTTTAAC 2580

AACAGGCGCA ATTACAGTAA CGACGCAATC GGTCAAAGCA GAAAAAATAC AATCAACTAA 2640

AGTTGACAAA GTACCAACGC TTAAAGCAGA GCGaTTAGCA ATGATAAACA TAACAGCAGG 2700

TGCAAATTCA GCGACAACAC AAGCAGCTAA CACAAGACAA GAACGCACGC CTAAACTCGA 2760

AAAGGCACCA AATACTAATG AGGAAAAAAC CTCAGCTTCC AAAATAGAAA AAATATCACA 2820

ACCTAAACAA GAAGAGCAGA AAACGCTTAA TATATCAGCA ACGCCAGCGC CTAAACAAGA 2880

ACAATCACAA ACGACAACCG AATCCACAAC GCCGAAAACT AAAGTGACAA CACCTCCATC 2940

AACAAACACG CCACAACCAA TGCAATCTAC TAAATCAGAC ACACCACAAT CTCCAACCAT 3000

AAAACAAGCA CAAACAGATA TGACTCCTAA ATATGAAGAT TTAAGAGCGT ATTATACAAA 3060

ACCGAGTTTT GAATTTGAAA AGCAGTTTGG ATTTATGCTC AAACCATGGA CGACGGTTAG 3120

GTTTATGAAT GTTATTCCAA ATAGGTTCAT CTATAAAATA GCTTTAGTTG GAAAAGATGA 3180

GAAAAAATAT AAAGATGGAC CTTACGATAA TATCGATGTA TTTATCGTTT TAGAAGACAA 3240

TAAATATCAA TTGAAAAAAT ATTCTGTCGG TGGCATCACG AAGACTAATA GTAAAAAAGT 3300

TAATCACAAA GTAGAATTAA GCATTACTAA AAAAGATAAT CAAGGTATGA TTTCACGCGA 3360

TGTTTCAGAA TACATGATTA CTAAGGAAGA GATTTCCTTG AAAGAGCTTG ATTTTAAATT 3420

GAGAAAACAA CTTATTGAAA AACATAATCT TTACGGTAAC ATGGGTTCAG GAACAATCGT 3480

TATTAAAATG AAAAACGGTG GGAAATATAC GTTTGAATTA CACAAAAAAC TGCAAGAGCA 3540

TCGTATGGCA GACGTCATAG ATGGCACTAA TATTGATAAC ATTGAAGTGA ATATAAAATA 3600

ATCATGACAT TCTCTAAATA GAAGCTGTCA TCGGAAAAAC AAGAAGTTAA GTGACAACGG 3660

TTTACATGTT GCTTAGCTTC TTTTATTATG CGTAATGATG TAAAAAGACG AATATTCATT 3720

TGTTTGTAAA AGTGGCATTT CTATGTCTTA AAAGTGACGA AACTTCAAAT GTGCCAAGTG 3780

TTGAATCACA TCAAAATCAT TTTTATTTAA CGAACATTAT GGATTTCTTA ATTTACTTAA 3840

CGATGATTCA AATATAGTTA AACAAGGTTT AATGTGAATG GAGCAATACG CCATCTATAA 3900

TAAAGCTGTA TGATTCAATG AATGTAATCG AACAAATCTA ATAATTACGA ATGGAGCATA 3960

CAACTATGAA AATAACAACG ATTGCTAAAA CAAGTTTAGC ACTAGGCCTT TTAACAACAG 4020

GTGTAATCAC AACGACAACG CAAGCAGCAA ACGCGACAAC ACTATCTTCC ACTAAAGTGG 4080

AAGCACCACA ATCAACACCG CCCTCAACTA AAATAGAAGC ACCGCAATCA AAACCAAACG 4140

CGCCTTCAAC TAAAGTGACA ACACCTCCAT CAACAAACAC GCCACAACCA ATGCAATCTA 4260

CTAAATCAGA CACACCACAA TCGCCAACCA CAAAACAAGT ACCAACAGAA ATAAATCCTA 4320

AATTTAAAGA TTTAAGAGCG TATTATACGA AACCAAGTTT AGAATTTAAA AATGAGATTG 4380

GTATTATTTT AAAAAAATGG ACGACAATAA GATTTATGAA TGTTGTCCCA GATTATTTCA 4440

TATATAAAAT TGCTTTAGTT GGTAAAGATG ATAAAAAATA TGGTGAAGGA GTACATAGGA 4500

ATGTCGATGT ATTTGTCGTT TTAGAAGAAA ATAATTACAA TCTGGAAAAA TATTCTGTCG 4560

GTGGTATCAC AAAGAGTAAT AGTAAAAAAG TTGATCACAA AGCAGGAGTA AGAATTACTA 4620

AGGAAGATAA TAAAGGTACA ATCTCTCATG ATGTTTCAGA ATTCAAGATT ACTAAAGAAC 4680

AGATTTCCTT GAAAGAACTT GATTTTAAAT TGAGAAAACA ACTTATTGAA AAAAATAATC 4740

TGTACGGTAA CGTTGGTTCA GGTAAAATTG TTATTAAAAT GAAAAACGGT GGAAAGTACA 4800

CGTTTGAATT GCACAAAAAA TTACAAGAAA ATCGCATGGC AGATGTCATA GATGGCACTA 4860

ATATTGATAA CATTGAAGTG AATATAAAAT AATCATGACA TTCTCTAAAT AGAAGCTGTC 4920

ATCGGAAAAA CAAGAAGTTA AGTGACAACG GCCTACATGT TGCTTAGCTT CTTTTGTTAT 4980

GTTCGATGAT TTGAGAACCC GAATTTTCGA TGGGTCCAAA TATGACGTGG AAGAGACCTG 5040

AATTTATCTG TAAATCCCTA TCTATCGGGT GTGAAGCACA ACGGGATCAG TTTTATTTAA 5100

CGAACATTAT AGATTCCTTA ATTTACTTAA TAATGATTCA ATGATTATTA AACATGGTTT 5160

AATGTGAAAG GTCAAATACG CTAACTATAA TAAAGCTGTA TGATTCAATA GACGTAAGCG 5220

AACAAATCTA ATAATTACGA ATGGAGCATA CAACTATGAA AATGACAGCA ATTGCGAAAG 5280

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 886 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

AGTAAAATTG CCGGTATGAT GGACACAAAC GGTGACCTTG GTCAAGGTGA ATTAGCGATT 60

AATCCACCtA AATCAGATTT gAACGAATTA CCTTGGGCTA CACGTAAAAA TAAACAGCCA 120

GCTTCATCCG AAAAAgGTTC AAGTGGTCAT CATGGTAATG CAGCAATGCC TCAAACCAmA 180

TTAGATTATC AAATATCTAT TGATAAGGTC GTTGAACAGG CGCAAAAAGC TGGTATTAAA 240

AAGCCGTTTT CAATCGTATA TCCAAGTGAT AAAAATGGTA CCTTTATTGT ATCTAATACT 300

GATCAATATA GCGGTAAAAA GCTAGGTACG ATTAAATATG ATGACTACGG TATTATTGCT 420

AAATGGTTTA CATGGGGCAT TCCGCTTCAC GAAGGTCATT TATTCGGCAT TTTAAATAAA 480

ATCATTAATT TATTTGTATG TATCGCTTTA TTAGTAGCCA TTGGCATGGG GTTTGTCTCT 540

TGGATAAAGC GTACAAAAAA TACTGCAGTA AAAGTACCAC ATCGCGTAAA AAAACCAGCA 600

TCTATATCAC TCATAATATG TTTAATTGTA TTAGGATTAT TAATGCCATT ATTTGGATTA 660

TCACTTATCC TTGTATTTAT AATTGAATTA ATATTATATA TTAAAGATCG TCGTGCTAAA 720

CAATAATGCA CTTAAAGTTT TGAACTGACG AAATTTACAA AATGgATTCT CGTCTCTCTA 780

ATTACtTAAA ACGGGgTtCy AaTAATAAAT CgTACTGaTG GgAAAGTTTT TACTTTTTAt 840

CTGtCCGAtT TTTTnGAAwT TGAAGATAAA AAAGCATCTA AAACGC 886

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

GGCATTTGTG TCCTTATATA AGGAACTGTG tTAAATACAT TACTGTTGTT AAGTTGTTTT 60

TGTAATTCAA AGAGCAGAAC AGAGTAACAT CATCAGTTGT AGTAAACGAT AATCCGGTAA 120

AACAACTAAA TGAAATAATG AAAGTCATTT AACCTGAACA TTAAAATATA TTTGTTTTTC 180

ATTAAGAATA ATTCAAGTAT ATTTAAATCG AGGTTAATTA TCGTATGAAA CGATGCACGT 240

TATAATAAAA ATGTATGATT CAAATTACGT AATGAAAACA ATCCAATATA TTAAGATTGG 300

AGCAAATAAA TATGAAATTT ACAGCATTAG CAAAAGCGAC ATTAGCTTTA GGAATTTTAA 360

CAACAGGAAC TTTAACAACA GAAGTTCATT CAGGTCATGC AAAACAAAAT CAAAAGTCAG 420

TAAATAAACA TGACAAGGAA GCATTATACC GATACTACAC TGGAAAGACT ATGGAAATGA 480

AAAATATTAG TGCTTTGAAA CATGGTAAAA ACAACTTACG TTTTAAGTTT AGAGGTATTA 540

AGATTCAAGT TTTACTGCCT GGAAATGATA AAAGTAAATT TCAACAGCGT AGTTATGAGG 600

GGTTAGATGT TTTCTTTGTT CAAGAAAAAA GAGATAAGCA CGATATATTT TATACTGTTG 660

GTGGTGTAAT ACAGAATAAT AAAACATCTG GAGTTGTCAG TGCACCAATA TTAAATATTT 720

CAAAAGAAAA GGGTGAAGAT GCTTTTGTGA AAGGTTACCC TTATTACATT AAAAAAGAAA 780

AAATAACACT AAAAGAACTG GATTATAAGT TGAGAAAGCA TCTAATTGAA AAATACGGAC 840

ATAACCTTGA TTTAAGATCT AAATTAAAAT TTAAATATAT GGGGGAAGTC ATAGAAAGCA 960

AACAAATTAA AGATATTGAA GTTAACTTAA AGTAAATCAT TACGAATAAT TAAAAGTAAT 1020

TGAAGCGGCT TAACGGTGAA ATGTAAATTG GTGCGCATAG CTTATACAAA AAGGATGCAT 1080

CAATCGATAT CGTCGTTAAG CCGTTTTGGT TTGTGTGTCA TGAATCCTAT CCCAATCTCC 1140

ATAAAGGTAA AATTTCCACC ACCAACATCA AAATTCTCCA CATCGCAACA TAACCAAATG 1200

TTATAATAAA TCTATTACAC AAAGAGATAA ATTACTTATT CAAAGGCGGA GGAATCACAT 1260

GTCTATTACT GAAAAACAAC GTCAGCAACA AGCTGAATTA CATAAAAAAT TATGGTCGAT 1320

TGCGAATGAT TTAAGAGGGA ATATGGATGC GAGTGAATTC CGTAATTACA TTTTAGGCTT 1380

GATTTTCTAT CGCTTCTTAT CTGAAAAAGC GGAACAAGAA TATGCAGATG CCTTGTCAGG 1440

TGAAGACATC ACGTATCAAG AAGCATGGGC AGACGAAGAA TACCGTGAAG ACTTAAAAGC 1500

AGAATTAATT GACCAAGTCG GTTACTTCAT TGAGCCAGAA GATTTATTCA GTGCGATGAT 1560

TCGTGAAATT GAAACGCAAG ATTTCGATAT CGAACACCTG GCGACGGCAA TTCGTAAAGT 1620

TGAAACATCA ACATTAGGTG AAGAAAGTGA AAATGACTTT ATCGGTCTGT TCAGCGATAT 1680

GGATTTGAGT TCAACGCGAC TAGGTAACAA TGTCAAAGAA CGTACTGCTT TAATCTCTAA 1740

AGTCATGGTT AATCTTGACG ACTTACCATT CGTTCACAGT GACATGGAAA TTGATATGTT 1800

AGGTGATGCA TATGAATTCC TAATTGGGCG CTTTGCGGCG ACAgCGGGTA AAAAAGCAGG 1860

CGAGTTCTAT ACACCACAAC AAGTATCTAA GATACTGGCG AAGATTGTCA CAGACGGTAA 1920

AGATAAATTA CGTCACGTGT ATGACCCAAC ATGTGGTTCA GGTTCACTGT TGTTACGTGT 1980

TGGTAAAGAA ACACAAGTGT ATCGTTATTT CGGTCAAGAA CGTAACAATA CTACATACAA 2040

CTTAGCACGC ATGAATATGT TATTACATGA TGTGCGTTAT GAGAACTTCG ATATCCGTAA 2100

TGATGACACA TTGGAAAACC CAGCCTTTTT AGGCAATACA TTTGATGCGG TTATTGCGAA 2160

CCCACCGTAT AGTGCGAAAT GGACTGCAGA TTCAAAGTTT GAAAATGACG AACGATTCAG 2220

TGGTTACGGC AAACTTGCGC CTAAGTCTAA AGCAGACTTT GCCTTTATTC AACACATGGT 2280

ACATTACCTA GACGATGAAG GTACCATGGC CGTTGTACTC CCACATGGTG TATTATTCCG 2340

AGGTGCTGCA GAAGGTGTCA TTCGTCGTTA TTTAATTGAA GAAAAGAACT ACTTAGAAGC 2400

TGTGATTGGT TTGCCAGCGA ATATTTTCTA TGGGACAAGT ATTCCAACAT GTATTTTAGT 2460

ATTTAAAAAA TGTCGCCAAC AAGACGACAA CGTACTATTT ATCGATGCAT CCAATGATTT 2520

TGAAAAAGGA AAAAATCAAA ATCATTTAAG CGATGCCCAA GTCGAACGTA TTATAGACAC 2580

ATATAAGCGT AAGGAAACAA TTGATAAATA TAGCTACAGC GCGACACTAC AAGAGATTGC 2640

GATTGATTTA GATCAAGTCC AACAAGATTT GAAAAATATC GATAAAGAAA TCGCAGAAAT 2760

TGAGCAAGAA ATCAATGCAT ACCTGAAAGA ACTTGGGGTG TTGAAAGATG AGTAATACAC 2820

AAAAGAAAAA TGTGCCAGAA TTGAGGTTCC CAGGGTTTGA AGGCGAATGG GAAGAGAAGC 2880

AGTTAGGGGA TCTTACAGAT AGAGTAATTA GGAAAAATAA AAACTTAGAA TCGAAAAAGC 2940

CTTTAACAAT ATCCGGACAG TTAGGTTTAA TTGATCAAAC AGAATATTTT AGTAAATCAG 3000

TTTCGTCGAA AAATCTAGAA AATTATACAC TAATAAAGAA TGGAGAATTC GCGTATAACA 3060

AAAGTTATTC TAATGGATAC CCATTAGGGG CTATTAAAAG ATTAACTAGA TATGATAGTG 3120

GTGTATTGTC CTCTTTGTAT ATTTGTTTTT CTATTAAAAG TGAAATGTCT AAAGACTTCA 3180

TGGAAGCATA TTTTGATTCG ACACACTGGT ATAGAGAAGT TTCTGGAATT GCAGTTGAGG 3240

GTGCAAGAAA TCACGGATTA TTAAATGTTT CTGTGAATGA TTTTTTTACT ATTCTAATTA 3300

AATATCCAAG TTTAGAAGAA CAGCAAAAAA TAGGCAAGTT CTTCAGCAAA CTCGACCGAC 3360

AAATTGAATT AGAAGAACAA AAGCTTGAAT TACTTCAACA ACAGAAAAAA GGCTATATGC 3420

AGAAAATTTT CTCACAGGAA CTGCGATTCA AAGATGAGAA TGGTGAAGAT TATCCAGATT 3480

GGGAAAATAG CAAAATAGAA AAATATTTAA AAGAGAGAAA CGAACGTTCT GACAAAGGGC 3540

AAATGCTTTC AGTAACTATA AATAGTGGCA TTATAAAATT TAGTGAATTG GATAGAAAAG 3600

ATAATTCAAG TAAAGATAAA AGTAATTATA AAGTAGTTAG GAAAAATGAT ATTGCATATA 3660

ATTCTATGAG AATGTGGCAA GGGGCTAGTG GTAAATCAAA TTATAATGGG ATTGTTAGCC 3720

CTGCATATAC TGTGCTTTAT CCAACACAAA ATACTAGCTC ATTATTTATT GGATATAAGT 3780

TTAAAACACA TAGAATGATT CATAAATTTA AAATTAATTC ACAAGGATTA ACATCAGATA 3840

CATGGAACTT AAAATATAAA CAATTAmAAA ATATAAATAT AGATATACCT GTATTGGAGG 3900

AACAAGAAAA GATAGGTGAT TTCTTTAAAA AAATGGATAT ATTGATAAGT AAACAGAAAA 3960

TGAAAATTGA AATATTAGAA AAAGAGAAAC AATCCTTTTT ACAAAAAATG TTCTTATAAC 4020

TTTGATAAAT ACATAGATTG CATAAGAATA AAATTTGTAT AATTTAACAT AAAAGTTGTA 4080

AAAGTAAAGT GAATTAAAAA CGAACATTAA ATTTAGGCAC TGTGAAAGCG CAGTGTCTTT 4140

TTTGTGTCGA AATTGTGTAC AGAATAAGTA GTTAAATAAA GATTAAGTTG AGATAAAGTG 4200

TTATTCGTAA ATAAAAGAGA GTAGATCGAT AGGAATTGAA TGATATTAGT TAACTATTTA 4260

TTAAATTACT TAATAATGAT TAATTTTTAG TTAAAGTAAG TTTAATGTGA AGCACGACCA 4320

TTGCTCATTA TAATGA 4336

(2) INFORMATION FOR SEQ ID NO: 547:

(A) LENGTH: 487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

TAAGCTATCT GAGATAATTG CTGATAACAT TAAACCGGCA ATTTCAGGTT TAATTTCAAA 60

GCCACGTTCT CTAAACATTT TGTATAAAAT TGTAGCTGTA CAACCAACTG GTTCAGCACG 120

ATAACATAAA GGACCAGCAG TTTCGAAATT TGCAATTCTG TGATGATCAA TTACATGCTT 180

AATTGTAGCA GAGGCAATCG TATCAGAACT TTGTTGGaAT TCGTTATGAT CAACTAAGAT 240

AACATCTTGA CCATCTAAAT CATCTGTTAA TAATTCCGGA GCAGGTACAT TAAATGTATC 300

TAACGCGAAT TGAGTTTCTG CACTCACATC ACCTAAACGG TATGCTTTGG CTCCTGAATT 360

ACCTCGAAGT TGTTCaAATT CTGCCaTAAT AATCGCAGAT GAAATTGCAT CAGTGkCTGG 420

aTTCTTATGT CCGAAAATAT ATGTTTTAGC CAnTGTCAAA TATCTCCCTT GTAAATTGTA 480

TTCTTTA 487

(2) INFORMATION FOR SEQ ID NO: 548:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 871 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

TTGGTGGTGC AGCAGTTATA GCAATTGTTT TAGCATTCAT TGGTAAGTTC ACTGCATTAA 60

TTTCTTCTAT ACCTACmCCA GTTATGGGAG GAGTATCTAT ATTACTTTTC GGTATTATTG 120

CAGCAAGTGG CTTAAGAATG TTAGTTGAAA GCAAAGTAGA TTTTGCGAAC AATCGAAATT 180

TAGTTATAGC TTCTGTAATT TTAGTTGTAG GTATCGGTAA TTTAGTATTT AACTTAAAAG 240

AAATTGGTAT CAACCTTCAA ATTGAGGGGA TGGCATTAGC TGCACTTTCA GGAATTATTT 300

TGAACTTAAT CTTACCTAAA GAGAAAAAAC AAAACAATTA AGATTTACAA ATTAAGGAGG 360

GCGCTTTTAT GAATCATTTA TTATCAATGG AACATTTATC TACAGATCAA ATATACAAAC 420

TTATCCAAAA GGCAAGTCAA TTTAAATCTG GTGAACGTCA ACTACCAAAC TTTGAAGGGA 480

AaTATGTCGC AAATTTATTC TTTGAAAATT CTACTCGrAC AAAATGTAGT TTTGAAATGG 540

CAGAACTTAA GCTAGGGTTA AAAACGATTA GCTTTGAAAC ATCAACATCA TCTGTTTCAA 600

TCATTAGACA TCCGTTTAAT AACTACTATG AAAAATTAGC GAATATTAAC ATCCCAATTG 720

CGAATGCTGG TGATGGTAGT GGACAACATC CAACACAAAG TTTACTTGAT TTAATGACGA 780

TATATGAAGA ATATGGATAT TTTGAAGGCT TGAATGTATT GATTTGTGGA GAcATTaAAA 840

ATTCACGTGT CGCACtAGTA ATTACCAnAG T 871

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

TCAATCTAAT ATATACTTCA TGACTTCCCG CCAAAGGCGC AATCGTAGGA TTAGTCTGTT 60

TATCGATAAG ATCTATTAAT ATTGTTTCTA CTTTAGATTC ACCTATTCCC GCAAATCTTA 120

ATAGTTCAGA ATGTATAATT CGATTATGGT TTATAAAATG TGACAACAAT TCATTTTTCA 180

CCATTGGTTG CATTTCTTTC GGTGGACCTG GTAATAAAAT AATTTGTTTG TTTTCAAAAT 240

TCACCATCAT TCCTGGAGCC ATGCCATGAT GATTTGTTAA TACAGTTGAA CCTTCAATTA 300

CTAAAGCCTG TTGTcTATTA TTAGGTGTCA TTTCTtGTCC TTGTTCCTCA aAAwAGCTTT 360

CAATATATTG AAAGAAGGCT CATCAATAAC TAAATCTnTA 400

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1523 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

ATACCTCCAG CTAGAATACC AGCGTATTTC ATAAAATACT TCCTCCATTC AACTATATCT 60

ATATTTAATT ATTTAAATTT CGTTGCATTT TCCAATTGAA AACTCATTTT AAAATCAAAA 120

CTCTAAATGT CTGTGTATTA CTTAAAATTA TACATATTTT GCTTATATTT TAGCATATTT 180

TGTTTAAACC TATATTACAT TATATCAGAC GTTTTCATAC ACAAATAATA ACATACAAGC 240

AAACATTTCG TTTATTATTT ATATCACTTA ACTAATTAAT TTATAATTTT TTATTGTTTT 300

TAAGTTATCA CTTAAAAATC GTTTGGCaAA TTCGTTGTGA CGCTTGTCCA TCTTCTAATG 360

TTTGTTTTAA TGCATCAATG AGTGCTGTTT GATTTTCAAC AATTGGACCT GGCAACTCTT 480

TTTTATAATC CATGTAAAAA CCTCTAAGCT CATCGCCATA TTTATCTAAG TCATATGCAT 540

AGAAAATTTG CGGACGCTTT AATACACCGA AGTCGAACAT GACAGATGAG TAGTCGGTAA 600

CTAACGCATC GCTGATTAAG TATAAATCCG AAATGTCTTC ATAAtCTGAA ACGTCTTTCA 660

CAAAATCATC ATGTTCATCA ATACGTGTCA CAACTAAATA ATGCATGCGT AAkAAAATAA 720

CATArTCATC ATCCAGCGCT TGACGCAAAG CTTCTATATC AAAGTTAACA TTAAATTGAT 780

ATGAACCTTC TCGAATCGCT TCATCGTCAC GCCAAGTTGG CGCGTACATA ATCACTTTTT 840

TATCTAATGG AATATTTAAT CTTGTCTTAA TACCATTAAT ATATTCAGTA TCATTGCGTT 900

TATGTGATAA TTTATCATTT CTTGGATAAC CTGTTTCCAA AATCTTATCT CGACTAACAT 960

GAAATGCATT TTGAAATATC GATGTCGAAT ATGGATTAGG TGACACTAGA TAATCCCACC 1020

GTTGGCTTTC TTTTTTAAAG CCATCTTGGT AATTTTGAGT ATTTGTTCCT AGCATTTTAA 1080

CGTTACTAAT ATCCAAACCA ATCTTTTTTA ATGGCGTGCC ATGCCATGTT TGTAAGTACG 1140

TCGTTCGCGG TGATTTATAT AACCAATCTG GTGTACGTGT GTTAATCATC CwCGCTTTCG 1200

CTCTTGGCAT CGCTAAAAAC CATTTCATTG AAAACTTTGT AACATATGGT ACATTGTGCT 1260

GTTGGAATAT GTGTTCATAT CCTTTTTTCA CACCCCATAT TAATTGGGCA TCGCTATGTT 1320

CAGTTAAGTA TTCATATAAT GCTTTGGGGT TGTCGCTGTA TTGTTTACCA TGAAAGCTTT 1380

CAAAATAAAT TAGATTCTTG TTTGGCAATT TTGATAGTAA TTTAAAAGTC GTATATATAC 1440

TATGTTCTAT CAATTTTTTA ATTGTATTTT TAATCATGTC GTACCTCCGA CGTGTTTTTG 1500

TAATTATATT AATATGTATG AGC 1523

(2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4923 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

CAGTAAGAGA TTTTCTTAAT TGAAAATAAT CTTACTGCTT TTTTAAATTT AATTTCGAGA 60

TTCAATATTA GTTTATCTCA TTGTGGCATT AATTGATAAA ATTGTTTTAA TGTTATAAAT 120

CAAAGTCtTC TTCAACAATT TCAATGTCTG CATCAGATCT ATGATATGTG AAAAAGCTAA 180

TTCTTATGCG GTCTAAATGC TCTAAATGGT GTCGATACTC TTCGATGGCT GCAACAATTT 240

ATGTGGACAA TAAATCTTTT TTCTGCGGAT TATCTAACTC ATAATCAACA TGTGTCACAT 360

TATAACGTGC TTTTTTAGAA AGGCTAGCTA AAATTTGCTC GTGAAAAGCA GTTAATGAAT 420

CTAAATCTAA TTTGATTTGT AATAGGAAAT TGTTATTAAG TAAATATAAG TCGTTTTGAT 480

AACGCGACAA TTTGTTTAAT ACTTCATAAG CTTGTCTAGT CGTCTGAACT ACTTCTCTGA 540

AAAGTATTTT CTTTCTATTC TGTTGGTGAA TATGTTTTTT TGTAATAGGA CGTTCTTCGC 600

TATAGTAATC ATAAATTTTC TCTAACTTTT CGACACGTTG TTTTAAATTA TGACTATCTT 660

GTTTAATATT ATTAAACTCC GTCGTATCAT TTAATACTAA TTTAAACCAC ATAAAAATAT 720

CTGAGGATAT ATTTAATGAA TTATAGTAAA TTTTTGTTTC AAATTTAGGT GGTAGAAACA 780

CAAAGTTAAC TAGAGATGAA CTTATGACAC CAATCATTAC AAGTACAAAC CTGTAAAAGG 840

CGGTAATATA GAAAGAACCG GTATGTTGTC CCATAATGAT TAATGCTGTT ACACTCGCCA 900

AAGTAGCAAC ATGTGCTAAA TTAAATTTAA ATAAAATAGC AATAAGTACT ATGACGGTAA 960

CACCCATAAT GATAAAATTA TCACTAAAAA TTGTTACCAT TGTAACAGAT AGTATGGCAC 1020

CTATAATGTT ACCCAATGCT TGATCAGAAA CTGTTTTAAA TGAACGATAA ATACTAGGTT 1080

GCATTGCAcA ACAGCACTGA CACCAGCTAA GGCTTTCAGA CCAACATCAT CCGGTAGTAA 1140

AGAAGCGATA GACATAGCTA AAATAATGGC TATACCAGTT TTAAAAATCC GAGCTCCTAG 1200

TCTCAAAAAT AATGACGCCC CTTTTAAGTT TATTGAATAT CTAATATTCG TATTCATTAC 1260

TGTTATACAC TTACTAGTTA CAAAATTCAA GCTTATTTAT AGTTGTTAAA ATAAATCATA 1320

CATAATACTG ATAGCGATGT AAAACTTTAG TCAGAGATTA AAATAGTATA AATTTGTAAA 1380

ATAAAAACTC ACATAGTGAC ATATCAAGTT AAACGTTAAT AGTTAACGAT ATAAAATGAA 1440

TCTACTATGT GAGCATTTGC TTTATTTTAA TTCAATTAAA AATATACTTC CTTAAAAGTT 1500

ATTTCATTTG ACTAAAAGCA TAGTCTGCAG CTTTTAAAGT TTGTTTAATA TCTTCTTCTG 1560

TATGTTCAGT TGTTAAGAAC CAAGCTTCAA ACTTAGAAGG TGCTAAATTG ATACCTTGAT 1620

TTAACATTAA TTTGAAAAAT TTACCGAACG CTTCGCCGTC AGAATGTTCA ACTTGATCAT 1680

AATGTGTGAC TTTTTCATCT GTAAAGTACA ATGTTAAAGA TCCATAAATA CGATTAATTG 1740

TAGCTGTGAT ATTATGTTTT TCGATTAATT TAAGTAAACC TTCTTCTAGT TGTTGGCCTA 1800

AGCTGTCTAA TTTTTCATAA ACACCGTCTT GTTCTAGTAC TTCGAGTAAT GCAATACCTG 1860

CTTTCATAGA TAACGGGTTA CCAGCCATTG TACCAGCTTG ATATGCAGGT CCTAGAGGTG 1920

CTACTTGTTC CATAATATCT TGACGTCCAC CATAGCCTCC AATTGGTAAA CCACCGCCAA 1980

CAATTTTACC AAATGCAGTT AAATCAGGGA TAACACCTAA TAAATCTTGA GCGGCACCGT 2040

AAATTTCATT AACCTCTTCT AAAAATCCAG GTTGAGGCAT TACCATTCCA AAGTTACCAA 2160

CAATTGGTTC TACTAATACT GCGGCAATTT CATCACCCCA AAATTCAATT GCTTCTTTAT 2220

AGGCGTTAAT ATCATTGAAA GGTACAGTAA TGACTTCACG TGCGACGCTT TCTGGAACAC 2280

CAGCTGAGTC TGGAGAACCG AGCTGAGATG GGCCGCTACC TGCTGCAACC AATACTAAAT 2340

CAGAATGGCC ATGATAAGAT CCAGCAAATT TTATAATTTT ATTTCTTTTA GTATATGCAC 2400

GTGCAACACG AATTGTTGTC ATGACTGCTT CTGTTCCAGA ATTTACAAAG CGAATTTTCT 2460

CAAGAGATGG AATTGCATCA CGTAATTTTT TGCTGAATTC AATTTCTAAT TCAGTCGGTG 2520

TACCAAATAA AACACCTTTA GCAGCTTGTT CTTGAATTGC TTTAGTAATA TGAGGATGTG 2580

CATGCCCCGT AATAATTGGA CCGTATGCTT GAAGGTAATC AATAAATTTA TTGCCATCGA 2640

CATCATATAA ATATGCACCG TGTCCTTCTT TCATAACAAC AGGTGCACCG CCTCCTACAG 2700

CTTTATAAGA ACGAGAAGGG GAATTGACAC CGCCTAGAAT ATATTCGTTT GAAAGTTGTT 2760

GTAAACGTTC ACTTTCACTA AAATTCATTT ATATCAACCT CTTTTAATTT AATATTTTCA 2820

TCTAATATCG TATCATAAAA TTATTATAAT GAAGAAAAAG GTGATTATAT GTTGCAAAAA 2880

GGAGAACAAT TTCCAATATT TAAATTAGAA AATCAAGACG GAACTGTCAT TACAAATGAT 2940

ACATTAAAAG GTAAAAAGGC GATTATATAT TTTTATCCTA GAGATAATAC ACCTACTTGT 3000

ACCACAGAAG CTTGTGACTT TAGAGACAAT TTAGAAATGT TCAATGATTT AGATGTTGCA 3060

GTATATGGTA TAAGCGGTGA TTCAAAGAAA AAACACCAAA ATTTTATTGA GAAACACGGA 3120

TTGAATTTCG ATTTATTAGT AGATGAAGAT TTTAAATTAG CTAAAGAAAt GGCGTATATC 3180

AGTTAAAAAA ATCATTTGGC AAAGAAAGTA TGGGCATTGT AAGAACGACT TTTATAATAG 3240

ATGAACAAGG TAAAGTATTA GATGTTATCG AGAAGGTTAA GGTTAAAACA CAAATAGAAG 3300

AACTTAAAAA CATTTTGGGG TGACATATAT GAAAGTTGTT GGGTTAAATC GTATGCGTGA 3360

AGTTGAAACT GAATTACAAC AACGCTTTTC AGATTTAGAT TTTAAATTTT ATAAAAAAGC 3420

ATCAGAAATA CCTGAGAGCG ACTTGGCTGA TTTAGATATA TTAGTTGGTT ATGATGGCGG 3480

TATCAATGAG GCATTTTTAC GACGTTGCCC GAATTTAAAA TGGATTGCAT GGTTTGCAAC 3540

GGGTGTAAAT ACATTGCCGT TAGATTATAT TGCAGATCAC GGCATACTTT TAACTAATGG 3600

AAAAGGTGTT CAAGCTAAAC AATTATCTGA ATACATTTTA GCTTTCATTT TAGATGATTA 3660

TAAAAAGATG AAACTATCAT ATGATAACCA ACGACAACAT ATATATGATT CGAAAATAAC 3720

TGGTAAACGC CTATCAGGAC AAACAGTTTT ATTTTTAGGT ACAGGTGCAA TTGCTACTAG 3780

AACTGCGAAG TTAGCAAAGG CTTTTAATAT GAATTTAATT GGTCTGAGCA AGTCAGGTCA 3840

TGCTGACATT ATTATAAATG CTTTACCAGA AACGCAAGAA ACGATTCaTT TaCTAAAGAA 3960

AAAACATTTT GAATTAATGA AAGATGAAGC ACTTTTTATA AATATAGGAC GAGGTAGCAT 4020

AGTTAAAGAA GCGCTCTTAA TAGAAGTATT AAAAAGTAAA GTTATTCGAC ATGCATATTT 4080

AGATGTGTTT GAAAATGAAC CTTTGAAACC TAATCATGAA TTATATGAAT TGGATAATGT 4140

AACTATAACA GCGCATATAA CTGGTAATGA TTATGAAGCA AAGTATGACT TATTAGATAT 4200

TTTTAAAAAC AATCTAGTTA ATTTTCTCAA TAAGAATGGT CTAATTGAGA ATGAAGTTGa 4260

TGCTAAAAAA GGCTATTAAA TGArATCATC ATGTAAATAT TGACACGCGC GCAATACTAC 4320

AGTTATATTT aTAGTAAgTt AATaATgATT ATATAAGAaA GATGGTgATA TAGATGAGTG 4380

TTGAAATAGA ATCAATTGAA CATGAACTAG AAGAATCAAT TGCATCATTG CGACAAGcAG 4440

GCGTAAGAAT TACACCTCAA AGACAAGCAA TATTACGTTa TTTaATTTCT TCACATACTs 4500

ATCCAACAsC TGaTGaAATT TATCAAGCAC TTTCACCTGa TTTTCCAAAT ATAAGTGTTG 4560

CGACAATATA TAATAACTTA AGAGTGTTTA AAGATATTGG AATTGTAAAA GAATTAACAT 4620

ATGGAGACTC ATCAAGTCGA TTCGACTTTa ATACACATAA TCATTATCAT ATTATATGTG 4680

AACAATGTGG TAAGATTGTT GATTTTCAAT ATCCACAGTT AAATGAAATT GAAAGATTAG 4740

CTCAGCATAT GACTGACTTT GACGTAACAC ATCATCGAAT GGAAATTTAT GGAGTTTGTA 4800

AAGAATGCCA AGATAAATAA TTTAACTTTG GTAGTATGAC AAATTAAAAA AGCGTTACTw 4860

ACTTCATATA AGTAAGCGTA ATATTTAAGA nGTTAAACGA CATGaAAGTt GTTTAACTTT 4920

TTT 4923

(2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 917 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

TCCGGCTTTA AAAACTTTTC CCAATTCCAG CTTGGGCCTT TGGCATTAAT ATTAACCTCC 60

TGGTTCGGAT TAATTGGGAA CCTAACCnTT TAGGCAATAA TTGGTTTAGG CAACTTCCAA 120

ATTGGTGGTT CAACCAACGT CTTTGGATAC CyTGcTCATT TAATTCTAAA ATGgTyrGAA 180

CGCATTTTGG TACCCAAAAt GgTGACGTTC GTTTGCACGG TCTAATAAAT TGTCTAAGTT 240

GTCGATTGGT TTCATTAATT GAaCACCATT TTGCTCTTCA GCAAGACCTT TGTCTACTTT 300

GCGATCCATT GTTTGTTCGA AAAGAATAGC ACCCAAAATT TTATCTGGTG AGAATGAAGG 420

TGAAGTTACC ACACGTGTAC GCATATCGTG AACAAGTTGG AACATTTCGT CTTCATTGCT 480

ATATTGATCT TCGTTTACAC CATATTCTTT AAGTGCTTTT GGTGTACTAC CACCACTTTG 540

GTCTAATGCG GCAATAAAGC CTTTTCCATT TTTCATTTTT TCTAATTGCT CTTTATTCAT 600

ACTTTCCACT CCTTAACTTT TCAATACACC TCCAGTATGA TAAAAATGAG AACATTTCTC 660

AAGTCATAAA CCTTGAAAAG TGTATAAAAT GTGAAAAATA ATTGTCAGTT TAATTAAAAA 720

TATTATTTTA TTCTAGGTAT GACTAACGCC ATTAATGACA TAAAGAAAAT ATGTGTAATA 780

ATCCAACCGA TTAATTCTGT CACACTAAAT TGAAAAATTG GACGTTGCGC AATAAATACT 840

AAAAAGGGAT ACAATGCTAT AAATAAGAAA AATAAAGGGA TATAACATAG ATAGTAAAGC 900

CTTTTAGAAG TATGAAA 917

(2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

ACTCCCATAT CCACTGGCAA GATTTATAAT TTGTAATTCT AAAGTATAAT AGCCTATATT 60

TTTCAAAATC TCTTTTTTTA TGATTAACAT CCCTCTAAGT GCACCTAAAG GTTTTTATGT 120

AATGTATTAA ATATTTCCAT TTATACATAT ACATCTTGTA TAAAAAGAAA GAACTCCATA 180

TATACTCAAA AGGTATACTG AAGCTCTATA TATTATATAA AATTATTATA CTATTTTGAA 240

AAACATAAGT AAATCACTAA ACATGATTTC TTTCACTTTT AGAAAACTTT TAATACTATA 300

AAAGCACCCA CTCAGTCACT AGTTTGGGCA GTTATTGTAT GCCTATTGaA CTCAATGCgT 360

ATATTACAAT ACCTTTTtCG CATATTCATA TAAGacTTTG CATCTTTAAG CTTAATTGCT 420

ATCTCTTTCT CT 432

(2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTTTGCTTTA TGTTAAATGG ATTATTaTTA GAATAAAAAA TCGGTGATGA GCTAAAAAAG 60

TGTGTAGGAT GTTTTCCkAA CCCAATTTTT ACATCCGAAG ATATCGAACA ATATCTTCCT 120

ACTTCTACAT TATTAAAATC ACTACCAAAT CCAATATAAC TGTATTCACC AATGTGAGAA 180

TTCCTGATTT TACACCATCT ATCTATATAG TTATTGCCAT CAAATTTTGA GTTTGTAATA 240

TACGCCAAGC GATGAATCTT AACATTCGAT TCTTTAGAGG ACTGGTTTTT CAGCAAACCA 300

ATTATCTTTT CAATCGCTAT CCTCATCGTC ATTTCCTCCA AGTATTTCGA TTGATAATAT 360

CTTTATAGCT TTGAATAATT TTAACTACCT TTGTCGAAAC GTTAGTGTCT TTATAATCAA 420

TAGCATCAAT CATCGGTTCG TTATTGTTTT GCATCTCTCT TGCTAGTTCA ACGGATTGGA 480

TTAGATTGTT ATAGGTAATA CCACCTACAA TAACCGTACC TTTATCTAGT ACTTCCGGTC 540

TTTCTGTGGA AGTTCGAATA AGGACACCAG GGAACTTCAA AATAGACGAC TCTTCTGACA 600

ATGTTCCACT ATCTGATAGC ACAACAAATG CATCTTTTTG CAATGCATTA TAATCAAAGA 660

AACCAAATGG CTTTAACTGT TTAACTAATG GATCAAATTC AAATTTACTT TCTTCAATTT 720

TCTTCCAACT TCTTGGATGC GTTGAATAAA TCACAGGCAT TTTATACTTT TTGGCAATAT 780

CATTTATCGC ATTCATTAAT GATTTAAAAT TCTTTTCATT ATCGATATTC TCTTCTCTAT 840

GCGCAGaTAC TAAAATGTAT TGTTGCGGTT CTAATCCTAG TTTATTTAAA ACGTCACTGT 900

GATTAATTTT ATCTCGATGC GCTTCTATCA CTTCTGTCAT CGGTGATCCT GTyACAAAGA 960

TATTCGCTTT ATTGAAGCCT TCATCTAATA AATAACGTCT GCTATGTTCC GTATAAGGTA 1020

GATTCACATC ACTGACATGG TCAACAATTT TACGATTGAT TTCTTCAGGT ACATTCTGAT 1080

CAAAGCATCT ATTACCCGCT TCCATGTGGA ACACAGGAAT CTTTAATCGT TTAGCAGATA 1140

CTGCTGCTAA ACAACTATTT GTATCACCAA GAATTAAAAG TGCATCTGGT TGTTCGCGTA 1200

ATAAAACATC ATATGTCTTC GCAATAATAT TCCCCAtCGT TTCTCCAnGt TACTTCCAAC 1260

TGCCTCTAAG TAGTGGTCCG GTTGTCTTAA TTCCAAATCA TCAAAGAAAA TTTGATTCAA 1320

TGTATAATCA TAATTTTGAC CAGTGTGTAC TAATATCTGA TTAnAAATAT TGAT 1374

(2) INFORMATION FOR SEQ ID NO: 555:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

TTACCTCTAG GCATGTCCCT TTCACGGTTT GCTTATGATA ACGTTATCGA CATTGTTAAA 120

TTGTCCTTTT TGAAAAAATA ATTCTGGTGA GATAGACGCT ACTTGGaTTT CaTCaGTTTG 180

TAAtAACGCA GtATAAtTAC CaTTACTAAA tTGaGTTAAT CGTTCaTATA AAGTACTAAT 240

AGGATAATAA ATGTTATCCG TTAAgCGCGC CGTATAGTTC ACTTGATACG TTTCGCCTTC 300

AACAATTGCT TGTTGGACAC GTTTAATATT AGTCATCATA ACCTCAGAAG ATTCAACAAA 360

TGAAAAATGA TACTTTGATA CATAAGAAGT TTGATGTTCA TATGTTGAAT TTATGCTTTC 420

CGCTTTTTCA AAACTATAAG CTGCTGCATA AATATCATCT TTAGCTAATG AATGTGTACA 480

CATAGCATGA TTAAAATACT TTGCCGCTTC GTAACTTAAA TATAACGAGA CATATCTACC 540

TTGTCGTkGt GCGCTTGTGC AAAGTGTATC ACTTCTCCCA CATCAGCCAA CTTAGTAGCA 600

ACATACTTCT TTATAAATCC CTTTAATTGA ATATGGTATT GCTTATATTC ATTTTCAGTT 660

AAATAGTAGC GATAATTATA TTCTATTCTC ACAGTAATCA CCTACCTTCG ATAAAAATAA 720

TTCAACTTGT CGATAACCGT ATTCACTCAA AATAGATTCA GGATGATATT GCACACCAAA 780

AACCGGAAAT CTAATATGCT CAAATGCCAT AATAATCGCT TCATCGTTTT TTGCTGTAAT 840

CTTTAAGCAA TTTGGAAAAG TCGCTCCGTC AGCAATTAAT GAATGATAAC GCATTACATT 900

GAAATTTTGA GGCAGTCCTT GAAAAATACC TTCATTGGTA TGGCGTAACT GTGTAGTATG 960

TCCGTGTACA GGATGATAGC CGTGAATGAT ATTTCCACCA AAATAAGACA CGATACATTG 1020

AAATCCTAAA CATACACCTA GTATAGGTAC ACGCTGATAA AATTGTTCTA ACACTTCATT 1080

CAAGATAGGA TAATCATCCG GaTTACCCGG CCCAGGCGAA ATAACAATTG CTTTTGGCTT 1140

CATATTAATG ACGTCTTCTA TCAGCAGATT ATCAATACCA ACAACTTGAA CTGTTAGTTT 1200

CGTTTGAGTC TTAATATAGT CTATTAAATT ATATGTAAAT GaATCATTAT TATCTATGAC 1260

TAGAATCATT GTATACTCCG TTCTAAATGT GTTTTATTTT TATAATATGT ATTGGATGTA 1320

GCTAAAACTT TAAAAGCATT GTCATTATCC TGACCTTGAT TTTAACTAAT ATATGGTATA 1380

TTCTATTCAT CGTACATAAA TGAATATCAG AGGTTCCTAG CTGAAACCCT CTATAAAAAA 1440

CTAGGCCATT GAAATTTCAA ACATTCGTTG GG 1472

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1054 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AGAACAGCAA GGATTACTTA CTGAGGAATT AAAGAAGGAT ATTTTAAAAC AGAACAAATT 60

ACAACGTGTT GAAGACCTAT ATAGGCCTTT TAAACAAAAG AAAAAGACAA GGGCAACTGA 120

GGCGAAACGT AAAGGGTTAG AGCCATTAGC GATATGGATG AAGGCACGTA AACATGAAGT 180

CTCAATTGAA GAAAAAGCAC AACAATTTAT AAATGAAGAA GTGCAATCGG TTGAAGATGC 240

TATCAAAGGT GCACAAGATA TTATTGCGGA ACAAATTTCA GATAATCCTA AATATAGAAC 300

AAAAATTTTA AAAGATATGT ATCATCAAGG TGTGTTAACT ACATCTAAAA AGAAAAATGC 360

TGAAGATGAA AAAGGTATTT TTGAAATGTA CTATGCATAT AGTGAGCCAA TTAAACGCAT 420

TGCTAATCAT AGAGTTTTAG CTGTTAATCG TGGTGAAAAA GAGAAAGTAT TATCTGTAAA 480

GTTTGAATTC GATACGACAT CAGTAGAGGA TTTCATTGCA CGTCAAGAAA TCAATCATAA 540

TAATGTAAAT CGCAGTTATA TTTTAGAGGC GATTAAAGAT AGCTTGAAAC GCTTAATTGT 600

CCCTTCGATA GAGCGTGAAA TCCATGCTGA TTTAACTGAA AAAGCTGAAA ATCATGCAAT 660

AGATGTTTTT AGTGAAAACT TAAGAAATCT ATTACTGCAA CCTCCAATGA AAGGTAAACA 720

AATATTAGGC GTAGATCCAG CATTTAGAAC AGGTTGTAAA TTAGCAGTCA TTAACCCATT 780

CGGTACTTTT ATAGCAAAAG GTGTGATTTA TCCGCATCCA CCAGTTTCTA AAAAAGAGGC 840

AGCAGAGAAG GATTTTGTAC AAATGGTTAA AGCGTATGAT GTGCAATTAA TTGCAATTGG 900

CAATGGTACT GCAAGTCGTG AAACAGAACA ATTTGTTGCA GATTTAATTA AAAAGCATCA 960

GTTGCCAGTA CAATTCATCA TTGTCAATGA AGCGGGCGCT TCAGTATACT CAGCATCAGA 1020

AATTGCTAGA GATGAATTTC CTGATTTTCA AGTG 1054

(2) INFORMATION FOR SEQ ID NO: 557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1057 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

AAATGTCAGA ATACAAGAAA AAAATAATTG AATTAATTGA AAGTAATTTA ACAGGATATG 60

AAATTTCTAA AAAAACTGGA GTTTCTCAAT ACGTACTTTC ACAATTAAGA CAGGGCAAAC 120

GCGAAGTAGA TAATCTAACC CTGAATACAA CAGAAAAATT ATATGAATAT GCCAATAAAG 180

TTTTGTAATT TAACTAATGT ATAAATTAAT CAAGCTATGT TTATTTGATT TAACTATTAA 240

TAAAAATCAT ATGGTGAATG GATATTATAA TAATTAAAAT ACAAAAATAG TAGATTCCAA 300

AAGGGAAAAT AAGTGTTAAG TTTTAAATGA TAAAAAAGAT TGGAATGGAT CGTCTTGAAA 420

TGCTCCCTTC AAAGTTTTCA TTTTTTCAAT GTCGACTTCG AAGGGGGCAT TTTCATTAAA 480

TTGTTATAGC TTTTTATATT TGTATAATGA ACATATAAGT TTAAGAAGGT GCGAGTGAAG 540

GAAATAAAAA AGCTCAAATG TACCAAATTG TTAATCTTAA TAAATCTCTA CTTTATAAAG 600

ATTGAATGGA CATTCGAGCG TTAATCAGTC AGGAGGGACT TTCCCTCCTA CAATTTAATA 660

ATAATACTTG CTTCACCACT ATACAAGGAG TGAGTTGTTA TGTTCAAAGT GAATTATTCG 720

ATTTTAAGTT ATTATCCAGA ATATAATATC GCAGTAAGTT GGCAACGTTT AAGAGAAGGA 780

AAAACAATAA AAAACAAGAT TTAATACTGC TGCGTCATGA GGCGCTTGAA CATTATTTGA 840

TGAATAAGTA TAATTTCAAC TATGATTATG CACATAAAAT TGTATCAAAA AAATACGATT 900

ATTCAATTTT TATAAAAaAG AAGGTGGATT AAATGCTTAC ATTAATAAAA TTGGAAAGAA 960

GATGaACAGG tTATAATATA TGraTATATa CCTGaAGATG aTATAAGTAC CGGGTAAAGG 1020

GTCCCGTACC TTTTTAATTA AAAAAGTTCC AGGGGGT 1057

(2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

CTGTGCTGTA TTTACtTTAA TTTGACGACA TTTGAGAAGT ATTATGATGG nTGTAGTTAT 60

TTTATGAAAG TAATGTATTA ACAATCGAAT TACTAAGTCT ATATTGGTAG GAATATCGAT 120

GTTTAGTTTA AATGGAATGC ACTATTTAAG TTTTTAATAT GGAGATGTTT GTGACTTTTC 180

GATGATTAAG ATTTTTATAG GTGTGCATCA TTTCAAATAA ACTTTGTGTT TAAAATTGAG 240

CTTAGGAAAT CGATAGGTTT AGATGAGGAT ATTGTTGAAG TTATGTGTCT TGTATCCTTA 300

GTTGTTATAA AAGCGCAAAA AATAGCACCG CTTTCTCTTT ATCTGTGTAG AAAGGATGCT 360

ATTATTGTAA AACAATAGTT TTAATTTnAT TTTCTGATaT ATCATATGTr ATTcTACCTG 420

TATCAATTTC TATCGAATTA TAACCATCAA AATTATCAAC TTTATCATCA AAGTCTATCA 480

CTTTTCCAAT TAATATTTTA TTATTAGTAA GCGTTAATTT GACTAATTTG CCTATGTATG 540

ACTGTAAATT CATATTTAAT CACTCCTTTT TAATATACGG AACTACATGA AAACCAGTTT 600

TAGAATAATG AACCTTACCT AATTTCGTTT CAATATATTT ACCATTCACA TAAGATTTAC 660

AAACTGGAAT ATCAATAAAT TCTTTTTTAG TCATCTTTTC ACTTTCATTA GAATCTATTA 780

TAGTATAACT TGGTAATAAA GATGAATTAT TTTTCTTATT ATTATATTCA TTTGTGCATA 840

AAATATGACG CTTTTGCTTA ACATTATTCA ATTTCATCGT CATTTTACCA TTACTTATCA 900

TTTCAAGCAT TTCTTTTTTA GCTTTTTGTA GAAAGGATGC TATTTTGTAA TTATTTTAAT 960

AATCTAATAC TTTTTATCTC AGTTTCATCA AACGAATAAA CAGCAAAATC AGTCTGTATA 1020

TCTACAACAA GATTTCCTGT TTCGCTCTCG AATTCATTTT CATAGTCAGT TACAAACCCT 1080

TCGTATTCTT CATTATTCAA AAGCGTGATA ATAACATCTT TACGATATGC ATCTnCAATT 1140

CTCAATACTT TTCACCTACT TATCAATATA AGGTACTATA TGaGcACCTG GTCTTCGAAT 1200

AATGGCACTT cCCTTTCTGG TTTCAATATA CACATTTTCG ATATGTATTT TTCCAATAAT 1260

TTGATTAAAA TTAATAATCT CTTTCAAATC AAATCGCTCA TCACTTAATA TTAGATTGCC 1320

TGTTGACATT TTTTCTCTTA ACAATTCATT CAATAAATCT ATAGAAAGTA TTGTATAGCT 1380

AGGCAATTTC TTATTATTTA AAATGGCTCT TTTTTTATTT TCATTATATA GGTGATGACC 1440

TAACATATAT CTATTTTATT TTCCGCAATT TATTTCTATT TTTATTTTAC CATTTTTAAT 1500

CATTTCTTTC ATCTGGTTTT TAGCTTTTtC CTGtAATTAT GCTTCTTTTA CTTCTACTTG 1560

ATATTTACCt TCACGCTCTT TAAAGAACTT GTCCCGCCAA TTGCCAACAT GTGGCACTGT 1620

GGTACTTCTA CACCAAGGAT GCATAGGTGG CGCATTCACA CCTGGTATCA TATCTTTAAC 1680

TTTAAATATT TTTCCGTTAA GTGAATGACA TAATTTAGAT GTTTTACTAT CTATTTTGGC 1740

AACATATTTA TATTCGCCAT CTTCACCAAG TTCTTTTAAA TATGTTAACT TTTGTGCTTC 1800

TGCATTTTCA GTAAATAGTT AAAAAAGCGT ATAAAAATAG CACCACTTTC TCTTTAkCTG 1860

TCTAAAAAGG ATGCTATTTA TCTTTTGAAT TTGAATTCTT TTTCGCTTTT TCTATACTTT 1920

CAAATTCTTC AACTAATTCT TTAAAAGATT CACTCAATTC TTTTGCAGTT ACATTTCCAT 1980

CTAATTGTGA ATCTAACATA ATTAAAATCA TCTCACTTTA TATTTAATCa TATTTATACT 2040

ATAAAGTTTT TTCAATAATT TTTCAATATG GCTATCATTA ATGATATTAA TATGCGTAAA 2100

ATATTTAGCA CAAAATTTAC TCACTATTTT ACCATGAAAC CTATTTGACT TGGTAATAAA 2160

TTTTACTTGT CCCTTATTAG TAACGATTGT CATTGATTTT ATTGATGGAT GCTTAAAAAA 2220

TGTAAATAAA TCATATTCTG AAAATCCTGA CTGTCCAGGA TGGTTATGTA ACATAACAAT 2280

TGAATTCGGT TTACTGTTAA ATAATAATTC GGTTGCTTGT TACCCTGGCA CAAAAGATAC 2340

ACTATCTTGA TTGACATATA CTTTTGTAAA TTTACCATCT TTTAACAAAT AAGCTACTTC 2400

ATTGCTATCA TTGTTTTCCA TGAGATATAC CTCCGTTTAT AGtCTGTCGA CTGATATTCC 2460

GAAGGTTAAA ATTTTTAAAG TAAACTTTCT TTATCCCCAT GCTACGAGTT CAGATTCAGG 2580

AAATAGCCCT TTACTAGTAT TTATGTATAT TCTGTCTATG GCATGAATAA AATAATTATC 2640

TCTTGTATTT tTTTCTAAAC TAGATTTTTC AGCATTGATA ACTTCAAGAC TATCTATATC 2700

CATTTGAATA ATACCAGGCT TAATATTTTC ATCATTATTA GGAAAATATT TATATGTAAC 2760

ACTTTTATCA TTAATTTCTT TTATTTTTAA TATTAGCAAT CATTTCCACC TCTAATTAAT 2820

TAAAATACTA TAATTATATT TTATTTCTGT AAGTTTATGT GCCTCTATAT AGTGTAAATT 2880

ATACTTATTC ATTAGATAGT GTTCAAGAGC TTCATGTTTC TACATTATTA TATCCATTTT 2940

TTTAATATTT TTCCCTTCTC TTAAACGTTG CCAACTTTGA GCCATATAAA AGTCAGGATC 3000

AAATTGTTTA AATCCACTTT CTAATAAATA CTTATTTTCA AATATATGTT CATAAACTCT 3060

TTGAATTAAA TTTTTATTTA TATTAgTATT TTTAGCAATT TTAGAAATCT CTATCTGTTT 3120

ATCTCGATTT CTAACTGAAT TATAATAAAT TTGAGCATGT CTGTTCCTTT TGATACCGTA 3180

TTCATCACTT TTATTATTAA GTGCACCTGA TTCAATAAAA CAACCTTCTA CTTGATATTT 3240

ACCTTCACGC TCTTTAAAGA ACTTGTCTCG CCAATTGCCG ACATGTGGCA CTGTGGTACT 3300

TCTACACCAA GGATGCATAG GTGGCGCATT CACACCTGGT ATCATATCTT TAACTTTAAA 3360

TATTTTTCCG TTGAGTGAAT GACATAATTT AGATGTTTTA CTATCTATTT TGGCAACATA 3420

TTTATATTCG CCATCTTCCA CCAAGTTCyT TTAAATATGT TAACTTTTGT GACTCtTCyT 3480

TTTCAACGAA TAATGAAAAA AGCATATAAA AATAGCATCG CTTTCTCTTT ATCTGTGTAG 3540

AAAGGATGCT TTAATACCaT GCTATTTTAT AATTTTcGGG AAATTcTTGC TTCTCGATAA 3600

AGTCTCTTAC TACAGAAAAA GACTTATTAC GATATAACAT AAAATATTCT TCATTTTCTA 3660

TTTCAGATAA TGAGAAATCT ATAACCTCTG CATCTTTTTT ATTAAAAGTT ACTGAACCTT 3720

TACCGTTACT TATATCATCT TCAGGTATAT ATTC 3754

(2) INFORMATION FOR SEQ ID NO: 559:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 815 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

ATTTAACTAA AACTATAaAT AATCAAATGA TATTGGAAGA TATTaGCATA GATATCGAAA 60

AAGGTAAATT GACTTCTTTA ATTGGACCTA ATGGTGCGGG TAAGAGTACT TTACTTTCAG 120

CTGATTATAA AAATAATGAC TTGTCGAAAA AAATATCTAT ATTAAAACAA ACAAACCATA 240

CTGAAATGAA TATTACGGTA GAGCAGTTGG TAAACTTTGG ACGATTCCCT TATTCTAAAG 300

GTCGTTTGAC GAAAGAGGAT CATGATATTG TCAATGATGC GCTAGATTTG TTGCAACTAC 360

AAGATATCAG AAATCGTAAT ATTAAGTCAT TATCTGGTGG ACAACGTCAG CGTGCATACA 420

TTGCAATGAC AATAGCACAA GATACTGAAT ATATTTTGCT AGATGAACCA TTAAATAATT 480

TAGATATGAA GCATGCTGTT CAAATTATGC AAACGTTAAA AATGTTAGCG CATAAAATGA 540

ATAAAGCGAT TGTCATTGTG TTACATGATA TTAACTTTGC GTCCTGTTAT TCAGATCAGA 600

TTGTAGCATT GAAAAACGGA CAACTAGTTA AGTCAGATTT GAAAGATAAT GTCATTCAAA 660

GTAGTGTTTT AAGTGATTTA TATGACATGA ATATTCAAAT TGAACATATA AGAAATCAAA 720

GGATTTGTTT ATATTTTAAG GATTGATAAT TTGGAGaCAC TTTAAAGGGG TGATGCGCCA 780

ATTAAAGAAG GGTTAAACGT AAAGCATTTA TTTAT 815

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 919 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

GAAACGAATA ATAAATTTAC TGAGTTATTA GTTGAAAAAG CTAATAAACA TGATGATGTT 60

CTCGATAmGT TGATTAATAT TTTAAAATAA GCGATACACA CTACTAAAAT TGTATTATTA 120

TTATGTTnAA TTGACnCCTC CTAAATTTGC AAAGATAGCA ATTTAGGAGG CGTGTTTATT 180

TTTATTGACG TCTAACTCTA AAAGATATAA ATTAGACATT TACAAATGAT GTAAATAACG 240

CAATTTCTAT CATCGCTGAT AACAATTCAT GGTTTAATAT GCAATGAGCA TATACTTTTT 300

AAATAGTATT ATTCACTAGT TTTAACAATC AATTAATTGG TATATGATAC TTTTATTGGT 360

TATTTTTATC CCATAGTGTG ATAATTACTA TTTTTCATTC ATAATAAAGG TTTAAAGCAT 420

GTTAATAGTG TGTAAGATTA ACATGTACTG AAAAACATGT TTAACATAAT GATATAAGGA 480

GTGACGTACA TGATCCGTCT AGGTAAAATG TCAGATTTAG ATCAAATCTT AAATCTAGTA 540

GAAGAAGCAA AAGAATTAAT GAAAGAACAC GACAACGAGC AATGGGACGA TCAGTACCCA 600

CTTTTAGAAC ATTTTGAAGA AGATATTGCT AAAGATTATT TGTACGTATT AGAGGAAAAT 660

GACAAAATTT ATGGCTTTAT TGTTGTCGAC CAAGACCAAG CAGAATGGTA yGnyGACATT 720

TATAAAGGAG CTGCTACAGA ATTATTCAAT TATGTTATTG ATGTAGTTAA AGCACGTGGT 840

GCAGAAGTTA TTTTAACGGA CACCTTTGCG TTAAACAAAC CTGCACAAGG TTTATTTGCC 900

AAATTTGGAT TTCATAAGG 919

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 518 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

ATCATATAAA CCGGCTGCTT CTAAAAACGA AAATACTGTT ACTGGACCTA AAAATTTAAA 60

CCCGTATTGT TTTAAATCTT TAGATAGTTG TGTTGCAGTA TCATCAACTG TGATACGATC 120

AGAAGCATGT TCATACTGCA AATCTTTAGG CTTACCATTT ACATATGACC ATAAAAATTT 180

ACTAAAACTA CCATATGCTT GTTCAATTTT TAAATACCCT TGAGCTTGAT TAACAATTGC 240

TTCTAATTTT TTACGATGAT GAACGATATT TGGAAAAGTC ATTAAGCGGT CGATATCTTG 300

AGCGGTCATT TGTGCTACCT TTTCTGGTTC GAAATCATAA AATGCTTCTT CATAGGCTTC 360

TTTCTTTTTT AAAATAGTTA ACCAAGATAG CCCAGCATGT TGTGaTTCTA ATGCTAAAAG 420

TTTAAACAAT GCCTTGCnAT CATAGAGCGG TTGTCCCCAT ACATGGATCm TGATAGTCTA 480

AGTAGACTGG GATCTTTAGT ACCAAATGCG CATTCATT 518

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1539 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

CTTATTTAAA AGTAAATCAA TCAATGTATT ATAATCCGAA TAGTCCGCAT AAAGCTGGTT 60

TGCaGGCAAA tCAATTACTA CAACAAGCAA AAACCCAAAT TAATGCAATG rTTaATTCAA 120

AAACAAATTA TGATGTTGTA TTCACTAGTG GTGCAcTGAA TCCAATAATC TTGCTTTAAA 180

AGGTATTGCC TATCGTAAAT TTGATACAGC GAAGGAAATA ATTACATCCG TGTTAGAGCA 240

TCCGTCCGTA TTAGAGGTTG TAAGATATTT GGAAGCACAC GAAGGATTTA AAGTTAAATA 300

CAAAGTCGGT TTAGTAACAT GTATGTATGT AAATAATGTA ACTGGACAAA TACAGCCTAT 420

TCCACAAATG GCTAAAGTTA TAAAAAATTA TCCTAAGGCA CATTTTCATG TAGATGCGGT 480

TCAAGCATTC GGCAAAATTT CAATGGATCT CAATAACATA GATAGTATTA GTTTAAGTGG 540

ACACAAGTTT AATGGTTTAA AAGGACAAGG CGTCTTACTT GTAAATCACA TTCAAAATGT 600

TGAACCAACT GTCCATGGTG GTGGTCAAGA ATATGGTGTT AGAAGTGGAA CAGTTAATTT 660

GCCAAATGAT ATTGCAATGG TTAAAGCGAT GAAGATAGCT AATGAAAACT TTGAAGCATT 720

GAATGCATTT GTTACTGAGT TAAATAATGA CGTCCGTCAA TTTTTAAATA AATATCATGG 780

AGTTTATATT AATTCTTCAA CTTCAGGTTC ACCATTCGTT TTAAATATTA GTTTTCCTGG 840

CGTAAAAGGT GAAGTATTAG TTAATGCTTT TTCAAAATAT GACATTATGA TATCTACGAC 900

AAGTGCTTGT TCATCTAAAC GTAATAAATT AAATGAAGTA TTGGCTGCAA TGGGATTATC 960

AGACAAATCT ATTGAAGGTA GTATAAGATT ATCATTTGGG GCTACTACAA CTAAAGAAGA 1020

TATAGCGAGG TTTAAAGAAA TATTTATCAT CATTTATGAG GAAATTAAGG AGTTGCTAAA 1080

ATAATGAAGT ATGATCACTT GCTTGTTAGA TACGGGGAGT TAACATTAAA GGGTTCAAAT 1140

AGAAAGAAAT TTGTAAATCA ATTAAGAAAT AATGTAAATA AGTCaTTAAA AGGACTTGAT 1200

GGGTTTGTCG TTAAAGGCaA ACGAGATCGT ATGTATATTG AACTTGAAGA CCATGCaGAT 1260

ATAAATGAAA TAACATATCG ATTATCAAAA ATTTTCGGTA TTAAATCTAT TAGTCCAGTA 1320

TTAAAAGTAG AAAAAACAAT AGAGGCAATA AGTGCAGCGG CAATTAAATT gCGCAGaATT 1380

TGAAGaAAAC AGCACATTTA AAATTGATGT GAAGCGTGCC CGATTAAAAT TTCCCCAATG 1440

GATACGGTAT GGAATTACAG CGTGGAATTG GGGTGGTGCC AGTATTGGAG CACTTCGCCA 1500

TATTTCCAGT GGATGTCCAA CGTCCCAGnC CCAGGAATT 1539

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 968 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

ATAnCGTATA CATGTGTTCT TTAAAATTGT GATAAGGAGT TTAGGATGGT TTATTTAAAA 60

TCAATAGATG CCATTGGATT TAAGTCTTTT GCAGATCAAA CCAATGTTCA ATTCGATAAA 120

GGTGTAACTG CAATTGTTGG TCCAAATGGA AGCGGTAAAA GTAATATTAC AGATGCTATT 180

ATCTTCTCAG GTGCAGAACA TCGCAAAGCT CAAAATTATG CTGAAGTACA GTTAAGATTA 300

GATAATCATT CTAAAAAGCT CAGTGTTGAT GAAAACGAAG TTATTGTAAC AAGAAGATTG 360

TATCGAAGTG GTGAAAGTGA GTACTACATA AATAATGACC GTGCAAGATT AAAAGATATT 420

GCCGATTTAT TTTTAGATTC TGGATTGGGA AAAGAAGCGT ATAGCATTaT CTCGCAAGGT 480

AGAGTTGATG AAATACTAAA TGCTAAACCA ATTGATAGAC GTCAAATTAT TGAAGAATCG 540

GCTGGTGTAC TTAAATATAA AAAACGTAAG GCTGAATCAT TAAATAAACT TGACCAAACA 600

GAAGATAATT TAACGAGAGT AGAAGACATT TTATATGATT TGGAAGGTCG CGTAGAACCT 660

CTAAAAGAGG AGGCAGCTAT AGCTAAAGAA TATAAGACAC TTTCACATCA AATGAAACAT 720

AGTGACATTG TAGTTACAGT sCACGATATT GATCAATATA CAAATGACAA TAGACAATTA 780

GATCAACGTT TAAATGATTT ACAAGGCCAA CAAGCAAATA AAGAAGCTGA CAAGCAACGT 840

TTAAGCCAAC AAATTCAACA ATATAAAGGT AAACGTCATC AACTTGATAA TGATGTTGAA 900

TCgCTTAATT ATCAATTAGT AAAAGCTACG GAAGCCTTTG AAAAATATAC GGGACAATTA 960

AATGTTTT 968

(2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

TTGTGTGTAT GCATTCAATG TGCTCTGTTT GTAAATGGCT AGCTATATAA TTTAgGATTC 60

GAGGATCGTC ATCGACAACA AGACATTGCA CCATAGCTAT AAACTCCCTT ATCTTTTTCA 120

TTTATTATAC ATGTAAAATA TTTTTGCGTA AAAAAACAAT TGTTCATATT GAGTTCATAT 180

TTCAACCTTA TACTGACGCT AAAGAAGAAA TAGGGAGAAG TGAATCGATA TGAAATTAGC 240

GATAAAAGAG ATTATGTTTT ACAAATTTCG TTATATTTTA ATCACATTAA TCATTCTTTT 300

ATTAAGTATT ATGGTGTTAT TTATTAGTGG TTTAGCTCAn GGGCTTGGTA GGGaGAATAT 360

TTCGTwATTT GAACACTTTG GATAATGATG aaTATGtTGT TCaAAAAATG AAAGAGCCGC 420

aAATTGaGAA ATCGCA 436

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2554 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

ATGTTTTGTC AATATCAATT GTTTGAGATA AATCCGCTTG TATAAAACGA ACTTTATCAT 60

CATTAAATTT GCTAGTTAAT TCATTTATAT CAGTACGATA ATATTGCACA TAAACTTCAA 120

ATCCATCAGT TAATAATTGT TTGACTATCT CAGAACCAAT TGAACCAGAA CCACCTAATA 180

CTAATGCTTT CATTACTTTT TAATCTCCAA ACGACTATCG ACTTGCTGAT CTAAATTTAA 240

ATATAACGAT GACGTTTCGT TAATACTATC TAACGTGATA TTTTCAACAA TGTCTAACAT 300

GTCAAACACG CTAACACCTT CAAAATACAA TTTAGTATAT TGATTAGCAA TATATTCAGG 360

TGAGTTTAAA CTTGATATGA ATTCACCTAT AAATTGCTTT TTCAAAAGTT CAAATGCTTC 420

TGCATCTTGG AAAtTGCCTT TTTTATCACG CAACTCATCT AATAATAATT TTTTTAATTT 480

ATCTGGTTCT TCAGTAGCAC TTGTCACGAT TGAAAAACTA TACGTCGGCT CTAGTACAAA 540

TTGATAACCA AATGTATCAT CGATAAGTCC TTCGTTTAAT AAATTCTGAT AAAAATCTGT 600

TTCTTCCCCA AAAATTAACT CAAAGAATAA TGACATTTCT AAATCACGTT GTACATATTT 660

TTGAGGCGCT TCTTGTAATG GTTTATTTTT AAAACCAAGC ATTAGTCTTG GTGATTGAAT 720

TTTCATAGAT TCAGTAACAA ATGCTTCTTT AACATCcTCC GGTTCATCAA CAAGTCCTCG 780

TTCGATTTTG GGTTGGTTAA CTTTATTACG AGCATCCTCG TGTTGTTTTA CTATTCgACA 840

TATTGCTTCA GGATCCACAT CGCCAACAAC AAATAAAACC ATATTTGATG GATGATAAAA 900

CGTTTCATAA CATAGATACA AATCATCTTT TGTAATATCG TATATACTTT CTACACTACC 960

GGCAATATCA ACACGTATTG GATGTTGTTG ATACATTGCA CGCAAtGTAT TaAACATTAA 1020

TTTATATCCA GGTTGCTCTT GaTACATTTT TATTTCTTCT GCAATAATAC CTTTTTCTTT 1080

ATCAACAGTT TCTTTTGTAA AATAAGGCGT TTCaACCATT GTAAGTAAAC GTTTAATGTT 1140

GTTTTCAATA TtATCAGTTG CACTGAACAA GTAGCTTGTA CGATCAAAGC TTGtAAACGC 1200

ATTTGCTTGT GCGTTATCTT CAGCAAACGC AGTAAATAAG cTTCTTCTTC TTTTTCAAAT 1260

AATTTATGTT CcTAAAAAGT GAGCAACTCC ATCAGGTACA GTAACAAATT GGTCTTGTCC 1320

AAGGGGTTTG AATTGATTAT CTAATGAACC AAATTGTGTA GTGTAAGTGA CAAATGTCTT 1380

TTGAAAACCT GGTTkGGGGA TAATAAATAA TCGTAAACCA TTTTCTAATt CTTGTTCGAA 1440

tACTCTTTCG TCTATTAATT CATAATAACG CTCTTTCATT ATTTATCCCC TCCTTTTGTC 1500

AACACATAGA TtGTATCTAA AAATGCTTTT TCAGCAACAG AAACAATATC TTCGCGACTT 1560

TTATGCATAA TCTCTATAAT ACTTTTCGGA CGATCTTCAG ATTCATATCG ATGAGAAATG 1680

ATTACTTTTT TAGCTAACTC TAATTTTTCT TCAGTGAAAT CTCCTGCTTT TATTTTTTCA 1740

AATTCACTTA TAATAGTGTC TTTTGCAGTT TCGTACTTAT CACTTGAAAC CCCACTCAAA 1800

ACAAATAAAT AGCCATTTTT GCCATCAATT TGTGAATGTA TAGAGTACGC TAAACTTTGC 1860

TTTTCTCGCA CTTCATTAAA TAAAACAGAT GAAGGATCTC CTCCAAACAT CATGTTAAAT 1920

ACAACAAAGG CAGCATATCC ACTTTGTCCA TATTGTGTTG GAAAACGGTA TCCCATATTT 1980

AATTTAGCTT GATCCACGTC ATCATATTCA ACAATATAAT CAACTTCTTC ATCGTGTAAA 2040

TGATGAGTAG AATGTTGGAA TTGATGTTTA TCGAATGGTT TAAGTGCAAA TTTTTCACGT 2100

ATTTGTTTCT CAACACTTTC AGGTTCTACA TTGCCGACAA CATAAACAGA ACATTGATCA 2160

TTATTAATCA TTGATTGATA TGTATGATAT AGTGTTTCAG CAGTAATATG TGGGATTTGT 2220

TCTAGTTGTC CTGTAGATAA GTATTTATAT GCTTCATTTT CAAACATATG GTCGAGTAAT 2280

TTTAAAAACG AATATTGTGC TTTATTATCT ACCATTGCTT CTATTTTTTT GGCTAATAAT 2340

GTTTTCTCTT GGTTAACAAA ATTATCATTG AATGCTTTAT TTTCAATTAA TGGATTCCAA 2400

ATGATTTCTT GtAATAAATC TAATCCTTGa TTAAATAATG AwTCACCGkT TCyTAAATAA 2460

CGkkCaTTAA caATTyCTAA tGaAAATGtA ATgACaTGCT GaTCTTTGAA TTTTGAAATT 2520

GTACTATTCA CATACGCACC ATATAAATCG GCTA 2554

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1424 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

TnTCGCTATT TTnAATTGGT TTTGTATGGT TTAAGTTATA TCAATATACA ACAnACCCTA 60

AAGCTGATAT CCCAGGTATC ATTTTTAGTA CGATTGGTTT TGGTGCTTTG TTATATGGTT 120

TCTCAGAAGC TGGCAACAAA GGTTGGGGTT CAGTAGAGAT AGAAACAATG TTTGCGATTG 180

GTATTATCTT TATTATTCTA TTCGTTATTA GAGAATTAAG AATGAAATCA CCAATGTTGA 240

ATTTAGAAGT ATTGAAATTC CCaACATTTA CATTAACAAC AATTATTAAT ATGGTTGTAA 300

TGTTAAGTTT ATATGGTGGT ATGATTTTAT TACCGATTTA TTTACAAAAT TTACGCGGAT 360

TcTCAGCATT AGATTCCGGA TTGTTATTAT TACCTGGTTC TCTAATTATG GGTCTACTAG 420

TTGCTGTAAT GACTTATGCA ACATGGGAAT TAACTAAATT AAATATGGAT ACACCATATA 540

TGACAATCAT GGGTATCTAT GTACTTCGTT CATTTGGTAT GGCATTTATA ATGATGCCAA 600

TGGTAACTGC AGCTATTAAT GCGTTACCGG GACGACTTGC CTCTCATGGT AATGCTTTCT 660

TAAATACGAT GCGTCAATTA GCAGGCTCTA TAGGTACAGC AATCTTAGTT ACTGTAATGA 720

CAACACAAAC TACACAACAC TTATCAGCTT TTGGGGAAGA GTTAGATAAA ACGAATCCTG 780

TTGTACAAGA TCATATGCGT GAATTAGCAT CACAATATGG CGGACAAGAA GGCGCAATGA 840

AAGTGTTACT ACAATTTGTA AATAAACTAG CAACGGTTGA AGGTATTAAT GATGCATTTA 900

TAGTTGCAAC GATATTTAGC ATCATCGCCT TAATTTTATG TTTATTTTTA CAAAGTAATA 960

AAAAAGCAAA AGCTACAGCT CAAAAGTTAG ATGCAGATAA TAGTATCAAT CATGAATAAA 1020

TAAAATAAAT TAATTGAAGT GTGACTAATC AAAAATTATG TTGTGGGGAC ATGATTTTTA 1080

AAGTATCGGT GCCAAATATG GTTATCGATA CTTTTTTTAT TTGTTGATTT ATAGAATGTT 1140

AGAGGAATTA TATTAAAATT TGGCATTGAC GTAGTAGGTC ATTAATAAAG AAAAAGCAGG 1200

AAGTGGGTCA ACGAAATGAA TTTTGTGAAA ATAACATTTC TGTCCCAATC CCTACTATAT 1260

AACATTATTT TAAACGAGGC ATGCGATTAC GGAAGAATAA GCTTATAACA AGTAAACCGA 1320

TGGTACAGCC AAGTAAAATG ATGCCGTTAT GAATAGCGTC ACTTgCTGTA ATCACTTGAT 1380

CTGGTGGTAC ATTTAAATAA TATTTTTTGA AAACATCTGC AATT 1424

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

TCTCCCATGT TCTGCTAAAT GACGCATCAC TTTTACTTCA TGAGGCGTCA ATACACGTCC 60

TTCACCAGCA TTCAAACCGA CAACATTTAA AGGCCCATAT TCAATACGAG ACAGTTTCGT 120

CACTTGATGA CCAAAATGTT CGAACATTCT TCTGACTTGG CGATTACGAC CTTCTGTAAT 180

TGTAATTTCA ACCAATGTTG TGTTTTTATC TTTATCTTGT TTCTTAACTT TCACTTCAGC 240

CGGTTGCGTC ATACCATCTT CTAATTCAAT ACCTTTTTCT AGCGCTTTCA CTTCTTCTCT 300

CATTAAATAA CCTTTTAATT TCGCAACATA TTTTTTCTTA ATTTGATATC TTGGATGTGT 360

CATTAAATTA GTAAATTCAC CATCATTTGT GAGTAATAAC AATCCAGAAG TATCATAGTC 420

ACGTCCTCTA TCATCAGATA CACTTGTkAT CACTTGAGTT GGkTTATGGA AkAAAATGkA 540

AAtTTTGTCT TCTAGTTCTA TTTTAATACC TTCAACTTCA ATCGTATCTG ATGGCTTCAC 600

TTTTGTTCCT AATTCAGTGA CAGTCGTACC ATTCACTTTC ACTTTTCCTT CAGAAATTAA 660

AGTTTCTGCC TTACGT 676

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

GAAACGGTTC TACCAAAAAA CAGTAAGGGC TAAACCCAAT CATGGTAAGA CAAAAAGTAC 60

AAATAGCCAT GCCCAAGTTG AACTCGCTGT ACGCCTATTT CTTTCTAAAA AGATAATAAT 120

AAAAGCCAAT ACTAAATTAA TGATGAATCC AATGGCTAAA ATAATAGTAA ATAACGTTCC 180

TAAATCGTTT GAAAATGTAA ATCGCATAGT CTTTTCTCCT ATAAAGAAAG GCACAAAAAA 240

ACATTTTGCA CCTTTCACGT CATATTATTT ATTCACAGAT AAAGTTAAAA TTGcATTGAA 300

TTCTTCTTCA TTATTTGGGA ATGTTCTTTC TTCTATTTCT TTAATAGTAA TATTTACTAA 360

TTTTAAATTT GTAGCTTCTT CAGAACTTAA AAAAGCATTA ATGTTTTTTT CTAATAACTC 420

kAAAGTCTCA GCTGtAAAaG TTTTAAGTTT AATT 454

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 894 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

ACGATATTAC CACCCTCTGA AATAACATCA ATCATGTGAT CTGTAAAGTC CCAAGGATGA 60

CTTGTTGTGA AACGAACTCT TGGAATCGCT ATTTTAGAAA TTGCTTGTAA AAGATCTCCT 120

AAGTCATATT CTATATCCTG TAAATCTTTA CCATAAGAAT TTACATTTTG ACCTAAAAGC 180

GTTATTTCTT TGTAACCTTC ACGAGCAAGT TCACGTACTT CATCTATAAT GTCTTCAGGT 240

CTACGGCTTC GTTCTTTACC TCTTGTAAAT GGAACAATAC AATATGTACA AAACTTATCA 300

TCAATAACGT CTCCTTCTTT AGACCATACT TCAACAACCA TTGCTTTAGA TAAGTATGCT 420

TCTTCTAAAA TTTCTGGTAA ATGATGAATA TTATGTGTAC CAAATATCAT ATCTACATTT 480

TGATACGATT TTAAAATTTT ATTCACTACT GACTCTTCTT GTGACATACA ACCACAAACA 540

CCGATTAAAA TATCAGGTCG TTCTTTTTTC AAATrCTTCA AATTACCTAT TTCACTAAAC 600

ACTTTGTTCT CGGCATTTTC TCTAATCGCA CATGTATTAA TTAAAATAAC ATCTGCAGTG 660

TTAATATCAG TCGTkGCTTG aTAGCCTAAT GCyTCmAGTA TACCAGCAAT GACCTCAGTG 720

TCATGTGCAT TCATTTGACA TCCATATGTT TTAATTAAAA ATGTACGCTC GTTCCCCATA 780

CCGCGATATT TTyCATCAAT TtGGgAAATC nCTATTATAA CGAACTTCTk GTtTACCnCC 840

TTTTTTnCGC TCCTTTAAAA TTAAGGCGGC TGATAAACAG GTCCAAAATA TTAC 894

(2) INFORMATION FOR SEQ ID NO: 570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

TATCAATCCC ACAGCACATG CTGAACAAGA TCAAACATGG GAGAAGATTA AAGAACGCGG 60

TGAACTTAGA GTGGGTCTTT CTGCAGATTA TGCACCAATG GAATTTGAGC ATACAGTTAA 120

TGGTAAGACT GAGTATGCAG GTGTAGATAT TGATTTAGCT AAAAAAATTG CGAAAGATAA 180

TAATTTAAAA TTAAAAATCG TCAATATGTC ATTTGATAGT TTGTTAGGAG CTCTTAAAAC 240

TGGAAAAATT GATATTATTA TTTCCGGAAT GACTTCAACG CCTGAACGTA AGAAGCAAGT 300

TGATTTTTCA GATTCATATA TGATGACTAA AAATATCATG CTTGTAAAGA AAGATAAAGT 360

TAATGAATAT AAAGATATCm AAGACTTTAA TAATAAAanA GTnGGGGCAC AAAGGGACTG 420

AACCAGAAAA AATCGCTCAA C 441

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

AAGTCGTTCA TCTTTTTCTA CAAGGGTGTA AAAATAATCA ATCATATCGT ATAACGCTTC 120

TTTACCAATG ATGTCATATG GTGTTGTTGT CATTTAATCA CCCATTTTCA AAAATTTACT 180

GTTACGAACT TAAGTTAATA TATAACTAAT ATAACATGAT TTTAAACATT TGAAAGAAAT 240

ATGCATATTT GCCAATTTAA TTTATATTGT TTGAAAGTGT TTCTTTTTTC TTGAAAAAAC 300

GTTGAACTTT ATTTAAAGGT tGATGATGTT CGAGGTTTAG TTCGTTtAAT AAAGATtGGA 360

ACTTTTGTAA ACCTTGATTA TAGTCTTTAA CTTCGAACTC TAACTCATAA TCCGTAGTAT 420

CGAAATACTC ACTTTTATCT AAAACCAGTA AATCACCTTT ATATTTAGTT TCTTGGCGAT 480

ATGTCGTTAA TGCACCAAGT ATTGATAAAG TTGTATCTTT TACACCAAAC TGTTCAACTA 540

TAATTTGACG AATGTCATCT GGAAGATTGT CGTTTGAAAT AATCAAGTTC ATCTCTGGTT 600

TAATGTCGAC GATATAGTTG TATTCTAATA GACCAACCTT TGCTGGTGTC TTTAAAGTCA 660

TTTCATATTG ATTGTCTTTA ACTCTTATGC GTAGTGCAGA GCGATGTTCC TTTAATTTGA 720

AATCGGGTGT ATCAATATAG TAATTGACTT GCTTAmAAAG CACACTGTCT TTAAAATATT 780

TCTCTTGCAA TTTATTATAG ATTGAtGCAG TTATCATTTG TtTAAATTCT ATtTCATGAT 840

TTGTTGCCAT GATATGTATA CACCTCGTAT CAAATTCAAT TTATCTTAAC TATATTATGA 900

ATGACAAAGT TGAATTTTAA AAGTAATTTC CTTTATCTAT TATCAATGTT AATTTGACCA 960

TTAAAAATAG TGTTCGTAAG TGTTTTGTAT TATTGaATTG TGTTAAAATG TTATGGAATA 1020

AGAGGAGGAT TAAGCATGsG TTTwTATATT AATGAAATTA AAATTAAAGA TGACATACTT 1080

TATTGTTATA CAGAAGATTC TATTAAAGGA TTATCTGAAG TAGGACAAAT GCTCGTTGAT 1140

AGTGATAATT ATGCCTTTGC GTATACATTA GATGATGGTA AAGCGTATGC TTATCTCATT 1200

TTCGT 1205

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 570 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

TGAAGAAATA GCAATGATGA AATGCCGTAT GTTATATGAG ACGGGGTCAT TTCTTGAATT 60

AAGAGAAGAA ACAATTGTCT TATTGAAAAC TGGCATACAA CAATATGATG CATTGATGAT 120

TTATTACGTG AAAAGTTTGA TTGGTTTGGG ACAATATTTT GAAGCGGTAG AAGTAATTCA 180

ATTTGCTAAG TCAAAATTAA TTGAAGATGA AAAACGATTG ACTCAGTCAT TAGCTGATTT 300

TGrTACGTTA TCAATGAGGG AACAGACGCA CTTGATTTTG AAGTTAATAG ACAATGGTCA 360

TTTTCAATTT CAAGAAACGG TATTATATAT ATkAAaAyCT AATaCGTACa GTtATAACCT 420

CATTAGTTTA ATGATTGAGT ATTTAAGGTT CGCAAATTGT ACACAAGAAC TGACAATTGA 480

AAAGTATGGT ATGGATGTAA CTTTTGTACC AGCTAATTTA AAAGGGCTAG AACATACAAC 540

ACTTAAAGAA AAAGTTATAC CTAACGTTAT 570

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 939 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

GTTGAATGGT TAGCAGCTGC AGTTGTATTA TATTTCTGTG GTGTAATTGT TGACGCTCAT 60

GTATCATTCA TGTCCTTTAT TGCAATATTT ATCATTGCTG CATTATCAGG TTTAGTCAGC 120

TTTATTCCTG GTGGTTTCGG CGCTTTCGAT TTAGTTGTAT TACTAGGATT TAAAACTTTA 180

GGTGTCCCTG AGGAAAAAGT ATTATTAATG CTACTTCTAT ATCGTTTTGC GTACTATTTT 240

GTACCGGTAA TTATTGCATT AATTTTATCA TCATTTGAAT TTGGTACATC AGCTAAGAAG 300

TACATTGAGG GATCTAAATA CTTTATTCCT GCTAAAGATG TTACGTCATT TTTAATGTCT 360

TATCAAAAGG ATATTATTGC TAAAATTCCA TCATTATCAT TAGCAATTTT AGTATTCTTT 420

ACAAGTATGA TCTTTTTTGT AAATAACTTA ACGATTGTkT ACGATGCTTT tATATGATGG 480

AAATCACTTA ACGTATTATA TTCTATtGGC AATTCATACT AGTGCTTGTT TATTACTTTT 540

ACTGAATGTA GTTGGTATTT ATAAGCAAAG TAGACGTGCC ATTATCTTTG CTATGATTTC 600

AATTTTATTA ATCACAGTGG CGACATTCTT CACTTACGCT TCATATATTT TAATAACATG 660

GTTAGCTATT ATTTTTGTTC TGCTTATTGT AGCTTTCCGT AGAGCGAATA GGTTGAAACG 720

CCCAGTAAGA ATGAGAAATA TAGTTGCAAT GCTTTTATTC AGTTTATTTA TTTTATATGT 780

TAACCATATA TTTaTTGCTG GAACGTTATA TGCATTAGAT ATTTATACGA TTGAAATGCA 840

TACATCTGTA TTGCGCTATT ACTTCTGGCT TACGATTTTA ATCATCGCTA TCATCATAGG 900

TATGATTGCA TGGTTGTTTG ATTATCAATT TAGCAAAGT 939

(2) INFORMATION FOR SEQ ID NO: 574:

(A) LENGTH: 1059 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

GAATTAATTA AATATTACAC ACAGCCTCAT TTTTCATTTT CAAATAAATG GCTATATCAA 60

TATGATAATG GAAACATTTA TGTTGAACTT AnGAGATATT CATGGTCAGC ACATATATCT 120

TTATGGGGCG CTGAAaGTyG GGGAAATATT AATCAGTTAA AAGATCGTTA CGTAGATGTG 180

TTTGGACTAA AAGACAAAGA TACTGATCAG TTATGGTGGT CTTATAGAGA GACATTTACA 240

GGTGGCGTTA CACCAGCCGC AAAACCTTCT GATAAAACTT ATAATCTTTT TGTGCAATAC 300

AAAGATAAAC TACAAACGAT TATTGGTGCG CATAAAATAT ACCAAGGCAA TAAACCAGTA 360

TTAACATTGA AAGAAATCGA TTTCCGTGCA CGAGAAGCGT TAATAAAAAA TAAAATATTA 420

TATAACGAAA ATCGTAATAA AGGTAAGCTT AAGATCACCG GTGGCGGTAA TAACTACACT 480

ATTGATTTAA GCAAAAGATT ACATTCAGAT CTAGCAAATG TTTATGTTAA AAATCCTAAT 540

AAAATAACTG TTGACGTCCT CTTTGATTAG TATATGAAGG TGACTTATAC TTCATGCACT 600

TTAATTCCAA ATCAGATTAT TTAAATGATA ATTTTTAAAG TGTATGATGT ATATAATAGG 660

TAAAATTTTC TATATATTTA AATGGAATTG GGAGTAGGAA TGTGACAGAA ATAGTATTTT 720

ATAAAATTTA TTCtTGTCAC TCCCCAACTT GCACATTATT GTAAGCTGAC TTTCCGCCAG 780

CTTCTATGTT GGGGCCCCGC CAACTTGCAT TGTCTGTAGA aTTTCTTTTT GAAATTCTCT 840

ATGTTGGGGC CCCGCCTATA ATTGAAAAAT GCTTGTTACA TGGGCATTTT CATTCGGTCA 900

ACTACTACCA ATATAATATT GtAGaGCCTA AGACATTGAT TTATTATGTC TTAGGCTCTA 960

TTCCTTCATT TAATGATTAA nTTATTATAG CAATACTTTA TTGTCCCATG ATTAGTGTTC 1020

TTTTAATGAG ACATAGTAAC TATAAAGTTT AATAATCGT 1059

(2) INFORMATION FOR SEQ ID NO: 575:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 574 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

GTTTGCTTTA GGTCCTGTTT CATATTTATA CTTCGAAGGA TTTACCTTTT TGaAGTCTGG 60

TTCAACTkGC TTTTTATTCT TTTCGAAATC AGCTGGTTGA GTAGTTATGA GTTCATTATT 180

TTTATTAGmA TAAATCTTAC CATTAACATA TTTATAATCT TTTGTTATAA AGTCACCATT 240

TCTGAATGGA ACTACTTGAT TATGACCTTT AGAGAATAAA TCAGTACCGA ACATTAAATA 300

GTTCTTCGTA TCTATACCAG CCAAATGTAA AATTGTTGGC ATTACATCGA CTTGACCAGC 360

ATATTCATTA TTGATACCAC CAGATTTACC AGGGATTTTA ATCCAGAAAC CAGTTCTGTT 420

TAAATCTGTA AATTTAGCCG GTGTGATTTT TTCACCTAAT AGTTTTTCCA TGGCATTGTT 480

ATGGTTTTCA GAGATACCAT AGTGGTCACC ATAAATCATA ATCACTGAAT TGTCATATAA 540

TCCTTTTTTC TTCAAGTCAT TAATATATTC TTCT 574

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 796 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

CAATGTTTTA TAGTACAATA TATTTTnAAT AATACTCGTT AAGGAGAATG ATATGATATC 60

AATTCACGCA ATTTCGACAG GAAAAATCCA AGATTTGCCT TATAGCTCGA AAAGACCGAT 120

GCGCTCTGCT TTAGATAAAA CTAAGATTTC ACAAACAACA TGGTTATCTT CAACTGGTTT 180

CACTGGTGAT GAACAGGCTT ATAAAGATCA TGGTGGACCA CATAAAGCAG TTTGTGGGTT 240

TAGTAAGCAT AATTATGCAC TGTATCAAGA TGATTTACCT ACACTACCTA CTCATGCGAT 300

GTTTGGAGAG AATTTAACAT TTGATTATTT AGACGAATCT GATGTTTACT TTGGTAATCA 360

ATATCGTTTA GGTGAAGCGT TAATTGAGGT TTCTGAAATT AGAGAACCAT ACTGGAAAAT 420

TCAAGCAAAA TATAATATTC CTGATTTAGT GAAGCGCATG TCTACATCTG GTAAAACAGG 480

TTTCTATTTC CGGGTATTAA AACAAGGCTA TGTATCTCCA AATGATCAGC TTTACTTAAT 540

ACAAGAAGCA CCAATCGAAC ATCGTTTATC TGTACAACAG CTTAATGACC TTTATTATAA 600

TGATAGACAA AATCAAGaTA TGTTACGATA TGCACTAAAC AATCCATTTC TGTCACCAAC 660

AAGACGCGAT AAACTTCAAA AAATGTATAA CAGAACATTG GAAATAATTA CCTTTCATTn 720

ATAAGTGTTA AATGAACTTT TCAAAACAnA AAGGAATCAA CTTCACACAT CGTTTGTATG 780

AATAGTCTTA TCTATA 796

(2) INFORMATION FOR SEQ ID NO: 577:

(A) LENGTH: 1095 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

AGAAATTATG ACAAAATATA AAGATGGAAA GTTAGTTTAT GCATCAGTCG AACCAGGATC 60

TTACGTAATA CATAAAGATG ATGCAATTAA ATATGACGAT TATTCTAAGT TAAAAAAATT 120

AAGTCAGCTA ACTAAACTTG ATCATCCAAA ACCAGTTCCA TATAGCGTaC TCAAATCAAA 180

TCTTTCGGAG TACCTTTAAC AAGCGTTTCA TTTATGACAC ATGGATCAAA GGATACTAAA 240

GATGAAGTGT TGCCGGCATT GGCCTATTTC ACTTTTTCAC CAAAAAATTA TGAAGACAAG 300

TCTAATCCAG ATCCAAAAGT TTTAAATTTA GTACATATGG ATTTCTTAAA TGCATCTAGT 360

GATTTTGGTA ACGCACATTT TGTTGTTTTA AGTAAATATA TTAAAGAGTA TGAATCAAAC 420

TATGAAACAG CGTCAGATGA TTCTTTAAAA TAGTATTTAC TGTGTGAAAA ATAAATAGTG 480

TACTACATTA AATAATCGCA ATAATAATCC CGATAAACAA TCAGCATTAC TGCTTATCAC 540

ATAGAGTTCG TAATAACTAT AACTCTATGA TTCGCAAATA ATAAATGATT GTCATCGGGA 600

TTTATTTTTA TCAATTTATA AAGTGACATT ACCTTGTTCA TCAGCAGGTT TGAAAACAGT 660

AATCACTGCA CTAATAATTG CTAAAATGTG TGGGATACCT GTCCAACAGA ATATTAAGTG 720

TAGAATACCT TGCATATTCT TGCCGGCATA AAATTTATGA ATACCAAAAC TACCTAAGAA 780

CAATGCTAAT AAAATATAAA TAACTTTGTT TACTTGCATT TCTTTCCCTC CAGTTGAATT 840

GCTTATAATG ACATTAGCTT CTCTTTTTAT TATACCCACT TTTAGTTCAA ACATTCTAGT 900

TTAAGCATTC CCAATCATCT AAATTTCAGT TATTCAATCC TTACAATAAA TTTAGGATTA 960

CATTTCAGTT GCATTGTATT ATTTTACGTG TGAAATATAC GTAATGAATC ACATGACAAy 1020

CTyCAAATTG AAAAATATAC ATTCTATGAT GTAAGGTCGC ATTTTTAATA TATTTACGTn 1080

AAAATAGTTT GGATG 1095

(2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

ACTGCCAAAA TAATCATAGC CATGTTCTAC AGCTGCTTTC GCTACAATAT CCAAACGCAT 120

TTCAAAACAA GCGGTACAAC GTAAGCCGCC TTCTTTTTCA TCAGCTAATT CTTTATCCTT 180

CACCATTTTC ACAAACTTAT GTGGTTCATA AGGTGCTTCA ATATACTTCA CATTCGCACC 240

AGTCTTGCGA TTAAAATCTT CCACAAATTG TTCTTGCACT TTAGCACGTC GTAAGTACTC 300

ATTTTTCGGA TGAATATTTG AATTCGCGAA ATAAATTGCA ATGTCTGCAT ATTGTGTTAA 360

AAACTCTAAT GTATATGTAC TACAAGGTGC ACAACAACTA TGCAATAAGa TTTTAGGTCT 420

GATTGCTTCT CTTTCCCACT GsCCGATTAA TnTCTTCAAC ACCTTGTCCA TAATTAATTT 480

GTnGATTTn 489

(2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

CGTACTGCAT CATTTGTTGA AAAATTTGCA AACTTCTTCA AGATGTTATG GCTTAGACTT 60

AAAGCGATGA AGCACTACAA AGCCTTAAAT AAAGAATCTA AGAAGCAAGA ATTTGAAAAT 120

TCATTCAAAG ATGTTCAAAA AATTATGCGT ATTGTGAATC ACAATATTAT TTTACGCTTA 180

AAAGAAGAAC AAAATAGTAC AAATGTACTT GAGGTTAGCT TAGTCATTAA TCATTACTAT 240

GATATGAGTC GCTCATTAAA GTGGCGTGCA CAACGTCGAA AAGAACGTCA AGAAAACAGC 300

AATCAAATCA TACCGCAAGC TATGTTCCAT AACCACAAAT TGGAAGCATT GTACTTACAA 360

CGTCATCTTT TAGATGAATT AATTCGCAAA AATAAAATCA ACAATATCGT TGCAGCTCAA 420

ATTCGAGAAA ATATCAATTa CAACGAAATT GTCTTGTCTT TACAGTCCAA ACATTaAGCA 480

AGaCwTaCaw TmCCCCCGTA CATATGAGAC AAAGTCATTA TCATCTCATA TGTACGGGGT 540

TTTTATATTC AACATCAAAA AATCAGATTG ATGAAAAGTA AATAACCTTT CATCAATCCG 600

ATTTGATTAT AGAATCTATT TTTTAAGTTT AAATGGAATT GTACATACGT TAACATTCTT 660

TTGATAAATT AAATACAATT TCATACGCAA ACTAGTTTGA TTGTGTAATA AATTATGCCA 720

ACGTTTCTTA GTAATAAATT CTGGTATCAC TACTGTAATC ATATAGTTTT GATCGTTGGC 780

TTTACGATTA ATCTTATCGA TAAAACGTGA AATTGGTCGT ATAATACTGC GATATTCCGA 840

ATGTAAAATA ACTAATCTTA CATCTGGGAA ATGACGTTTC CATTTCTCTT GGAATGCTTT 900

TGCGTAATAA ATAGACTTAT CAACTGCTGT TGTAATACTT GTTATCGGCA CAATTGCTAA 1020

ATTACGATCT ACCACGTCCA CATTAAGAAC ATCAATGTCA GAACGTAATT GTTCTGCGAT 1080

ATCTCGATAA TGkTTGkTAA TTTTCAAGAA GAAAATCACC ACGAACGGCA AGAAAATAAG 1140

TATCGGCCAT ACTTGGCTAA ATTTAGTTAT GAGTAAAATC cATAAnAACA ATAAATGTCA 1200

CGATACCACC AAGTAAGTTC ACAGACAACT TACTTAACCA ATTCTTAGGA CGTTCATGAA 1260

TCCATTTAAT AACCATACCG AATTGTG 1287

(2) INFORMATION FOR SEQ ID NO: 580:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

GCCTCCTTTC CTATATCCAT GGGTGTCCTA GTTGGGAATG GCTTATTCCC TATCCCAAAC 60

ATCTGTCAAT TCAAGACTAT CACTGTATAC TAAATCGCCT nTCTATACnT CCATnCATTT 120

CATTTTCCAG TTGGAACAAT TTGTTTAATT ATTTTAAATA TCATTATCAA TCCAGAAGTA 180

TTTACTATTC ACTTTTACAA TAATCAATCA TTTAACTACA CATGGGTAGT CGGTGGTTTG 240

CTTGGGGTTA GCTTTTTAAC TGGCAATTTA TTGTTATTGC CAAAATTAGG TGCAACATTA 300

ACTGTAATTG CAACAGTTGC GGGTCAAATT ATTATGGGTG TCATTATTGA TACATTTGGA 360

TTATTTGGCG CTACAATTCA TGATTTTAAT TTAATTAAAG CAATTGGAGT ATTGTTACTC 420

ATTGTCGGCA TCGTCATAAT GAATCAATTT AACAAGAATA ATTTATTACT AACTGATCAA 480

AAGTATTTAC TGTTTTGGCT TCTATTAGGA TTTATTTTTG GTTTCTTTCC ACCTATTCAA 540

ACGACAATTA ATAGTGCTTT AGCTAGTCAT ACTCATTCAC CAGCCTTTGC ATCATTAGTA 600

TCATTTACAA TTGGGTCAAT AGCGCTATTG ATTTTAACCG CTATTTTTAA TCGTTCTTTA 660

AAACTAAAAA CAAGTCATTT AAAATTCGGT AAATTAAAGC CTATCTATTT TACTGGCGGT 720

ATACTTGGCA TGGCTTTTGT AACAGCTAAC ATTATCTTAA TGCCTCATAT GGGTGCAGCA 780

TTAACAACAC TTATTGGGAT GTTTGGCCAG ATTCTAATGG GCATATTGAT AGATCACTTT 840

GGATTATTTG GTTCACCTAA AATAGCAATG ACATCCAGAA AAACTATTGG TCTATTATGT 900

ATTTTGACAG GCATTATACT TTTAAGATTA TTTTAAATTA ACTTTTAGCT TATCATTTTA 960

ACTTGTAATT ATTTTTAAAA GTGATAAGCT ATTTTTTTGT GGTCTAAAAA TCTTTAGAAA 1020

CAACTCATTC TTAAGACCTA AATTAATGTT ATnTTTTAAT AATTTACACC AAATTAATAG 1140

CAAAAATTAT GTTATTCGTG CTAATATTTC ATAGTTGGTT ATTCAATTAA TTAAAAATAA 1200

GTCAAAATGC ACAACTTTTT ATn 1223

(2) INFORMATION FOR SEQ ID NO: 581:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

CACCTTTTTA TCATGCTTAG TTATCAATAA ATCTATATTT TGCTGTTTTA CAATTTTTTT 60

AACTTTATCA ATCTCATTAT CTTGGACTAA ATAAATATAT GATCTTGCAT CTGTTGCTAG 120

AGCTTGTTCG TGTTTTTCTG ATAAAACATA TGTGATGGAA GCGTGAATAA TAATGCCTAA 180

TGTAACAAAA CTGATAATTA ATATACTGCT TATCAATAAC ATTAAGCGGT GGTGAAACTT 240

CATCATTGTT CTTTAGGTCT TTCCAATTTA TAGCCTAAGC CACGCACAGT TTTAATAAGT 300

TGTGGCTTCT TAGGATTATC TTCTAATTTA TCTCTTAAAT GACTGATATG TACATCAACA 360

ATTCTTGAGT CTCCTGCAAA TTCATAATTC CATACCGTAT TTAACATATG CTCTCTCGTA 420

ATGACTCTGC CTTGTCTTTC TATCAAATAA AGCA 454

(2) INFORMATION FOR SEQ ID NO: 582:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 452 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

TTTATAAGAT TTTATTTACA AATAATTGGT TTTCATATGT ATAAACACTT TTGACTTTCA 60

AATCTTAACG ATAATTCTAT TACAATACAA TCCCCTATTA GAATGATTTA TGTAATAAAA 120

AAAGCGGAGT TTCCCCCAGC TTTTCTAAAC GACTACATAA AATATAAGAT TGCAATTAAA 180

TGCAATAGTG ATGCTATTAC AATAAAAATA TGCCAAATCA TATGAAAATA TGGTCTATTC 240

TTTTGTGCAT AAAACCATGC ACCAATTGTA TAAGACACAC CACCTAAGAA AATGAATAAT 300

ATGAATATCC ATGATGTGCG AATAAAAATA ATTGGTAACA AGATAATACC TACCCAGCCC 360

AAAATCCCCC AAAGTGTCGT TCCCCATAAT AA 452

(2) INFORMATION FOR SEQ ID NO: 583:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

CGCTTTTTGC AATAAGTCAT TAGCCGCTTT TAAGCCTTCT TCTTTTCGAT CTACAACAAG 60

TAAAATAAAT GGCTTTAACG CTTCTTCTTT TTCACTTTCA AGCATATCTG GTTTTTGAAC 120

CATTTCAAAT GGAGATTTCA ATCCATTATT ATCGCTCATT TCAATAATTG CATCATACTG 180

TGCTTGTGAC ATACTTGCAA TAGCCTGTTT TGCATTTTCT TGAAGGAAAT ATAAGTTTTT 240

CAATTTAGGA TGCTTATTTA ATGTACTTAA TGTAATCGGT GTAATGTCTT TCTCATAAGA 300

CACTTCAATC ACTGTACTAT TTGTTCTACC AGGAATTGGT GGTTTTTCAT GAATATGCTT 360

TGATACTTCT CCAATTCCAA CGACAGATTG ATTTTTCGTT CGATTATAAA AAATAATATT 420

GTCGCCTTCT TCTAACTGAG TATAAAAATG ATAACCATTA CGTTTAATAC CGTTGTACGT 480

GTGCGTATAA ATCGTATATT GGTTTCCAGG TTCAAATTCT TCAGTTTCAG CTAAAAAGAA 540

ATAACGCGGT ATCTTAATTT CGCCTTTACC AAGACCACTT ATTAAATCAA ACTCTTCTGC 600

AGTGATTTGA TTGAACAATG TCTCTTTCAT ATnACTTATA CGAAATTCCA AAGCTTCACT 660

ACGCTTTAAA TAATCTGCTG TTAATGGTTT CAATTGTTCA TTAAAACGAA ACTGTACACG 720

TATTTTATTT TGTGCACCTG TTTCAACACT AATAATTTCA CCACATCCAA GTAGTCCAGT 780

ATCCGTCTGA ACTTGATAAA AGATGACTTG ATCTCCTACT TTAGCCTTTT TAAACGCTCT 840

AAATCCTTGA GATGGGTTAA AATGTGCGCC TGATTCAAAT AAAGCTGTTT GTCCTACTAA 900

CGGTTCATTA TGATTCCAAC GGTTATATCC ACAATTCAAC CAAAAATAAT TCGTTTCTGC 960

TGTCATCTTA ATACTCCTTA ACCTGAATAA ATTTTAGAAA CACTATGAAT TACATTCTTT 1020

tAGTGTTTCT TATGCAGTTG GACGCGTATG CGAACAACTG TATACCCTTT GTTCACTGCG 1080

ATTTTAATCG CATTTCCTAT AACATTGTAG CGCCCAGGAC ATTAATTTAC GTCCCAGACC 1140

CTTATCGTTT TCACTTCTAA GTAAGTCGAA CTATTTTGCT TTACAACAAG TGCGACTCTA 1200

AATACAGTTG GACACACATA CGAGCAACTG TATACCTTTT AATCAGTTTT CTATATTTTA 1260

TTTATTATAT CTGTCTTAAT GATAAAAATT GTTACAAACA GTTTAACATA TTTAGCTACC 1320

ATGATACCAC TATGCTTGCn TATCTCTATA GCGCCATTGA TACACATTTT TAAATATCTA 1440

TACTGCCGTT AGAATTTTAT CATGTCTnAA TT 1472

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 787 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

GGTAGTGAAT GGGGTTCAAG ACAACAGTAT TGGAAGTACG AATGAATCAC AGTTTTTAGG 60

AAATTATATT GTAATTAAGC ACGCAGAAAA TGAGTATAGC TTAATAGCTC ATTTACACCA 120

ATATTCAATC ATTGTGAATG AGGGGCAAAA TGTTAAATAT GGTGATATCA TTGGGAAGGT 180

TGGGAATTCT GGCAATTCTA CTGAACCTCA TATACATTTT CAAGTAATGA ATGATAAGAA 240

TATTGAAGCA TGTACATCTT TAAAAATTCG ATTTATAAAT AATCGAGAAC TTATCAAAGG 300

GGATGTGGTC TGCGGATTAC AAGCTGAATG ATGGCGATAC TTATAAAATC TCGACACTAT 360

AAAAATGGTA TAGTGTCGAG ATTTTCTTGC TTATTTAGTT AATTCAAAGT GCACGCCGGA 420

TTCATTAGAA GTCGACGTAT TTTTGTTTGT AATAGAGTAA CCGGTCATTG AAATTTTAGA 480

TTCAATATCT GAAGCGGAAT TTGTAGATTC AGGATTATAG AAGCTACATT CATAAGTGTT 540

ATCATCTTTC TTTTTAAGTA TAAACATACC TTTGGCTTTA ACTTCGACTT TAGTGTTGTT 600

AATGTCAAAA GTTTGAGTGC TATTACTATA ATTAACACCA GCCCAAACCG ATTCATTATC 660

TTTCACAACG GGGAAGTCAT CTTCTTGCTT AACGACGTnA CTTCATCTTT CTCTGTCTTA 720

AAGACATCTT TAGATAAGCC TGGATACAAC ACATATCCAT ATTTATTGTC AGAATTAGAA 780

TGCTTTT 787

(2) INFORMATION FOR SEQ ID NO: 585:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

ATGCTAAATT AGGGGGAATA TTTACGATAA AGAGACCAGA AAAATAATAA AACACATGCT 60

TAAAATGAAG ACTATTTTTT ATTACAAGAA AATGTATCTA GTAAACTTAA AGTAGCAAGA 180

CCTAATAAAT TTAATGCATG TTGTGCACCT TTTTTACCTT GGCCAGCTTC GAAATGTTTG 240

TAAGCAGCTA CACTTAAAAT GCCTATCGTT GATAGTGATG CAAGGCGAGA AATGTTTTTA 300

TTGATAAAGC TAGCTGAGTA TAAAGCAGCA GTAGTTGCTT CTGCAATGCC GACGTATTTT 360

ACAAGTTCTT TTTGCAAGCC AAAAGTATGT TCAAACAGTT CAATCATACC CTTATCTTCT 420

TGCAATTTAG GTTTACTGGC TTGGTATAGC TCTTTCGCAA GTTTTAAATT CGTTGCGTAA 480

CGCAAAATCA TATTTAATTC CTCCCAATAT TTGATTTTTT GTGAAAGATG ATTACTTTAT 540

CATTTTTACC CGTTTCTATA AAAATGAATC AATTATGTAA CGTATGTGTA GTTTAGGAAT 600

GTTTGCTATG GAAATATAAT TCTGTTCACT CAAAATGTAT GAAATTAATG TGTAGTTTTG 660

TCGAGTTGCT CTTTTAATTT GGTTAGATTG TTTTTTAGAG AAGCGGTACT ATTTTTAAGT 720

GCATCAACAG ATTTACCTTC GTTTTGAGAC ATTGAGTTTA TTACAGCACG AAGTTCTGTT 780

TCTAGTATGT CaGCGTCGCt TTAGCATTAG AACTTAaTAt TTAtAcTCTT 830

(2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

TTAGGACGTT TTTACAATCA GTACAATGAG CTCATTGTTA TTAGTCCTTT AACGGCGTCT 60

TTTAATGCTG GCGCTACATT TGGGCGATTT CATCATTTAA TTGATACTGA AACTTTAGCA 120

AAATTAGAAC ATGAAAAAGG ACATTATTAT CAGAAGATGA TATGTGATGA CAATGTAGAA 180

ATGATTTCTA TAAATAACAT ACCGAAATAT CCGAGAAATC ATAATGTATT AACTAATCAT 240

GACTCATACG AATATTCATT GAATTTAGGA AGTAGTAATA GTTATTCAAA GTATGAGCTT 300

ACCTTAGATG ATATTTATGT TGGTGCTACC TTTtAACAAA TTATATTTAT ATTCTAGCCm 360

ACtAAATAAA AGGGkaCtaT TTGaATCaAA CmATaTGtAT TAACCTTTTT TA 412

(2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4709 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

TTCAGTTTGA AATTAATCAT ATAAATTTCT TATGGGAGGG TTGATATCTT AATGATTAAC 60

ATTATTTCAG CTATAGGATC TATTGGAACA TTTATTATGG CTTTATTTTA TTTTGTATCA 120

GTTTCAGTTC AACTTTATCA AATGAAAATT AGCTTTCTGC CAGCTTTAGG TTTTAACCAA 180

ATTTTATTAG AAAGGGAGGA GGATCAACTT AATATAATGA ATTCGGCAAC AGAAGAGCAT 240

CATCATAAAG ATTATATTAA ACTATATAAT TTAGGTGGCG GTGCTGCTAA rAAAATTGCA 300

ATAGAGGTTT TATTGGGGAA GGATArAGTC ATTCAGAAAA AATACGTGCA TATTkTACCT 360

AGTAAAGAAG GGTACATGTT ACCAATTAAT AAAAATGTGT ACGAAGAATT AGAAAGAACG 420

ATTGAsAACA ATGGTCATGA AGCTGATTTG AATGTACGTA TGACTTATTA TCATAATGTA 480

AGTCGCAAAC AACAGGAAGT TATATTAAAA GGTCAAATCG ACCGTTTTAA TACTTATAAT 540

AATAAAGAAA TTTATGATTT GCAGTTTATC TAAAAATTGA TTTAAGAGGG TAGTTGTTTA 600

TTGCGAAAAA TATCATTCAA TTTTAATGAA ATAATGGCGT CATTACTATA AAATATTACT 660

TTATGTTGTA ATGCATTTTT CTATAAGATA GAACTAAAAG GAGGGGCAAA GATGCAAATT 720

AGACAAATAC ATCAACATGA CTTTGCTCAA GTGGACCAGT TAATTAGAAC GGCATTTGAA 780

AATAGTGAAC ATGGTTATGG TAATGAATCA GAGCTAGTAG ACCAAATTCG TCTAAGTGAT 840

ACGTATGACA ATACCTTAGA ATTAGTAGCT GTTCTTCAAA ATGAAGTTGT AGGGCACGGT 900

TTACTAAGTG AAGTTTATCT TGATAACGAG GCACAACGGG AAATTGGATT AGTGTTAGCA 960

CCTGTATCTG TTGATATTCA TCATCAAAAT AAAGGTATTG GGAAGCGATT GATTCAAGCA 1020

TTAGAACGAG AAGCAATATT AAAAGGATAT AATTTTATCA GTGTATTAGG ATGGCCGACG 1080

TATTATGCCA ATCTAGGATA TCAACGCGCA AGTATGTACG ACATTTATCC ACCATATGAT 1140

GGTATACCAG ACGAAGCGTT TTTAATTAAA GAATTAAAAG TGAACAGTTT AGCGGGAAAA 1200

ACAGGTACCA TAAATTACAC ATCTGCTTTT GAAAAAATAT GATTTCAAGC TAGGATTACA 1260

TTAGGTAGAG TTCATATTAA TAATAAAAAA TGTTTGCAAT CAAATCGTAC GTTGTCGTTT 1320

GTAATTCTTA AAATAGCAAT AAATAAAATG TTTGTTAGTA AAGTATTATT GTGGATAATA 1380

AAATATCGAT ACAAATTAAT TGCTATAATG CAaTTTTAGT GTATAATTCC ATTGACAGAG 1440

ATTAAATATA TCTTTAAAGG GTATATAGTT AATATAAAAT GACTTTTTAA AAAGAGGGAA 1500

TAAAATGAAT ATGAAGAAAA AAGAAAAACA CGCAATTCGG AAAAAATCGA TTGGCGTGGC 1560

TTCAGTGCTT GTAGGTACGT TAATCGGTTT TGGACTACTC AGCAGTAAAG AAGCAGATGC 1620

AAGTGAAAAT AGTGTTACGC AATCTGATAG CGCAAGTAAC GAAAGCAAAA GTAATGATTC 1680

GTCAAACACT AATAATGGCG AAACGAGTGT GGCGCAAAAT CCAGCACAAC AGGAAACGAC 1800

ACAATCATCA TCAACAAATG CAACTACGGA AGAAACGCCG GTAACTGGTG AAGCTACTAC 1860

TACGACAACG AATCAAGCTA ATACACCGGC AACAACTCAA TCAAGCAATA CAAATGCGGA 1920

GGAATTAGTG AATCAAACAA GTAATGAAAC GACTTCTAAT GATACTAATA CAGTATCATC 1980

TGTAAATTCA CCTCAAAATT CTACAAATGC GGAAAATGTT TCAACAACGC AAGATACTTC 2040

AACTGAAGCA ACACCTTCAA ACAATGAATC AGCTCCACAG AGTACAGATG CAAGTAATAA 2100

AGATGTAGTT AATCAAGCGG TTAATACAAG TGCGCCTAGA ATGAGAGCAT TTAGTTTAGC 2160

GGCAGTAGCT GCAGATGCAC CGGTAGCTGG CACAGATATT ACGAATCAGT TGACGAATGT 2220

GACAGTTGGT ATTGACTCTG GTACGACTGT GTATCCGCAC CAAGCAGGTT ATGTCAAACT 2280

GAATTATGGT TTTTCAGTGC CTAATTCTGC TGTTAAAGGT GACACATTCA AAATAACTGT 2340

ACCTAAAGAA TTAAACTTAA ATGGTGTAAC TTCAACTGCT AAAGTGCCAC CAATTATGGC 2400

TGGAGATCAA GTATTGGCAA ATGGTGTAAT CGATAGTGAT GGTAATGTTA TTTATACATT 2460

TACAGACTAT GTAAATACTA AAGATGATGT AAAAGCAACT TTGACCATGC CCGCTTATAT 2520

TGACCCTGAA AATGTTAAAA AGACAGGTAA TGTGACATTG GCTACTGGCA TAGGTAGTAC 2580

AACAGCAAAC AAAACAGTAT TAGTAGATTA TGAAAAATAT GGTAAGTTTT ATAACTTATC 2640

TATTAAAGGT ACAATTGACC AAATCGATAA AACAAATAAT ACGTATCGTC AGACAATTTA 2700

TGTCAATCCA AGTGGAGATA ACGTTATTGC GCCGGTTTTA ACAGGTAATT TAAAACCAAA 2760

TACGGATAGT AATGCATTAA TAGATCAGCA AAATACAAGT ATTAAAGTAT ATAAAGTAGA 2820

TAATGCAGCT GATTTATCTG AAAGTTACTT TGTGAATCCA GAAAACTTTG AGGATGTCAC 2880

TAATAGTGTG AATATTACAT TCCCAAATCC AAATCAATAT AAAGTAGAGT TTAATACGCC 2940

TGATGATCAA ATTACAACAC CGTATATAGT AGTTGTTAAT GGTCATATTG ATCCGAATAG 3000

CAAAGGTGAT TTAGCTTTAC GTTCAACTTT ATATGGGTAT AACTCGAATA TAATTTGGCG 3060

CTCTATGTCA TGGGACAACG AAGTAGCATT TAATAACGGA TCAGGTTCTG GTGACGGTAT 3120

CGATAAACCA GTTGTTCCTG AACAACCTGA TGAGCCTGGT GAAATTGAAC CAATTCCAGA 3180

GGATTCAGAT TCTGACCCAG GTTCAGATTC TGGCAGCGAT TCTAATTCAG ATAGCGGTTC 3240

AGATTCGGGT AGTGATTCTA CATCAGATAG TGGTTCAGAT TCAGCGAGTG ATTCAGATTC 3300

AGCAAGTGAT TCAGACTCAG CGAGTGATTC AGATTCAGCA AGCGATTCCG ACTCAGCGAG 3360

CGATTCCGAC TCAGACAATG ACTCGGATTC AGATAGCGAT TCTGACTCAG ACAGTGACTC 3420

AGATTCCGAC AGTGACTCAG ATTCAGATAG CGATTCTGAC TCAGACAGTG ACTCGGATTC 3480

CGATTCTGAC TCCGACAGTG ATTCCGACTC AGACAGCGAT TCAGATTCCG ACAGTGATTC 3600

CGACTCAGAT AGCGATTCCG ACTCAGATAG CGACTCAGAT TCAGACAGCG ATTCAGATTC 3660

AGACAGCGAT TCAGATTCAG ATAGCGATTC AGATTCCGAC AGTGACTCAG ATTCCGACAG 3720

TGACTCGGAT TCAGATAGCG ATTCAGATTC CGACAGTGAC TCAGATTCCG ACAGTGACTC 3780

AGACTCAGAC AGTGATTCGG ATTCAGCGAG TGATTCGGAT TCAGATAGTG ATTCCGACTC 3840

CGACAGTGAC TCGGATTCAG ATAGCGACTC AGACTCGGAT AGCGACTCGG ATTCAGATAG 3900

CGATTCGGAC TCAGATAGCG ATTCAGAATC AGACAGCGAT TCAGATTCAG ACAGCGACTC 3960

AGACAGTGAC TCAGATTCAG ATAGTGACTC GGATTCAGCG AGTGATTCAG ACTCAGGTAG 4020

TGACTCCGAT TCATCAAGTG ATTCCGACTC AGAAAGTGAT TCAAATAGCG ATTCCGAGTC 4080

AGTTTCTAAC AATAATGTAG TTCCGCCTAA TTCACCTAAA AATGGTACTA ATGCTTCTAA 4140

TAAAAATGAG GCTAAAGATA GTAAAGAACC ATTACCAGAT ACAGGTTCTG AAGATGAAGC 4200

AAATACGTCA CTAATTTGGG GATTATTAGC ATCAATAGGT TCATTACTAC TTTTCAGAAG 4260

AAAAAAAGAA AATAAAGATA AGAAATAAGT AATAATGATA TTAAATTAAT CATATGATTC 4320

ATGAAgnAAc rCCTTAAAAG GTGGCTTTTT TACTTGGATT TTCCAAATAT ATTGTTTGAA 4380

TATAATTAAT AATTAATTCA TCAACAGTTA ATTATTTTAA AAAGGTAGAT GTTATATAAT 4440

TTGGCTTGGC GAAAAAATAG GGTGTAAGGT AGGTTGTTAA TTAGGGAAAA TTAAGGAGAA 4500

AATACAGTTG AAAAATAAAT TGCTAGTTTT ATCATTGGGA GCATTATGTG TATCACAAAT 4560

TTGGGAAAGT AATCGTGCGA GTGCAGTGGT TTCTGGGGAG AAGAATCCAT ATGTATCTAG 4620

TCGTTGAAAC TGACTAATAA TAAAAATAAA TCTAGAACAG TAGAAGAGTA TAAGAAAAGA 4680

TTGGATGATT TCAATATGGT CCnTTCCCA 4709

(2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1554 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

CTTTTTTAAt TAwCgGaAtA TTGtCaTgaT tAcAcTTCGt TAGGGTTTAc gTCGtAATTT 60

CATTTaaTAA gCgCTTCAcC ATTAAAtGTG gTAmCCTTTA ATTCGCCAGT AGAAACATCA 120

CAGTAACTAA GCGCAATTTC AGGTTGATTC ATAACAAAAC TTAAAATATA GTTATTTTGT 180

CGTCTAACCA TACCTTTCGT TTGTTTCGGA TCTTCCATCT GTTCACAAAT AGCTACTTTA 300

TATCCATTAT TAACAAGTGT ATCTATATAA CTATCTGCAG AATGATACGG AACACCACAC 360

ATCGGAATTG GATTTTCTTT TTTAGCATCT CTTTTAGTTA AAGTAATTTC AAGTAyACGT 420

GATGCCTCCT TGGCATCTTC ATAAAACATT TCATAGAAAT CACCTAGTCT AAAAAATAAT 480

AAGCAATCTT GGTATTCTGA TTTTATTTTT AAATATTGCT GCATCATTGG TGTAACATTA 540

GACATATTAT TTCTTCACAA CCCTTGTCTC TTTTTAAAAT TTGTCTTTAC AATATATTCG 600

TTTGTAAGyT TTTTAATTAT TAATTATTTA ACTTATACAT TTTAACATAC TTACTTTTAC 660

AAACCTATTC ATACCATATA ATCACGAAGC ATCTTAAATG TATAAGAAAA CGCCTCAAAC 720

CTAATAAAAT GTGTCAATAG CATGTTTAGA ATTAAATTAA AATTCTAACA TTCAAGACAT 780

TTAATTAAGT AAGGGCGTTC AATATTAAAA TGAACAATGA CTCTGTTTGA AATCATATAT 840

CATAAAATTA TTTTATAAAC CTTTGAAGAA TACCACGTTT TTTTAGAGTA ATTAATAAGA 900

AATAACTTAT AATAGATCCG ATAGCACTTG aGACTATGaA CGTAATCATT AACGGTTTAA 960

TGAAGAAGTC TTGAAGCCCA AGGaAATATG CTAATGGtAT aCaAATTAAA cTTCCgATGA 1020

CaCCAGTTCC aAGTACTTCa CCGACCGCGG CCaTAAATAT ATGTTTACGA TATnygTAAA 1080

ACATACTAGC CAATAAAACT CCAATCATAC TACCCGGAAA TGCAAAAGst GTACCAGTAC 1140

CAAAAAGAAC TCTTAAAATT GATGATATAA GCGCTTGAGC TAATCCATAC CAAGGACCTA 1200

CTATGACCGC ACTTAATACA TTTACAAAAT GCTGTACTGG TGCTGCCTTA ACTGGTCCTA 1260

GAGGAATGAT GATAATACTG CTTAATACAA CATTTATTGC AATTAAAAGT GCAGTTATAG 1320

CCAGTTTTCT TGATTTCATA TGATTGTTCT CCTTTTTGTT TGTAATTAAT CACTATGCTT 1380

GGCTTTATTA TGGTCATTTA AACGTGTTTC CATTGTTGAT ACAAACATTT TCAATAATTG 1440

ATTCGCTTCA TATTGTGAAG TTTGAAACTG TTCAACTATG GGCAATGTAT TTATTTCTGC 1500

TTCTAtACTC TGAATGGtAT GTTCCGACTG nTCCAGCGCA TTTGTTTCCC GnAA 1554

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 638 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

TTTTGACGAA AAAAGTTGAT TTACAAATAT ATAAACGTTG TGATTTCAAT GTTTGTATAG 60

TATATACATG ACAGCAACTT GGGAAAAAAA GGAAGGTAAC GAAGGTTTAT TAACTGTTAC 180

TGTTCCTGCA GAAAAAGTAA ACAAAGCrCT GAGAGATCCC CTCATAATTT CCCCAAAGCG 240

TAACCATGTG TGAATAAATT TTGAGCTAGT AGGGTTGCAG CCACGAGTAA GTCTTCCCTT 300

GTTATTGTGT AGCCAGAATG CCGCAAAACT TCCATGCCTA AGCGAACTGT TGAGAGTACG 360

TTTCGATTTC TGACTGTGTT AGCCTGGAAG TGCTTGTCCC AACCTTGTTT CTGAGCATGA 420

ACGsCCGCAA GCCAACATGT TAGTTGAAGC ATCAGGGCGA TTAGCAGCAT GmTATCAAAA 480

CGCTCTGAGC TGCTCGTTCG GCTATGGCGT AGGCcTAGTC CGTAGgCAGG ACTTTTCAAG 540

TCTCGGAAGG yTTCTTCAAT CTGCATTCGC TTCGAATAGA TATTAACAAG TTGTTTGGGT 600

GTTcGAATTk CAACArGTaA GTtAGtTGCT AGAnCCCA 638

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

AAAATATTCC CGTACATTTT GATGTCTGTA GGGGCTTTTT TGACTTTAGG ATTTGTCATT 60

TTTTCAATTC ATAAAGGGAG ACGAACGAAA AATGAATCAG CACGTAAAAG TAACATTTGA 120

TTTTACTAAT TATAATTACG GCACATATGA CTTAGCAGTA CCAGCATATT TACCGATAAA 180

AAACTTAATA GCTTTAGTAT TGGATAGTTT GGACATTTCA ATATTTGATG TCAATACACA 240

AATTAAAGTG ATGACGAAAG GTCAATTACT TGTTGAAAAT GATCGACTCA TTGATTATCA 300

AATCGCTGAT GGAGATATTT TGAAGTTACT ATAGGAGGGA AAATAGATGG TTAAAAATCA 360

TAACCCTAAA AATGAAATGC aAGATATGTT AACGCCTTTA GATGCTGAAG AAGCAGCTAA 420

AACAAAATTA CGCTTAGATA TGAGAGAGAT TCCTAAGTCT TCAATTAAAC CAGAACATTT 480

TCATTTAATG TACTTATTAG AACAACATTC TCCATATTTT ATAGATGCTG AATTAACTGA 540

ACTACGTGAC aGTTTCCaAA TACATtATGA CATTAATGAc AATCATACAC CTTTTGATAA 600

TATTAAATCA TTTACTAAAA ATGAAAAATT ACGTTACTTA CTCAATATCA AAAATTTAGA 660

AGAAgTAAAT CGTACACGCT ACACATTTGT GTTGGCACCA GATGAATTAT TTTTCACAAG 720

AGATGGATTA CCCATTGCTA AAACAAGAGG GTTACAAAAT GTTGTTGATC CATTACCTGT 780

GTCAGAAGCT GAATTTTTAA CAAGATATAA AGCGCTGGTT ATCTGTGCAT TCAATGAGAA 840

AACTAAAGTT ATTGAAGCGG CAACGTTAGA TTTACTAACG GCATTTTTAG ATGAACAGTA 960

TCAGAAACAA GAACAAGATT ATAGTCAAAA TTATGCATAT GTACGCAAAG TAGGACATAC 1020

CGTTTTCAAA TGGGTTGCTA TCGGTATGAC AACGTTAAGT GTTTTATTAA TTGCATTCTT 1080

AGCCTTTTTA TATTTTTCAG TAATGAAGCA TAATGAGCGC ATTGAAAAAG GATACCAAGC 1140

ATTTGTAAAG GATGtTATAC GCAAGTACTA AATACGTATG ATGATTTAGA TGGTaAAAAt 1200

TgaTAAAGAG GCACTTTACA TTTATGCCAA AAGTTATATC CA 1242

(2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 744 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

TTCCAGATAG AGCCTTAGTT GCTGCCGCTG AATTGTCTGA TCGTTACATC ACTGATCGTT 60

TTTTTACCAG ATAAAGCGAT TGATTTAGTT GACCAAGCAT GTGCAACAAT TCGTACGGAA 120

ATGGGATCAA ATCCAACTGA ATTGGATCAA GTTAATAGAC GTGTCATGCA ATTAGAAATT 180

GAAGAAAGCG CACTTAAAAA TGAATCTGAC AATGCGAGCA AACAGAGATT ACAAGAACTA 240

CAAGAAGAGC TTGCCAATGA AAAAGAGAAA CAAGCAGCAC TTCAATCTCG TGTAGAATCA 300

GAAAAAGAAA AAATAGCAAA TTTACAAGAA AAACGTGCGC AACTAGATGA AAGTAGACAA 360

GCGTTGGAAG ATGCACAAAC AAATAACAAT TTAGAAAAAG CTGCTGAACT ACAATATGGA 420

ACAATTCCTC AATTGGAAAA AGAACTTAGA GAATTAGAGG ATAATTTCCA AGATGAGCAA 480

GGTGAAGATA CAGATCGAAT GATTCGTGAA GTTGTAACAG ACGAAGAAAT TGGCGATATT 540

GTCAGCCAAT GGACAGGCAT ACCAGTTTCA AAATTAGTTG AAACAGAACG TGAAAAATTA 600

CTTCACTTAA GTGACATCTT GCATAAACGT GTTGTAGGTC AAGATAAAGC GGTTGACCTG 660

GTTTCAGATG CAGTAGTTAG AGCAAGAGCA GGTATTAAAG TnCAAACAGA CCTATTGGTA 720

GTTTCTnATT CCTAGGTCCn ACTG 744

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

TTGTTATAGT GTCTGAATCT GTGTAACTCT TGCCCATGTG TTCTGAGTAA AGCACCCACT 60

GTTTATTTAC TTTTCGTTGT AGTCTAGCTT CGTGTAGTAG TTTGTTTAAC TTTTGTGCTG 120

ATATACCGTA GTCTGCCGCG ATTTGAGTTG TGGCTAATGT GCCAGTTGAT TTTAAGATTT 180

CATCAACATA ATCTGCTTTG GGTTTTAGCT CTCCAATTTC TTGTTGTAAA AGTAAGTTTT 240

GCTCTTTTTC TTTCTTATAC TCAGTCAACA CTGTAATGAT GTAGTCTGGA TCTTTTAATG 300

TTTGTTCAAT TACATTGTCT GTTGCGTATA TACCGTGTTT GCGAATAGCT GGTaGGACAT 360

CTGATGTTAC CCAGCGTTTG AATTTTCTAG CGGTTTCTCT AATTTTTTCG TTTTTGCTTT 420

GTTTAGAAGC ATCGAAGATT AGACTGTATA ATCCTGATTC GTTGATAATG ATCATATTTC 480

TGTTTTGACC TGATGCACTA AATTGGTGCG TCAGTTTGTC CTCGCTATCA ACATGATTTC 540

TAATGGCATT GTCTGATCTT GCATATCCTA AAATCTCAGC AATATCTTTT CCTACAAAAT 600

AAGGTTCGTT TTCAATTTCT ACTGTTCTTA CTGGTAGCTC TTTAAAATTA AATGTTTGTA 660

ATGCTTGCAT TTGAGTATCC TCCTTTTTCC TCAACACCCA CATTCAGCAG ACGGTTATCG 720

CAATGACTAT CGAATGTATT TAAACGCGGC TCATATCATC GCCAGcTCTC GCTCACATCT 780

GCTCAATGTG GATGTTGATA AGCGTGGTTA TATTAAGAAG TGAATGTTAC TGATTCACTT 840

TCCGCCACTC TGTTAAATCA GTAACTTTGT TATCGCTTTC AACACCGTTA AGCTTGTCTA 900

ACGCTTTCAC TACTTTTTGG AACTCTTTGA TAGCACTtCG TAGCTTTTTA GTAATTTCAT 960

CTTCTACCAT TTCCAAACCA GCAAATGCGT CTTCGTTATT CATGCTTAGA TGTTTGTTGA 1020

AAAGATCTCG AGTGTATCTT ATTTCTTTAA GTGATTTATC ATAAGCTTCA ATTTGTCCTG 1080

AAAGGTTATG ATATTTTAGT TGTAGTTTTA CTAATTTTAA TGATTGGTCT TGCATTTGTT 1140

ATGTCTCCTT TAAGATGTTT GTTTGCGTTT CGTGTACTTT GTGGGTAAAA AAATATCTCC 1200

AATATTTTCG TCAAAAAAAT CAGCGATAAT AAACATCTCA TCATTCTTAA ATTGATGCTT 1260

TCCTAATTCT TTTAAACGAT AACCTTCAGT TGATATATTC AAGAGGTTTG CTAAATCTTC 1320

TTGAGTACAC TTTCTTTCTT TTCTCAACTT TATTAAATTC CATTGCATGT TGTCACCTCC 1380

CGCTTTACAA AACCTACTAT ACACGATACG GTACTTGnGT CAACATAAAA GTTTGCTTTT 1440

CGTGTATTT 1449

(2) INFORMATION FOR SEQ ID NO: 593:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

ACCAAAAACA CTTTCTAAAG AAATTGTTTC AGAACCATTT GCTAAAAACC AATTACGTGA 60

AAAAGCTCGT CTAACTAACA TTAAAGGTTT AGAGATTCCA AGAGTTTCAT ACACTTTAGA 120

CGATGATGAT TTCATTACAG ACGTAGAAAC AGCAAAAGAA TTAAAAGCAA AAGGTGATAC 180

AGTCAAGTTC ACTACTAATA AATTCAAAGT ATTTGCTGCA ATTTCAGATA CTGTAATTCA 240

TGGATCAGAT GTAGATTTAG TAAACTGGGT TGAAAACGCA CTACAATCAG GATTAGCAGC 300

TAAAGAGCGT AAAGATGCCT TAGCAGTAAG TCCTAAATCT GGATTAGAAC ACATGTCATT 360

TTATAATGGA TCTGTTAAAG AAGTTGArGG AGCAGACATG TATGATGCTA TTATTAACGC 420

TTTAGCAGAT TTACATGAAG ATTATCGTGA TAACGCAACA ATTTATATGC GATATGCAGA 480

TTATGTCAAA ATTATTAGTG TTCTTTCAAA TGGAACAACA AATTTCTTTG ACACACCAGC 540

AGAAAAAGTA TTTGGCAAAC CAGTAGTATT TACAGATGCA GCAGTTAAAC CTATTGTGGG 600

AGATTTCAAT TATTTTGGAA TTAACTATGA TGGAACAACT TATGACACTG ATAAAGATGT 660

TAAAAAAGGC GAATATTTGT TTGTATTAAC AGCATGGTAT GATCAGCAAC GTACATTAGA 720

CAGTGCATTC AGAATTGCAA AAGCAAAAGA AAATACAGGt CCATTACCCA GCTAAGCCCC 780

AAAAGGTTAA TGTAACAGCT AAGGCTAAAT CAGCTGTAAT ATCAGCCGAA TAGGGGTGAT 840

GAAATGAGTT TAGAAGAAAk TAAATTGTGG TTGAGAATTG ACTATAATTT CGAAAATGAT 900

TTAATTGAAG GTCTCATTCA ATCGGCTAAG TCTGAATTAC TATTAAGTGG GGTnCCAGAT 960

TATGACAAAG ATGACTTGGA ATACCCGCTT TTTTGTACAG CGATTAAATA TATCATTGCA 1020

AGAGATTATG AAAGTCGTGG ATACTCAAAT GACCAATCTA GAAGCAAGGT GTTTAATGAA 1080

AAAGGATTGC AAAAAATGAn TTTGAAATTA AAAAAGTGGT AGGTGATTTT TAAATGGAAT 1140

TTAATGAATT TAAAGATCGC GCGTATnTTT 1170

(2) INFORMATION FOR SEQ ID NO: 594:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

TGAAGGGTGT TTTGTTTATG GCCAATTGCT GTGTTATTAA AnCGAATGTT TCGAATGGAA 60

ATCATTCCGG AAGAGGACAT GTCTTCAGCT TCTGATTTGA AAGCACAGTT TTATCGCGGT 180

ACTTTGCAGC GCTTTTACCA AtCnTTGCAC GCAGAAAAGC TTACACCTTA TGTTATGTCT 240

TATGACGATA TCATTTCATT TTGTAAAGAA AACAATATCT CTGAAGTAGT GACTGCGGGT 300

GATATTATGA GTTATCATCT TGAAGAATAT GATATTTTAC ATCAACGTTC TTTATTCAAT 360

GAAGCACGCA TTGCCGTTAC TTTGATACGT GGGAATCATT ACTTTAAAGC GAGTAAAACA 420

ATGAATCAAC AAGGGGAGCC ATACAATGTT TTTACTAGTT TCTATAAAAA ATGGCGACCT 480

TACTTGAGGC ATAGAGACGT ATATCACTAT GATTTAAAAT CATTCGAAAA CTTTGTCATT 540

GCATCACCTG ATGATTTAGT GTTTGATGAC ATAGCATTTG GATCCTCACA aATAATTGAA 600

CAGatAAATG GCAACATTTT TTAGATCAAG ATATACAGAA TTACGAAAGC GGAAGAGACT 660

ATTTACCTGA AGTATTAACA AGTCAGCTAA GTGTTGCTTT AGCATATGGA TTATTAGATA 720

TTATTGAAAT TTTTAATGAT TTATTGGCGC GTTATGATGA AGATGAGGCA AACTATGAAG 780

CATTTATACG TGAACTCATT TTTAGAGAAT TTTATTATGT GTTAATGACA CAGTATCCTG 840

AAACCTCATA CCAAGCTTTC AAACCTAAAT ATCGACAGAT AAAATGGTCG CAAAATGAAG 900

CGGATTTTAA TGCATGGTGC GAAGGGCAAA CAGGATTTCC AATCATTGAT GCAGCAATAA 960

TGGAATTGAC ACAAACTGGT TTTATGCATA ATCGAATGAG AATGGTTGTG TCGCAATTTT 1020

TAACCAAAGA TTTATTTATA GATTGGACAT GGGGAGAAAA ATTCTTTAGA AAGCACCTTA 1080

TTGACTATGA TGCAGCATCA AATATTCATG GATGGCAATG GTCTGCTTCT ACAGGTACGG 1140

ATGCAGTGCC GTATTTTAGA ATGTTTAATC CAATAAGACA GAGTGAACGC TTTGATGCTA 1200

AAGCTTTGTA TATCAAAACA TATCTTCCGA TTTTTAATCA AATTGATGCA AAATATTTGC 1260

ATGATACACA ACGCAATGAG TCCAACCTTT TTGAACAGGG GATTGAATTA GGTAGTCATT 1320

ATCCAAGACA AATGGTAGAT CATCAAGAAA AACGTACACA AGTTTTAGCT ACATTTAAAG 1380

CGCTAGACTA ATT 1393

(2) INFORMATION FOR SEQ ID NO: 595:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1484 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

TTAACTTGAA AGATTTCCCC GACATCTATA ACTTGTATAA TGTGTATATG TCGTTTTTAG 60

AAAAATTAAA AAAAGAATAT CTTGATTGGT ATAATCAGAC CTTAGAGTTT TCTAATTTAT 180

CAAACAATGT AGTAAGwATA GATACTCCTT TTAAAGATAA TTCTTTAGAT AATTTAATAA 240

TTTACGCTTT ATACGATCAG TCCAGAGACA TGATTACACT GACAGATGAC GGCTATACTA 300

TATtTGATTT AGAAAATAAT GGTATTTCTT TAAATAAATC AAAAAAACGT AAAAAGATTT 360

TTGAAGAGCA CCTTTCAGCT TACGGTATTA AATATAACGA TAAAACTCAC GAAATTTTTG 420

TTCAAACTAA CTTTAAAAAT TTTAATAAAT CGAAACATAA TTTATTACAG TGCCTTATAT 480

TTGTTAATGA TATGTACTTA CTTTcTAATC CTAAGTCACA GAACATATTT ACAGAAGATG 540

TTGCAAACAA ATTGGATGAA CATAACATTT ATTACGGAAG AGATTTACCT ATTATAGGAA 600

GCAGTGGTGT TGTTCATAAT TTCGACTTTT TTATTAGCGC TAAGAAAAAT CAAAAAGAAA 660

AATTTATCAA TGCTATTTCT AACCCTAATA ATTCTATGAT TATTAAGTCG AAAATAACGG 720

ATGCTATGCA AGCAAAAAAA ATAAAAAGAC ACAGGCAAAA TGAGTTTATT TTTATTTTAA 780

ATGACTCAAA AAAAGAAATA AATGAACATA ATAAAAATCT TCTTCATGAA AACTATATTA 840

GTACAATAGA TTATAGCGAA TTAGATGAAA AGATAGGTTT ATTGATTTAA TATATATAGA 900

CGTGATAATA TCAATGTTTA TATTAAATGA AACGAATTTG AAAATTTCGA AACAGCTTAA 960

GATAGCAAAT TGAATAGCCT TATTGATAAT GCAGAATCGT CTACACTTAG TTGAACAAAT 1020

TCTATGAGAA TAGATATTGT TAAACTATTT GGGTAGGCGA TTTTATTTTG ACAAGAGTCA 1080

GAAGATTATT TAGTTCATAG TTTAAGTTAC AAATGGCTAA ACTTTATGAA AATGGTATGA 1140

CTAGAATCGA AATTATACTC GAATACGATT TAACACTCTC AATCTTCTCG AACTGAATAA 1200

ATACTGGGTC ATTCAATCAT CAAGACAACT TAATAAGTGA TGATAAATGT TCATACCATT 1260

TTGCAAATAT AACCAGATAC TCTCAACAAA ATGTAGAGTT CAAAATTAAA AATGTCCCTA 1320

ATTGGCACAT TGCTGTATGA TAATAAATTC AACTTAGATT TCAACAATAT AACTAATGAT 1380

GCTTATATTT ACCGCGATAT CAAACCAAAC AGCCCATCCA CAAACAAATT AGAATATATC 1440

mTGTTAATAA TAGTAAATGA TATATCTTCC AAAGACCGCA AACT 1484

(2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

CTTTATCaTT AAATGCCaTT TTGaATCCTT CTTGAATTTG TTTGATTTCC TTTTCAGTAT 120

TATTAACCTT GTTCAAGACA GTGCCATTAA TTTTCTTCTT GAGTGGACCA ACCTCATCTT 180

TATTAGTTGA TTCATGAATC GTTAATCCAA TGTGTGGCTG TATTCTATAA CCATCATTCG 240

CTATAGTTGA AACATATTGT GaTAATTGTA ATGGTGTATA GGTATCATAT TGACCAATTG 300

ATAAATCTAG ATAATTACCT GGATTATTTG TTAATGGTTC GATTTGACCT CTTGTTTCAT 360

TTGGTAAATC TATCCCTGTT TTCACACCTA AGCCTACTTG ATTTAATCCT CTTCTTAGCT 420

TTTGGGCAGG TGAACTTATG TCTGAAGGTA AAGCCATACC AGAATAATAA GGGTCTCCCG 480

CTAATTTTAA TGCTGTTTTA AACATATATA CGTTTGATGA ATGCATCAAA GCTTGCTTAT 540

CATTAATAGT TACATGCCCG TTTTTATTGA AGTATGATCG TTTTGTCAAA CCACCTTGGA 600

AATGTAATGG TTCATCGACC ATTGTTTCTC CAACTTTGAT AGCTTTATTC TGATAACCGG 660

CTAATAATGT TCCACCTTTT ACAGAAGATC CAACCGCAAA TTGAGAAGTA AACGTACCAA 720

TGTCATAATC AGTCATTTTA CCACTCTTAT TAATCTGCTT TCCGGCAAGC GCAAGAATGT 780

CTCCATTTTT AGGATTTTGT ACAACCATCA TTGcATTATC CATATCTTTG GCACCTTGAC 840

TGCGAsTTCT TAATTTGTTT ATCTAATAAT GCTTCTACTT CTTTTTGAAG ATCTATATCG 900

ATCGTTAATT TCAAATCTTG ACCGCGAGCG CCAGGrTTTA ACACTTCTGA AGATGTAACT 960

TTACCAGATT TGTCCGTTGT GTATTTCATT TCTTTCTTCT TACCACGcAA TACATCTTCA 1020

TATTGATATT CTAGGTAAGA TTTTCCAACA CGATCATTGC GTGAATATCC TTTGGATAAG 1080

TAATGTTCTG TCAATTCTTT TGGaATACCT TCAGCAGGTG TCGATACATC TCCGAATATA 1140

CCTCTTAAAG TATCGCCATA TGGATATTTT CTATCCCAAT CCATAGACGT GTTAACACCT 1200

GGTAATTTGG AAAGTTGCTG AGAAACTGCT GCATACTCTT TTTCACTGAC ATCTTCATTT 1260

TTTATCATTT GTGGATCTAA AACTGTTCCT GGCATTCATC TCTCGAAAAA TAGCTAAAAC 1320

TTGGTAAATC TTTAGAAGAC AATTCATCTA ATTGTGGATT TTCCGGATTT CGGATAACAG 1380

TTGGTnTATC CATAATGGAT CCTGGTTTAA TACCTTCCAn CnGGCGAACA TAGCC 1435

(2) INFORMATION FOR SEQ ID NO: 597:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

AGAAAAAGAT TTAGAAAAGA TTACCATTCG CGACATAACA ACACGCGCTG ATATCAATAG 120

AGGGACATTT TACTTACATT ACGAGGATAA ATATATGTTA CTCGCAGATA TGGAAGATGA 180

GTATATTTCA GAACTAACGA CATATACTCA ATTTGATTTG TTACGCGGTT CTTCArTTGA 240

AGACATTGCG AATACTTTTG TAAATAATAT ACTCAAAAAT ATTTTCCAAC ATATTCATGA 300

TAATTTAGAG TTTTATCATA CTATTTTACA ATTGGAACGC ACGAGTCAAT TAGAATTGAA 360

AATCAACGAA CATATTAAAA ATAATATGCA ACGTTACATT AGTATCAATC ATTCTATCGG 420

AGGCGTTCCA GAGaTGTATT TTTACAGTTA CGTTTCCGGA GCAACAATTT CaATTAnnTA 480

AATACTGGGG TAATGGACAA ACAGCCCATT TTCAGT 516

(2) INFORMATION FOR SEQ ID NO: 598:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1955 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

AGTACTTTAC CATGAGGTAA GACTTTATTC CCTGCTTTTA TAGATTGTGC TTTTATTTGT 60

GTGCCAGAAC CAATAGtAct GGTcTAATGA TTTTGCACTC ACATTATCAA TAGCTTTTTG 120

TTTGTCTTGA CCTTCAACAT CTGGCACTTT ACTATACTCT GCATTAGATG TGTCATCTTT 180

TGATTTACCT ACATTTAAAT ATTTCAAAGT ATTTTCCATT ATTGGTTTAA ACGCTTTACT 240

AACACCTAAT TCATAAGCTT CTTGGTCATT TTTTTGTGCC AAGCTCATAC CAGCGTATAC 300

AATAACTTTA GGATTTTTCT TCGGCGCGTC ACCCATAAAA CTTACAAAAT ATGGGTTTGG 360

ACCTTTAACG TATCCACCAC CATTAGGTGC AGCGACTTGT GCTGTACCAG TCTTACCTTC 420

GACCTCATAA CCATCAATAC GATAGTTTGC AGCGTGACTC TTCTTACTAT TCACAACTAA 480

ATCCAATTGC TTTTCAACTT TTTCAGCAGT ATCTTTTGTT ATTGGTTTGC CTGCGATTTG 540

TTTTTGCCCT TTATAAAATT GTCTTTTACT AACAGGATTT TCAACGCTAT TCACAAACCA 600

TGGTTTTAAC ATATTACCAT CATTAAAGAA CGCTGATTGC GCTTGTAACA TTTGAACAGG 660

TGTTACTGTT GTCGATTGAC CAAATGATGA CGTTTTTTGt TGCAACTCAT TACTCCATCC 720

AATTTGaCCA GGTGCTTCTC CATCAAACAT ACCTTTAGTT GaTTTTCCaA ATCCaAATCG 780

TTCATACCAA GATTTCATTT TGTCTGCACC AACTAAATCT TGTAAATGCA TCATCAATGT 840

ATTAGATGAA TAAGTAAATC CGAGTGACAT TGGGATTTCA CCCCAACCGA CTCTATTCCA 900

AAAAGCACCT TCTTGAATAG CAGCTGCTAA CCCATATGAT TTAAATGTTG ATCCAGGCTC 1020

GTATGTGTTT TGATAAAGGT CATTTGCCCA CTTTTTACCA AAGTCTTTAC CAGTTTCAGG 1080

ATTAAATGTT GGTCGCTGAC TGTATGcTAA AATTTCTCCA GTTTTGGCAT CCATGACAAC 1140

CGCAAATAAA TCTTTCGGCT GGTATCTTTC AACCATGCCA TCTAAAGCTT CTTCAACAAA 1200

TACTTGAATA TTTGAATCGA TTGTTAAATG GACATCATCA CCACGTTTAG GCTGCTTCTC 1260

TTTTTTAGTA TTTGGTGCGA TATATCCCCA AATATCATGA ATATATCTCA ATGATCCTTT 1320

AGATCCACTT AAATAACTAT CAAAAATCTT TTCAACTCCA AGTGCACCTT TAAGTTCACC 1380

AGTATCCGGA TTTTTCTGAG CTCTACCAAT TAAGTGTGAT GCAAAATTGC CATTTGGATA 1440

AAAGCGTTCT GTTTCAGGCA ATAAAGAAAT ACCAGGCAAA TTCATTTTCT CTATTTTCAA 1500

TTTGTCCTGA TACGTTAAAT TTGTTCCTTT GCGTCCAAAT TCAATTTGGA AAGCTTTCTT 1560

TTGACTAAGT CTCTTTTCAA TTTCCTCTGG CTTCATATTA ATGACTGTAG ATAATTTCTT 1620

TGCAGTCTCT TTTTTATCAA CTACATGCCT AGGTTTTTTA GAATTGGCAC TCGCCTTTTT 1680

ATCTATTACT GCAACAAGTT TATATCTTTC TACATCTTCT GCTAGCACTT TACCATkACG 1740

ATCATATATC TTTCCTCGTT CTGGTTGTTG TGCATTCTTA ACTAAATACT TTTCATTTGC 1800

CTTCATGACT AAATCTTGAC CATTAGAATG TCCAGTAATC ATGATATATG AAATTCTTAA 1860

AACCAATATA AAAAAGAGCA GTCCGAATAA ACCAACAAGT AGGACTGCCC CTATTTTATT 1920

TTTTTTAATT TTAATTTTTT TGGTCGCCAT TACTA 1955

(2) INFORMATION FOR SEQ ID NO: 599:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 704 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

TAGCAAGAGT AGGTGATAAC AGTTCTTTTA ACGTGTTTGC TGCTTGCTCA TTTCTTGGCT 60

CATTGTAGAC TAAAATATAA TAAGCGTTTT CAAATAAGTG CTTTTTAGCA TTTAGTACAC 120

CAGATTTATG ACTACCAGCC ATTGGATGAC CACTGACTAA ATGAATATTA TGCTTTAATA 180

AATTGCATTC GTGTTGCTGT ATCATTGCTT TAGTACTACC AGTATCAGAA ACAATAACAC 240

CAGGTTTAGT TGGCATATCT ATAAGCTCGC TAAGATATTT ATTTGTGATA GCAACAGGTG 300

TTGCATAAAT AATTACATCG GCTTTTTTAA TAGCTTCACT ATAATTTAAA CATTTTTCAT 360

TATTAGTATT AGGGTTATGG TATTTTATAT TGCTAGCAAG ACTTCCACCA ATTAATCCAA 480

GCCCAACAAA TAAAACTGTT GTCATATAAA TCACCTTATT TCGAAATTTT CAGAATAATA 540

ACATTGTAAA TGAGCTGTTG ACACAGTGCA ATAGTAAATA AAAATCGATA ATAGCATTAA 600

TAGATAAACG GAGATAAATC ATCTACAATA AAGAGTATAG TAACACAATG GCAACGGAGG 660

GGTAAATCAA TGGAACCAAT ATTAGAAATG ATtAAAACAT TAAC 704

(2) INFORMATION FOR SEQ ID NO: 600:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

CCTCTAAAGG ATCACGAACC TTTTTCATCG TGACTAAGCC TATAATACCC TTAAAcCTAT 60

TATTATTAAC TTTTACCTCT GTGTATTCCC TATCAATTAG GCGACGCCAG TGACGTTTAT 120

CTATATACTT TACTTTCACA GTCACCAACT CCTTGTCATT ATTATATAAA ACTACATAAA 180

TGATGTCATG TCATGATACA GTTTTATAGT TTTTGTTAAT CATATGAAAA TATTTATTAT 240

TATTTTACTA CAACTCGCTT CAATTTACTT AAAATAGACA ATATTAATTA GATAGTACAC 300

ACATTTCTTC ATAAAAGTGA TTTTTCAAAA ATATAAATAA CACACTCTTA TCGTTTTCAA 360

AATCATTTAA TGCTATTTTC ATTAAAAACA GCTGAAGCAT CAAATCTATT CTGATTCAAT 420

CAAGAATACA TATAAAAATG AAGTGACTCA AAGGTTTATT AACAACCTTC AAACCACTTC 480

ATTGATCACT TTTATTTTAA AGCATATTTT TCGATTACTG ATTTAAGATG CGGATATTGC 540

GTAATTAATT CAGATTGCTT AAACAATTCA AACTGCTTAA ACTCAAATGC CGGTTGACAC 600

ATACAACCTA CTAAACTAAA AGTATTTGAT ATTTCGATTG AAGAAGCAAA AATTGTTCCT 660

TTAGGCACTA CATATTGCAA TACATCTCCA TTTTGGATAT CAGTACCCAA TGTTGCAGTC 720

GTATATTCCC CATCCGGATT TATCATATGA ATTGTTAGAG AATCGCCAGC ATGATAGTAC 780

CATACTTCAT CAGCATCAAT TCGATGAAAA TGCGAAATAT TGTCATCTGT AAGTAAAAAA 840

TAAATACTAC TAAACGGCGC TCTGCGTCCA TCTTTCAATA CTTCTCGAAT TGTCTCTCTA 900

TAGAAACCAC CTTCAGGATG TGATTCAAGT TGCAATTcAT CaATCCATTG TTCTGCTGAT 960

TTCATTATTT CAAATCCACA TTATGGAATA CGTTTTGTAC ATCTTCTAAA TCTTCTAATG 1020

CATCGATTAA TTTTTCAAAT GTTACTTGGT CCGCTTCAGA AAGTTCAATA TCTGTTTGAG 1080

GAACGACTGC AAATTGAT 1158

(2) INFORMATION FOR SEQ ID NO: 601:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

TGATACTTAT TTTTCAATAT TATTTGGAAT AAAnTCTTnT AATTGTGGTG TGAAATAAAC 60

ACCGAAATTC TTTTCAGATT CATCTTTTcC ACTACCTGCA TATAAAATAC CAATCAGTyC 120

ATGTTTAGAA TTCAATACAG GAGATCCTGA ATTACCTGGT TGTGCATACG CATCAAATTC 180

CATAAACGTT CCACTGATAT GGTTAATCGT TCCTGTCGAT TCAAACATTT TATATTTTGT 240

TTGTGCACCC TTTGGATAAC CAATAACAGA AATTCTATCT TTCACTTTTG CTCCGTCTGC 300

AAATTTTGTA TAACTAACGT TCTTATTAAA ATTCAAACCT TCTGTACTTG TTTCATGAAC 360

ATGAACTATC GCAAGGTCTT CTTTTCCGGG ATATTCTACA ATGTCTTTAA CGTCGTAGTT 420

TCCTCCGCCT TTACCTTTAC TCGAATGATG TGCTGATACT CTATTTTTAA AAATATCATT 480

ACTTTTAGCG ATATGTTTGT TAGTTACGAT TGTATTTTTA CCAACAACTA CACCAGTACC 540

ACCCACAAAT GCTACCACTG aATTGTATGG TTCCTTAGTT GCATCGGTAA TTTCTTTGAC 600

ATTCTTTTCT GCTTTGGCAA TTGAATGArG CTGATTAGAA ATATTTTCAG CAAAACCAAG 660

AGATGTTAAA ATAGTTAAAG CAGTTAAACC TTTAACCATT ACATTTTTAT TCATATTTTA 720

CCTCCTTCCA AATTTATTTT nATAGTTAAT GTATCTAGAT ACACATTTAC TATATACATT 780

TTAAATAAAA ATATTnATTA AATATTAATT AACCACTTAT nAACGTT 827

(2) INFORMATION FOR SEQ ID NO: 602:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 796 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

nGGnACGTAA AGTATTTATG TTAAATGGCA nAAATATATG AATGATGAGT TACCTGGATT 60

ACCAATGTTC CAAGGTAAAT CGATAACTAT TGTTAACGAT AAAGTACGAA ACTTAGACAT 120

CGACGATTTT GTCGAGGTTT ACTTATATGG GGGGATGTTA TGAATAATGT ATTGTTAGAG 240

GTTAAAGATT TAGAAACATC ATTAAAAATA AATAATGAAT GGTTAGCAAC TGTTGAAAAT 300

ATTTCTTTTG AATTATCTAA AGGAGAAGTT TTGGGTATAG TAGGGGAATC TGGTTGCGGT 360

AAGTCCATAT TAAGTAAGTC AATTATTAAA TTATTACCAG AAAAGATATC TAAACTAAGT 420

AATGGAGAAG TTATATTTGA TGGTAAACGA ATCGATACGC TCAATGAGAA GCAATTGCTA 480

GATATTCGAG GAAATGATAT TGCTATGATT TTTCAAGAAC CTATGACTGC TTTAAATCCT 540

GTATTTACCA TAAAAAATCA ACTTGTGGAA TCTATAAAAT CACATAAAAA AATTTCTAAA 600

AAAGAAGCAA ATAAATTAGC AAAAGATTTA CTAAAAAAAG TTGGAATTGC TAGACAAGAT 660

GAAATATTAA ATAGCTATCC TCATCAATTA TCTGGTGGTA TGAGACAAAG AGTAATGATT 720

GCAATGGCCA TTTCATGTTC TCcTAAATTA TTAATTGCTG aTGAACCTAC AACAGCATTG 780

GATGTCACGA TTCAAG 796

(2) INFORMATION FOR SEQ ID NO: 603:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1618 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

GGATGTGTTC ATCCCAAATT GaAAcAgAaA TTTATGATCA AAtGATGTGG ATTGGTTTTA 60

AaCCATTCAa AATTaCCAAT ATTAmaCAAG AATCTGAAGA CATTAAATCA TTTtACAGTT 120

GAAACTGAAG AATATGACTT TAGTGAATTT ACACCAGGCC AATACATCAC AGTTGATGTT 180

TCTAGTGATA AACTTCCATA TAGAGCTAAA CGTCACTATT CTATCGTATC AGGTGAAAAA 240

AACCATTTAA CTTTTGGCGT TAAACGTGAT GTCACAACAG AACATGAAGG CGAAGTTTCA 300

ACAATTTTAC ACGATGAGAT TAAAGAAGGC GATATGATTA ATTTAsTGCG CCTGTAGGTG 360

GATTCGTATT AGAGAATACG ACTGAACCAC AACTTTTCTT AGGTTCAGGT ATTGGTGTTA 420

CACCTTTAGT AGCTATGTAT GAAGCTGCCT CTGCCAAAGG TTTAGATACA CAGATGGTTC 480

AAGTTGCTGA AAATGAACAA CATTTACCTT TCAAAGACAA CTTCAACAGT ATCGCAAGCC 540

ATCATGACAA CGCTAAATTA TATACACACT TAnAgATAAA CAAGGCTATA TTGGTGCTGA 600

AGAATTACAA GTATTTTTAG CAAATAAACC TGAAATTTAT ATCTGTGGTG GTACAAAATT 660

CTTACAaTCT ATGATCGAAG CACTTAAATC TTTAAATTAC GATATGGATC GCGTACACTA 720

ATATGAAACT TAATCAACGT TACGTAAAAG TATTTGCATT ATATTTCGTA AGTATTGTTA 840

CTGCAAATAT TATTGTTAAA AATAATAATT TAATTAAAAC AtTGATACAA ACCATAGCCG 900

GGTACACGGT CTTTGCAGTT GGTTTGAAGT ATTTAACTAA ACGTAAAAAT AAATGACATC 960

TATACCAAAA CAGCTATGAC TTTACTTTGT CATGGCTGTT TTTTAATTGG GAGTAGGACA 1020

GAGATGATAT TTTCGCAAAA TTTATTTGGT CGTCCCACCA CAACATGCAT TGATGTATGC 1080

TCACTGAATT TCATAAGAAA GGAGTTCACA AGATGACCGT AGATATTGGA CGGATTTATG 1140

ACAATAAAGA TAATACCGAC GCTATTCGTA TCCTAGTCGA TAGAGTCTGG CCGAGAGGTA 1200

TTTCGAAAAG AACTGCTAAC CTAGATTATT GGTTAAAAGA CATTGCCCCT TCTACTGAGT 1260

TGCGACAATG GTTCCAACAT GATCCTAAAC TTTTTGGAGC TTTTAAAGAA AAATATGAAA 1320

AAGAATTACG TGATCAGGAT GCGCAAAAAG ATGCTTTTGA AAAATTAAAG GATATTGTAA 1380

ATCAGCATAA TCATGTTCTA TTGTTATATG CAGCAAAAGA TACTAAACAT AACCAAGCTG 1440

TAGTACTACA GCAGTTGCTC AATACTTAGT TATATATGTT TATCGTGAAT CACTATAAAT 1500

GTCGCTAACT TCATTTCTAA TATTTATTTT TAAAAAGCAT AATTACTACA ATTAATTGGA 1560

ACTTTAATAA TTACTAAACT TGGAACAATA TTTTACTTTA ACAAAATAAA GTTTTAAA 1618

(2) INFORMATION FOR SEQ ID NO: 604:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

ATTATAATGC AAATATTGAA GCATTTAAAA CAGTCGCTAA AGCAGTAGGC AAAGAGAAAG 60

AAGGCGAGAA GCGTCTGGAA AAGCATGATA AAATATTAGC GGAGATTAGA AAGAAAATTG 120

AACAGAGTAC GTTAAAATCT GCATTTGCAT TCGGTATCTC AAGAGCAGGT ATGTTTATTA 180

ATAATGAAGA TACATTTATG GGACAATTCT TAATTAAAAT GGGTATTCAA CCTGAaGtcA 240

mAAAArAmAA AACTACGCAT GTTGGTGAAC GCAAGGGTGG TCCTTATATA TATTTAAATA 300

ATGAAGAACT TGCCAATATC AATCCAAAAG TTATGATTTT AGCCACTGAC GGAAAAACGG 360

ACAAAAATAG AACGAAATTC ATTGATCCTG CAGTTTGGAA ATCATTAAAA GCTGTGAAAG 420

ATAACAAAGT TTATGACGTT GACCGAAATA AGTGGTTGAA ATCAAGGGGG ATTATCGCAA 480

GTGAAAGTAT GGCAGAAGAT TTAGAAAAAA TTGCAGAAAA AGCAAAATAA AAATACAGCG 540

TGTGATGATT TACCTGAAAG TTTATTTCGA ATAAATTTAA TTACATAACC GACAAGGATT 660

GTTTTAACAG TTCTTTTAAT GAATTGGCGC ATCGTTACAT ACCTCATTTC TCTATATCTT 720

ACGAACTATA TACCCATTCA TATATGCTTT TTAAACGTCA TTGTCACAAT TTAATTTTTA 780

GGGAATATAA TATAACCATC TTTATCTGCT TTTTTAGTAA AAATGACAAA AATTGCATGT 840

ATTATTGaGA TGATGGTAGG GATACCTGTC CAGAAAAATA ATAAGTGAAA AAGACCTTGT 900

CCAAATTTAT CAGCATAAAA TTTATGaATA CCTAAACCTC CAAGAAATAA TGCAACmATa 960

ACATAAATGG CTTTATTGAC TTTCATTTGT AAtCCTCCTT AACTATAATT CTACTTAAAT 1020

TCGTTGTGAA AACCAATATT TCTAACTTTA GAATTTTCAA ACTTTCTAAA ATTATAAGTA 1080

TATCTTTTTA AAATAAGCTA GAATTTCTAT ATAATAAATG TTAATAACGT AAAAGGGAAT 1140

GATGACATAG TGATACGTCA AGCACGTCCA GAGGACCGAT TTGATATTGC GAAGTTAGTT 1200

TATATGGTTT GGGATGATAT GGAATTAGAA TTGGTAAAGC ATCTACCTAA AGACATGGTA 1260

TTAGATGCAA TTGAAAAAAG CTGTGTTGAT GCAACATATC GAACTTTTTA TCAGCATATT 1320

TTAGTTTATG AAGTAGAAAA TAAAGTAGCA GGTTGTATTA TTAGCTATAG TGGTGAAAAT 1380

GAATTGAAAT ACGAAAAAGC ATGGGAACTA CTTGACTTGC CAGAAAAAAT AAAACAATAT 1440

GGCACGCCAT TACCTGTAAA AGAAGCTAAA GACGATGAGT ATTATATAGA AACAATTGCG 1500

ACATTTGCAG CATATAGAGG TAGAGGCATC GCGACAAAGT TATTAACGTC ATTACTTGAA 1560

TCAAATACAC ATGTTAAATG GAGTTTGAAT TGCGATATTA ATAATGAAGC AGCATTAAAG 1620

TTATATAAAA AAGTAGGCTT TATATCTGAT GGACAGATTG AATTATACAA GCACATGTAT 1680

CATCATTTAA TTGTTAAATA AAATACTCGA CAGTTCGATG TAAGTCGATT GCCGAGTAGT 1740

ATCATTTTCT ATTAAATGCC TGCAAATAAT GCACTAATAT AAATACCTAA TGCATATAAT 1800

AAACCGAAAA ATGTATTTGT TTTACCAGCA GCAGCCATTG CTGGCATCAT TGTAGGCGGT 1860

GTATCATTCT TCTTGAAACG TCTGATAACT TTAACAGGCA TTGGGAATGA TAACAACGCA 1920

AGTAAGTAAA ATAATGAGCC ACCAGGTTTA ATAATGATCG TAAGTACAAT AAAGGCATAA 1980

GCGATAAAGT ACATGATTGC CATAAATGTT AAAGAAGCAT TTTTACCTAA TAGAATGGGT 2040

AAAGTTTTGC GACCACTTGC TTTATCTTTG ACACGGTCGC GAATATTGTT AGCCATATTA 2100

ATTAAACCGA TAGTG 2115

(2) INFORMATION FOR SEQ ID NO: 605:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1003 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

TATGTCTCAA ACTCAAATTA ATCAAATGTT CCAGCAGAAA AACATGTCTA CTGAATTAAA 60

ACGTCGTTAT GCACAACGTT TATTACAGTT TCCACATGTA CACAATAAAG AATACTTGAA 120

ATCTTATGCT AAAAACCCTA AAGAAACTAA AGATAGTTAT ATTTCTGGTT TTAAAGAGAA 180

TCAATTGATT AAAATAGAAG CGATTAAATC ATTGTTTGCA ATGGATAAAT CTCCATTAGA 240

ACATGTTAAA CCTGCTACAA AACCAGACGC TTCTTGGGAT GAGATGAAAC AAAAAGCAGT 300

TGAAATTGGT AAAGCTGATA CTACATCGAA TAAATTTGGT ATTAGAGATC AATACTGGAA 360

ATTAATTCAA GAAAGTAAGC GTAAAGTTAG ACGTGACTAC GAATTCAATG TTAATTCTCC 420

AGAATTCCAA GATTTAGAAT TACTTGTAAA AACAATGCGT GCTGCTGGTG CAGATGTTCA 480

ATATGTAAGT ATTCCATCAA ACGGTGTATG GTATGACCAC ATTGGTATCG ATAAAGAACG 540

TCGTCAAGCA GTTTATAAAA AAATCCATTC TACTGTTGTA GATAATGGTG GTAAAATTTA 600

CGATATGACT GATAAAGATT ATGAAAAATA TGTTATCAGT GATGCCGTAC ACATCGGTTG 660

GAAaGGTtGG GTTTATATGG ATGAGCmAAT TGCGAAACAT ATGAAAGGTG AACCACAACC 720

TGAAGTAGAT AAACCTAAAA nTTAAAATAC AAATAGCACA TAACTCAACG ATTTTGATTG 780

AGCGTATGTG CTATTTTTAT ATTTTAAATT TCATAGAATA GAATAGTAAT ATGTGCTTGG 840

ATATGTGGCA ATAATAAAAT AATTAATCAG ATAAaTAGTA TAAAATAACT TTCCCATCAG 900

TCCAATTTGA CAGCGAAAAA AGACAGGTAA TAACTGATTA TAAATAATTC AGTATTCCTG 960

TCTTTGTTGT TATTCATAAT ATGTTCTGTT AACTTAATAT CTT 1003

(2) INFORMATION FOR SEQ ID NO: 606:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1097 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

GCTnTTATAT TTAAAAAATT TATTnGCGGA TAATTACCTT TATTAAATCC CACCCATTAG 60

GAwTaCGAGT AATAGGACTA ATACTGGAAT CACATAATGT AACATAACGT CCCTCCTTTA 120

ACTTAATTTT AATTGTAATC AAATTTGACA ATAAGTCAAA mCATTAATAC CTATGATArG 180

TATCATTTAT TAACATATGT ATCATATTTT TAATCTTGCG TAATTTTTAT CGTTAACTAT 240

CTTTTGTCAT TTTAATTATG TTAAGATAAT AGTAGTTATA GAAGTTCAAT CTATAGGAGG 360

CATAGCATGG ATATTCCAAA AATCACGACA TTTTTAATGT TTAATAACCA AGCTGAAGAA 420

GCTGTTAAAC TATACACAAG CTTATTTGAA GATAGTGAGA TTATAACAAT GGCTAAGTAT 480

GGTGAAAATG GACCTGGTGA TCCCGGGACT GTACAACACT CAATATTTAC ATTAAATGGA 540

CAAGTATTCA TGGCGATTGA TGCTAATAGT GGCACAGAAT TACCAATGAA TCCTGCGATT 600

TCATTATTTG TTACAGTAAA AGATACTATT GAAATGGAAC GACTATTTAA TGGATTAAAA 660

GATGAAGGTG CCATTTTAAT GCCAAAAACG AATATGCCAC CATACAGAGA GTTTGCTTGG 720

GTTCAAGATA AGTTTGGAGT AAGTTTTCAA TTAGCATTAC CTGaGTAAAA GGATTCGCAC 780

AGCtTGgAAT GATAAAGAAA CACTTTTTCT TATGCATGCG TTTTACCTAT GTATTTCTAT 840

TTTAAGTACA CATTAGCATT TTAGTTTCGC TCATTTTTAA AATCACAAAG ATAATTTGTA 900

ACTTAAATGA TGATACGTTA TTTAAAAACA CGATACTTCG TTTCAATGAA CGCATTAAAT 960

AATAAATAAA CACCTCACCA TAAGAAAGGA CTACTTTCTT TTGTGAGGTG TTTatTTGTC 1020

GACAACTTGA TTATGATTGT TTCATTTTTT GAATAAGTTC ATAATCAGGT GTAGCATACA 1080

AAGTTTTTTG ATTGTCA 1097

(2) INFORMATION FOR SEQ ID NO: 607:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2031 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

GAGGTCTAGC ATGTCTCGTT CAAAAAAATA CTTTTACTTA TCTAGCTTAA TGATTATTTT 60

AAGCTTTTTC TTTAATACAA ATAACGTTTT CCTAAGTGGA CTTTTTAATT CTTTTATTAA 120

ATTAATACTT TTCTGCAGTG TTATTAACTC AATTGTACTA ATTTTGTCTA TAATTTTTGC 180

AGATCGTTCA ATTAAATCAC TAAAGCCTGA TGCAGATTGG ATTAGAATTG CGAGTAAAAG 240

TTTGCCTTGG aTTATTCTAA TTGTTATTTT AGTACATATC TTTTCAATTG TTCGTACATT 300

CGGTTTTATT TAAAAAAGTT AATATGTCAT TGTAGCCTTA ATACAAAACA ATACAATGTA 360

TCATGCTATA ATGAGTAAAA CAATTTGATA ACGTTGTTGC GTATAAAAAA TATTAGATTT 420

TCGAAATCAT AACTATGCAT CTAATCGCTA TAGTTATACA ACAAGATATA ACATATAATG 480

AGGTTTGATA ATGCATCGAC AATTTTTGTC GTCGCGTTGC CAAAACCTCT TTTTTAAATT 540

TTTAGGCGCT TTATTACGTT ACCTCATTTC TTTTCTGAAT ACTGACGGAG GTTTTCCAAT 660

CGGAACACTG ATAGCCAATT TGACTGGTGC CTTTGTAATG GGATTGCTAA CAGCCTTAAC 720

AATTGCATTT TTTTCAAACC ATCCGACCCT AAAAAAAGCT ATTACGACTG GTTTTCTTGG 780

TGCTTTAACG ACTTTTTCAA CATTTCAATT AGAATTAATA CATATGTTTG ATCATCAACA 840

ATTTATAACT TTACTACTAT ATGCTGTAAC AAGTTATGTC TTTGGTATTT TGTTATGTTA 900

CGTCGGTATA AAACTAGGTG GTGGTTTATC ATGATATCAA TCATTTTAGT CATGATTGGC 960

GGCGGTTTTG GCGCAATTGC TAGAAGTGCC ATTACTGATT ATTTTAATCA TAAATTTACT 1020

TCAAAGTTAC CTATCGCAAC ATTGATAGTA AATCTAGTTG GTAGTTTTTT AATTGGATTA 1080

ACTATAGGCT TATCAATTTC AATCTCATGG TTCCCTGCGT TCTTTGTTAC CGGTTTTTTA 1140

GGTGGCTTAA CAACTTTCTC AACGTTAGCC AAAGAACTTA CACTAATGAT GACGCCAAAA 1200

TTTAATATTA ACCTTTTTCT CAATTATTCA CTTTTACAAT TCATCATTGG ATTTATAGCT 1260

TGTTATATTG GCTATCATAT TTAAAAATAA AATGCTTCAT TCAGCAAATA GGTAAATTAC 1320

GACACCTTCC TGAACGAAGC ATTTTTTAAT TTTCATGCAA ATTTTTAAGC ACCATATAAT 1380

GCCTACCAAA TTTCAATAAT CTTTGTTGCC GTTTAAATAA TGTGAATGTC AATAAATTCT 1440

CCAAACTAGT CGAAAATAAA GGGAGTGGGA CATAAATCCC TAAAAAAACA GCAGTAAGAT 1500

AATTTTCAAT TAGAAAATAT CTTACTGCTG TTCTCTATTT ATACAATACT TCGTATTGAa 1560

TGGcTTCGCT TTCCTAGGGT GCCGTCTCAG CCTCGGcTTC GACTGGCACT GCTCCCTCAG 1620

GAGTCTCGCC ATTAATAcTA CGTATTAACA TGTAATTTTA CTTTTACATA CTTTAAAAAA 1680

TAAGACACTT TGCCCAACTT ACACTACCAA TAGAAACCTC TGTTAGAATT CCTCAAAATG 1740

ATATTTCGCG ATATGTTAAT GAAATTGTTG AAACGATACC TGATAGCGAA TTCGATGAAT 1800

TCAGACATCA TCGTGGCGCA ACATCCTATC ATCCAAAAAT GATGTTAAAA ATCATCTTAT 1860

ATGCATATAC TCAATCTGTA TTTTCTGGTC GAAGAATAGA GAAATTACTT CATGACAGTA 1920

TTCGAATGAT GTGGTTAGCT CAAAATCAAA CACCTTCTTA TAAAACTATT AATCGTTTTA 1980

GAGTGAATCC TAATACTGAT GCGTTAATTG AATCTTTATT TATTCAGTTC C 2031

(2) INFORMATION FOR SEQ ID NO: 608:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 687 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCCCCGGGAA TCGAACCCGC GAnCTCCTGC GTGACATGCA GGCGTGTTAA CCGCTACACT 60

ACGAGACCTA TTAnATTAAA AACTATGTAT TGCGGGAGGC GGATTTGAAC CACCGACCTT 120

CGGGTTATGA GCCCGACGAG CTACCGAACT GCTCCATCCC GCGCTAATAT TATTTTGAAT 180

TACCTAATTA ATATACCATA ATCAAAAACC TAAAGTsrrG AACTTTTTGA ATTTAATTTA 240

AATGTTATCT CTTAAATAAT TACTTAAATA TCGTAGCAAC ATGTTCTCTG TTGAACACAA 300

ATATTAGTAT ATTCATTTTT GTAGTGTACG TCAACGACAT TTTCAAAGTT TTTTGTGTAA 360

AAAAACGCTT CTTATTCCCT TTTATCATAT AAGTGTCTAA TAGTTGTCAT AAATAGTGkT 420

AAAGCATTTA AAAAGGTATA GGAGTTATAA AGTTTACAAC GCCTATACCT TCTGAAAAAG 480

AAATTATAAA AGCTTGTTAC ACCGCATATT CTTTCAGTCA GCGACTACCA ATATAACATT 540

GTAGCCCtAA GACATTGCTT GACGCCTCAn TTACAACAAT TTTTCAAAAT CAGCAGCTAC 600

CTACTGACAC AACATAACAC AACCCnTACA CTAnCTATCG TGTCATGTAA TCTTGCATCC 660

GATCTTGCAA CGCTGTAAAT GTTTCGA 687

(2) INFORMATION FOR SEQ ID NO: 609:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

GTGTTGAATA CTTTGACAAA ATGAAATCAT TTGTTCTTTC GTTTCAAATT TAACTGTTTG 60

AATTAAATCA GTTCGTTTTT CGTAGTACTT CGGCGTTGTG TTCATATTCA TTTTTTCTAA 120

AAATAAACTA GTAAACAATG CACCTTTAAG ACTCTGACTG ACAACGTGTG GTGCTAAAAA 180

GAAACCTTGA TACATTTCAA GCAATGCATT TAATGATGCA CCCGCTTCTT TACCAATACC 240

AGGTGCTGTC AATCTATAAC CACATCGTTC AATTAAATCT TTTCTACCAG CAATGTATCC 300

ACCAATCTTA GCTAAACCAC CGCCAGGGTT TTTAATTAAT GATCCTGCTA TTAAATCGGC 360

ACCACATTCT ATAGGTTCAC GTCTTTCAAC AAATTCCCCA TAACAGTTAT CCACAAATAT 420

TAAAATATTA GGATGCACGT TTTTCAACCT AGTAATTACC TTTTCAATTT CATCTAGCGG 480

AATTGAAGGT CTTTGATCAT AGCCTTTCGA ACGTTGAATC GCTATTACTT TGGTGCGCTC 540

AGAAACCCCa TCTAACACAC TTTCAATATC GATCTTACCT TCTTTAAGTG CAATATCTTT 600

ATACGATmCG CCATGCTCCA TTAAACTTTC AATACCATTT CCGTTTACGC CAATGACTTC 660

ACTTTGTAAT GCAATAGTAA TCGCATGCGT ACCTGAAATA ATTTGCGGAC GAACAATTGC 780

ATCTTCTGCT TTAAATGCCT GCGCATATAT TTCTTAATTG AACGAATTTA GAACTAATCG 840

TAA 843

(2) INFORMATION FOR SEQ ID NO: 610:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 775 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

GATTATTATA AACCGAATGA AACAAAAAAG TTTTTACATA TTTTCAACAA CTTTATTTCA 60

ATAAAGCATC AAGTTGATCT AAAGTTTGAT TCATACCTTG TTCAACACCC ATGTTTATGA 120

CTTGTTGAGC GGCTTCTTTT GTTGGAAATA CCGATGTTGA TGTCACTGTC GTTTTCGTTG 180

TATTGCTCTT GGAAAATGAC AAAGTAATTT TCATGCTTGG CATTTTTGTA TCTTTTGCAC 240

CTTGAGGTGT CGCAAATGAG TCAATATATT CAATTAAATA TGGACGCTTA ACCGTTTTAT 300

ATTCTGCTAA TGTATAGCTG GTCATTGTAG GTGTTTTAAT CGCATAAAAT GCATCACCGC 360

CTGAAACAGC ATTAAAGCGA AACACTTTGG TACTAGCGTC TTTTGGAtGA AACCATTTTT 420

CAAATAATGC TTTkGTCGTA TAGGCATCAA ACACCTTTTC AATCGGTGCT TCTATCGTTC 480

TTGAAAAAAT AATTTTATTA TCTTCAACTT TAATCGTCAT CTTCCCACTC CCTATCTTTT 540

ATATTTACTC ATCTTAACAT GCATTGAGTA ACATATGTTA CCAAATCATT TGTTATAAAC 600

TATAGTAATA TTAATCATTC CCTCTGTnGA AATTGATAAC TACGAAATAA AAAACACACT 660

CTATTCAGCT ATTAACAGTT GAGTAGAGTG TGCAAACCTG TTGAATTAAT GCGCTAACAT 720

TTCTTCTTTG ATTTGGTCTT nATnTAATTT TGAAGGATAA TATGTTGGCC AGTTA 775

(2) INFORMATION FOR SEQ ID NO: 611:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 728 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

ATCAAAATTT GATACTAAAG GGCTCACGCT ATTTTATGTA TTTATTGGAT TGATTATGTT 60

TGTGGCAATG TGTTTATTTA AAGTAGAAAA ACATGTTTCT TCACCATTTT TACCTGTGGT 180

TGAATTTAAT CGTTCGATTA CTTTAGTTTT TATAACTGAC CTTCTAACAG CTATTTGTTT 240

AATGGGATTC AATTTATATA TTCCAGTCTA CCTTCAAGAA CAACTAGGAT TATCTCCATT 300

GCAAAGTGGA TTGGTTATTT TTCCTTTATC TGTAGCTTGG ATTACATTGA ATTTTAATTT 360

ACaTCGAATT GAAGCAAAAC TATCAAGGAA AGTTATTTAC TTACTATCAT TTACATTGCT 420

ACTAGTAAGT AGTATTATCA TTTCATTTGG TATTAAATTG CCGGTACTTA TAGCATTTGT 480

GTTAATTTTG GCAGGATTAA GTTTTGGATA TATTTATACG AAAGATAGTG TGATTGTCCA 540

AGAGGAAACT AGCCCATTAC AAATGAAGAA AATGATGTCA TTTTATGGAT TAACTAAAAA 600

TCTTGGGGCA TCAATAGGTT CAACAATAAT GGGATATCTT TATGCGATAC AATCAGGAAT 660

CTTTGGTCCA AACTTACACA nTGTGTTAAG TGCTGTTGCT GTAATTAGCA TGGGCTTATn 720

GTTTTATG 728

(2) INFORMATION FOR SEQ ID NO: 612:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 913 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

TATCAGAGCA AATAAGCAAG TTAGATAAAA AGATTTCTGA CTTACAATTA ATTAGACGCT 60

CTGTATGTGA ATTTATTAAA GGACTCTCTC TAATAGATAC CAGCATTTTA AACAAGACAC 120

TACAGTCACA ATATGATAAA GAAGCATCTA TAAAATATGG TCATACGAAA GCATATCAnT 180

CATTTATTAG ACGTAAAGAC AGCTTACAAT CGCAGGATAT CAGACATAAA TTGACAACTA 240

TCTTCAATAA ATTTAATCAT ATGTCTTTGA GTCATTATCC AATCCAAGAT TGTAGTGATC 300

TCGTATTTGA GTGGAAGGCA TTTATGAACA CTATCGCTGA TTTTGmTGAT GAAACATTAT 360

GCTGTATTGC TAAAACATAT GAAGATGATA CGCGTTTCAA AGATTACTTT AATTCATATG 420

ATAATCAAAA TTTAGCATCA TACATTTCAG AAGCTGTTAA TTATTTTTTG AGCAATGTGA 480

ATAAGAGCGA CAATTTTTAA TCCTCATACA GATGCTACAA CACTGAATAC ACCAACTAAA 540

ATAATTGTTC AAAGTAGAAA ACTAATCATT TATTCTCTAA ATCAATAACT ATATTAAAAG 600

TTATACCTTT GCAAAGCGAA TTAGTATAGG TTACCGAAAG GAGAAAGGAT TAGGTTCCAT 660

TCGATTTATA AAAAAATATA TTTCGAAACA TACAAAAGCG CCAGAAGATA ATCATTTCCT 720

TCAATGCATA TTCAACTAGC TCAGGTTTAC TCTTTAAGCC AAGCTTTGTC ATAATATGCG 840

TCTTATGTGC TTCTACTGTT TTCACAGATA CAAATAATTT CTCTGCAATT tCTTTATTCC 900

CGTAACCTTT GGC 913

(2) INFORMATION FOR SEQ ID NO: 613:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 654 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

ACAAGTGTTG ATGTCATAGT AGCGTCAAwT GTGCTTTATT TCTGGGACAC ATTTAAATTT 60

TTCCACCCCA TTACTTGGAG CTTAATCTTT ATTACAATTT TACTATTATT AAACATTTTT 120

TCTGTAAAAT CATTTGGAGA AACTGAGTTT TGGTTATCAT TGATTAAAGT GTTAACAATT 180

ATCGTATTCG TTATTTTTGG CTTTTTAATG ATTTTCGGTA TCTTAGGTGG TCATACATAT 240

GGATTTGAAA ACTATACAAA AGGCCAAGCA CCGTTTGTTG GTGGTATCTC TGGTTTCTTA 300

GGCGTATTAT TAGTCGCCGG ATTTTCGGTT GGTGGTACAG AAGTAGTAGC AGTAACTGCT 360

GGTGAATCAG ATGACCCTAA AAAGTCTATG CCTAAGGCAA TTAAACAAGT ATTTTGGCGT 420

ATTCTTTTAT TCTATGTCTT ATCAATTGCA GTAATTGGTG CAATTATTCC GTACACAGAT 480

CCATCATTAT TAAGAGCAAG TAGTTCAATA AGTCAAAGCC CATTTACAAT TGTATTCGAT 540

AGAGtAGgCA TAGCCTTTGC AGCATCAGTA ATCAACGCGG TTATTTTAAC TTCATTATTA 600

TCCGCTGCAA ATTCAGGTGT TTATACAACA GGCAGAATGT TGTATTCCTT AAGT 654

(2) INFORMATION FOR SEQ ID NO: 614:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

TCGATCTTTA TTGATAATAA TTAAATTGTC GCCTTTAAAA TGTGATATTA ATCCTGCGGC 60

AGGnTGTACA ACGAGTGATG AACCTAGTAC AACAAGGGTG TCAGCATGTT CAATTTTATT 120

TAATGCCCTT ATGATGGTAG GTTGATCTAA CATTTCACCG TATAATACGA TGTCCGGTCG 180

ATAAGATTTA TGACATACAT TACAATAAAA ACGATTTAAC GTGCCATGTA ATTCATCAAC 300

ATGTTGACTT CCAGCGTCTG AGTGCAAACC ATCGATATTT TGCGTGATGA CACCTAAAGA 360

TTGTTGATTA CGTTCTAATT TTGCAATCCA ATCATGAACG ATATTGGGCA TCGTATCGAC 420

AAATAGTAAG CGCTTATGGC AGAAATTGAT AAAACCTTCA GGATCATCTT CTAAATAATC 480

ACGGCTTAAC AAGTATTCTG GCGAAAGCCC ATCTTTTGaA ATTTCATCAA ATAAGCCACC 540

CATTGaACGG AAATCTGGAA CGCCACTTGC GACAGATACA CCAGCACCTG TAAAAAATGT 600

AATACGATTC GAACTATCTA TAATATGTTT TAGTGTCTCT AA 642

(2) INFORMATION FOR SEQ ID NO: 615:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

TTTCCCCnCC CCnCCAAATA TCCAAnGGAA CTTTAATAGT CCAATTGGCA CAGTAAAACT 60

ATGGCATTTT ATAAGTATAA TATATCTGTA ATTTATGGTC AATTAGTAAA TTGTTTTTTA 120

TTTGAAACAT ATTTCACATc AAAATCACAA AGACTTTTAG ATTTTGtTCT AAAAATCTCT 180

TAATAATTTA TTTAATGAGA AGAGTTGCTT ATATAGTAAA TTGTGAAGCC GTTAAAACAA 240

CGTTACAAAA CCTATATCTT TAATACGGAA CCATATGGTA TGAATCAAGG AATACTTAAA 300

CTAAAACTTC TCTATCAGAT TTATTTGTTG CGAAATCAAC AACTTTAATT GCTTGCCCTT 360

CATTTAATGG ATAATTTGCT TGCGTAATTT TAACTTTTAC AATTTGACCT ATGAGTGATT 420

CGTCACCTTC AAATTGTACT TTCATATAAT TATCTGCATA TCCAACTAAT GTACCTTCTG 480

TGtCACCCTG TTCCTCAGGA ATTACTTCAA GCACATCTTG ATCAAATTTA GACGCATATA 540

ACTTTCCGAG TTGATTGCTT AGCGTAATTA ACTTATGCAC CCGTTCATTT TTAATTTCTT 600

CATCAATTTG GTCATCCATT CTTGCAGCTG GCGTGCCAAT TCTAGGAGAA TAAGGGAAAA 660

CATGCAGTTC AGAGAACTTA TGCTTTACGA TAAAATCATA TGTTTCTTGG AACTCAGCTT 720

CAGTTTCACC TGGGAAACCA ACAATTACAT CACTCGTAAy TGCCAAGTCT GGTAAAGCTT 780

TATGCAATTT TGTTAATCGT TCTGAAAATC TATCCATTGT ATACTTACGT CTCATACGTT 840

TTAATACTGT ATCTGAACCA GATTGTAATG GAATATGCAA ATGACGCACA ACTTTTGTTG 900

AACGTTCTAA AACGTCAATT ACTTCATCTG TAAGTTGACT TGCTTCAATT GAAGAAATTC 960

CTTTTAAATC TTGACCATAT CCACCTGTAT GAATTCCCGT CAATACAATT TCCTTATATC 1080

CTGAATTCAC TAGTTGCGTC GCTTGTTCAA CTACTTTTTC CGGATCTCTT GAACGCATTA 1140

AGCCACGAGC CCATGGAATA ATAcAGAATG TGCAGAAGTT GTTACAACCT TCTTGAATTT 1200

TTAATGACGC 1210

(2) INFORMATION FOR SEQ ID NO: 616:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 652 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

TAATAAAATA CAATACTTTT CAATACAGAG AATCCCGCAA TGTCGGGATT CTTATTTATG 60

CTGATTTTGT TTTTGTCTAT GATCAGGGAC TTtCAGGGAC TCAATTAATT ATCACATTCA 120

TATTTTCTTA TGACCAAATT GATACATATG ATGCTATTTA ATGAGAAAAT TAGGCATCAC 180

TTGGTTATTG AATTTCCTTC ATTAAACTTT CCAGCTCAAT TTAATAGTTA GTCGACTATT 240

ATTCATTAAA CACTTTTTAA TCATAAAAAA GTGTTTTTGa TAATTCACTa CCaAAAACAC 300

CTTCTTACTT ATAATTCTAT TTGTTCACCA TTTCTAATCT TATCGGCTAA ATCATTCAGT 360

TTTCTTAATC GGTGATTTAC ACCTGATTTT GAAATTGGAC CAGTTGATAC CATTTCTCCA 420

AGCTCTTTCA ACGAAATTTC TTGATGTTCT ACTCGAATTC TAGCAATCTC TCTCAACCTG 480

TCTGGTAAAT TTTCAATACC AATTTCTTTA TCAATCAATT TAATGCTCTC AACTTGTTTC 540

ATCGCAGCAC TAACTGTTTT ATTTAGATTG GcCGTTTCAC AATTAACGAG TCGGTTAACA 600

GAATTACGCA TATCTCTTAC AATACGTACG TCTTCAAATT TTAATAACGC TT 652

(2) INFORMATION FOR SEQ ID NO: 617:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 798 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

TnACCACTTT AAAATAGCGC TTAATAAAtG AAGGGGGCAA GTCTTATGAC GtTTTACaAT 60

TTCATCaTGG GTTTTCAAAA TGrTAACACA CCATTTGGTA TATTGGCCGa ACACGTTAGT 120

TCTAATTACA CAGATCATCA ATTAATTGAA ACTACAAATA GAGCTATTAG CTTATATATG 240

GCAAATTAAT TTGAGTAGTA CCAATTATGA TGTATTAGTG CATCCCAAAT ATCTTTTGTT 300

TTAAAGTTTA TTTCATCATT TCTTATCGAA AATGGTGTAA TAATGTCTTT ATCTAACCAA 360

GTGTTGATAA GTTCATTTGG TACACCATCT AACAACATTT CACTTTTACT AATTATAAAA 420

CATTCCCAGT CAAGTGAAAC ATTTTGTGGA TTCACATAAT TACATTGATT ATGATTATCC 480

ATAAACACTC ACTCCTTTAA AATTCTGTAC TCTTCATTGC GTTTTACCCC GTCACATTAT 540

CTTTTAAACT AAAATCATCA TTACTTATGA AAAAAATGTA CATCAAAAGC AAAGGTTTTC 600

GCTACCGAAA AAGTTTAAAT AATGGTttAA TATATttGGT ACTCATTTTA ATAAAAAGAG 660

AATACATTTT GAGCTATCAA TACTTTTTAT TGAAGAGGTG TTATTsyTGG CTAAAACGTT 720

ATATTTAATG CGCCACGGAC AAACTTTGTT TAATTTTAAG GGACTAATTc AGGGATTTGG 780

AGATTCGCCG CTAACAGA 798

(2) INFORMATION FOR SEQ ID NO: 618:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

ATACGCTCAA TTGATAAAAA TTTAATATCT GCCATTTGTA TACGCATCGC TTCGAATGTT 60

TCCGTTGCAA TATCAAATGA TAATTGTGAC TGGAACCTTA AACATCGAAT CATACGTAAA 120

GCATCTTCTT GGAATCGTTC CTCAGCTATA CCTACAGTTC TTATTATTCG ATTATTAATA 180

TCTTGTTGAC CATCAAAATA ATCATACAAT TTGTATGCTG TATCCATTGC TATCGCATTC 240

ATCGTGAAAT CTCGTCGTTG CAAATCTTCG TATAAATCAC GAACAAATGT AACACCACTT 300

GGTCTACGGT GATCGACATA ATCTTCTTCA GCCCGGAATG TTGTCACTTC ATAATTTtCA 360

TCATtAAAaa CTACATTtAT CGTGCCAtGT yCTTnACCTA CAGGTATCGT ATGACTAAAG 420

ATAGATTCTA TTTCATCCGG CGTTGCACTT GTTGTGATAT CTATATCATG AATATTTCTT 480

CCCATGACAT AATCTCTTAC AGAGCCACCT ACATAATATG CTTCAAAACC ATTGTCTTGA 540

ATTTGTTCTA ATATAGGCCT TGCCTGTTCA AATAATGATT TATCCATATT ATTACTCGCC 600

TTTACTTTTG TTATGCTCAT TTAGCATTTT TTGATAATAA TACTCATATT GATCTGTAAT 660

AAGTTCTGAT CCAAAACGTT CAGCAATATC TGCTAGCATG TTTTTCTGAA GTTTGTTGTA 720

ATCTACGACA AATCCAGTTT CACCATGTTT AATAACCTCT TTAATTCCAC CGGCATTTGA 840

ACCAATTGGA ACGACGCCTG TwTTCATAGC CTCAAGTAAA GTTAGTCCAA AGCTTTCTTT 900

TTCACTTAAT AATAATACTA AGTCAGATAA TTGGTAAAAT TCACTTACGC AATCTTGTTT 960

CCCTAAAAAT AAAACATCCT CTTCTACGTT TAACTCTTTC GTCAATTGAC GCATTGGCAC 1020

TAATTCAGGA CCATCTCCAA GTAAAATTAA TTTACTAGGT ATCTTTTCAC GTACTTTTGC 1080

AAATGTTTCT ATAATAGTAT CTATGCGTTT TACTTGTCTA AAATTCGATA CATGTATTAA 1140

CACTTTTTCA TCTGGTGCTA TACCAAATTG TGATTTTAAT GCTGTGTTAT GTTTAGTTGG 1200

AAACTCATTT TCACGTACAA AATTATAAAT CGGTATAATT TCTTTGTTAG TTTCAATAAT 1260

TTCATGTGTT TCTTGTGCTA AAGATTTACT CACACTTGTC ACAATATCAC TTTTTTCAAT 1320

GCCAAATTTA ATTGCACCTT GGAGTGAATG ATCATAGCCC AAAACAGTAA TATCAGTACC 1380

GTGTAGCGTT GTCATAATTT TTATATCTTT ACCTGACATC TCACGAGCTA AAATCCCACA 1440

AATTGCATGA GGTACAGCAT AGTGCATATG CAACAAATCA AGATCATATT CTTTAATAAC 1500

TTCAGCGATT TTAGTACTTA ACGTAATATC ATACGGTGGA TACTGAAATA CTGCATATTG 1560

ATTCACTTCA ACTTGATGAA AAATCATATT CGGTAATGGT TTTCTTATTC TAAACGGGAT 1620

ATTTGAAGTG ATAAAATGTA cTTCGTGACC TCGCTCTGCT AATTTAATTC CTAATTCTGT 1680

GGCAATAATT CCAGAACCAC CCATGGACGG GTAACATGTT ATACCTATCn TCATTCGCTT 1740

GCCCATCCTT TCTTTCTATT TCTCnCTATG ATnCTCGATG CGTAGA 1786

(2) INFORMATION FOR SEQ ID NO: 619:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 844 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

ACAGGTATGG ACTTnGCTCA AATGACACGA CATTATTTAT CAAGACCTAT TGCTATAATC 60

TTTTGGATCA TTGCAGAACT AGCAATTATC GCTACAGATA TTGCTGAGGT TATTGGTAGT 120

GCTATTGCTC TTAATCTCCT ATTTAACATA CCTTTAATCG TCGGTGCACT AATAACTGTA 180

CTTGATGTAT TTTTACTACT TTTTATAATG AAATATGGTT TTAGAAAAAT TGAAGCTATT 240

GTTGGTACAT TAATTTTCAC AGTGTTATTC ATCTTTATAT TTGAAGTCTA TATTTCATCA 300

CCACAGTTGA ATGCTGTGTT AAATGGATTT ATACCACATA GTGAAATCAT TACAAATAAC 360

TTACATTCAT CAATTGTACA ATCTAGAACA TACTCAAGAC ATAACAATGA AGAAAAAGCG 480

CAAGGaTTAA ATTTGCTACG ATAGATTCGA ACATTCAGTT ATCAATCGCA TTTGTAGTCA 540

ATTGCTTATT ATTAGTGtTA GGAGCATCAC TATTTTkCAA CTCAAATGCT GACGATTTAG 600

GTGGTTTCTA TGATTTATAT CACGCCTTAA AAACTGAACC TGTACTAGGT GCAACAATGG 660

GTGCAATCAT GAGTACATTA TTTGCAGTTG CATTATTAGC GTCAGGTCAA AATTCAACGA 720

TTACTGGTAC TTTAGCAGGA CAAATTGTAA TGGAAGGATT TTTAAGATTA CACATACCAA 780

ATTGGTTAAG ACGTTTAATT ACACGTTCTC TTGCTGTCAT TCCTGTTATC GTATGCTTAA 840

TCAT 844

(2) INFORMATION FOR SEQ ID NO: 620:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 574 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

TGTATTGCAG TCATGCCATA AATTTTTTGA ATAATAAACG GAGACGCAGA AATATAAGTA 60

AATAATATTA CAAATGTCAT ACCTTGGAAT GAGCATTGGT AATACAAAAC GTGGCGTCTT 120

CAnTAATATT TTGAAGTTTT TAAACATTGT CTTTAaTCCA CTACTTGACT CACGATTTGT 180

CACTGTTAAT GATTCAGGTA CTTTTAATAA AGAACCTATG ACCATGACGA AGCCAAAGAT 240

AGTCAGAATG ACAAAGACCA TACGCCAGAC AGAATAATTT AAAATTATGC CCCCTATTGT 300

TGGCGCAACA ACTGGTGCAA TACCATTAAC AAGCATCAAT AATGCCATAA ACTTAGTTAG 360

TTCATTACCA CTATACATAT CACTTGCTAT AGCTCTTGAA ATAACTGCTG tGCGCCACCT 420

GTCACTCCTT GAAGaAATCT TAATGCAACC ATCAGCCAAA TATTATGTAC AAAAACAATA 480

CCTAAACTTG CTAATGTAAA AATAATCATA GCTATAATAA GCGGCTTTCT GCGCCCAGTT 540

GAATCTGAAA TTGGACnAGC AACCAAATTA CCAA 574

(2) INFORMATION FOR SEQ ID NO: 621:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 523 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AAGCAAGAGA GAGTACAACA TTTATATGAT ATTAAAGACT TACATCGATA CTACTCATCA 60

GAAAGTTTTG AATTCAGTAA TATTAGTGGT AAGGTTGAAA ATTATAACGG TTCTAACGTT 120

GTACGCTTTA ACCAAGAAAA TCAAAATCAC CAATTATTCT TATTAGGTAA AGATAAAGAG 180

AAATATAAAG AAGGCATTGA AGGCAAAGAT GTCTTTGTGG TAAAAGAATT AATTGATCCA 240

AACGGTAGAT TATCTACTGT TGGTGGTGTG ACTAAGAAAA ATAACAAATC TTCTGAAACT 300

AATACACATT TATTTGTTAA TAAAGTGTAT GGCGGAAATT TAGATGCATC AATTGACTCA 360

TTTTCAATTA ATAAAGAAGA AGTTTCACTG AAAGAACTTG aTTTCAAAAT TAGACAACAT 420

TTAGTTAAAA ATTATGGTTT ATATAAAGGT ACGACTAAAT ACGGTAAGaT CACTATCAAT 480

TTGAAAGATG GAGAAAAGCA AGAAATTGAT TTAGGTGATA AAT 523

(2) INFORMATION FOR SEQ ID NO: 622:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1871 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

AGAAGTGTGA nAAAAATTTA AnAGAGATAT GCACATAGAT GACGCATTGC TATATCCAAG 60

CAATTGAGAA AGCTGCTGAT GCTCCAAATC aCGGAATGAG GGAACCATGG AGAGTTGTGC 120

ATGTTCCGAA AGACAGATTA GGAGATATGA GTAAGGATAT TTCTAAATTT GCATTTCCTA 180

ATGAATTAGA TAAGCAACAA TGTCATTATG ATGCAGTTAC GAAACTAGGT GGCATGTTAT 240

TGCTTATTTT AAAAACAGAT CCAAGACAAC GTCAAAATGA TGAAAACTAC TTTGCATTTG 300

tGCATATGCA CAAAATCTTA TGTTGTTACT TTATGAAGCG GGAATAGGTA CATGTTGGAA 360

aTCGCCATTA TATATCTATG ATCCTAAAGT AAGnAAACAC TTGGTATAAA GnAAGATGAA 420

GTTCTTGCTG GATTCTTATA TTTAACGGAT TTAGAAGnAG ATATGCCTAA AGCACCACGT 480

AAAAATAGAA ACTTAATTAC ATTATATTAA TATGTATAAT TATAGAAACA TTAATAAAAG 540

CTGAGTCATG AATTGATGGA CATCTATCGA GTTAGAGATT TAATCTAACT TACTAGAGTC 600

GGTACAATAA CAGTCTCAGC TTTTTATTGT GCAGTATATA CACATTTTTA TTTTAGTATT 660

TATTtAAAAG TTtCTGCTaA AAATGATTCA ACTTGTTCAG GTGACTTAGC ATTTGCTGAA 720

TGAAGGTGTG CAATTTTATC GCCGTTTTTA AATACTAGCA AGCTAGGGAT ACCCATAACT 780

TCATTTTCAA CAACTACATC TTCTAATTCA TCACGATTAA CAGTATACCA TTGGTAATCA 840

CCTGCCTCAA ATTTAACAAT TACAGGTGTA TCGCTATTAA TTACAGATTT AAATGATTCA 960

TTACTTTTGA TTGATTGCAT TGTAACAACT CCTCTAGATA GTTTAATAAT TTTTATTATA 1020

GCTAAATTTA TATCATAATA AAAAATTTTA GCTTCAAAAT GAAAGCCTTT TGCTTTGGAA 1080

AATGATATAT TTATTTTAAA TACATAAAGG AGGTTGCAGT CGTATGATTA AATTTTACCA 1140

ATATAAGAAT TGTACAACTT GTAAAAAGGC AGCAAAGTTT TTAGATGAAT aTGGCGTAAG 1200

TTATGAACCA ATTGATATCG TTCAACATAC ACCTACAATA AATGAATTTA AAACAATAAT 1260

TGCAAATACA GGCGTAGAAA TTAATAAATT GTTTAATACA CACGGCGCGA AATATCGTGA 1320

GCTTGATTTG AAAAATAAAT TACAAACTTT ATCAGATGAT GAAAAGTTAG AGTTGTTATC 1380

ATCTGATGGT ATGTTAGTAA AGCGTCCTCT AGCAGTAATG GGCGATAAGA TAACATTAGG 1440

ATTTAAAGAA GATCAATATA AAGAGACTTG GTTAGCGTAA GTGaAATGTA AGCGTTTACT 1500

AAATATCTCG ATATTTAGAT TCATTACATG TAAAATGAAA TAAGCTATAC AATTGTTAAT 1560

TTTTATAAAT ATAGTTGAAT AGCATCTAGC CTTATGGCAT CATTAATGAT GTAAAGATTA 1620

ATTAGGAGGG GATTCTCTTG GCAGTACCAA ATGAAyTGAA ATATTCAAAA GAGCATGAAT 1680

GGGTTAAAGT TGAAGGTAAT GTAGCAATAA TTGGAATCAC AGAATACGCA CAAAGCGAGT 1740

TAGGTGATAT TGTTTTCGTT GAATTACCAG AAACAGATGA TGAAATTAAT GAAGGGGATA 1800

CGTTTGGTAG CGTAGAATCA GTTAAAACTG TATCAGAATT ATATGCACCA ATCTCTGGTA 1860

AAGTAGTTnA A 1871

(2) INFORMATION FOR SEQ ID NO: 623:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

TTGCTGTAGA AGATAAAGAG TCCCATCAAT GGATAGGCTT TATAGGTTTG AATTATATTC 60

CAGAAACAAG CGATTATCCA TTTAAAGAAT TACCGCTTTA TGAAATAGGT TGGCGCTTGT 120

TGCCAGAATT TTGGGGAAAA GGATTAGCAA CTGAAGGCGC AAAGGCAACA TTGAAGTTAG 180

CAGAAGAACA TCAAATATAC GATGTCTATA GTTTTACAGC AGAAGCAAAT AAAGCTTCAC 240

AACGTGTAAT GGAAAAAATT GGCATGACAG TGTATGATCA TTTCGAATTA CCCAATCTAA 300

GTAAGTATCA TTTATTaAAA AGGcAAGTGC GCTATTACAT TAATCTTCcG AAAGTGGAAA 360

ATTAgGGGGT GtTTnGTkTn ATTTTTTTAA n 451

(2) INFORMATION FOR SEQ ID NO: 624:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 665 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

CGATAGTTAT CTAAAGCCAT TTTnGATTGT GTTATGAAAT CTAATGATGC GTGATAATTT 60

AATGCrACAT AACGrTaATA TAAAATATCA ATAGTGAACA TTTGAGCAAA TAATGAAGTT 120

GTTGCTCCCA TATGCATCTC ATTTTCATCA GTTTTCCCAT AAGTTAAAAC AATATTTGAT 180

GCCTGTGCTA CGGGATTATC CCTTGTACTA GTAATTGTAA TTATAGGTAT ATGGTAGTCA 240

TCAATAACTT TAACCATTGA TTGCATTTCA CTTTGCGTAC CATTGTTAGT AATAAGAATA 300

aCACTGTCGT TCGAATTGTG AGTTGCTAAT AATGTAGCAA AAATATGTGT TTCTTGAACA 360

AGTTGAATAT TAAGACCTAT TCTTGATAAC TTTTGGTATA AGTCGGTAGC AACTACAAAA 420

GATGCGCCAA AACCATATAT AAAAATCGTC TCAGAACGTT TTAAACAATG ACATATTTGA 480

TCAATAGTTT TATCATTTAA TTCGTTATTT GCATGATTAA GTGCGCGTGT AGTACGTGTA 540

TGGAGTTTAG TTCTTAAAGA TTCTGTGCTT TCGTTATTCA TTAATTCAAC ATTGTAAATT 600

GATGATGCTT TAGGAACATA TTTAGATATA TTTATTTTCA AGTCGTGAAA ACCGCCATCA 660

GTAAT 665

(2) INFORMATION FOR SEQ ID NO: 625:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

GATGCCAATT AACCGTGCAT ATAATGTTGA GAAGTTAATC GAAGCAATTC AATATTATCA 60

AGAAAAAACA AATCGTCGTG TTACTTTTGA ATATGGTCTG TTTGGTGGTG TGAATGACCA 120

ACTAGAACAT GCAAGAGAAT TAGCACATTT AwTAAAAGGC TTAAACTGCC ATGTTAACTT 180

AATTCCtGTC AACCATGTTC CAGAAAGAAA TTATGTGAAA ACGGCTAAAA ATGATATCTT 240

TTCGGATATT GACGCAGCTT GTGGTCAATT AAGAGCAAAG GAACGACAAG TAGAAACGAG 360

GTAAAGACAA ATGCTAGAGG CACAATTTTT TACTGATACT GGACAACATA GAGATAAGAA 420

TGAAGATGCG GGTGGTATTT TTTATAATCA AACTAATCAA CAACTTTTAG TTCTGTGTGA 480

TGGTATGGGT GGCCATAAAG CAGGAGAAGT TGCAAGTAAA TTTGTTACAG ATGAGTTGAA 540

ATCyCGTTTT GAAGCGGAAA ATCTTATAGA ACAACATCAA GCTGAAAATT GGTTGCGTAA 600

TAATATAAAA GATATAAATT TTCAGTTATA TCACTATGCA CAAGAAAATG CAGAATATAA 660

AGGTATGGGT ACAACATGTG TTTGTGCACT TGTTTTTGAA AAATCAGTTG TGATAGCAAA 720

TGTCGGTGAT TCTAGAGCCT ATGTTATTAA TAGTCGACAA ATTGAACAAA TTACTAGTGA 780

TCACTCATTT GTTAATCATC TTGTTTTAAC GGGTCAAATT ACGCCGGAAG AAGCATTTAC 840

ACATCCACAA CGTAATATTA TTACGAAGGT GATGGGCACA GATAAACGTG TGAGTCCAGA 900

TTTGTTTATT AAGCGATTAA ATTTTTATGA TTATTTATTA TTAAATTCAG ATGGATTAAC 960

TGATTATGTT AAAGACAATG AAATTAAGCG TTTGTTAGTA AAAGAAGGTA CAATAGAAGA 1020

TCATGGTGAT CAATTAATGC AATTGGCATT AGATAACCAT TCGAAAGATA ACGTTACTTT 1080

CATACTCGCG GCTATTGAAG GTGATAAAGT ATGATAGGTA AAATAATAAA TGAACGATAT 1140

AAAATTGTAG ATAAGCTTGG CGGCGGTGGC ATGAGTACCG TTTATCTTGC TGAAGATACG 1200

ATACTTAACA TTAAAGTTGC AATTAAGGCG ATTTTTATAC CACCTAGAGA AAAAGAAGAA 1260

ACATTAAAAC GTTTTGAACG AGAAGTACAT AACTCATCAC AGCTATCACA TCAAAATATA 1320

GTAAGTATGA TCGATGTTGA TGAAGAAGAT GACTGTTACT ACTTAGTAAT GGAATATATC 1380

GAAGGTCCGA CTTTGTCTGA GTATATTGAA AGTCATGGGC CATTAAGTGT TGACACAGCG 1440

ATTAATTTTA CGAATCAAAT ATTGGATGGC ATTAAACATG CGCATGATAT GCGTATTGTA 1500

CATAGAGATA TTAAGCCACA AAATATATTA ATTGACAGCA ATAAAACGTT GAAAATATTT 1560

GATTTTGGAA TTGCTAAAGC TTTAAGTGAG ACGTCTTTAA CTCAGACTAA TCATGTGTTA 1620

GGTACTGTGC AGTACTTTTC GCCAGAACAA GCAAAAGGTG AGGCAACGGA TGAATGTACA 1680

GATATTTATT CTATAGGTAT kGTGTTATAT GAAaTGCTTG TTGGTGAACC ACCCTTTAAT 1740

GGAGAAACTG CAGTTAGCAT TGCGATTAAA CATATTCAGG ATTCTGTGCC AAATGTGACA 1800

ACAGATGTAC GTAAGGATAT TCCGCAATCT TTAAGTAATG TCATTTTACG CGCTACAGAA 1860

AAAGACnAAG CGAATCGTTA CAAAACAATT CAAGAAATGA AAGATGATTT GAGTAGTGTT 1920

TTACATGAAA ATCGAGCGAA TGAAGATGTC TATGAACTCG ATAAAATGAA AACGATAGCG 1980

GTACCTTTGA AAAAAGAAGA TCTAGCAAAG CATATTAGTG AACATAAGTC GAATCAACCT 2040

AGCCAGAAGG TACGGTGTAC GAACCAAAAC CTAAAAAGAA ATCAACACGA AAGATTGTGC 2160

TCTTATCACT AATCTTTTCG TTGTTAATGA TTGCACTTGT TTCTTTTGTG GCAATGGCAA 2220

TGTTTGGTAA TAAATACGAA GAGaCACCTG ATGTAATCGG GAAATCTGTA AAAGAAGCAG 2280

AGCAAATATT CAATAAAAAC AACCTGAAAT TGGGTAAAAT TTCTAGAAGT TATAGTGATA 2340

AATATCCTGA AAATGAAATT ATTAAGACAA CTCCTAATAC TGGTGAACGT GTTGAACGTG 2400

GTGACAGTGT TGATGTTGTT ATATCAAAGG GCCCTGAAAA GGTTAAAATG CCAAATGTCA 2460

TTGGTTTACC TAAGGAGGAA GCCTTGCAGA AATTAAAATC GTTAGGTCTT AAAGATGTTA 2520

CGATTGAAAA AGTATATAAT AATCAAGCG 2549

(2) INFORMATION FOR SEQ ID NO: 626:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

TGCTTACTTC GCCTTCAATA CGTACTAATT CATGTCCACA ACTTGGACAA TGGGTTGGCA 60

TATGATATGT GACAGCATCC TCAGGTCTAC GTTCTGGAAT ACTACGTACA ACTTCAGGTA 120

TGATGTCACC TGCTTTTTTC ACTACAACAC TATCACCAAT TCGAATATCT CTGTCATGAA 180

TTAAATCCTC ATTGTGCAAA GATGCTCTTG aTACAGTTGT ACCAGCTACT TTTACTGGTT 240

CTAAAATAGC AGTAGGTGTG ACTACACCTG TTCGTCCAAT ACTTAATTCA ATATCTAATA 300

ATTTAGTTAC TACTTCCTCA GCTGGAAATT TATAAGCAAT GGCCCATCTA GGAGATTTTT 360

GTGTGAATCC CATCTCATCC TGTTGATCTA AATCATTAAC CTTAATAACA ATCCCATCAA 420

TATCATAAGG TAATGACTCT CTTTGGCTTG TCCATTTTTC AATATACTCT AAAACACCAT 480

CGATATTATT TACACGCGCT CTATTTTTAT TCGTTGTAAA ACCTAATTTA TCTAACTCAT 540

CTAATGCTTC ACTTTGCGAA CGCGCATTGA AATCAGTGAA ATCATTGACA CTATATATAA 600

ATACGCTTAG CTTTCGTTTT GCCGTTAATT TAGAATCTAA CTGTCTTAAT GATCCCGCAG 660

CAGCGTTTCT TGGATTnGCA AATAACTGCT CATCATTTTT TTCTTTTTCT TCATTTAATC 720

GTAAAAATGA ACGTCTCGGC ATATATGCTT CACCACGAAC TTCTACATTT AATGGtTCTT 780

TCATTTTCAA AGGTATCGCA TGAATTGTTT TTaAATTTTC GGTAATATCT TCACCTGTTG 840

TTCCATCACC ACGTGTTAAA CCTTGaACGA AGTATCCATC AACATATTTC AATGATACTG 900

GTTGGTCGAA TTTTCTCAAA TCATCCTCAT TAAATGCATT CCCTAAACTT AACATTGGCG 1020

TGTCATGGTT GACTTTATTG AAAGAGGCTT GGGCTTCACC GCCAACTCTA ACTGTTGGAG 1080

AATCTACAGT CTTATACTCA GGATGCTCCT CTTCTATTTT AATCAGTTCA TGAAGTAATT 1140

TGTCATATTC ACTATCTGGT ACAGATGGAT TATCCTCTAC ATAGTATTCA TAACTGTATT 1200

GATTTAATAA ATCATGTAAC TCGTTCACAC GAGACGATAA ATCAGCCATC CCTTAATCCT 1260

CCTTTTTTtC AATTGGTGCA AATTGCGCTA ACAAACGTTT TGGCCCTTGT GATTTAAAGA 1320

TAATATCTAG TTCGATTGAG CCATTTTTCT CGTTTACATT ACTCACCATG CCTTCTCCCC 1380

AGGCTTTATG CATCACTTTG TCACCTACAT TCCAATCAGA TGACAATACT TGTTTTTTCG 1440

TTGACGTTGT TCGTTGACTA AATCCGCGTT TAGCAAAAGG TTTTGCCTTA GGTTGTATCG 1500

TTTGTCGTTT GCCACTTGAA TGATTTTCTA ATAGTGATTC TGGAATTTCC TTTAAAAATC 1560

TGGATGGCAT ATTTGACTGA GGGCGACCAA ATAACATTCT TGATGTCGCA TGAGTGATAT 1620

ATAACACCTC TTCAGCCCTT GTAATTGCTA CATAACAAAT ACGACGTTCT TCTTGCATTT 1680

CATGATCATC TTCACTCTTA ATCGCTCTAA TATGTGGGAA TAAAGATTCT TCCATCCCCA 1740

TTATAAAGAC AATTGGAAAT TCAAGGCCCT TAGCCGAGTG CATCGTCATT AGTGTTACGC 1800

CATTTTCAGT ATCTGCCTCA TCAATATCAG CTACTAACGA TAAATCCGTT AAAAAGTTAA 1860

TTAATGACTG TTCTTCTAAT GGGGTATTTT CCTCATAGTC TTTTGGTACT GACATAAATT 1920

CATCGATGTT TTCTAATCTA CTTCGAGATT CTAATGTATT TTCACGTTCA AGCATTTCTC 1980

GATAGCCAGA CTTTTGTAAT ACTTCATCAA CTATTTCATG AATTTCTAAA AATTCTTGTT 2040

CTTTTATCAA GCTTTGGATT AACTCGTAAA AATTAAGACA CTCTTGTGTC ACCTTTTTTG 2100

aCAATCCGAT AAAATCAGCT TCTCCAAGTG CATCAAACAT ACTGATATTG TTTTGAAGTG 2160

CATAGTTTTG AACTTTTTCA ACAGATGAAG GACCTACACC TCTTTTTGGA ACATTaATAA 2220

TACGTTGCAA ACTAATGTCA TCATTACTAT TGGCAATTAT ACGCAAATAA CTTAATAAAT 2280

CTTTGA 2286

(2) INFORMATION FOR SEQ ID NO: 627:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

TGACATTAAA AGTTGGGTGA AnAAACAAGG CATACTTTAG TTAAGCTTGA TGAAAATAAC 120

AATGGAATTA ATGCGATTAT TCAAAAAGAA AAAGCAAAAG ATTTAGATAT AAATTATTCT 180

GCTAAAGGTA CTACCAATTG TATTATTTAG TGGAGAATTA GACAAGCTGT AGCAGCGTTG 240

ATTATTGCCA ATGGTGCTAG AGCTGCTGGA AAAGATGTAA CTACCTCCTT ACTTTTTGGG 300

GGCTTATGCC nTTAAAAAAG TGCCACCGTT AATGTTAAAA GCAGTTGCCA AAATGTTTGA 360

TTnATGTTGC CCCAAAAGAT TTACGATGCC CCTTCCCAAA 400

(2) INFORMATION FOR SEQ ID NO: 628:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 453 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

AATAATTTGG GCGCTnTTTG CGTCGGGATA TTATACCGCT TCCTTAATTG TTCAACATTG 60

TAATCACTGT TTTTCAATTG ATATTTTGCA GAGTAAATTG GTACTTCTGG GTTATATGAC 120

ACTTCGTCCT CTTTATAGTT TTCCAATTCT TTGAAATTCC CGTATTGTAC AAAGAAGTTA 180

AATTCTTCGA TTTCTTTTTT TACTTTTTCG TCATCGATTG GTTTTAATGG AATCATTTTA 240

TTAkTTTCCA TTTTCACAGG ATATCTTTTT GTATGATTGT GTGTCATTCC ATCGCTATCT 300

TCAACAACTT CTCTAACAAT ATAATGCCCT TTAGCCGTTC TAGTATTTCT GTTAATTTCT 360

AAAACTGCTC CTCTrGATTC CAGATTTTCT CCTTTTAATT GGATTTTCAT TTCAGATCTA 420

ATTAGcCAAG TACCTTTATC ATCTtTTTTA AAT 453

(2) INFORMATION FOR SEQ ID NO: 629:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

TCATATGCAT TTGCAAAATA AACGCCAGAA GCAAGGTTTA GAATTGGGCC GTCCGTTTTG 60

CTCAaTTCAC TTGcATTCAA TAATTCATGC TGATCATGAT CAATTTGCTT ATCTAATTCT 120

GCaATTTTCT TCATTTGCTT ATCTGATTTG TTTTCTTTCG CCATCATTTG ATCACGACGA 180

GCTAATGGTA CTAATACTTT ATCTCCATAT GTGTCAATAA AGTTATAAAA ATAATCATCT 300

GTTTTTGATA CAAATCCAGC ACGCTCTTCA GTTTCACGAT ATAAATCTAA GAAAAGATTG 360

AACTCATCAC GTTCAAGGAA TCTGACTTTA ACACCATAGT TTATCGCTTT ATTAATATTA 420

CGTTTACGTT GACTATCAAA TGTCTTTTTC AATGTTTCGG GTGTTTTACC TTCAAGGTTT 480

AATACGCCCA TCCATCGTAC TTGGCTCGAT GTATCATACT CAGTTGTAAA GCCATGATGC 540

TCGTAACCAT GTGATTTAAA CAAGTTTACT AGGGCATCAT TTTTCTCGCG ACCTTCAAAT 600

GGCACGATAT CTTTATCATA TAGATGATAT AACCAATACG GATCTAATTT AACATATAAA 660

CATTGATGTT GCTGTAAATA TTTATCTAAC TCTTTTAAAT AATAATCAAC TAATCCTAAA 720

TCTGAAAAAT CCATTACTGG ACCACGATTC GAATAGTAAA CATAACTTCC CATAGTAGGA 780

ATTTTAGAGA AAAGGCTTGC TGCAATTACT TTGTTATTGT CGTCTTTAAT ACCTAATAAA 840

ACTACTTCAA AGCCATCATT CTCACGGGTA ACTATATTTT CTTTTACTTG GAAATAATGA 900

CTTTCCAATG ATGGATTTTG TACAAAGTTG TCAAATTCGG TAACAGTTAA CTCTGTAAAT 960

TTCATGTTTT GATAATTCCt TCCTAAAAAA TTCTGTCTTT AACTTTTTTA AGTGCGGTAT 1020

ATGCTGCGTA AACAGGTTTA TTAATTGGTT TAATAAAGTC ACCAACATAT TCmATAATTT 1080

CAGCATTGTA ACCTTTTTTG AATTTAACTA CACCAGCATC TTCAGCATCT TCTGTAAATT 1140

TrCCACTAAC ACCATAGAAA TTATAACGGT CAATGCATGA TTTAATGCAT AATTAATCAT 1200

TTCCCATTGC ACTGCATAAC T 1221

(2) INFORMATION FOR SEQ ID NO: 630:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

TGGCCCAAnT AACACAAGTA ATTGCTGCTA ATGGTAACAT CACAAAAAAT GAAATCGTAA 60

CTACAAATGT TAAACCTTGG AATACACCAA CCATTTCTGG TAATCGTTTA CTATAGTATC 120

TATTGTGAAT CCAAGTAATA ATAGCTGAAA TAATAATACC ACCTAGAATA TTCGTATCCA 180

ATGTGGCAAT ACCTGCAATT GATTTTAAAC CAGGTACATT TTCAACGCCT TTTTCTAAAT 240

TAGCGCCAAA CGTATGTGGC CATTGTGTTA AAATGGCATT TATAAATGTA TTAAACATTA 300

AGTAACCCAT CAATGCTGCA AGTGCTGCAT GACCTGGTGC TTTTTTAGCT AAAGAAAGTG 360

TTACTGACCA AAATTTAAAC CAAAACGTAT GTTGATCTGC TAAACTCCCC ATGATTGTAG 480

GATTTTTAAA TAATGTCGCA AAGCCAAGCA CTATCCCAAA GAAAGCGAAC ATTAATACCG 540

GTACAATCAT TGCACTACCG AAACGCTTTA TCGCATTCAT CTTCTATTCC CTCCATATCA 600

TCTTTCCTAA CAATACATCT AATTAGATTC ATTTATAAAT AGATGTCTTA CTATTTAAAT 660

ATAATATATA GTAAACGCTT ACACACCTAC AACGACATTG ACGTATTTTG AAAGTATTTT 720

GTATAATCAG ATTATCTTTT CATATAGTGA AAATTTTTTC ACGACCTTAT ATATGACATC 780

GTTGTATTTG TAATACATTC GTTTTAAACG CATAATCAAA CCTATATCAA TACACAAATA 840

TATATAATGA CATACAAGAT TTTAATGTAA TAACGATCTA TTACACATTT ATTTTCAAGG 900

AGGTTGAATA TGTTTTTAGA TGAACACATT AATCGAAACT TTGATAAACT TAATGATAAT 960

GATTTACATA TCGCTCACTT TATCAATACA CATATAGATG AATGTAAAAA TATGAAAATA 1020

CAAGATTTAG CGCAATTCAC ACATGCCTCG AATGCAACCA TTCACAGATT TACACGCAAA 1080

TnAGGTTTTG ACGGTnATAG TGGATTTAAA TCGTACCTTA A 1121

(2) INFORMATION FOR SEQ ID NO: 631:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4005 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

AACCTTCCAT TTTACTTGAT CGATAACATC AGTTCTGCTT TACAAATCTC TTCATTAATA 60

TGCGTCTTAA AACCATGAAA TTTAACATGT TCCGATAAAT GATAATCTTC TACAAGTTGT 120

CGATATTCTG ACAAACCATT TCCATGTCCA TAAATATTCA ATTGAATATT GGGATGTTTT 180

GTTACTAATT GCTTGATTAC TTCAATTTGA TGTTTAATTT GTTTATTTTC AACGAGGCGA 240

GCAATTGATA TGATATGATT TTTCTCCTTT TGATTGATGT CAAATTGATA CTTTAAATTT 300

GCCACGTAGC CAACCGGAAT ATTGATAACT GGTATTTTAT TTTCAATATA TTGTGAAATA 360

TCTTGGCATT GCTTTTCTGT TGATACAACA ATCGCTTTAT AACGTGTTAA ATTATTAAAC 420

ACTGTTTTAT AAAAACTTTT TATACCATTA CCGGCACCGG ATAAATGTGT ACTATGGAGC 480

ACAACAATAA CTGGAATACT TTGATTTAAT CCCGCTATAA CATTTCCTAA TTCATGAGGA 540

CGATCTAATA TGATTTGATC ATTATTTTTA CATAATTGAT GGAGAAAATA TTGAACTAAT 600

TCATCTTCTG TATCAAAAAA TTGTTGATGC TGGTCTTCAT TTAAGATAAC CTTTGTGAGC 660

TAGTAATTTT CGAGTACAAT CCGTTGTCCT TCACCTAAAA TTCGAGAACA ACTTAAAAAG 780

CCTCTTCCAT CATACAATTC GCGTTTTACT TTTCTTCTTT TATGATCAAA ATAATTCACA 840

TAATTTAATT GATGATACTG TTTATCTAAA AAATGAGCAT ACATTACAAA TTGCTCTTCA 900

TCATATATTC TGACATCATT TGAATTTTCC ACAAATTTCA ATGTGTACCT ACATGACTTT 960

TCCCAATACT GTATCCAGTT AACTTGCTTT GTCTTTTTAT AATTGATTGC TTTTTGAAAA 1020

TAGTCATACA TTGTAAATAC ATCATTTTCA ATCTGATGTT GCTTCGCATA TGTGTATGAA 1080

TAAGGATTCC ATTTAACATA TACACATTTT GAAGATATGC CGTGTTGTTT GAACAACTTC 1140

AATCTATTTA TTTGCGCTTT TTCTACACCT GTAATTTTAC TTTCTAAAAT TGTTCCTAAA 1200

ATGTAATTCA TATTATCGCC TCATATAAGT TTTATTCCGT ATCTTTATTG TTTATTTTAT 1260

ATGAAAAATA CATCTATTGC ATGTGTAATT ATAAAAAAAC CAGGCCACAA GGACCTGGGT 1320

CATATTGTAT TATTTGTTTT GTTTTTTGCG ACGACCGAAT AACAATAATG AACCTAATGC 1380

TGCAAATAAT CCACCAAATA ACGTTGCGTT ATTTGAGCCG TTATTTTCAC TACCTGTTTC 1440

TGGTAATGCT TTTGCTTTAT TGTGATGGTC TTTAGTAGTA CTCATTGGTT TAACAGGTGT 1500

ATGTTTTCCT GCATCCGAGT CTGAATCGCT GTCTGAATCA CTGTCTGAGT CTGAGTCGCT 1560

ATCAGAGTCT GAGTCGCTGT CCGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTGTCTGA 1620

ATCTGAATCA CTGTCTGAGT CTGAGTCGCT ATCTGAGTCT GAATCGCTGT CTGAATCTGA 1680

GTCGCTATCT GAGTCTGAAT CGCTGTCTGA ATCTGAGTCG CTATCTGAGT CCGAATCGCT 1740

ATCTGAATCT GAGTCGCTGT CTGAGTCTGA GTCGCTATCT GAGTCTGAAT CGCTGTCTGA 1800

GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAATCTGA 1860

GTCGCTATCT GAGTCTGAAT CGCTGTCCGA ATCTGAGTCG CTATCTGAAT CTGAGTCGCT 1920

GTCTGAATCT GAATCACTGT CTGAGTCTGA GTCGCTGTCT GAGTCTGAGT CGCTGTCTGA 1980

GTCACTATCT GAGTCTGAAT CGCTGTCTGA TGTATCTTCT TCGAAGTATC CGTTATCAAG 2040

TGTGAAATCA TCATGATCCG TAATTGTTAC GTCAACTTCG CCACCATCTG CATCTTTATC 2100

ATCTTCAGTT GTATTTGTAA CTGTTTGTGT TAAGCCAGCA GGCTTTTCAA AAATAACTTT 2160

GTATTTACCG CTATCTAAAT TATCAAAGCA GTATTTACCA TTTTCATCTG TTTTAGTTGT 2220

TCCAATTACT TCGCCTTTTT CATTTAATAA AGTAACTTTA ACATCTTTGA TACCTTTTTC 2280

AGTTGAATCT TGTTTGCCGT CTTTATTACT GTCGTACCAA ACATAATCAC CTAAACTATA 2340

TTTTGGTGTT TTATAGAAAC CACTGTCTAA TGTCATGTTA TCTGCATCTT TAATGACACC 2400

TGTTGTTGTT AAACCATTAG AATCTTTTTC AGTATCATTT CCAGAAGTTA CTGAAGTTGG 2460

TTGATATTTA CCATTTTCAT CTGTTGTAAC TGTTTTTAAA ACTTTGTCGT TTTCATCTTT 2580

TAACGTAACT GTTACACCTG AAATGCCCTT TTCATCTTTA TCTTGAACAC CGTTTTTATT 2640

TGTATCTTCC CATACATAGT CACCTAAGTT GTAAGTCGGT TTGTAGAAAC CAGAGTCAAT 2700

AGTATCGTTA TCTTTATCTT TAATGACACC TGTTGTTGAT GTACCATTTG AATCTATACC 2760

TTCATCAGTT CCTGAACCTA CTTGTGTTGG TGTGTAACCT GATGGTGTTT CGAATTCAAC 2820

TTTATAAGTT CCATTTTCTA ATCCAGTAAA TTGATATTTA CCATCTTTAT CTGTTTTAGT 2880

TGTTTGTAAA ACTTCACCGT TTTCATTTTT CAATGTAACT GTTACGCCTG AAATACCTTT 2940

TTCAGTTGAA TCCTGCTTAC CATCTTTATT TGTATCTTCC CATACATAAT TACCTAAATT 3000

ATATTTTGGT GTTTTGTAGA ATCCACTATC TAATGTCATG TTATCAGCAC CATTAATAAC 3060

ACCTGTTGTT GTTAAACCAT TAGAGTCTTT TTCAATGTCG CTACCAGATG TTACTGTAGT 3120

CGGTGTATAG CCTTCTGGTG TAGTAAATTC AACTTTATAA TTACCATTAT CTAAATCAGT 3180

AAATTTATAT TTGCCATCAG CGTCTGTTGT AACTGTTTTT AaCAgTTACC GTTTTCATCT 3240

TTTAATGTTA CCGTTACGCC AGATATACCT TTTTCATCTT GGTCTTGGAT ACCATTTTTA 3300

TTTGTATCTT CCCAGACATA GTCACCTAAG TTGTATTTAG GTTTGTAAAT ACCTAAGTCT 3360

GCAGATAAGT TATCTTTGCC ATTAACTGTA ATAACTGAAG ATAAGCCGTT TGAATCTAAT 3420

TCTTCGTTAT TACCTTGTTT TGAAGGGGTT ACTTCATAAC CTTTTGGTAA GTTTGAAAAT 3480

TCTACACGGT AATCTCCATT AGGTAAGTTT GGAATCAAGT ATGACCCATC TTCTTTAGTA 3540

ACTGCTTCTC CTACTTTTGT ATTTGTATTA TTATCAAATA CAGTTACAGT TACATTGCCA 3600

ACGCCTTTTT CTCCTAATTC TTGAACACCG TTTTTATTAG TATCTTCCCA TACGTAGTTA 3660

CCAATTTTAT ATACTTCTTG ACCAGctCCG CCACTTTGGT TATTAGTAAA TCCTAAAGCA 3720

TTGCCAGTAG AAACGGATTT ATTACCTGTT GAAGATAAAG TAGCCATTTG AACAAGTGTT 3780

GGGCTTTCGC TATTTGTATA TTGGAATTTT GTATTAACCA TTACAACATA AGCAGAATCT 3840

GCATTTCCAA AATCAATAAC AGCGCTATTG TtGTCGCCAT ATGTAATTTT CTGCAAGTAT 3900

TGATTTGTTA CATCTGTAAG CTCTTTAGTA TTCACATCGT ATCCTTTATT TAATGTATAA 3960

CCTTTAGGAA CTTGATATAT TTTTATATCT GTTACATCTT TATTT 4005

(2) INFORMATION FOR SEQ ID NO: 632:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

TATTAGGTTA CTCTAGTTTC CAAAGCGGGA ATTTTAATGT TATTAACAGC AAGGACAGCA 60

AAAGCAATAT CGGCGCATTG ATTGAAAATC CAGGAATATA TCCTTTTATG TCTGGATATG 120

AAAACTTGAA GTTATTGAAT GAATCAAAAA ACACTCAAGA TATCGATAAA ATTGTCTCAC 180

AACTTCATAT GGATGAATAC ATTCATAAAA AAGCTAAAAC GTATTCTCTT GGTATGAAAC 240

AAAAATTAGG AATTGCTATA GCATTTTTAA ATAAACCTCA ATTCATTATC TTAGATGAAC 300

CAATGAATGG CTTAGATCCA AAAGCTGTGC GAGATGTACG TGAATTGATT GTCCAAAAAG 360

CGCAAGAAGG TGTTACTTTC TTAATTTCGA GTCATATTTT AAGTGAATTA GTTAAAATCA 420

CAAACTCTAT CCTTATTATT AACAAAGGTA AAATTGTTAC AGAAACATCG GAAGAAGAAC 480

TTAAACAATT TAAAGATAAT GATTTAGAAA ATGTATTACT AGAAATCATA GAAAGGGAGG 540

ACCAAGCATA AAATGGGAAC TTTAATTAAA CAAGAATGTT TCAAATTATT TAAAAAGAAA 600

TCAACTTTTA TCGCACCTAT TGTCTTTATT CTACTAATGG TTGCTCAAGG TTATATTGCT 660

ACAAAATACA ATGAAATTTT TACGCCACAG GAATCTTTCA CATCTGCTTA TAATGGTTTT 720

TCATGGTTTG CATTTTTATT AATTATTCAA GCAAGTACAA TCATTTCAAT GGAATTTCAT 780

TACGGTACGA TTAAAAATTT ACTCTATCGT GAATATTCAA GAACAACTAT GATTGTTAGC 840

AAAATCATCA CATTATTTAT TATTTCTTTA ATTTATTTTG TTATTACAAT TATTGCTTCA 900

ATTGTTATTG GGTCTTTATT CTTTAATGAT TTAAATATAT TTGAAAGTAG CGGTAATCAA 960

TTATCTTTAT TGAATCAATT ATTATTAGTT AGTTTAGGCA CATTTGTTGG CGTTTGGTTA 1020

GTTTTAAGCT TAACGTTGCT ATTATCATCT GCAACAAATT CAACGGGAGT AGCCATTGCT 1080

GTAGGTATTG TTTTTTATTT TGCAAGTTCT ATTTTAGCAG TTATTCAAAC GGCACTTTTA 1140

GAAAAAATAG ACTGGCTAAA GTGGAATCCT ATTAATATGA TGAATATTAT GCTTCAAACA 1200

GTTGAAAAAG GCTTTAGTAA GTCGACAAAA TTAGAACTTC ATGAATTGTT TATTGGTAAT 1260

ATTGCTTATA TTTCTATTTT CTTAATACTT GTAGTATTTA TTTTCAAGAA GAAAAATATT 1320

TAGTAACTTA AAGTATTAAA TGTCTAAATA CACACATATT CCATCGTAAT TCAAAATCAT 1380

TTTCAAATCC CTTCACCCAA ATAATGGTGC GGGGATTTTT TCATCCAAAT TTTGGAAATT 1440

(2) INFORMATION FOR SEQ ID NO: 633:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

GCTGACATAA TTGCATCAAA TTTCACATCC CCATAAAAAT CGCTACCACA TAACCTACGA 60

TAATACCTAC AAGAACTGGA ATTAAAGATA GGAATCCTTT AAAAAATCCT TGAACGACTA 120

TTGTTACAAG CAAGGTTATC ATTGCAACAA TTAAGAAACT GATATTGTAA CCTTTCATAT 180

CTCCAGGATT TTCATACATT GCCATATTGA CTGCAGTAGG CGCTAAGCTT AAACCAATTA 240

CCATGATGAC TGGTCCAACA ACAACTGGTG GTAATAATTT CATTAACCAT GCTGTCCCAC 300

TTAATTTGAT TAGAATCCCG ATGATGACGT ACATAACACC ACTCATGaAT AATGCTACAA 360

GCATGTCTCC TAAGCTATGC GTACTTAATC CCGTGATAAT TGGCGTGATA AATGCAAAGC 420

TAGATCCCAA GTATGCTGGT ATTTGCGCCT TCGTTATTAA GATATAAAGT AATGTACCGA 480

TTCCCGAAGC TAGTAACGCT GCTGATATTG GTAGTCCTGT TAAGAATGGT ACTAGTACTG 540

TTGCGCCAAA CATCGCAAAT AAATGTTGTA AGCTTAAAAA TGCCCATTGC GCTGGTTGTG 600

GTTTTTCATT TACATCTAGT ACGGGTTTTA CTGTTCGTTC AAACATTTCA TCATTTTGCA 660

TAATATTCAT TTCCTCCGAT AATAAAAAAA TCTCTTTACA TCAGTATATG TAAAGAGACA 720

AAAAGTGTGA CAAGTTGCTA CAAGTCATTT TCGTCCATAG AAATTGACTT ATAGTTGTCG 780

AACATGAGGG TATTATTAGA TAAACAAGCA TATGAAAACT TATTTATCAT TCAACTCCCC 840

CACCTTTTTC AGTCTCTCGT ACTGAATTAA AAGGGGtATT ATTTAATTAT AACTGCATTT 900

CTTTGATCcA TTtCTTCyAA ATAGACACTT ACCGTTTCCT CTTTAGAAGT AGGTAwATTT 960

TTACCAACAA AATCTGCTCG AATTGGTAAC TCACGATGTC CTCGATCAAC CAAAGCAGCT 1020

AAACCAATTT TAATAGGTCT AGCATTTAGC AAAATAGCAT CAAGTGAAGC ACGAACCGTT 1080

CGACCAGTAT ACAGCACATC GTCAATAATG ATGACTACTT TATCTGTAAT ATCTGTGTCG 1140

ATGTCTATTG CGTCTTTTGT CGTAAGTGAT GACATGTGcT CTATATCATC TCTAAAGTAT 1200

GTAATATCAA TTGTTCCAGT AGGTATACGT TGTTGCTCAA TTTGATGAAT TTtATCTTGT 1260

ATACGATTCG CTAAATATTC ACCTCTTGTn TTGATACCTA AAAGATTAAA TTATCAGTAC 1320

CTT 1323

(2) INFORMATION FOR SEQ ID NO: 634:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 761 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ACCCATCTCA TCGTATTTTG AATTTAATAG ACGAGATCGA TGTATATCTG AATTCATCCC 60

AACTATGGAT TAATGTTGGT ACATCATtAA cGCATAACCA ACATTTTGAG CAGTTGTTTT 120

ATAAGTAACG TGATTTTTAT CTAATTGCCC TCTTAATGCG TCCTCTGTAA ATTCAACACT 180

ATCAGAACCA TTAGAGGTCG CTTCATATAA GTTATTAGAT GCAATATGTG CTAAATCGCT 240

ATTGATTTTC AATGGTTTTA ATCCTTTTAA TTTTCTCATT TCATTCGTTA CTTCATAAAG 300

AGAAATTAAT TGATTTGGAT TTTGCTCAAC TGGACGCTTA TTATGCTCTT CTGACGTAGA 360

ATTAGAATTT AATTGATAAG GTTCAATATC TGCTAACATT TCTTTTGTTA AAAATCGTAC 420

ACTTAGCACC TTTTTCGATT GTTGATCAGA ATACACTTGT GCATATATGT CGCCATATTT 480

AATCaGTGTT TGTGTTTTTA AATCTTCATC TGAAAGTTCA AATTCATATT TTTTACCATC 540

AACTTTAAAG GACGGTTCTG GATTAATACT TGTATGATTA AAAATTTCTG CAGAATGTTG 600

TCCTATTTTT AACGGACTAA CATTGACTTT CTCACCTGTA GCATACACTG AAACGATTTC 660

TTCACGTTTA GTTGAAACAA TGTAATAACT GTTTTTGTCT TTAAACACAT AATTTTTGTA 720

rCCATCTCTA AAAGGGTAGA CrCGATCTGC TTGTCCAAAT T 761

(2) INFORMATION FOR SEQ ID NO: 635:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 827 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

nTAAATATAT TTATATATTA TAGAATAGAA AGACCTGAAG ATTGAATATC TTTCGCAAAG 60

CCTTTAACTG TATCTACTGA TAATTCGTTA ATATCGCGAC CTAAGTTTGT ATTCACTTTT 120

TTCACAACAT CTGCTGGGCA TGTAATAATA TCTGCACCAA TTTCATCAGC TTGAATCACA 180

TTGAATAATT CGCGGCAACT TGCCCATAAT AATTTAACGC CGTCTTTACT ATGCGTAACT 240

TTnACAGCCT CTkTCATTAA TGGTaATGGA TCTACGCCTG TAtCTGCAAT ACGTCCTGCA 300

AATACTGAAA CATATGTTGG CACACCTTCA GTTACTGCTT CAGTTATTTC TTTAACTTGT 360

TCAATTGTGT AAACAGCCGT AACGTTTAAT CTCACATTGT CAGCTGAAAG TTTTTTAATT 420

AAAGGAATCG TTGATTCACC TTTTGTATTT ACAATAGGAA TTTTAACAAA TACATTTTCG 480

CCATATTGTT TTAAAATTGC TGCTTCTTTk TCCATAGTTT CTAAATCGTC TGCAAATACT 540

TCAAATGArA TTGAAGCATC TGGAATTTCT TTCACAGCTT CTTCAGCAAA AGCTTTGTAA 600

TTTTTATAAG CTGCTTTCAT TnCTTCAATA TCTGCACCGk CCGCAAATAC TTCTACATTT 720

AGTTTAGCCA TATAAyATAG CCTCCTTGAT TCTTATTAAA ATTTTAACAA CATCTGCATG 780

kCTTTTTCTT ACAACCATTT GTAAAAAATG ATTTTTATTT CTTtGTT 827

(2) INFORMATION FOR SEQ ID NO: 636:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1478 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

TTAGTCGGTA TAACCATCGG CTAGGTGGTT TTTGTATTAA AAAAGTGGAT aCCAAAATTT 60

ATTAATAATT ATTTTAATGT TAGAAAAAAA CTAAATAAAA ACTCGCTAAT GATATCCAAT 120

AATATGTATA CAAAACGAGA CATATATTGC ATATGATTAA CGAGATACTG AAAATATTTT 180

ATCACCCCTA AAATGATTAT TCATTTTCAG CGGTAATTCG ACCTAAAGTC AAACTTACAA 240

TAAAACCGAT GATAAATACT ACTAATGAAA CGAACCACAT CACGATATTA GTTGGTAAAC 300

CTGGAAATAC TGCAAAGAGG GAGCCAACAA CAAAACCAAT GATTAATGCA AAAGTCATTA 360

GTTTATGATG TGTTAGGAAA TACTGGATAA TTTTGCTTGA AATAATGAAT CCAGCAAGCA 420

CGCCAAATCC GACTGCAAGT AATATAGGAA GACCTGCAAA GTTAAGTTTA ACAACTTCAG 480

ATATTGCTAG CATGACCGTA CCATAGACGC CAAATACTAA TAACATAAAT GACCCTGAAA 540

TACCTGGGAG TAACATAGCA CTAGATGCAC ACATACCTGC AATAAAATAT TTAATAATAA 600

GACTAGTTGA TAGAGTAAGT GTTTCTCCAG CATGTTTATC ACCATTATTC ATTAATGTAA 660

TAACAATTAA GATAGCGATA CCAGCTATAA CCATCATGTA ATGTyTAGTT GTAAATGACG 720

TTTTATAGTT AGAAATTTTC AATAAATATG GAACGATACC AATGATTAAT CCACCAAAGA 780

AAAACATAGT TGGAATATGG TGTTGGCTTA ATAAATAATT AAAAAGATTA CTTAGTGATC 840

CCATTGCCAG TAACATTCCA ATTATAATGG GGATTAAAAA TGTAAAACTT GGCCAAAAAC 900

GTCGTGAGAA TATGCCGCTA ATTGAAGCGA TAAATTGATT GTAAATACCT AACAATAATG 960

CGATAGTCCC ACCGCTAACA CCAGGTACCA AGTCACTCGT TCCCATAGCA AAACCTTTTA 1020

GAATATTAAT CCATTTAAAT TGTTGCATGA ATAACTCCTT TCAAACGATT GGAATAAAAT 1080

CATAAATAGC ATCATACCAT ATTACAAATG TCCTAGTGAA ATGATAACAT ATTTTAAATT 1140

CATAAAATCC ATTGAGAAAT TATGTGCACT TATTATCATT TATATTTTTA AAGAGAGCGG 1200

AGGTATAAGT AAGTTATAAT TAACTGAACG CATTATTACA AAGTCTTTTT GACTACAAAT 1320

TAAAATTATT ATAAACTAGT TAAGAAAACT TTATATTTTA CGGAGGGAAT ATAAAATGGC 1380

ATCAACATTA GAAATyAAAG ACCTACATGT GTCTATTGAG GATAAAGAAA TCTTAAAAGG 1440

TGTTAACTTG ACAATTAACA CTGATGAAAT ACATGCGA 1478

(2) INFORMATION FOR SEQ ID NO: 637:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1995 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

ATTACAGCAT CTTCTCTAGG TAGATTATTA AAAGATAGAG GTCTAAATGT AACAATTCAA 60

AAATTCGATC CATACTTAAA TGTTGACCCA GGTACAATGA GTCCTTATCA ACATGGTGAA 120

GTATTCGTAA nGGATGATGG TGCAGAAACT GACCTAGACT TAGGACATTA CGAAAGATTT 180

ATTGATATTA ATTTAAACAA GTTTTCAAAT GTGACAGCCG GTAAAGTGTA TTCACACGTA 240

TTGAAAAAAG AACGTCGTGG TGATTACTTA GGCGGAACAG TTCAAGTTAT TCCGCATATT 300

ACAAATGAAA TTAAAGAACG TTTATTACTT GCAGGGGAAA GTACGAATGC AGACGTTGTT 360

ATCACTGAAA TTGGCGGTAC AACAGGTGAT ATTGAGTCAT TACCGTTTAT TGAAGCGATT 420

CGTCAAATTC GTAGCGATTT AGGTAGAGAA AATGTTATGT ATGTTCACTG TACATTACTG 480

CCTTATATTA AAGCTGCTGG AGAAATGAAA ACGAAGCCAA CACAACATAG TGTTAAAGAA 540

TTACGAGGCT TAGGTATTCA ACCAGACTTA ATCGTTGTAA GAACTGAATA TGAAATGACA 600

CAAGATTTAA AAGATAAAAT TGCATTATTC TGTGACATTA ATAAAGAAAG TGTTATTGAA 660

TGTCGTGATG CAGACTCTTT ATACGAAATT CCATTACAAT TAAGCCAACA AAATATGGAT 720

GATATCGTTA TTAAACGTTT ACAATTAAAC GCGAAATATG AAACACAGCT TGATGAATGG 780

AAACAGTTGT TAGATATCGT TAATAATTTA GATGGTAAAA TTACAATTGG TTTAGTAGGT 840

AAATATGTTA GCTTACAAGA TGCATATTTA TCAGTTGTTG AATCATTGAA ACATGCTGGA 900

TATCCTTTTG CCAAAGATAT TGACATTAGA TGGATTGATT CAAGTGAAGT AACAGATGAA 960

AATGCAGCCG AATACCTTGC AGATGTCGAC GGTATTTTAG TACCAGGTGG ATTTGGTTTC 1020

CGTGCAAGTG AAGGTAAAAT TAGTGCAATT AAGTATGCTA GAGAAAACAA TGTACCATTC 1080

TTTGGTATTT GTTTAGGAAT GCAACTTGCA ACAGTTGAAT TTTCAAGAAA CGTATTAGGC 1140

TTACCAGAAC AAAAAGATAT CGAAGATTTA GGTGGTACAT TACGCTTAGG CTTATATTCA 1260

TGTTCAATTA AAGAAGGCAC ATTGGCACAA GATGTTTATG GTAAAGCGGA AATTGAAGAA 1320

AGACATCGTC ATCGTTATGA ATTTAATAAT GACTATAGAG AACAATTAGA AGCAAATGGT 1380

ATGGTGATTT CTGGTACAAG tCCAGATGGA CGTTTAGTAG AAATGGTAGA GATTCCGACA 1440

AATGtTTCTT TATTGCTTGT CAATTCCACC CAGAATTCTT ATCTAGACCA AATCGTCCGC 1500

ACCCGATTTT TAAATCATTT ATTGAAGCTT CATTAAAATA TCAACAAAAT AAATAAATTT 1560

GCTAATAAAA CCGGTACTTT CATTGTTAAA CATTGAAAGT ACCGGTTTnT CGTATAATTT 1620

TAATATTATG TTAGTGACAA GGTATGAAAT AACAATAGTG ACTTTTATAA TTCTAAGTCT 1680

CTTGTCATTT CAATCATTTG TGTATAAATG TCATAGTATA CATAATTCAA TGCCATCGCA 1740

TGTGGTyGGA CAATCTTATC GTAATCTTCA GTGTAGACTA TAGGTcTTGG TGTAGATAAA 1800

TCGATAAAAT GTACGAGATG ATCAGGGAAA TCATCTGTTT TAGGTTTGTT GCTTATTAAG 1860

ACCACATCGA TATCTAAGTC GATAAGTTTT TGAATATCTA ATGCAACTTG ATyATTATAA 1920

AATGGTGCGA ATAATAATAC ACGATCAGTT GAGTCAATTT CTTTAAwkTC TTTAATAGCG 1980

TaAGTTTnCG GCTAG 1995

(2) INFORMATION FOR SEQ ID NO: 638:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

ATTAGTGATG AAAGTCAGAT TGAAGCTTTA TTAACAGCTG AAAAATATTC AGAAATGATT 60

GGTGAATAAT CACCGTGTAA CTCCTTAATC TAAGATTGAG GAGTTTATTT TTAGTCTGAG 120

AAAATAAATG ATATGAAAGA AAAATTATTA GGTACTATTA TTTGGAGTAT TGCTACATTT 180

TATTATTCAA GAATGATGGA AATAATGAAT TTAGCTATTT TAAAAATAAA AATTGGGGGA 240

AGTTAATATG CTAAACATTC AAGACGTTAn CATnCTTTCT AAAAAGGAGC AAAAAGCATA 300

TAACCGTTTC GTAGAATCTG TAGAAAACGG TAATTTACCA GTACTACCAT GTATTGAAAT 360

GGATCTAAAA GAGATGCAAG AAGAAACATT AAACCAGAGT AAGATTGGTG GAATGCCATT 420

TTTAAAATCT TTTAAAGATA TACCATTAGA TGAAAATAAT GTACCAATGG TATTGCTAGC 480

ACAGATTAAT TTGGATGATC TTCCAGAACA ACAAGAATTA TTTCCTGTAA AAGAAGGGAT 540

AAACAATATA AACTCAAGGC TTGTTTATAT AAAAGAGCCA ATTACAGATT TATCACTCGA 660

AAATATTCAA GCGCATTTGA AGTCATTAGA TGCTGATAAT GAGGATATCC CGTTCAGTGG 720

AGCATTTTCT ATAGAATTTA GATTGTCGAA ACAAACTATT ACATGTACTG ATTATAAGTA 780

CGATGAGGAC GTGCTTGCAT TGTGGAATAA AGTCAATCCA TCCTTCGCGC TAAAATCAAT 840

GTTTGGTGGT TATGATGAAT TGATGGAACC TGTGTGTAmC AywTTTACTG CTAAGgAACC 900

ATTTAATCAA CTTGGTGGTT ATCCATATTT TGACCAAATA GATCCAAGAA CGAACGATcA 960

AGAACTGAAA ATGTATGATA GAGTCTTACT GCAAATTGaT TCTACAAGAG ATGGTAATTC 1020

TTCGATTATa TGGGGTGaTT TAGGTATTGc CAATATCtTA GTGaAATCTA CTGrACCTTG 1080

aGGcTAtGaa GTTTTGAATG ATTACCT 1107

(2) INFORMATION FOR SEQ ID NO: 639:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 904 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

ATTCATATTA TTATAAATTA TTTCTACACC ATCCCAATTG AGTTGTTTTT CATAATTTAA 60

ATGTAATTCC ACTAACTCCC TACCAATTTC AACAAATCCA TATACATCCT TTAATATCGG 120

TATTCGCGGA AAACCTTTAC TCAAATCACT TGAATATTTG TTCACATAAT ATTTATGATG 180

CAAAATTGCA TATATATAAT ATACTATCTC TTCTGAATTA AGATTTATTT TCTTTTTAAA 240

AGAATTAGgA AATATTATCT ACArGCCTCA AACTATCTTT ACCTTTGtAT GTAGCAAAGC 300

CTTkGCCATT ACCAATAAAt TGGAAATTAG GTAATATGTC CGTGATCATA GCCGAGAATT 360

CTTTATTCAT TCCCTGTCCT TGTATATAAA TCACCTGTCC AGTATTCTCC ATTATATTAT 420

AATATCTACT TGGCATTTCC ATAATATTTT TGTCGTACAC TATCCATTTT TTTGTAAATG 480

GTCTATGCAT AAATTTAACA ATTCTCTCTG GATTAATTGA AATATTTTTT CCTTTAGAAA 540

ATTTTTGGGT AAGTCCTCGT GTCCAACTaA TaAATGTTTC ATCTTTGTTC ACTAAATTTA 600

TACGTTCTCT TGAATCTAAG ATATCAATTA ATCTATCTAT TTCAGAATTA TAGTTATCTA 660

CAAGTAATTT TGcATTTACT AATGCTTTTT CATTCGAAAA ATTTGTTACC CAATTATCTC 720

TTGCTGaATT TACTCCATTA AATkGAkCTA AATATATAGA ATTTTCAATA TCCTTGGAAT 780

CATACATTGG TAAATAATTC CCCATAGTTT ATGTCTCGGT GATTAATCCA ATCATTGGGG 840

AAAG 904

(2) INFORMATION FOR SEQ ID NO: 640:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

CGATGTCTTT ACTATTAGAC TTAGCCATTG GTTTCACCTC TCCAAAAATT GTAAATGTGT 60

ATCATCAATA TGAAAGTTAC ATAAAACTGA CATATTTCTT TAAAATATCA ACGCCATTGA 120

TAACTTCCTG TTTTAATTGA TACGCTGTAA CAAAATACTA TAGTTAGTGC TTACATGTAT 180

ATGTTAAAGC AAGCAGTGGT AAATGTAAAT TATAATTATT CATTAACTTT GCAATATATT 240

AAATCTTTTA TTCATAGAAG ATAAATATCA AATCAATCAT AATTATTTGA CAACAAATAG 300

CTAACGATTG TTTTAATCTA CATTTGGCTT ATAGCATTTT AAACCTATAC TCTATTTTGA 360

TACAATATAA GTGTAAAATC AATCATAAAA AGGATATTCA ATATCTGCAT CCAAGAAAAA 420

CATTACAATT ACCTTT 436

(2) INFORMATION FOR SEQ ID NO: 641:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 442 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

GTTATTAAAT TCAGAGTGGT AGCAAATTAA AGTTAnTCAA GAGTTAAGAT GAATTTAATT 60

CATGAACACG TCTATTATTT TTATAATTGT AGCAAATAAA GCTTTACATC AAGGAGGTAA 120

TTAAATATGT TCAAAAAATA TGACTCAAAA AATTCAATCG TATTAAAATC TATTCTATCG 180

CTAGGTATCA TCTATGGGGG AACATTTGGA ATATATCCAA AAGCAGACGC GTCAACACAA 240

AATTCCTCAA GTGTACAAGA TAAACAATTA CAAAAAGTTG AAGAAGTACC AAATAATTCA 300

GAAAAAGCTT TGGTTAAAAA ACTTTACGAT AGATACAGCA AGGATACAAT AAATGGAAAA 360

TCTAATAAAT CTAGGAATTG GGTTTATTCA GAGAGACCTT TAAATGAAAA CCAAGTTCGT 420

ATACATTTAG AAGGAACATA CA 442

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

CCAATTTTGG TATGAATTAT ACAGATAATT CnGCGCCCGG AGGATCATTT GCTTATTTAA 60

ATCAATTCGG TGTGGATAAA TGGATGAATG AAGGGTATAT GGCATAAGGA GAACATTTTA 120

ACTACTGCCA ATAACGGAAG ATATATTTAT CAAGCTGGAA CTTCATTAGC CACACCTAAA 180

GTTTCGGGAG CACTAGCTTT AATCATTGAT AAATATCATC TTGAAAAACA TCCAGATAAA 240

GCGATTGAAT TGTTATATCA GCATGGGACA TCTAAGAATA ATAAACCATT TAGTAGATAT 300

GGGCATGGTG AGCTTGATGT GTATAAAGCA TTAAATGTAG CAAATCAAAA AGCAAGTTAA 360

TAAATCAAAG GAGTTTTTGA TTATGGCAAA ATTAGTTACT GAAAACATTT CGAAGCGGTT 420

TAAAAATCAA GATGTATTAA AGCATATTAA TATCACTTTA GAAAATAACG AAGTTTATGG 480

ATTACTTGGT ATTAATGGAG CCGGTAAAAC GACACTTATG AAAATTATAT GTGGCATACT 540

TCAACAAGAT TCAGGGGAAA TTAAATTAGA TAATAGACCA ATGACACGAA ATGATTTGCA 600

CAAAGTTGGT TCGCTTATTG AAACACCTGC GACATATAAT CATTTAAGTG CACAAGATAA 660

TTTGAAAATT GTGTGTTTAA ATGAAAGCGT TGATTTCaGC GAAATTAATA GTGTTTTAAG 720

CTTAGTCAAT TTAAATGTCG ATAAAAAGAA AAAGGTTAAG GACTTTTCTT TAGGTATGAA 780

ACAAAGACTT GGAATTGCAA TGGCaTTAAT TAAAAaGCCA GAAATTTTAG TATTAGACGA 840

ACCATCTAAT GGTTTAGACC CATATGGAAT CCAAGAACTT AGAGAACTTC TAAAATTATT 900

AACAGAACAA GGTACTAGTA TTATTATTTC AAGTCACATT TTATCTGAAA TCCAAGTTTT 960

AGCAGATCAT ATCGGTATTA TTCATGAGGG TGAGCTAAAA TATCAGCAAA GAAATAACAA 1020

AGATGAAAAC TTAGAAGAGA TATTCTTCAA AATAACGAAA GGTGATTACA AATGATACAT 1080

TTAAAGATaG AAGGTATCAA ATTTAAAAAt TCTTTCAGTA TGTATGTTTT ATTAATAAGT 1140

CcGcTGGTAT TTCTTTGTTT TGCTATTTTC ACAGTCTTAT TCGCCAAAAG TAATACGGGA 1200

ACAGCGAATA GTGTGTCACC ATATATAACT TTACTATTTA ATATTTGGCC AATTGCTTTC 1260

ATCCCGATTG TATTATGTAT GGCTTGTAAT TCGTTATTTA AAATTGAAAT GAGAAATAAA 1320

TCATTTAATT ATTACTTAAG TAATAATTGG TCGATTACAA AAGAAATAAG AGCAAAGATT 1380

TTCATTTTAT CAATAGCATT TTTGGTACAT TGCTTTTTAG TATTTATTAT TGCTTATATA 1440

TTGATGTATG TAGTATCTCT ACCATTGATA CCGCTCAACT TTTTATTAAC TCGATACTTT 1560

GGTGTGTTCG TATCAATATT AATAAACTTA GTATTATCAG TCATTTGTGT CTTGTTTTTA 1620

ACATTGAAGA GTTTATTTTG GGTGTTGCCG TGGGGGATAA TGCAGAGAAT CCCGCTTATT 1680

ACGCTTGGTA TACTACCTAA TGGtTTAGTT GTAAACCATA ATTCAAAATA CTTTAATGAT 1740

CTCAATGCCT TATATATTTC GATTATTGTT AGCATCATTA TTTTCGCGAT AGTAACATTT 1800

TTAAATAATA AGAAAAGTTG GCGATTAAAA TGATAATTAA CGAATTAAAG TCATGTAAGT 1860

TGAAATTTTC TAAGCAAGCG CTCACATTTG TACCCATTAT TGTAACCATA TTGTTTATAT 1920

TATTTATAAA TTGGTATTTA AACGTAAATT TATGGAATGG TCGACAAATm AGTTTGTTTA 1980

CAGCGAGTTT TAATGCAATT ACATCGCTAT TAATTTCTAT AAACGTCTAT CAAGTTATCA 2040

ATTTTGAAGA AAATATTGGT CACTTTAATC ATATTTTAGG AAAAGCTAAT AGGCTAAATT 2100

GGTTAAATGC ATCAATGATT TTTACTTATA CTATTACAGC CATATGTATT CTATTAGCAT 2160

CAATTAATTT ATTGTGGCAT TCACATGATA TGAAAATAAC ACTTATGTTT ATAGGcGTaT 2220

CATTGTTTTT CAATGTaATT ATATTACTGC TACTTTTTAT TTTTAGTATT TTCATTAAAG 2280

ATGTAATGGC TATTGTTGTC GGAGTTTTAA TGTTTATTTT TAACGTTTAT TTTGGATTAG 2340

AAGTGCTTGG AGATCATTCG TGGTTCTATT TACCAATCAC ATATGCTACA CGTTACGTTT 2400

ATATGTTTAn CGAAGGGGAG TATACCAGTT ACATTAACAT TGGGCAATCT ATATnATTAT 2460

CACGnTGCCG AT 2472

(2) INFORMATION FOR SEQ ID NO: 643:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 646 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

ATAATATAGG AATTATTTCG ATnACAGATT TTACGAATCG TGCTACGATG CAAAATGAAn 60

ATAAAGATCC ATATGGCGAA AAGTTAGCTT ATGGAATTGC TTTTAATGGC AGTGTGGATA 120

TGCAAGGGGA TAAACAAGTC ACAATTCCAA AATATAGTGT AGTTACAATT ACTGGCGAAA 180

ATAGTAAAAA TTATCGTGTT ACCGCCGATA ATAAGACTTA CTATGTTAGT AAAGATAAAT 240

TAGAATATTT TAACCCGGCA GGTTTATATC AAACGCATAG TTTTAAAAAA TTAGCACCAT 300

ATATGAAATC AAATTATAGT AATTACTATG CATACTTTAA TAGTCAATTA CATAAAAAGC 360

CACAACAACC GATACAATTA CTTTTCAATG ATAATAATCA GTTATACGGT TTTGTTTATC 480

CAATTGTAGA TAAAAAAGAA TTAAAAGATA AGTTTAATAT TAACAATAAC ATTTGGATTA 540

CTAAAGTTGG GAATGGATAT TGTATTGCCA ATTTGAAAGA AGACAAATGG ATTTATATTG 600

AATTGTAGGT GTAAAGATGC TAGATAATAT TATTTTATAT TTTAAA 646

(2) INFORMATION FOR SEQ ID NO: 644:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

TAATATCGGA ATTTGATAAT GAAGATATCT AATTTTTTAA TATTCGTAGC TTTTATTTTT 60

CTACTTATTT TATGTTTATT TTTAATCTTA CAAATGACAA ACCATTAAAA GTAGCATCCC 120

AACATCAAAC AAAAAAACAA TTCATCAAAT AAAAATCGCT ACAAAACCAA GTCATTAAAC 180

ACGCAATAAT TAAAATTTTC CACTCATTAT AATTCTGAAT TCCAAATGTC GAATTCCGAA 240

AACCAAACTC CAAATTCCAA AAACGCAACT CCAAAATTAA AAGCATTTCC CTACCATTCG 300

GGAAATGCTT TTTACATACT GgATTACTCT GTCATTAATG ATTTTACAAC GGgAAACCAT 360

GTCGtCATGT ATGACCaAAG TAGCGTCGCT AtCaTaAgGt GGTTCGGATC TTTATTGGAT 420

AATnAT 426

(2) INFORMATION FOR SEQ ID NO: 645:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645:

nTTATTTACC CACAACATGT TGCGACATTA GGTAAATGGG TACCTTATTT ACTTGGTATT 60

GTTATGTTAG GTATGGGATT AACAATTACA CCTAATGATT TCAAAATGGT CTTTAAAGCA 120

CCTAGAGCAG TAATTATTGG TGTCTGTCTA CAATTCAGTA TTATGCCCAC ATTAGCATTT 180

ATAATTGCAA AGTCTTTTCA TTTACCACCT GATATTGCTG TTGGCGTAAT ATTAGTTGGA 240

TGTTGTCCGG GTGGGACATC AAGTAATGTA ATGAGTTATT TAGCCAAAGC TAACGTAGCA 300

ATATATCTAT TTGCAAATGA ATGGTTGGAA GTATCTTTCG TGAGTATGTT GTGGTCAGTT 420

GTTCAAGTTG TATTAATTCC AATTGCTTTA GGTATTGTTT TGCAAATTAT TAATCGTAAA 480

ATTGCTGAAA AAGCTTCTAC AGCTTTGCCA ATTATATCAG TTGTTGCTAT TTCATTAATT 540

TTAGCAATAG TTGTAGGTGG CAGTAAGCAC CAAATCTTAA CTACAGGATT ATTAATATTT 600

TTAGTAGTTA TTTTACATAA CGTATTAGGG TATACGATTG GATATTGGTT AGCTCGTCTT 660

TTAAAATTAG ATCGACAAGA TCAAAAAGCA GTCAGTATTG AAGTTGGAAT GCAGAACTCT 720

GGTTTAGCTG TGTCATTAGC aGCATTGCAT TTTAATCCAA TTGCAGCAGT ACCAGGCGCA 780

GTGTTTAGTT TCATTCATAA TATAACAGGG CCTATTTTAG CAAAGTATTG GTCAAAAAAG 840

TTATAATTGC ACTAATAGAA TGAAGTGGTC ATCGGACTAT GTTAAGCTTT GATAAAGAGA 900

AAAAATAGAG GAGTAAATAT ATGTATAGAG CAGTTATATT TGATTTCGAT GGAACAATAA 960

TAGATACGGA ACAACATTTA TTTAATGTTA TTAATAAACA TTTAGAGATG CATAATGCCG 1020

ATCCTATAAG CATTGATTTT TATCGTTCTT CTATTGGAGG AGCAGCTACA GATTTGCATG 1080

ACCATTTAAT TAAAGCGATT GGTTCGGAAA ATAAAGATAA ACTTTATGAA GAACATCATC 1140

TTACTAGTAC AACATTACCG ATGATTGATA CGATTAnATC ATTGATGGCA TTTTTAAAGC 1200

AACGTCACAT TCCTATGGCA ATTGCCACAA GTAGTGTGAA AGCGGAAATA ATGCCCACCT 1260

TTAAAGCATT AGGTCTAGAC GATTATATAG AGGTAGTTGT TGGTAGAGAm GATGTTGAAC 1320

AAGTTAAACC TGACCCTGAA TTATATTTAT CTGCAGTACA ACAATTAAAT TATATGCCGA 1380

CACAATGTTT GGCTATTGAA GATTCTGTAA ATGGTGCAAC AGCCGCGATT GCAGCTGGAT 1440

TAGATGTTAT TGTTAATACG AATAAAATGA CAAGCGCACA GGACTTTTCT AATGTAGATT 1500

ATGTAGCAAA AGATATTGAT TACGATCAAA TTGTAGCGCG TTTCTTTACG AAATAGGAGG 1560

CGTATCATGA TGGGTTACAT TATATTGTTT TTTCTAGCTG GTCCAGTAAT TTTAGGCGTT 1620

GGAAATTTGG TGATTGGTCC TATATTTAAC AAACAGACAC CATTTCGCGT GCAAGTAAGA 1680

TCTTTTGTTG kTGGkTCmAT GrTTTACTTA ATACTCGCAA CAATTGGCTA TTTTTTACTA 1740

TTACAAGGTA AACTTTAACG AGAAAACCAC CTTACCTCAT TAAATGGACG ACCATATGTA 1800

TGTGAAATGG TAGAACGTTC ATGTTTATGT ATGAGATAGG GTGGTTTAAA TAGTTACATA 1860

TATTTTAATA ATAACGTCAC GATGATAAGT ACAATTAAGA TAATATCTAT GCCTACCATA 1920

ATTGTAGCTC TTGTTGCAIT ACTTCCTTGT TCTTTTGCTG ATTTCATAGC ACGGTAGTTT 1980

GGCACAAAGC TAATAATTAG TAAGATTAAT ACAATTACAC CAATTAATGC TGTTGTCATG 2040

ATGAACGACC TCCTTTATTT TTTTCAATCA ATTCCCAAAT AAACGTAGCA ATCACACCGA 2100

CAATAATTAA TGCAATCGGT AAAGTCGTAC CGAGTTTAAT CTTGCGCTCT GGAGAATTAA 2220

TAATAGTAAA TACTGTAAGA CAAATGAGTA TGAAAGCAAG TGTTGCAATA ATAGTTCTTC 2280

CAACTAAATA TAGGATGTCA GGTTTTTCCA TACCGATATA ATTTATGATG AAAAATGCTA 2340

CAGCAAAGAG TACCGATATT TTTGTAGCAC GTAGCAGTAT TTGTTTTAAC ATTGATATAC 2400

TCCTTTTTAA TATTATTAAA ATTATATCAT AATTACCAAG AATAGCTGAA GTTGTATGTG 2460

ACTCAACGGT ACTTGAGCAA CTTTTTTAAT TTTTTAGAAA AATCACAAAA TAATTGTTTG 2520

CAAAGTTGCA AAAGCCTGCT ATAGTAGTTC TGTAAACGAT TGCATGGTAT GCAAATATTA 2580

ATGTACCAAA ATCGATAATT TATAGTATAA TTACGGCAAT AAGTTTTTTT ATGGATTTAT 2640

TTAGTATCAA TCAGAGATGG GGTAAGAAGT TATGGAGAAC AATGAACTAC AAAGGGGATT 2700

GAGTGCCCGT CAAATTCAAA TGATTGCACT TGGTGGTACG ATTGGCGTGG GGCTTTTCAT 2760

GGGTGCGACA AGTACAATTA AATGGACAGG CCCATCAGTT ATCCTTGCAT ATTTAATTGC 2820

GGGTATCTTT TTATTTTTAA TCATGAGAGC AATGGGGGAA ATGATTTATT TAAACCCTAC 2880

AACAGGATCA TTTGCAACAT TTGCAAGTGA TTATATACAT CCTGCAGCAG GTTATATGAC 2940

AGCATGGAGT AATATATTCC AATGGATTGT AGTTGGTATG AGTGAGGTCA TCGCAGTAGG 3000

AGAATATATG AAGTTTTGGT TCCCGGAATT GCCAACTTGG ATTCCTGGTG TTATTGCTAT 3060

TTTATTATTA ATGGCAGCGA ATTTATTCTC GGTAAAAGCG TTTGGAGAAT TTGAATTTTG 3120

GTTTGCTTTA ATTAAAGTTG TAACAATTAT TTTAATGATT ATTGCTGGTT TTGGTCTTAT 3180

nnTCTnTGGT TTTGGAAATG GTGGCCATGC GGTAGGTATT TCTAATCTAT GGACAAATGG 3240

C 3241

(2) INFORMATION FOR SEQ ID NO: 646:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

AGGCGTCAAC TCAGATGGTT TAATAATTGC CGTATTACCT GCTGCAATAG CACCGATTAA 60

AGGTtCGAaC ACTAGTtGAA AAGGATAGTT AAATGGTGCA ATGATCAAAA CTGTTCCATA 120

AGGTTCTTTT TTGATATAGC TTTTTGTTGG AAATAAATAT AAAGGTGTGT CTACATTkTT 180

TGTTTTAGTC CAGTTTTTAA GTTCcTTACG GGCAATTTTG ATACTTyTCA AAGTTATGCC 240

AATATCGCTC TCGTATGATT TAATAGCTTT GCTTAACTTC TTTAATTGCT CTTTTCTAAA 360

ACTAATATCT TTAGTTTGTT GTGTATTGAA AAAAGCTTTA CTGTCATAAA ATTTTTGCTC 420

AATGATATTC ATAATGAAAA GAACCTCCTT ATATGATTAT TTTGGAAAAA GCGATTAATT 480

GATTTGAATG TTGTGGCCGT TAATTTTAAA TGGTCTTTCG AATTATATAT GTTGAAAGTT 540

GAAAATAGAG CGATGAATCG TGTACATAAT AATATTTATA ACTTTAATCA TAACGAAAAA 600

GGTAGGAAGA AAACAAAAAT TTATACTCAA CATCGCAAAT ATTTTAAGAA AATGTAAAGA 660

CAAAAGGGGA ATTGTATAGA AATCACTAAT CTGTGGGTTA GGGTAGCTAA AGGAATAAAA 720

ACTACTATTG AAAAAGGGTT GTAAATTAGT CAAACGTAAA TAAAAAACAG TTCATTGAAA 780

GTGAAATAAA TTCTACTTTA ATGAACTGTT AGTTAAATAC AACATGTCTA TAATTAGACA 840

GTAATATAGT ATTATTTTGT TAATGCTTCA GTGATTTGAG GTACGATTTG TTTTTTTCGA 900

GAAACGACAC CAGATAAGAA GGCCATGTCA TCTTCTAATT GAACATTGAA TGtTCGCCAA 960

CTTTATCTTT TTCAGCACCT ACAACTAAAA TTTTAGAATC ACTATTAATG ATGTCAGTAA 1020

CAACAAGTAC AAATAAGTCA TATTTTTCTT GTGCACTTAC AGCTAACATT TCTTTTTCTA 1080

rATCTTCTTT ACGATTTAAC ACTTCGTCAA GGTCAACAGC ATTAACTTGT GCAATACGAG 1140

TCACATAGTC ACCCATAGTA AATGATTTAG CATCCATGTT TAATAAGAAT TCAACTGATT 1200

TATCAGTTGT TGAAGCACCT GCTTTtAACA TATCTAAGCC GTACTTTTGA ATATCAACTT 1260

TAGCAATATC TTTnAATTCT tCAGCTGCTT TAACATCTTG TTGTGTACAT G 1311

(2) INFORMATION FOR SEQ ID NO: 647:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1498 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

CATATACTTT TTCATTTCTT TACGAGATAC TTTACCAGAG GATTTAGACT TCATACGCTG 60

ATCCATATGT GCTTGCGTTT CAGaATGTCC ACAAACACAA CGATATACCG CTTCTTTCCC 120

TTTACCAAAC AACGTTAATT TCTTTTTACA GTTTGGACAT CTTGCATTTG TTTTGCGCTG 180

TACATTCTTT TTCGTCTTAC AAGATGGATC TTGGCACACA AGCATCTGAC CATTTTTAGT 240

TTTAACTTTA ATCATGAATT TACCACACGT TGGGCATTCT GTGGTTGTTA AATTATCGTG 300

TTTATATTTA CGATCACTAT TTTTAATCCC ATTTACAACA TCTTTCGTAA AATCTTTCAT 360

CCATTGTGcA GTTAAAAGTG GCGACGTTAA TTCTTCTGGT GCTAATTCTA ATATTTGTTT 480

ACCTTTTGAC GTTACTTTAA TTTTACCGTC TCTTGATTCA ATGGCATTCA TATTAAATAA 540

TTTATCGATA ATGTCGGCCC TTGTTGCAAC TGTGCCGATA CCACCTGTTT GTTTTAAAGT 600

TTGCGCATAT TTTTTATCCT TCAATTGAAT AAAGTTCTGA GGGTTCTCCA TCGCTTTTAA 660

TAACGAACCT TCATTAAAAT ATTCTGGAGG TGTTGTTTCA TGTTCTCTAA TATTTGTTTT 720

TGAAATCTTC ACTTCATCGC CTTCTGAAAA AGGCTGTTGC ATCTCTGTAA TAGATTCACC 780

TTGTCTAATA GATTTAAAAC CTAAAACAGT TGTTACATTC TCTTTCAAAA CAAATGTGTG 840

CCCTGCAACC TCTAAAGTTA CAGTTATCGC GTCATACTCG TGCGGAGGCA TTAAAGCTTC 900

TAAAAAACGC TCGACAATCA TATCGTATAA CTTTAATTCT CTATTACTTA AGTCTGACAT 960

GACAGGTCTC ACTTCTGTAG GAATAATTGC ATGGTGATCA GATACTTTTT GATTATTAAA 1020

TATCGACATT TTTGATGAAA ATGTTTTAGA CATTAATGGG CGTGCTTGGT CTTTATATGT 1080

TGTTGCCATC GTCACCTGAA TACGTTCTTT CATAGTATCT ACCATATCAG TTGTTAAATA 1140

GTTTGAATCT GTTCTTGGAT AGGTTACGAC TTTATGTCTC TCATATAAGC TTTGAAGTGT 1200

ATTCAATGTT TCTTTAGGTC CAATTTTATA ACGTCTATAC ATATCTTGTT GTAAATCTGT 1260

TAAATTGTAC AGTGATTGCG GATACGACTT CTTATGTTTA GTAGCAACAG ATTTAATCTT 1320

ACCATCGACA TTTTTCAAAT TATTAACCAT CTGTTCTAAA GTTTCTTTAw TGGtATATCG 1380

CTGATTTGaw TCTAGCTGAA AATCAAACCC TTTTACCGTT AATGATAATG TAAAGTATTG 1440

TTGTGGnTTG AACTGATTAA TCTCTTGTTG GTCGTGTAAT TTACTAAATT GAAACGGn 1498

(2) INFORMATION FOR SEQ ID NO: 648:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1044 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

TAAAACAATT CGTTTTATTA ATACAGTTTG TAAAAGTATT CTCTTAGTAC TAATAGCTAA 60

TGTAATGATA GAAAATACTA GTGTTATTAA AGATTTGAAT AAAATAAAAG AAACTGAGAA 120

ATATTGGAAT GTATTAGATG ATTATTACAC GATTGAATTT GCACCTTATC ACGAAACAAA 180

ACAAAGTTTG ATTGATAATA TGGTGCGATC AGAACAATTA GTAAAGGCTA GTGAAGCAGA 240

AAATAATGCG ATTTTATTCA AACCAAAGGG TGACTCCGTT GACAATGACA ACTTTTCGCC 300

TCAACCTGAT ATTCCGATAA AAAATCAAAA AAATAATGTC GAAGTAATTA TTCCACAAAA 420

GTTTCATGCA ATGCGTAATG AAATCAATCA AGCATATCAT TCATGGTTTG AATTTGTACA 480

AAATAAAAAT AATAAAGAGA ATAAGTTATC TATACAGTTT ATCAACAAAA ATGATTGTCG 540

AATTTTTTCA TTTGATGCAC GAGATAGTCG CCATTTGTCA TTTATAGAGG CGCCAATCAT 600

TGTGAATGTT CAGGCATCAG ATTTATCGaA TGATTTttAT TATGCCATGa TCaGTCaAGG 660

CGGGTATTTa TTCaAAAATT ATGaCGCGCT AGTAAAAAAT ATTGGAAAAG TATCCATCTT 720

GATGGGGAAA TCCAGTGGAA TAACCAATTA TAAAGATAGC GTGATGGAAA TGTATCATGA 780

AAACAATTTG AAATTAACAG TACTCAACTT TTCACAAATC ATTATCGCAA TCATTTTAAT 840

AATTATTATT TTATTTGATG TGAAATATTA TTTTGAACAG CATCGAAAAT TACTCGTAAT 900

CAAAAAGCTA TATGGTTATT CAACATTAAG AGCCAATTAC CAATACTTAT TAATAAATAA 960

TATAGTTGTT ATTTTTATTG GAATATTGAC GAATGTAATT TTACATTCTC ACTATATAAT 1020

GATGTTATTT GCAACGATTC TTGT 1044

(2) INFORMATION FOR SEQ ID NO: 649:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649:

GAACATATTG GGTTATGCAA GGnGGTCACT CTTCACACTT ATAAACAACA TTTTAATAAT 60

GTAAAGTTTA ACCAGCTAAC ACTTTTGTTA GCTGGTTTTT ATTTTCCTTC AATTTTTAAA 120

TGGTTAAGTC CCCTTCTATA TCTTATAAGA CAATCATTAT AATCAATTCA ATTAATACAT 180

TAACAACCAC AACTAATAAA TATAGTAACT TCAAAATCCA TATTTATGTC TAAAGATAAT 240

CTCAATGTTG TTCACGTCAA TAAAATTATC CCTAGGTTTT TAAAAATTGT ACATGTTTAA 300

ACAATCAAAA GTGTACATTA TTAAATTATC ATTTCCAGTT AGATTTAGAA AACATTCACA 360

CCACGCATGG ACCAACGTAT TCGTCTTcAT TcATTTTAG 399

(2) INFORMATION FOR SEQ ID NO: 650:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650:

GTACTAGGTT CTAnGATTCC CTACTGTAGT CATAGATATT TTCCAAACAG AGCCTGACAA 60

CTTTTCATTT TTAATAGTGA TCACTATATT AATCGCTATT GCAATTTATG CATGTCGATT 120

TGTTTGGGTT TATTTCTGGT ACAAAGATTT TTATTTCCCG AAAAATATAC AATCTTATCT 180

AGACGAGGAA CATGATTCAC ATGAAACACC ACCTTCTCGA GTGCGTTACG CATTTATTAT 240

GACCATGTGT GGTATTCACG GTACAATTTC ACTTTCAATG GCACTTACAT TACCATTTAT 300

CATTACAAAA GGACAAGCAT TCGAATACCG TAATGATTTA TTGTTTATTG CATCTTTCAT 360

GGTATTAATT AGTTTAATCT TAGCGCAAAT TGTTTTACCT TTAATTACAC CATCTGCCGA 420

AGATACTACT TTTAAAGGTA TGACTTATCA ATCTGCCAAA ATTTTCATTG TTCAAAAAGT 480

GATCCAGCAT TTTAAAAACG AAAGTAAAAA AGACAAAAAC GATACAAATT ATCGCCCAGT 540

ATTAAACCAA TACTATGGAG AATTGTTATT TTTATTAAAT TCAGAACCTG ATAATCAAAA 600

TACrAAAGAa CTCAAACGTT TAGAAGATAT TGCaAAAGTA ATCGAAACAT CTACACTTGA 660

GCGTTTAATT GATAAAGGTA AGGCAACATA TCAGGATATT AATAATTACC GCAATATTGT 720

CGAATTAACA GAGACACACC GTACTGC 747

(2) INFORMATION FOR SEQ ID NO: 651:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651:

ATACAATACT CTTTTATTAT TCAATAAGCC ACTTCCTATA GCAAATGTTT AACTTTAAAT 60

ATTTTTCGAT GCTAACAAAA AATCACACTA TCATCTTTTA AAATGAAAGT GTGATTACAA 120

GCAAATCTGT AAAATTTATA AAGCAGAAAC AATTCAACTT TATCATTATG ACATTTCAAT 180

TAAACCTTCT ACATTATAGT TCCAAGCATC TTACACATGA ATGCAAGTAT TTAACGATTT 240

AATTGTGACA TAGCCTGTTG ATATTGTGTT TCATTGATAT AATTTTGTTG CTTCATTTTT 300

TCTAAGTTCG TGCTTACACG TTGCGTAAAA TTCTCTGACA TATTATTGAT ATTATATACG 360

CTAGGTGCAT TGACTTTACT AGCTAAAATA GCGCTTTGTA AAACTGTTAT GTGAGACATT 420

GTTGTACTAT TTTTATTCAC GGTTGTTCCA AAGTAATGGT TTGCTGCGCC CTCAAGCGTA 480

TATTGATTAT CCCCAAAGTA AATATTATTT AAATAAAAGC TTAAAATTTC GTTCTTATTA 540

TCATTATCAT AAAAATAATT TTTGACAACT TGTTGTGTAA TGGTACTACC ACCTTGCACA 660

TCTCTGTCGC TAATCGTTGA AAATAAAGCT CTAGTTGTAC CTTTCAAATC GAATCCATGA 720

TGATTGTAGA ATCGTTCATC TTCCATTGAA ATAAAGGCAC CTTTAACATA CTCTGGCATG 780

TTATCAGCTG ACACAAAACT ACTTTTATTT TCAATTTTTC TTAGTTCATC CACATTATCG 840

CGTGTAGATA AAAAATACAT GATACCAATA AACAATGCGA TAATGATTAG AATGGTTAAT 900

AATATTTTTA ATAGTATTCG TTTACTTTTT TTCTTTTTCG GCGGTTTGCC AACTGGTTGA 960

TAATACGTAT TATAGTGAGG TTCGTGTTTC ATATGCTCAA AATGTTCATT TGAGTTTGAG 1020

TACCTATCGC TTCTTTTCAT GCGTTTGCTC CTTCTTTTAA AACTCACTTA GtATATACCT 1080

TGaGTTTACC AGTACTATCA CAAATAGGCT ACACTTTTTG GGAAAATCAG TCCAAGGGCT 1140

TACAATCGTA TACGCCATCA TACTTACTTT TTTGTTTTTT GAAAAAATTA TAGATAAATC 1200

ATTGCAATTT TAAATATTAA TCATGTCAAA TATTGTTATA TTTTATAAAA ATAAAAGACC 1260

ATCCCTATTA AATGCCAATA GAGACGACCT TTTATTTGTT ATTCATTTAT TAAAACTAAA 1320

ATCCATATTT CATTTCAAAC GAAAATATAT AAATTTTAAC AATCGrTAAC CAC 1373

(2) INFORMATION FOR SEQ ID NO: 652:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 859 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652:

GGCAGATAAT TTAGTCATTG TTGAATCGCC TGCAAAAGCA AnAACCATTG AAAAGTATTT 60

AGGTAAGAAA TATAAAGTTA TAGCTTCAAT GGGACACGTC AGAGACTTAC CAAGAAGTCA 120

AATGGGTGTC GACACTGAAG ATAATTACGA ACCAAAATAT ATAACAATAC GCGGAAAAGG 180

TCCTGTTGTA AAAGAATTGA AAAAACATGC AAAAAAAGCG AAAAACGTCT TTCTCGCAAG 240

TGACCCCGAC CGTGAAGGTG AAGCAATTGC TTGGCATTTA TCAAAAATTT TAGAGCTTGA 300

AGATTCTAAA GAAAATCGCG TTGTTTTCAA CGAAATAACT AAAGACGCTG TTAAAGAAAG 360

TTTTAAAAAT CCTAGAGAAA TTGAAATGAA CTTAGTCGAT GCACAACAAG CGCGTCGAAT 420

ATTAGATAGA TTAGTTGGCT ATAACATCTC GCCAGTTCTT TGGAAAAAAG TAAAAAAAGG 480

GTTGTCAGCG GGTCGAGTTC AATCTGTTaG CmTTCGTTTA GTCATTGACC GTGAAAATGA 540

nATTCGAAAC TTTAAACCAG AnGAATATTG GACTATTGAA GGAGAATTTA GATACAAAAA 600

aAAAGATGTT GAGAAAATTA CAGCTGCATT AGATGGAGAT CAATTCGAAA TTACAAACGT 720

GACTAAAAAA GAAAAAACGC GTAATCCAGC AAACCCATTT ACAACTTCTA CATTACAACA 780

AGAGGCGGcA CGTAAATTAA AcTTTmAAGC AAGAAAAACA ATGATGGTCG CACAACAATT 840

ATATGAAGGT ATAGATTTG 859

(2) INFORMATION FOR SEQ ID NO: 653:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653:

TTCAACTTCG TTTGGAAATC ATGTTCCTCA ATTGTTGGAC TTAAACGAAT TTCTTTAACA 60

TTGATAATTT TTTGTTTCTT TTTCATTTCT TTTTCTTTTT TCTGTTGTTC GAATTTGAAT 120

TTACCGTAAT CCATAATTCT TGCAACTGGT GGTTTCGCAT TCGGTGCAAC GACCACTAAG 180

TCTAAATCTA CACGTTCAGC CATTTCTAAA GCTTCACGCT TTGATTTAAC ACCAATTTGT 240

TCACCATCTT GACCGATTAA ACGTAATTCT TTTGCACGAA TTTTGTCATT GATTTGAGTT 300

TGATCTTTTG CTATGGTTGA CACCTCCAAA ATTTTTACGA AATTTGCACC AAGCAAAAAG 360

GAAGAGCAGG TATAAAATAC CCGCTCTTCC TTATACACAG TTATGTGTAA TGTGATTAAC 420

CTGCCAACTG CTTTATGCGT CGCTACAGGT GAGAAGCGGG TGCTTCTACT TGGTTCGTTT 480

CGTATTCAAC GTTATTAATC ATATCAACAA TTCACATTTA AGTCAACACT ATAACTGTAA 540

TTATTTTTAT TTTAACCTTT TATTTCATCC ATTGACACGT CTTGACGTAA ATCTACTTGT 600

TCTAATGGAA TTTTTTTCGT TTTATATCGA AGCTTATGAT AAATAAAGAA TGCTAAAAAT 660

ACTGGAATTC CCATATACGT AATTAAGAAG CGACTAAAAT TAAAATCTCC TGTnTTAATA 720

AAGTCAACAT CTTGCCCAAn AAnTACT 747

(2) INFORMATION FOR SEQ ID NO: 654:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

TTGTGCTTCT TTTTTAGCTT CTTGAACCTC TTGTGCCTCT TGTGATGTAT CACTyAAATT 120

ATTTGCACTT GCTTCTTCTT TTATCGCTGC TTGTTGTGCT TTCAATGCCA CTGCTTTTGr 180

TTCTTyATTT GATACAGCCA CACTTTTATC CGCTTCTGCT TGTGCTTCTC TTTTAGCTTC 240

TTGAATCTCT TGTGCTTCTT GTGATGTATC ACTTAAATTA TTTGCACTTG CTTCTTCTTT 300

TATCGCTGCT TGTTGTGCCT TTAATGCCGC TTGCTCATTT TTAGATTTGT TTAAAAATCC 360

TTCAACACGT TCTTTTGTAT AGGCAACCGT TTCTTCAAGT TGCGTTTTTC TTTCTTCAAA 420

CTTTTGCGAC AGTTCTTGTn CTTTGACTTT nAAATCATCT GCTTTTTGAT AAACTTTATT 480

TTAAAATACC AACCTAAAGC C 501

(2) INFORMATION FOR SEQ ID NO: 655:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655:

CACCTTGTCA TAATTAATTT TTTGATTTTT CATTTTACTG ATAATAGGTT CAGCATTAAT 60

CATGATTTAA CCTCCCACAT TTAATCATTA ACTTCTATTA TATATGATTC ATATTAAATG 120

TCAGTCAAAA AAGTTAGAAA TTCATTTTAA TGCATTTATA TTTCGAAAAT CCCTTATGTA 180

TCTAAAAGCA TTTTTTAAAC TTGAATTTTA AAACACTAAA CAACACATAC GTCTCTGTGT 240

CATTTTCATT TTTTGTATGT CATATATATG TTTACTTCAT TTAAATCAAT TTCATCTTAT 300

AATTTATCGT GTATTTTACA AAAGATTGAC TTCAATTCAT CGTAAAAGTT ATACTTTTGC 360

CATTTTTTAA TGTAACATGG TGTTAGTAAT AAAAATAATA CATTGAGGTG TTTTACATGA 420

CAGCATTATT CCCTTATATC GCTTTTGAAA ATTCAAAAGA AGCCCTTGCA TATTACGAAG 480

AAGTATTTGG TGCAACTGAC GTTAAACGTT TAGAAGTTGG CGAAGAACAA GCGTCACATT 540

TTGGTATGAC TAAGGAAGAA GCGCAAGAAG CAACTATGCA TGCTGAATTT GAAGTGCTTG 600

GCGTAAAAGT GTTATGTTCT GATTCTTTTG GTCGCGCTGA CAAAATTaAT AATGGCATAT 660

CATTATTAAT TGATTATGAT GTTAACAATA AGGAAGATGC TGATAAAGTT GAAGCATTCT 720

ATGAGCAAAT TAAAGATCAT TCTTCAATTG AAATAGAATT ACCGTTTGCT GACCAATTCT 780

GGGGTGGCAA AATGGGCGTC TTTACCGATA AATACGGTGT TCGTTGGATG 830

(2) INFORMATION FOR SEQ ID NO: 656:

(A) LENGTH: 539 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656:

GTATCCATGG GCCCGTTnCG CACAACATTT GGnACAATTA GGTACACGnG TTGTCaTCGG 60

TCGTTTCGGT ATAATTTTAT CGAATGaAGG CGGTGCGTTA CAAACAATGA AACTACCATA 120

CGAATATTAC ATTGGTGGTA AATTAGGTTC TGGTCAACAA TGGTATTCAT GGATTCATAT 180

CAATGATTTA ATTCAAGCTA TTTTATTTTT AATAAATAAC GAGTCAGCTA GTGGTCCGTT 240

TAATTTAACT GCACCTATAC CTGAACGTCA AAATTTATTT GGCTACACTT TAGCAAGAGC 300

TATGCATAAG CCTCATGAAA CTTGGGCACC AAGTCTTGCA ATGCGTCTCA TACTTGGTCA 360

AATGTCAACA GTAGTATTGG ATACTCAAAA AGTATTACCT aATAAAATTC AAGCATTGGG 420

aTTCCAATTT AAATATAGTA ATTTAAAAAT GGnACTTGAA GATTTAATTA AAGAATAATC 480

AATACCATTA ATGAGCATTA GAAACAACAT ATGTACTAAA TGTAATGTCT AGAGCGACT 539

(2) INFORMATION FOR SEQ ID NO: 657:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657:

ATCAAGTTGA ATATCATCCA TATTTAACCC AACATAAATT GArATTATAT TTGGCAGCAC 60

AACGTATCGT gATGGaATCT TGGTCACCAT TGATGAATGC ACAAATTTTA AATGATGAGA 120

CAATTAAAGA CATTGCTCAA GAATTAGGAA AGTCACCTGC CCAAGTTGTT TTAAGATGGA 180

ATGTGCAGCA TGCTGTGGTT ACAATCCCTA AATCGGTGAC ACCAAACAGA ATCTCTGAAA 240

ATTTCCAAAT ATTTGATTTC GAATTATCAG ATGAACAAAT GACGCGAATT GATGGTTTAA 300

ATCAAGATAA GAGAATTGGA CCTGATCCAA AAAAATTTGA AGGCTAGATT AAAATCGCTC 360

AACTGATGAA AAGGTTAGAT GAATTGTCAG GGCTTGGGAC ATTAAGTTCT TAGGCAATGT 420

AAAAAAGCTG ATTTCTATTA ATTATTTGAT AGAAATCAGC TTTTTTGATA TGTATTTTAT 480

AATGTACAGC TCGTTGAGCT GCTATTTTCC TTATATTAAG TGCCATTAAT ACAAAACCTA 540

GCTCTCGTTT AACTTTATTT AtTCCTCGAA CTGACGTTCG AGTTAAACCC AAAATAGCCT 600

CTGGTTCAGA AAGCTTTTGA TTAATTTGGA CTTTAAAGTA TTCCCAATTA TAATTCTTCA 720

TGATTtTCTT ATTGGATTTT GAATTTGGTT TCATGCATTG TTGCCTCAAA GAACATGCTG 780

AACAGTCATC GCATTCATAT AGTTTGAAGT CTCGTTTAAA ACCATATCTA TCATTACGGT 840

ATGCATATCT TTTAAAACCT ATTCTTTTGT TATTAGGACA TATAAATTCA TCATTAAGTT 900

CGTCATATTT CCAATTTTGA GTGTCGAAAA TGTCACTTTT AAACTTTCTA GTTTTATCtT 960

TAATAAACAT GCCATACGTA ATAAGTGGCG TTTTATTAAA ATCATCTATA ATGGCCATAT 1020

AGTTTTGGCT CACTACCCAT AACCTGGCAT CAGCTACCAA ATGAACCGAA GGGATTTTTG 1080

GAATCCATTG GTTGAAAAAA TGGGAA 1106

(2) INFORMATION FOR SEQ ID NO: 658:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658:

TTTTAACTTT ACTCTTTGAT TTAAAGAGTG ATAAATGTTT ACAGTTTAAT TAAAACTGCA 60

TAAGAACTTC TAGCTTTTCT CTTTCGTTCA AAGAGAAGCA GCTGTTCGCA GTTTAATCAA 120

AACCACATAA AGCTTTTAAC TTTACTCTTT GATTTAAAGA GTGATAAATG TTTACAGTTT 180

AATTAAAACT GCATAAGAAC TTCTAGCTTT TCTCTTTCGT TCAAAGAGAA GCAGCTGTTC 240

GCAGTTTAAT CAAAACCACA TAAAGCTTTT AACTTTACTC TTTGATTTAA AGAGTGACAA 300

ATGTTTACAG TTTAATTAAA ACTGCATAAG AACTTCTAGC TTTTCTCTTT CGTTCAAAGA 360

GAAGTTCTAA TACCACCATA TCGTGCGATC GGGAACGGTA 400

(2) INFORMATION FOR SEQ ID NO: 659:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1899 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659:

ATAATTACAA TGGCTACTGC AATTATTGTT GGAATTATAT ATTTCAGTTT AGTCATCATT 60

TATGCTCCCT TGATTTCAAA TTCATATCAT TAGTTTACCA TATTGAAGAT GATATAATAA 120

AACTTTAACT GAGCTTCATG GGGCACCAGG TTTTGAAGAA GAAGTAAAAA ATTATATGAC 240

TCAGCAAATG GCGCCGTACG TAGATGAATT TATTGAAAAT CGTATGGGTG GATTTTTTGG 300

TGTGAAAAAA TCTAAAAATC CAAATGCAAA ACGTGTAATG ATTGCAGCAC ATATGGaTGA 360

AATCGGATTT ATGATTACAA ATATCACTAA AAATGGAATG ATTCAATTCA CAAATTTAGG 420

TGGTGTTGCA AATGATATTT GGCAAGGACA ACGCTTAGTA ATTAAAAATA GAAATGGCGA 480

TAAAATTATC GGTGTTGTTT CTAATATACC TAAACATTTT CGTACTGGTA GTGAAGGTGC 540

ACCGGAAATT AAAGATTTAA CATTAGATAT AGGTGCTCAA AATGAAGATG AGGTGCGTGA 600

gCGCGGAATA GATATAGGAG ATACAATTGT ACCTCACACG CCATTCACAC AGTTATCTGA 660

ACATCGATAT AGTGCTAAAG CATGGGATAA TCGTTATGGT TGTGTCTTGG CAATTGAAAT 720

ACTAGAATTA TTAAAAGATA TAGAATTAGA TGTAGACTTG TATGTTGGCG CAAATGTTCA 780

AGAAGAGGTT GGATTACGAG GTGCGAAAGC ATCTGCAGAG ATGATAGACC CAGACGTTGC 840

ATTTGTAGTT GATTGTTCAC CTGCCAATGA CGTTAAAGGA AACCAACCAT TATCTGGTGA 900

ACTTGGTAAA GGGACGTTAA TTCGCATAAA AGACGGTACA ATGATTTTAA AGCCTGTATT 960

TAGAGACTAT TTATTAAAGT TAGTAGAAGC ACATGACATT GAACATCAAT ACTATATGTC 1020

ACCAGGTGGA ACAGATGGTG GAGAAATTCA TAAAGCTAAT ATTGGTATTC CGACTGCAGT 1080

TATTGGTGTA TGTGCACGAT ATATTCATAG TACAGACTCA GTATTTGATA TAAGAGACTA 1140

TTTTGCAGCT AGATCTTTAC TTTCAGAAGC CATTTGTAAT TTAGATAATA ATCAAATAGA 1200

AACATTACAA TATAAATAAT CGGGTAATAA CAACTATTAT CTCTAAATAG TTATATATAA 1260

TCATTAATTA AGGAGACATA AAAATGAAAC AACTTGAATC AGAACAACAA TTTGAATCTT 1320

TAAAACAAGG TGCTACAGTA TTTGAATTCA CTGCAGGCTG GTGTCCAGAT TGTAGAGTGA 1380

TAGAACCAGA TTTACCGGAA TTAGAAGCGA GATATCCTAT GTTTGACTTC GTATCAGTAG 1440

ACCGTGATAA ATTTATGGAT ATTTGTATTG AAAATGGTAT TATGGGTATT CCAAGTTTTC 1500

TAGTATATAA AAATGGAGAA CTGCTTGGAA GTTATATTGG AAAAGAACGA AAATCAATTG 1560

AACAGATAGA TGCATTTTTA GCTCAATACG TGTAATTTAG ACTAGAGAAA AACGGGGTAA 1620

TACTCGTTTT TCTCTGTTAC TATGTGTTGA TTTATTGTAA ACTATTATAA GGTGCGAAAT 1680

TAGGAGTGTT ACATATGAAT ACCTTTCAAA TGAGAGATAA ATTAAAGGAA CGTTTAAGCC 1740

ATTTAGACGT TGATTTTAAA TTTAATCGTG AAGAAGAAAC TTTGCGTATT TATCGAACAG 1800

ATAATAACAA AGGTATCACG ATTAAACTTA ACGCTATAGT CGCAAAATAT GAAGATAAAA 1860

AAGAAAAAAT TGTAGATGAA ATTGTTTATT ACGTTGATG 1899

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3774 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660:

GTATAATATC CTTTCAATCT GTTTTCATAT TTTATATATT TTTTAAATAT AAGTGCTAAA 60

TGTTTTAACT AAAGCATAGA TTGACAAGAT GTTATACAGA ATTTCAAATT CTATCCAATA 120

TTGTTCGAAG TGTAGTATCA CTGGATTGGT ATTAAACAAT GTAAAGGAGA GATTGCAAAT 180

GCCGTATAAT TACAAGAAAC AAAATGGAGA GTTAATGTCT GTAATGAGCC AAGGTGAAAA 240

GTTTATTCAT CAATCACCCG TTAATGATGA ACTTAGTGCA TTGATTAAGT TATTAATTTC 300

TAAAATTAAC GGTTGTCATT ATTGTGTTGA TATCCATAAA AAAGAATTAA AGGAATTGGG 360

TGTAaCACAA ATGAAAATTG ATGAAGTCTT GAGTTTTAGA CATTTAGATT TATTTACTGA 420

TCAAGAAAAA GTGACGCTTG AATTTGCAGA AATGTTAAAT TCAATCAAAG ACTTTAAGAA 480

GTTTGAAATT ATTGACCGGC TAAAATCATT TTATGATGAA GAACAAATTA TTGATCTTGT 540

CTTTGTTGTA AACCAAATTA ACGGTTGGAA CAGATTAAAT ATTATTAGTG ATAGACTATA 600

ATTGTTCATA TAAATGCAGA GTTTCATCTC GAACGCTATA TCATAACAAA TCATGCCACT 660

ATACAGGTCA AATCTTGTAT AGTGGCATTT TAATTTATCC CTTTGAATAC TGTTATTTAA 720

CGAATATCGG TCCACCTGGT CCAACAGGGA TACCTAATAG GAACCAAATG ATGACAAATA 780

CTGTCCATAC AATACTTAGC GCGATTGAAT ACGGCATTAA ACTAGAAAGT AAGGCTCCGA 840

GTTTCATGCG TTTATCGTAT TTTTGTGCAT AAGTTAATAA TAAAGGTAAG TACGGCATCA 900

TCGGTGTAAT TGGATTGGTA ATTGAATCGC CTACACGGTA AATGACTTGT GTGAATGCGG 960

GATGAAAGCC GATAAGGATT AACATTGGTA CGAATATCGG TCCTAAAATA CCCCATTTAG 1020

CCGATGCGCT TCCGATTAAC ATGTTGACCA TTGCACTCAG TACAATAATA CCTAGTATCA 1080

ATACAATACC GTTTTGATGT TCTAATAATT TGGCACCTTT AACAGCAGCG ATAATTCCTA 1140

AATTACTCCA CTTTAAATAC GCAAGTAGCT GTGCTGCAAA AAACACAATA ACGATAAATG 1200

TTCCCATTGA TCCTACAGCA TCGCCGAACA TTTTACCTAA GTCTTTTGTA TTTTTAATTT 1260

CTTTGCTTAA AATCCCATAA ACTAATCCAG GTACTAAAAA TACGACAAGA ATAATTAATC 1320

CGACACCGTT AATTAATGGC GCATCGTCTA GTAAGCTGCC TGTTTTAGCA TTTCTTAAAA 1380

AGCTATGTTC AGGAATGGCT GTAATAATTA ATAAAATAAT TGTGACTATG AAACTGATAT 1440

CATCATGCAT TAAACTGTCA TCATATTTTC CTAATCTAGG AATAATGAGC TTAGTTGTAA 1560

CTAGCAATAT CGTAGGAAGT AATACAACGA CACTCGCTGC GATAAAGTAC CAGTTCATAG 1620

CAACGTTTGT TTTAATAGAA TCTGAAACGA TACGTGTTGC CGGTTCTGTA AATGAATAGA 1680

CCAAAGCATC TTGCATACCA ACAACTATAT TTGCTGCAAA TCCTCCAACA GCGGAAGCAT 1740

ATGCCATCGT TAGTCCAGCG ATAGGGTGAT AGCCAATTTT AATAAAAAGC ATTGCTGCAA 1800

GCGGCGGCAA GATAATTGTC GCAGCATCGC CGGCTGTACT ACCTAAAATA CCAATTAATA 1860

TAATAGTCGG TAAAATTAAG AAACGTGGTG CGCGATTCAC AACAGAAATC ATTAACTTAT 1920

CGAAGTATCC TGTTTTCTCT GCAACACCAA TACCAATCAT CACTGCTAGT ACTAAGCCTA 1980

ATGCTGGGAA CTCTGAGAAA TTTTTAATCG TATCATTCAT TATCATCGTA AATCCATCAT 2040

GGCTAATTAT ATTTTTAATA TAAATGGTTT GATGCGTACC TGGATGCTTA ACAGATACAT 2100

TAAATAATGA GATAACCCAT GTCATAATGG CTAAGCCCAC ACACATTAAA AAGAATAAGA 2160

CGCTAGGATC TGGCAATTTA TTTCCGATTT TTTCAACACT ATTCAAGAAA CGATTGACGA 2220

TAGACCCCTT TTGTTGATGT TTTGATGTCA TCAATTATTC CCCCCTTTGT TAAATATTTA 2280

AAGTGTAACA AAAAATACTC TCAAAAGTAA CAATTTTCAG GAAATAAAAA AACTAATATT 2340

GTTAAATATT TTGAGTTATT CAATAGAAAG TGTATAGCAG AGTAGTTAAG ACTGCCTGAA 2400

GACTTATCTA TTAGGTTTAT GAAGCATCGA ACAGTGGAAA ATAAGGACTG TAAGTTTAAG 2460

ATATGTTGTA TAGGAGTGAC TGAATGAAAC GTTTGGAAAA TAAAGTAGCA GTCGTAACAG 2520

GAGCAAGTAC AGGTATCGGT CAAGCTTCTG CAATCGCTTT AGCTCAATAA GGTGCGTATG 2580

TATTGGCGGT AGACATAGCT GAAGCGGTAT CGGAGACTGT CGATAAAATT AAAAGTAATG 2640

GTGACAATGC GAAGGCGTAT AATGTGGATA ATGCAAGCGA ACAACAAGTG GTAGACTTTG 2700

TGTCTGACAT AAAGGAACAG TTTGGAAGAA TCGATGTGTT GTTTAATAAT GCCGGTGTGG 2760

ATAATGCGGC TGATAGAATT CATGAGTATC CAATAGATGT GTATGACAAG ATTATGAATG 2820

TAGATATGCG TGGGACATTT TTAATGACGA AAATGATGTT ACCTTTAATG ATGAATCAAG 2880

GTGGCTCTAT TGTTAATACG TCTTCATTTT CCGGACAAGC AGCAGACTTG TATCGCTCTG 2940

GATATAATGC TGCGAAAGGT GCAGTGATTA ATTTTACAAA ATCAATCGCA ATTGAGTATG 3000

GCCGTGATAG CATTCGAGCC AATGCGATTG CACCAGGTAC AATTGAAACC CCGTTAGTAG 3060

ATAAACTGAC AGGTACGAGT GAGGATGATG CAGGTAAAAC ATTTAGAGAA AATCAAAAAT 3120

GGATGACTCC GCTGGGACGT TTAGGTAAAC CAGAAGAAGT TGCTAAATTA GTAGTCTTCT 3180

TAGCATCTGA CGACAGTTCA TTCATAACTG GAGAGACGAT TCGAATTGAT GGTGGTGTGA 3240

AATTATTTAA AATCGATATC CAGTGGAAAA GAATTTGGCA TGAAGTAGGC AATGTATGCA 3360

TATTGTCGCA ATGAAAGACA TTTAAAGCGG AGATTAATTA ATCTTTGAAA ATCACATATT 3420

GTTCATTTGA AGTGTATTGC TTAAAGCTTG TTTTAACGTA TTGTAGGTCG TGCATCTAAT 3480

TTATCAGAAT CTCGAGTTCA AACTTTTGGA GTATCTTTAA AATAAGCTGT ATTTTGTCTA 3540

TTCTAATAAA TTAAGGAGAA TTTTATGTTA AAAGAAAAAG AAAGTTTTAG ATTGCTATAT 3600

CAAGCTATAA GAGAGATTGC AGATAAAATT GGAGATAATC AGTTAGAAAC TAATTCCGTT 3660

AGTTTATTtAT tATTGGACTT TGATTTTGAA CATGAAGTAT TTGATGAATT GTATCTTGTG 3720

ATTTtAAAAT ATTTAAATAC AGTAAGTATA GAGAACATAA GTCATAGTGA GCTT 3774

(2) INFORMATION FOR SEQ ID NO: 661:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1078 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661:

TACTGGTTTT GGATTTTGGA GGTAATACAG TACCTAATAG TAATnATGGT GTCGTCAnAA 60

TTATATCTTT CCGTGATGTT CTTACTCATT AGAACATCnG CCTTCAGAGG AATCATGATA 120

CGAGGAATAA GAAATTTAAA TGTGAGCGAA GTCAATATAG TATTTGCGAT TATTTTTATT 180

AACTCCATTA TTATTGTTAG TTTGATTTTT CGAGGATAAC TTCAATTTTT GCATTTTGAG 240

GTTTTTTAAC ATATCTATTT GCATCAGTTG ATGGCAACCT TTTACTTAAA TCTATTGTGT 300

AGTTATTGTC TGCACCTGTT ATTTTAATTT GTCCTTTATT ATAAGAATTA TTATATAATT 360

TTTTACTTTT AATTAATGTT TGACGAATAC GAAAATCTAA TTCTTTTAAA GTTAAAACAG 420

GCTTATTGCC TTCATAAACT GGAAATCCGC CAGTAAACGT TTCTGCTTTA TCTTTATATG 480

TTACATTCAG TTTATAGTGT TTATCGTTAG ATGTTGCTGC AGGAGTAACA CCACCAGTAA 540

ACGTTTCTTG AGATAATGCA AAAGaATCAA TGGTTTCTTG GTCTTTTATG CyAAAAATAT 600

CAACGCTTTT ATTTCTTAAT TGGTTGATAT TGCCCCAACT TTCAGGTCCA TAAACTTGAA 660

TATGACTATA CCAAGaAAAC TGTAACAACG TTGCATGAAT CgTACCGTTA TCTTTTTGCC 720

ATAACGTACT GTTAGAGAAG GTTAAATATT TTTGCGAGTA ATATTTAGTT AACTCATTAA 780

CGTTAGTTTC GTTTTGATTT ATATAATtAAG cTTTCGCTTC AGATGAAGAA TTGATAkGTG 840

TATTAGGAAA TTGTGTAGAT GCTGTACCTA ATAGTAACAA TGTTGTTGAT AAAATAATTT 900

ATAAAAAGGG GTTAATTAGA TAATTGAAAT TATCCGCATT TACAAAAGGT AATAGGTTAG 1020

TTAGATTTTT CGAGTATGAC TcAATTTCTG CATTACGAGG ATTTTTAACA TAACGGTT 1078

(2) INFORMATION FOR SEQ ID NO: 662:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662:

AACTTGCTTT TTAGTATCTA CGTTAATATT AATAGCTTTA ATTTCACTTG TATTAATTAA 60

ATCAGCTGTG TAAATACCTG CTTTCAAATC GATAACTTTC TTTGTTCCAT TTTTAAAGTA 120

AACAGTATAT TTCGCTTGCT TCGATAGTCT TAAATCTATA TCACTAATAC CTCTGTCTGA 180

TTTTAAAACT GATTTAACTC TATCCTCTAA ATCTTTATAA CTAATATTTT GATTCTTATT 240

AAATGTTAAG CTTGATAAAA TATTTTGGCT TGTACCGTTC ACAGTGaTTG CATATGGAAC 300

ATGGACTTTA GAATATCCAT GGTGTAACGA ACTTGATGAT TTATCTAATG GCTTAGCTGC 360

GGCAGACGCT TCATTATTAT TAAAGTTTGC ACCTGTTGAT GCTAAAACAC CTAATGCTAA 420

AGTTGTTGTA ATCAATGACT TAAATTTCAT AAATTATCTC TCCTTTTTTG TGTAATTCGT 480

ATTTGCAACT TAATTATAGC CAGACTTTCT CTATTTTTTG AATTAACTGA ATATTAATAA 540

TAAATTATCT TTAACAATAA TTTTTTAACA CTGTTAAAAG TTCTTTTAAT TTTGATTAAC 600

TAATTAATTT ACAATACCTA AAATGTTGTT TGGTTTTGTT TATACCAAGC TTCAAACTTA 660

AATGTCATAA CAACATTCAT TTCTTAATTC CTATTAGATT TGTCGATTAT ATTTACAGCA 720

TCTTTATACT CAAAAAACAT TTACTTAAAA ATATAAATTC GATTTAATAA TTAATTTAAA 780

TTTAGTTAAT CAATTTTGCA TCTATTTTGT TGTAAGCTAT ATAAAAGGAG TGATAATGAT 840

GGTGAAAAAA ACAAAATCCA ATTCACTAAA AAAAGTTGCA ACACTTGCAT TAGCAAATTT 900

ATTATTAGTT GGTGCACTTA CTGaCAATAG TGCCAAAGCC GAATCTAAGA AAGATGATAC 960

TGATTTGAAG TTAGTTAGTC ATAACGTTTA TATGTTATCG ACCGTTTTGT ATCCAAACTG 1020

GGGGCAATAT AAACGCGCTG ATTTAATCGG ACAATCTTCT TATATTAAAA ATAATGATGT 1080

CGTAATATTC AATGAAGCAT TTGATAATGG TGCATCAGAC AAATTATTAA GTAATGTGAA 1140

AAAAGAATAT CCTTATCAAA CACCTGTACT CGGCCGTTCT CAATCAGGGT GGGACAAAAC 1200

TGAAGGTAGC TACTCATCAA CTGTTGCAGA AGATGGTGGC GTAGCGATTG TAAGTAAATA 1260

CAACAAAGGC TTTGTTTATA CAAAAATAGA GAAAAATGGT AAGAACGTTC ACGTTATCGG 1380

TACACATACA CAATCTGA 1398

(2) INFORMATION FOR SEQ ID NO: 663:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663:

TTGTAATTGG AACGTACGAA CTTTTCTAGG TAAGAAACGT CGAATCTCGT CCTCATTATA 60

ACCAACTTGT AGTCGTTTAT TATCTAAAAT AATTGGACGA CGTAATAAGC CAGGATTATC 120

TTGAATGATT GAATATAAGT CTTGTAATGG TAGTGAATCA ATATCAACAT TTAATTTTTG 180

GTATGTTTTA GAACGTGTAG AAATGATTTC ATCAGTACCG TCTTCAGTCA TTTTTAATAT 240

TTGCTTAATT TCATCAATTG TTAAATGTTC AGAAAAAATA TTACGCTCCG TATACGGAAT 300

GTCcATGTTC tTGkTAACCA TGCTTTCGCT TTTACGGcAA GATGTGcAaC TTGGtGaAGT 360

aAATAATGtT ACCATACATC TCACTCTCCT ATTTGAATGA ATAAAATTCA TTGCTTAAAA 420

TTTAGTTATA GATCAAGAAA AAACATTTTT TTCTAAAATT CTTAATCGTT ACTATTTATT 480

ATAACTATCT AACATTAAAA TTAAATGAGA AAAACCTAAT TTTTCAGATA AGTTTCTACA 540

CTTATAAAAA AGATTATTAA TCCCTTTGTT AGTAGTAAGT TATACGTATA TTCTAACACA 600

TCTTACATTT TTAAGAAATA CTGTTATAAT GATAATTATT AAAATATTAC TAAGAAAGTA 660

GGCATTTAAA TGGAGACATT ATTTTCAGGC ATCCAACCTA GTGGAATTCC TACTATTGGA 720

AATTATATTG GCGCACTAAA ACAATTTGTT GATGTGCAAA ATGACTATGA TTGTTATTTC 780

TGTATCGTAG ATCAACATGC AATTACAATG CCACAAGATC GTTTAAAATT ACGTAAACAG 840

ACCAGACAAT TAGCAGCGAT TTATTTAGCT TCTGGTATAG ATCCAGACAA AGCAACATTG 900

TTCATACAAT CTGAAGTCcC TGCACACGTA CAAGCAGGAT GGATGTTAAC TACGATTGCT 960

TCTGTTGGAG AATTAGAGCG TATGACGCAA TACAAAGATA AAGCTCAGAA AGCAGTTGAA 1020

GGTATACCTG CTGGTCTATT AACATATCCA CCTTTAATGG CAGCTGATAT TGTTCTTTAC 1080

AATACTAATA TCGTTCCAGT TGGAGATGAC CAAAAGCAGC ATATCGAATT GACTCGTAAC 1140

CTTGTAGATA GATTTAATAG TCGCTATAAT GATGTGCTTG TGAACCTGAA ATTCGTATGC 1200

(2) INFORMATION FOR SEQ ID NO: 664:

(A) LENGTH: 787 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664:

TGTACCTTTT GCTTTAATAA ATACTGTTTC TTTATCATAA TTAGGTTCAG TTAAGAAATT 60

AAATTGTAAG CTTTGAGTAA TATTTTTTTG ACTATCACTT GTTGTAGCTG TACGTGTATA 120

CATTTTAGTA TCACCATCAA GATTCTTCTC AGAAACTTGT TTGATTTCAG AATTAATCTT 180

TGCAAATGAA GTAGCTGGTA ATACAGTGAA AGTAGTCGAT AGTGCTAAsG wACAAATTGT 240

GATATTTTTA CATAGTTGTT TAATCATTAG TAATCCGCCC TTTCAATATT ATCCTTCTTT 300

ATAAGGTTTA TTGTCATCAG AATATTTATC AACGACTTTA ACTGTTTTAT TTTTCCAATC 360

AACTTCATAA GTGACAATTA ATCTTTGACC ATCTTTATTT TtcTCTAAAA TTGGAGGTGC 420

ATAATGTATy CCAGGTCTGT TTTTCAAAAT ATCTTGATTT CGTGTGTATG TTACTTCAAA 480

TTGCGTTTTC TCATTTGACT TTTCATTAGA TAAATAAGTT AAAAATTCTG GATTAAAGCC 540

ACTTCTTACT AATGCTGGGT ATCTATATTT TGAAGCAAAG CTTAGTTCaG GGTTTTCTAC 600

AGTAGCAATT CTCGTATTTC TATAGAATAA TAATTCATCA TTTCTATTTT TCACTTCTCC 660

ACCATACTTC AAGTCATTCG CAATAACTGA CCAGTGTACA TGgCCAGTTn ATTTATTTTT 720

ACCGCTGGCA ATTGTGTCAT AATTTGCTGC ATCATCAACT AATCGTTTTG GAAGTAGCTA 780

TTTGCTG 787

(2) INFORMATION FOR SEQ ID NO: 665:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665:

TTATCTGTCA TTAACCACTG GTACATGTGA ACCCGGCnTn AATCAATATA TATATTTAAA 60

AGCAAAGGCG CGCCATGTGC CTTTtTTnTA tTTTGTATAT CTGTATCAAA ATCGATTTGA 120

TTAAAATCCG CTTTATTTTA TCATCTATTC AAATGATTTT AGTGCGCTTA TTTTACTATG 180

GCATTATTGC CTAACCTGTT TGAGATATAT TAATATTTGA TGATTCGTAT TCAAAGTTTT 240

CATTTAACAT GTATTTAGTA TCATGATAGC TGCTTCATTG ATGATATACT ACCTACTTTT 300

CAGAGGCAAT ATTGAACAAT TCTTCATCAT GACTATTTTC CATCACATAA CTATGCTTAG 420

CGAACGCTAA CATATCTTTA TCATTATTCG CATCTCCGAA GGCCATGAGC TCTGAAGGAG 480

ACATTTCCCA TTTATCTAAC AATCGTTTTA ATGCCTGnCC TTTAGTCATG TTT 533

(2) INFORMATION FOR SEQ ID NO: 666:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666:

GACTTCTCTT GCACTAAAAA TTGCTCAAAT TGCTCGCTGT CATAACCAGG CGGTGTTTCC 60

AACCATACAT ATATGCCACC TTTAGCATGA ACAAATGGCA AATCAGCTTT TGCAAGCATG 120

GCTTCGAATC GGTCACGACG TGTTTTAAAT ACATTGCTTT GTTCTTCTAA AAAATCATCA 180

TAATGGATTC AAAGCATATA TTGCGGTCAT CTTGTAAATG CACCAAACAT CCCAGCATTT 240

GTGTGCGTTT GGTACTTTTT CAAAGCTTGA AATCATATCT TTATTACCAA CTGCCAAAAC 300

CGACTCTGAA AACCTGGACA TGTTGATGAA CCTTTnAGAC AAGGGAAGAA ATTTGCAATC 360

GCAACATCTT TGCCCATTTT nCCGAAGCAA GTGnGACTAG 400

(2) INFORMATION FOR SEQ ID NO: 667:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667:

TCTCCAATGC TACTCAAATT AAAAAGGTTT TAAATATTGT TAATTCTGAT CCAGAGCGAA 60

AGATTGTTAT CGTTTCTGCT CCAGGTAAAA GACATGATAA TGATATTAAA ACAACTGATT 120

TGTTAATCAG ATTATATGAA AAGGTCATTA ATCATCTTGA TTATCATGAT AAAAAAAGAG 180

AAATTATTCA GCGTTATGAT GATATTGTAA AAGAATTGCA AATGGATGAA AGTATTTTAC 240

GGACGATAGA TGTGACTTTG GAACATTATA TAAATCAATT AAAAAATGAA CCAAAGAGAC 300

TATTAGATGC ATTACTTTCT TGTGGTGAAG ATTTTAATGC GCaAyTGAtA GCyTTATATA 360

ATAAtAGTCa gGTtACCAAC AAmATwTATA TCCcCGAAGG AAGCGGGTAT TT 412

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668:

TTACTCGTTA AAGATATTGT AAAAGATGAA GTGACAGAAT ATGACATTCA TCAAATGTTA 60

CCGCATCCGA TTAATATGGT AAGGGTTAGA CTTTTTGGTG TGAAATTAAA AGAGATTATA 120

GCTAAAAGTA ATAAACAAGA nTATATGTAT GAACATGCAC AAGGTTTGGG TTTCAGAGGG 180

AATATATTTG GAGGATATAT TCTTTATAAT TTAGGGTACA TTCATTCTAC AGGGCGTTAC 240

TATCTGAATG GAGAAGAAAT CGAGGACGAC AAGGAATATG TACTAGGTAC GATAGATATG 300

TATACGTTCG GTCnTATTnC CCAACATTGA AGGATTACCA AAGAGTATTT AATGCCAGAG 360

TTTTTCAGAG GTATATTTAA nGAAAATTAT TGGCTATTTA 400

(2) INFORMATION FOR SEQ ID NO: 669:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669:

TGTTCGATAT TTTTAAATTT ATCTTTTAAA TACAACAACT GTTTCCGTAA TGATTTAACT 60

GTTTTATGAC TAATGCCATT GAATATTTCT AGCGTTTTAT TTAACTTATC GATAATCGCA 120

TGTAAATCCT TCAAAATGTC TTTTGTTTCA AAAGTAAATA CATTATGGAA GCGATGAATA 180

TCATCATCAT AAACATCAGA ATCATTGATA ATCGTAAATA TCGTTGAGAA CAATTGCTCA 240

TTTAACTCAT GAATCTCATT CATACTAGCC TTCAAGCCAA AAATATCAAT TGGTGCAATA 300

TCTAATTTTT CCAAAATTCG CTGCTTTTCC AGTTGATCAA TTGCCTTTAA CAATTTTTCA 360

TTTTCGTTTT TACCAATCAA ACCAAGCTGA TATTTAATAT CAGCATAACT CAACTCATTT 420

GTCACTTGAT TTAAGGCATA GTCTGGTAAG CGATGTGCTT CATCCACTAT ACAATCATCA 480

AACAATTGAT ATATTGAATT TTCAACATCA GAATGaATTA AATGTGCATG ATTTGTAATA 540

CCAATTTGaA TGTTCTGTGC ATTTCGCTTA ATAAAATTAT aATAATGAAC ATCGTGACGT 600

GCCGGTACAT ATGTTTCAAT TTTCTGGTcA AAATACATCT TTTGACCACC TTTTAAATTT 660

ATATTCACtT CGTAATTACT TGTGTCATCT TTTAAAATTT GACTAATAAG CCCCAATGAA 780

ATGTAATCaC TTtTACTTTT AATCAATAGT GCATTAATTT TAAAATTCAA CGCTTCATTC 840

ATTGCTGGAA TATCTTTTTC TAACAATTGA CTTTGCAGTA ATTTAGTATT GGTAGAAATC 900

ATGACATGCT TCCCAGTTTC AATATTATAC ATCAAGGCCG CAAGTAAATA TGCTAATGAT 960

TTACCACTGC CTAGTGATGC TTCAATCATT GCTTTTTCAC TATGCATGAG CTGATCTAAT 1020

ATAGTTTCCG CTAAATATAA TTGTTGCGGT CGATATGTTA AGCCAAGTTG ATCTACAGCT 1080

TTGCTATATA AAGACTTCAA GCTGCCATTA TAATTTGTTG TCGGCTTTTT AAAATCAACT 1140

TGCTTACGAT AGATAATCTG TTCGAACTTT TCGTACGATT TATCCAATGG CTTTGCATCA 1200

TATTGCCTAA CCATCTCAAA GAAAATATCA TACAAA 1236

(2) INFORMATION FOR SEQ ID NO: 670:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1819 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670:

ACAsAATTAT TGACCAATAT GACTCGTGGA CTGATATGTT TAAAGCACTA CTGCATGAAA 60

CATTTAAAGC ATATGGCGTT CTATTTATAG ATGCGCAGTT TGAGCCGTTA AGAAAAATGG 120

AAGCGCCTAT GTTTAAAAAG ATTTTGAAAA AACATCAGTT GCTTGATGAT GCTTTTAGAG 180

CAACACAACA ACGTACTCAA AATCAAGGCT TGAATGCGAT GATACAAACA GATACAAATG 240

TTCATTTATT CTTACATGAT GAAAATATGC GTCAATTAGT tTCGTATGAT GGTAAGCAyT 300

TTAmATTAAA TAAAACAGAT AAGACATATA TAAAGGAAGA AATTATAAAT ATTGCGGAAA 360

ATCAACCkGA ATTATTTTCT aATAATGTAG TGACAAGACC ATTAATGGnA GAATGGTTAT 420

TTGAACACGG TGGCATTTGT TGGAGGACCG AGTGAAATTA AGTaCTGGGC TGAACTAAAA 480

GATGTATTTG AACTATTTGA TGTTGAAATG CCtATCGTGA TGCCAAGGCT TAGAATTACT 540

TATTTAAATG ACCGTATAGA AAAATTACTT TCGAAATACA ATATTCCATT AGAAAAAGTG 600

TTAGTCGATG GTGTTGAAGG AGAAAGAAGT AAGTTTATTA GAGAACAAGC ATCACATCAA 660

TTTATTGAAA AGGTAGAAGG TATGATTGAA CAACAGCGTC GTCTAAACAA AGACTTATTA 720

GATGAAGTGG CGGGGAATCA AAATAATATT AACCTTGTGA ATAAAAATAA TGAAATTCAT 780

ATACAACAGT ATGATTATTT GTTAAAACGT TATCTTTTAA ACATTGAAAG AGrAAACGAC 840

GAAAGAATAT GGAATCCACT TCAAATTTTG AATGATTTTG GGACAGATGT GTTCAAGCCC 960

TCCACCTATC CACCACTTTC TTACACTTTT GATCATATTA TTATAAAACC TTAATATACC 1020

AAGGGTTTAG CCCGATTTAT CTTAATGATA AATCGGGCAT TTTTTTGTTT TTTAAAATAA 1080

ATTTCACAAA TTTTGTATAA ATAGTGGTGG ATAGTGGGGA GATGTGGTAA ATTATATATA 1140

AGGTGAGGTG ATAAAAAATG TTCATGGGAG aATACGATCA TCAATTAGAT ACAAAAGGAC 1200

GTATGATTAT ACCGTCCAAG TTTCGTTATG ACTTAAATGA GCGTTTTATT ATCACAAGAG 1260

GCCTTGATAA ATGTTTATTC GGTTACACTC TAGACGAATG GCAACAGATT GAAGAGAAAA 1320

TGAAAACCTT ACCTATGACA AAAAAAGACG CACGTAAGTT TATGCGTATG TTCTTCTCTG 1380

GTGCTGTTGA AGTAGAACTT GATAAGCAAG GGCGTATTAA CATCCCTCAA AACTTGAGGA 1440

AATACGCTAA TTTAACTAAA GAATGTACAG TAATCGGTGT TTCAAATCGT ATTGAGATTT 1500

GGGATAGAGA AACTTGGAAT GATTTCTATG AAGAATCTGA AGAAAGTTTC GAAGATATTG 1560

CTGAAGATTT AATAGATTTT GATTTTTAAA ATGGAGGAAT TGAAGtGTTT CATCATATCA 1620

GCGTTATGTT AAACGAAACC ATTGATTATT TAAATGTAAA AGAAAATGGT GTGTACATTG 1680

ACTGTACGCT AGGTGGAGCG GGACAnGCCC TTTATTTACT AAATCAATTA AATGACGACG 1740

GAAGATTAAT AGCAATCGAT CAAGACCAAA CTGCAATTGA TAATGCTAAA nGGGTATTAA 1800

AGGATCATTT GCATAAAnG 1819

(2) INFORMATION FOR SEQ ID NO: 671:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 609 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671:

ACCAATTATT GGACAGGAAT TAGCAAAAAA TGCAATGCTT GCATTAATCT ATGCATCGAT 60

AGGTATCATC ATCTATGTAT CATTACGATT TGAATGGCGC ATGGGTCTTT CATCTGTATT 120

GGCATTATTA CATGATGTAT TCATTATAGT AGCGATTTTC AGTTTATTTA GAATTGAAGT 180

AGATTTAACA TTTATCGCCG CTGTATTAAC AATTGTCGGT TATTCAATTA ATGATACAAT 240

CGTAACGTTT GACCGTGTAC GTGAAAACTT ACAAAAGGTT AAAGTGATTA CGACAACAGA 300

ACAAATTGAT GATATCGTTA ATAGATCAAT tAGACAGACA ATGACACGTT CAATTAATAC 360

AGTATTAACA GTTATTGTAG TAGTAGTTGC TATACTATTC TTCGGTGCTC CTACGATATT 420

TGCCGTTCCG CTATGGGGAA TAATGAAAAA ACGTCAGTTG AAAAAATCGC CGAAACACAA 540

ATTAGTTGTA TATAAAgAAA AGAAATCGAA CGATGAAAAG ATTTTAGTTT AAAAtGaATT 600

AAGCGGTAT 609

(2) INFORMATION FOR SEQ ID NO: 672:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672:

CTTAAAACAG CAATTTGAAC GTTTACAAAA TGAACAAATC TTTGTTTATG TTTGTCATGG 60

TAATCACGAT CCTTTATCAT CAAAGATTTC ATCAAACTGG CCAGATAATG TtnTTGTATT 120

TTCAAATAAA GTTGAGACGT ATGAAGCAAT TACTAAATCT GGTGAAACAA TTTATATTCA 180

CGGATTTAGT TATGAAAATA GAGCAAGTTA TGAGAACAAG ATTGATGAAT ATCCATCAAG 240

TCAAGGCCAA AAAGGCATAC ATATTGGTGT CTTGCATGGT ACGTATAGTA AATCTTCAGT 300

TAACGAAAGA TATACCGAGT TCATTTTAGA AGATTTAAAC AGTAAATTGT ATCATTATTG 360

GGCTTTAGGT CATATACATG AACGTCAACA ATTAAGTGAT ATGCCTGTAA TTAACTATTC 420

AGGTAATATT CAAGGTAGAC ATTTTAATGA GCAaGGTGAA aAAGGTTGCT TATTAATCGm 480

GGGTGACCAC TTAAAATTAA AGACTAAATT TTATCCTACA CAGTATATTA GATTTGAAGA 540

AGCAACTATT GAAACGGATA AGACATCTAA GCAAGGTTTA TACGAGGTCA TTCAAAACTT 600

TAAAGAACAA GTGAGAGAAG AAGGAAAAGC CTTTTATCGT TTAACGCTTG TTATTAATAG 660

TGAGACATTA ATTTCACCTC AAGATTTATT ACAAGTTGAA GAAATGATTA CAGATTATGA 720

AGAAAACGAA AATCAATTTG TATATATTGA TGAGTTAAAA ATACAATATG CACAAAATGA 780

TGAGTCACCT TTAGTTAATG AATTTTCAGC GGAATTATTA GTCGATCAAA CTGTTTTTGA 840

TAAAGCGATG TCAGATTTAT ATTTAAATCC AAGGGCATCT AAGTTCCTAG ACGATTATGG 900

AACATTCGAC CATACAGCAT TAGTTAATCG TGCTGAAGAA ATATTAAAAG CTGAAATGAG 960

AGGTGAACAA AATGATAATT AAATCACTTG AAATTTATGG TTACGGTCAA TTTGTTCAaC 1020

GTAAAATTGa ATTTAATAAA AACyTCaCTG AAA1TTTTGG TGAAAATGAA GCGGGTAAAT 1080

CGACGATTCA AGCATtCATC CATTCGATAT TATTTGGATT TCCAACTAAA AAGTCTAAAG 1140

AGCCAAGACT AGAACCACGT CTAGGTAACC AATACGGTGG TAAATTAGTA CTTATTCTTG 1200

TATATTTACC TAATGGTGCT GTGCGTGATG ATGCTTGGTT ACAAAAGAAA CTTAATTATA 1320

TTTCTAAAAA GACATATCAA GGTATCTTTT CATTTGATGT ACTAGGGCTT CAAGACATTC 1380

ATAGAAATCT AAATGAAAAA CAATTGCAAG ATTATTTATT ACAAGCmGGG GCTTTAGGAT 1440

CAACTGAaTT CACGTCAATG CGCGAAGTGA TTAATCGTAA AAaAGATGAA TTATATAAAA 1500

aATCAGGTAA AAATCCGATC ATTAATCAAC AAATTGAGCA ATTAAAACAA CTAGAAAGTC 1560

AAATTCGTGA AGAAGAAGCA AAGCTAGAAA CATATCATCG CTTAGTAGAT GATCGAGATA 1620

AATCATCACG TCGATTAGAG AATTTAAAGC ATAATTTAAA TCAATTATCA AAAATGCATG 1680

AAGAAAAACA AAAAGAGGTT GCTTTACATG ATCATTCACA AGAATGGAAG TCTCTAGAAC 1740

AACAGTTAAA TATTGAGCCA ATCACATTCC CAGAAAAAGG TGTGGATCGT TACGAAAAAG 1800

CACGAGCGCA TAAGCAATCG TTAGwAAGAG ATATTGGTTT AAGAAATGAG CGTTTAGCTC 1860

AACTTAAAGA AGAAGCGACT CAATTAGAGC CAGTTAAACA ATCTGATATT GACGCCTTCA 1920

TTAGTTTGAA TCAACAAGAA AATGAAATTA AAAATAAAGA ATTTGAACTT ACTGCAATCG 1980

AAAAGGATAT TGCGAATAAA CAACGTGATA AAGATGAATT GCAATCAAAT ATTGGTTGGT 2040

CTGAAACGCA TCATGACGTA GATAGTTCAG AGGCAATGAA AAGTTATGTC AGTGAGCAAA 2100

TCAAGAATAA ACAAGAACAA GCTGCATACA TTAAACAATT AGAACGTAGT TTAGAAGAAA 2160

ATAAAATCGA AGATAATGCG GTTCATAGCG AACTAGATTC TGTTGAAGAA AAATAGTTCC 2220

TG 2222

(2) INFORMATION FOR SEQ ID NO: 673:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 406 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673:

TTGCAGGTAT CATTTTTTTA ATGCCATATG GATTATGTTT TCTACCGTTT TATAAGCAAA 60

AAAAGAAAAA ACAGACATTT AAAAAATACA TGGTTTACAC TACGATTGGT TTGTCAATTT 120

GTCTAGGCTT ATCTCTAGTT TTGGTTCACA CTACGAAAAT TTATATGGAC GAAGGTGGCG 180

TAAGATACTA TTACGGTAGT TTTGTAATGA AACAAGCGGG CGGTTATGCT TATTTAGCTT 240

TAGCGGTACT TTCAACGTTG TTAATTGTTG CGAAAAAAGC TACAAATAAA AATAAAGAAA 300

TCGAAACCGT CGACAATACA AATATAACGG AAAGATAATT AAGGGAGTGC TCATTCAGGA 360

(2) INFORMATION FOR SEQ ID NO: 674:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674:

CCACTTTGTG GATTTTCTTT ATATTCTCCA CGCTTGtACT ACAACTTCTT TCGTTTCTGT 60

TTCATCACCG ACTGCCGCAT TCGTTAGCAC ATGTAATAAC TCTTTTGCGG TTAATACATT 120

CTCATCTATA ATCTTATCTT TTTGTTCTTG TATATATTGC TTGATGTGCG GCTTTTTCAA 180

TAACCTACAC GCTGTCACAT GTGCGCTATT TGCGTTATAT CCTGyTTTTA TGGCACTTTG 240

TGTTACATTC AGTGTTCTAA TATACTCATT CACAAAACGT GCTTGCTTTG CAGTTAACTC 300

ACTCATTTTA TCACCCCCAC AATTTTATCT AATATGGTTT CATACCATAA TATTACAGAT 360

TGTTCTGAAC AATCTAAGGC ACTACTAATA TCTTGATAAC TAAGTCCTTG TATAAGGGAG 420

TCAAAAATAT AAAACTCTTT ATCGGTCGCT AATCTGTCAA CAATCATTTC TATGTGATTC 480

TTTATAATAT GATCATTGAC ATTATCGTCT GTCATCAATT CGTCAGAATC TTCATCACCT 540

ATTAAAAAGA AATCATCAGT ATTTATTTCA TCATCGCCCC GTTAACTAGC TTTGAAGTCT 600

TTAGCACACT TGCATATACC GGCTGTCGTG CTGGCkAGAT ACTAGCATTG AAGTGGTCTG 660

ATATTGATTT TGAAAACAAC ACGATTAGTA TTACTAAAAC ATATTACAAT CCAAATAATA 720

ACAAGAAGAA ATATCAGATA CTTCCCCCTA AAACTGAAAG TTCTATCGGT AAGATTTCCG 780

TTGACCCAAA TGTAATAAAG GtGtTGCGtG ATTATAAGAT AAACGTTCAA AATAATTGGA 840

AAAACGAATT ATATAATGAT AACCATTGTA ATGAAAAAAC TATCAATGTG GATACAAACC 900

ATTATGTCAC GTACCAGCAT ACTCAAA 927

(2) INFORMATION FOR SEQ ID NO: 675:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675:

GATGTTAAnA TAAGTACATC ATTTTGACTC CCAAATATTG GCTTTAGACC TTGAAATGCT 60

CTCATAATGG CATCAGGTAC cAGGGGTTGG GaCCAGGTGT TAATAACAAC GGTTGATGAT 180

AATACATTTA TATGCCTCCT ATAAATAAGA TTTCACTATT TTAGCAAATT TTCTGAAAAT 240

TTAAAAGCCT AAAAAgtGAT AACGCTATAT TGTCGAACAA ACGTTATCAC TTAACGATTT 300

TATTTGGCCT GAATGATGGG ATAGATTTTT ATGTCCACAT TATTTCTTAC AGCATTTGAA 360

ATCATGCAAT TATTATCTGC AATTGTTATC AATTTTGGTA ATCGCTTTTC TAATTGTGCT 420

ATTTGATCAC TTGGAATTTG AATTTGAGGA TGGTGCACAA TTTTTGACAT ACTGAATTTT 480

CCGTTATTTA AACAAGCTGT TCCAATCGAT TGTTGTkCAA TTGAAATATC TGTGAACTTT 540

GCACGTTCAA GAGTAGCTGC TAATGAGATG ATATAACATG ATGAAGCGGC TGATACTAAC 600

ATTTCATCGG GATTTGTTCC TATACCAACA CCACCTAAAG AAGCAGGTAT AGAAATATTC 660

TCTGAAAGTA TGTCGCCTTG AACGTTTCCG ACATTGTTAC GACCACCTTG CCAAGAAGTT 720

TGGACTTTAA AGTCATGTTG ATGCAATTGC TTTAACCTCC AATATAATTG TGATAGTTTA 780

ATTTTAGAAT AGTTTATCAA AGTTTAACAG AAAGGTGACT TATCAATGAC TCTGAATAAA 840

CTGAAAGATG AATTACAAAT TGTTTCGCAC CGTGGATTGC CGAGTGATTT TCCTGAAAAT 900

ACAATGGTCG GTTATCGAGA GGTAATGGGG CTCAATGTTG CTATGTTAGA AATAGATGTT 960

CATTTGACCA AAGACCAACA TTTTGTTGTG ATACATGaTG AAACAATTGa TAGAACATCG 1020

GaTGGtArGG GGCGTAwTGc TGaTTACACA TTATCGCAAT TAAAATCATT TGATTTTGGT 1080

AGTTATAAAG ATGTTGCTTT 1100

(2) INFORMATION FOR SEQ ID NO: 676:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 460 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676:

ATTAATTTCA TATGGAAATA GTTGAACTAA CTGCGCTGTA TAAGCTTCAA CAGTTTGATG 60

AATTAACGAT TGATCTTCAA TATATCCGTA GAACAAATCT TCAGTACAAA CTACTTTACC 120

TTTATCAGGT TTAATTGCAC CTGCCAACAA TTGACCTACC AACGCTTTGG AAGATTCAGG 180

TTCACCAATT ATACCTAATG CTTCTCCTTG ATAAATATGT AAACTAATAT TGTTTAAATC 240

GATATCTTCA GCATCATATC CAAAAGGTAA ATACCATTTC TTATTCTGTT TATTCCTATA 300

GTAGTGTGTT ACTTTTAGTA ACTTTAAAAC AATTGAACTT CCCATCTATT TTCATCCTTC 360

CCCCACGCaA AAATACCTTT TAATCTTnCT ACTTTAAAAT 460

(2) INFORMATION FOR SEQ ID NO: 677:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677:

GTCAAGTTTT CGGCTAGATT TTAAACGCTC ATCACTATGT AGAATGAAAC TTTCGAAAAA 60

CTGTAAATCA TCATAACCTT TTACATAAAC ATAACCTTCG CCACCAATTG CTTGAATTAA 120

ACATTGGGCG GCCATTTGAA TTTCTAAAGA TTGTTTTTCT AGCCTATTAA AGATACCTAT 180

TAGTTGTGTG TTTAAGATTT TTGACATCTT TATCCTCCAA TCTACTTATA AAATATTGTA 240

ATTAATGACT ACATATTATG CAACGGCTTA AATTGTATAA AAATGTATAC GTTTGCATTT 300

AGTATAACTA TCGCATTTTT CAAAAAATAC ACATTTAATC TGCAGTATTT CAATGCATTG 360

ACGCTATTTT TTTGATATAA TTACTTTGAA AAATACGTGC GTAAGCACTC AAGGAGGAAC 420

TTTCATGCCT TTAGTTTCAA TGAAAGAAAT GTTAATTGAT GCAAAAGAAA ATGGTTATGC 480

GGTAGGTCAA TACAATATTA ATAACCTAGA ATTCACTCAA GCAATTTTAG AAGCGTCACA 540

AGAAGAAAAT GCACCTGTAA TTTTAGGTGT TTCTGAAGGT GCTGCTCGTT ACATGAGCGG 600

TTTCTACACA ATTGTTAAAA TGGTTGAAGG GTTAATGCAT GACTTAAACA TCACTATTCC 660

TGTAGCAATC CATTTAGACC ATGGTTCAAG CTTTGAAAAA TGTAAAGAAG CTATCGATGC 720

TGGTTTCACA TCAGTAATGA TCGATGCTTC ACACAGCCCA TTCGAAGAAA ACGTAGCAAC 780

AACTAAAAAA GTTGTTGAAT ACGCTCATGA AAAAGGTGTT TCTGTAGAAG CTGAATTAGG 840

TACTGTTGGT GGACaAGAAG ATGATGTTGT AGCAGACGGC ATCATTTATG CTGATCCTAA 900

AGAATGTCAA GAACTAGTTG AAAAAACTGG TATTGaTGCA TTAGCGCCAc ATtAGGTTCA 960

GTTCATGGTC CATACAAAGG TGAACCAAAA TTAGGATTTA AAGAAATGGA AGAAATCGGT 1020

TTATCTACAG GTTTACCATT AGTATTACAC GGTGGTACTG GTATCCCGAC TAAAGATATC 1080

CAAAAAGCAA TTCCATTTGG TACAGCTAAA ATTAACGTAA ACACTGAAAA CCAAATCGCT 1140

TCAgCAAAAG CAGTTCGTGA CGTTTTAAAT AACGACAAAG AAGTTTACGA TCCTCGTAAA 1200

TACTTAGGAC CTGCACGTGa AGCCATCAAA GAAACmGTTA AAGGtAAAAT TAAAGAGTTC 1260

GGTACTTCTA ACCGCGCTAA ATAATTAATA TTTAGTCTTT AAGTTATTAA TAACGTAGGG 1320

AATAAATAAA ACAGTTTGAT TTTAAAATGA AAGCGTAAAA ATGGTAAAAT ATATCAAAAT 1440

TGATTGTGAT A 1451

(2) INFORMATION FOR SEQ ID NO: 678:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 668 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678:

nGTATTGAAG CGGTTAAACA AACACCTAAT GCAACTGACG AAGAAAAGCA GGCTGCTGTT 60

AATCAAATCA ATCAACTTAA AGATCAAGCA ATTAATCAAA TTAATCAAAA CCAAACAAAT 120

GATCAGGTAG ACACAACTAC AAATCAAGCG GTAAATGCTA TAGATAATGT TGAAGCTGAA 180

GTAGTAATTA AAACAAAGGC AATTGCAGAT ATTGAAAAAG CTGTTAAAGA AAAGCAACAG 240

CAAATTGATA ATAGTCTTGA TTCAACAGAT AATGAGAAAG AAGTTGCTTC ACAAGCATTA 300

GCTAAAGAAA AAGAAAAAGC ACTTGCAGCT ATTGACCAAG CTCAAACGAA TAGTCAGGTG 360

AATCAAGCAG CAACAAATGG TGTATCAGCG ATTAAAATTA TTCAACCTGA AACAAAAGTT 420

AAACCAGCTG cACGTGAAAA AATcAATCAA AAAGCGAATG AATTACGTGc TAAGATTAAT 480

CAGGATAAAG AAGCAACAGC AGAAGAAAGA CAAGTAGCAC TAGATAAAAT CAATGAATTT 540

GTAAATCAAG CCATGACAGA TATTACGAAT AATAGAACAA ATCAACAAGT TGATGATACA 600

ACAgTCAgCG CTgATAGCtT GCTTTAGTGA CGCCTGACCA TATTGTTAGA GCgCTGCTAG 660

AGATGCGT 668

(2) INFORMATION FOR SEQ ID NO: 679:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679:

GATCCAAATT TAAAAGGAAA AATAGCCTTT AACGAATTTA CGAAACAAAT TGAATGTTTA 60

GGGAAAGTGC CATGGAATAC TAATTTTAAG ACACGTCAAT GGCAAGACGG TGATGATAGC 120

AGTTTAAGAA GTTATATCGA AAAGATTTAT GACATACACC ATTCAGGTAA AACAAAAGAT 180

ATCGTGGGAT GGACATAAAC GCCTTGAAAA GTTATTTATC AAATACTTAG GTGTTGAAGA 300

CcTGaAGTGA ATAGAACAAC TACCAAAAAA GCATTGACTG CTGGAATCGC TAGAGTAATG 360

GAGCCTGGAT GTAAATTTGA CTATATGCTT ACACTTTATG GTCCTCAAGG TGTAGGTAAA 420

TCTGCTTTGC TAAAAAAATT AGGTGGTGCA TGGTTTTCTG ACAGTTTAGT TTCTGTTACA 480

GGTAAAGAAG CTTATGAGGC CTTACAAGGC GTTTGGCTAA TGGAAATGGC AGAACTTGCA 540

GCTACAAGAA AAGCTGAAGT TGAAGCTATT AAGCATTTCA TATCTAAACA AGTTGACCGA 600

TTTCGTGTTG CTTATGGGCA TTATATTGAA GATTTTCCAA GGCAATGTAT TTTCATTGGT 660

ACAACTAATA AAGTTGATTT CTTAAGAGAT GAAACTGGTG GAAGACGTTT TTGGCCAATG 720

ACTGTAAATC CAGAGAGAGT TGAAGTGAAC TGGTCTAAAC TAACCAAAGA TGAGATTGAC 780

CAAATTTGGG CAGAAGCTAA ACACTATTAT GAACAAGGAG AAGATTTATT CCTTAACCCT 840

GAACTAGAAG AAGAAATGCG TTCAATACAA AGCAAACATA CTGAGGAATC TCCATATACA 900

GGCATTATTG ATGAATATCT TAACACACCm ATTCCtAGCa ATTGGGATGA CTTAACTATC 960

TTTGAACGAA GACGATTTTA TCaAGGTGAT GTTGATATGT TACCaACAGG AAATGTaGAT 1020

TACGTTAAAA GAAATAAAGT CTGTGCGCTT GAAGTGTTTG TTGAATGTTT TGGTAAAGAT 1080

AAGGGAGATA GTAGAGGATC TATGGAAATT AGAAAGATTT CAAACATCTT AAGACAATTA 1140

GACAATTGGT CTGTATATGA TGGTAATAAA AGTGGGAAAA TTCGATTTGG AAAAGATTAT 1200

GGTGTACAGA TAGCTTATGT AAGAGATGAA AGTTTAGAGG ATTTAATATA AGAAATATTG 1260

AATAAATATG CATTTTAGAG TGTTGTATCA GATGTTGCAT CATTTTTTGA GTGATGCAAC 1320

ACGGGAGTGT AAAAAGTAAT CGTAGGTGTT GTATCATTTT TGGTGATGCA ACATTGATGC 1380

AACAAATGAT ACAACACCTC TTTCCTTTCT AGCTGTAGGG TTCAACCCTG TTTGTTTCCA 1440

ATGTTGCATC AAATTCACTA TAAAGTTTAA AAAGTAGTGT TAGGGAGTAA AGGGGTATAG 1500

GGGTAACCCT CTAACAGCTA TTTTTAAAAG TTTGGCAAGA ATTGATACAA CATCGGAACA 1560

CAAATATAAA TTTTGTATAC AAGGTGAATA AATGAAAGAA TCGACATTAG AAAAATATTT 1620

AGTGAAAGAG ATAACAAAGC TAAACGGTTT ATGTTTAAAA TGGGTCGCAC CTGGAACAAG 1680

AGGTGTGCCA GATAGAATTA TTATTATGCC AGAAGGAAAA ACATATTTTG TAGAAATGAA 1740

GCAAGAAAAA GGAAAGTTGC ATCCTTTACA ArAATATGTG CATAGACAAT TTGAAAATAG 1800

AGaTCATAAA GTATATGTGT TATGGAATAA AGAACAAGTA AATACTTTTA TCAGAwTGGT 1860

AGTGAACATT TGGCGATTGA CTTTCAAACC ACATAGCTnT CCAAAG 1906

(2) INFORMATION FOR SEQ ID NO: 680:

(A) LENGTH: 948 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680:

AATTATTTGA ATAAATTAGC AATTAAAGAG TTGATTTGTC AGTTTAAGyA TTTGAGTGCA 60

TTTGAAAAAG ATGTCATGTA TTTAATGTGT GAACAATATA AGCCGAGAGA AATTGCTCAA 120

TTGATGCATG TAAAAGAGAA AGTGATTTAT AATGCCATAC AACGATGTrA AAATAAAATA 180

AAACGTTATT TCAAAATGAT TTGAAAAGCG CCTTAGGACG TGAATTGAAT TATAACGTGT 240

TACTTACTGA TGGTTTGACA TTTGTTATAA ATTTTATGTA TAGTATACTG GTATTATAAT 300

GAATAAAGGT GAATTATTGT GAGAAAAATA CCTTTAAATT GTGAAGCTTG TGGCAATAGA 360

AATTATAATG TTCCTAAGCA AGAAGGCTCG GCAACAAGAT TAACCTTAAA GAAATATTGT 420

CCAAAATGTA ACGCGCACAC AATTCATAAA GAATCGAAAT AAATACATTC GAAATAATAC 480

TTTGATAATA TGTTCAAAGG ATTTGGAGGT TGAGCAGATG GCTAAAAAAG AAAGTTTCTT 540

TAAAGGCGTT AAGTCTGAAA TGGAAAAAAC AAGTTGGCCG ACGAAAGAAG AGCTATTTAA 600

ATATACTGTA ATTGTAGTTT CTACTGTTAT ATTCTTCTTA GTCTTTTTCT ATGCCTTAGA 660

TTTAGGAATT ACAGCATTGA AAAATTTATT ATTTGGTTAG AGGAGTGAAG ACATGTCTGA 720

AGAAGTTGGC GCAAAGCtTG GTATGCAGTG CATACATATT CTGGATATGA AAATAAAGTT 780

AAAAAGAATT TAGAAAAAAG AGTAGAATCT ATGaATATGA CTGAACAAAT CTTTAGAGTA 840

GTCATACCGG AAGGAAGAAG GAAACCTCCA GTAAnAAGnT GGCCAAGCCT AAAACCGCCT 900

GTTAAAAAAA ACCATTCCCC TGGGnTAnGG TTTTAAGTGG GAATTTAA 948

(2) INFORMATION FOR SEQ ID NO: 681:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 863 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681:

ACAnATAATA ACAAAGCGCT TGCTAGTACC TCTTAAAAAG ATGATGCTAG CAAGCGCTTk 60

TCTATACTAT ATATTATTTT TCTAAAATTT TAACACCCTC TTGAGTGCCT ACAATAACTT 120

GATCTGCCAT ATCTAAGAAG TATCCTGTCT CAAACACACC TGTCAGATGA ATTAAATACT 180

TATCAGTTAT AAATGCGACA TCTTCGTTTA CACGACGTTC TACTTTTATA TCAGCGTATG 300

ATTCAATTTT ACGTAATATG TGATACCAGT TAAATTTATC CACCTCTACT GGTAACTTAA 360

ACGTCTCACC TAAGTATTGA ACTATTTTCG TTTCATCGAC AACCACAACA AAACGCGATG 420

CCATTTCATC TATAACTTTC TCTCTGAACA GCGCACCACC GCCACCTTTA ATTATATTTA 480

AAGATGGATC TACTTCATCA GCACCATCAA TTGCTAAGTC GATATGATCA ACATCATTGA 540

TTTCACATAT TTTAATACCT AATTCTTTTG CTAAAAATGC AATTTTATTA GAAGTGCATA 600

CACCTGTAAT ATTGTAACCA CGTTCTTTAA TTAGTTGCGC CATTTGAGGT AAGAGTAATT 660

CCATTGTACT TCCTGTACCA ATTCCCAGCG TCATGTCACC ATTGATTkGA CTTAAAACAT 720

CATTTAATGT CATTAACTTG AGTGCTTTGA CATCTTTCAT GAAGGTAGCC TCCCATATTT 780

AtGTAATCTA TTCAATTCAT ATTTTACATG ACTCGTATAA ATTAACATAC CCTTATnGCT 840

AACCATTTGT GTTAAACATA TCG 863

(2) INFORMATION FOR SEQ ID NO: 682:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682:

TTCATTTTTG TTGTTCAGCA ATTTTGGTCC GAATTTCAAT TCATCAGATG ATAGCTCTAT 60

TAATTCTGTA GAATATTCTG CtACAACAAT TTCATAAATA TGGCCTTTTT CTTCCATTAT 120

TATTTCATCa ATTATTTCAT AATTCAATTG TTGTAATGTT TGTCTTAAAT TTTCAGTTTG 180

GATATTACTT TGTAAAATCA ACCTTGGATG TTGACTTAAC TTATCTTGCC CATCTTTTAA 240

AATTTTAGCA ATAAGTGGTC CGCCCATACC ACAAATTGTG aTATTATCGA TTACGTCCTC 300

AGGTTGAATA ACACTTAAGC CATCCCCTAA ACGTACATCA ATTCTATCTA CTAATTGGTT 360

TGCAGCTACA TTTTTCACAG CAGCTTGAAA AGGGCCTTGA ATAACTTCTC CAGCAATAcC 420

GaTTCGCATA AATGGTTTTG AATTGCATAG ATTGGCAAAT AAGCATGATC TGAGCCAATA 480

(2) INFORMATION FOR SEQ ID NO: 683:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 689 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683:

CTGCAAAAAA TATTGGTATA ATAAGAGGGA ACAGTGTGAA CAAGTTAATA ACTTGTGGAT 60

AACTGGAAAG TTGATAACAA TTTGGAGGAC CAAACGACAT GAAAATCACC ATTTTAGCTG 120

TAGGGAAACT AAAAGAGAAA TATTGGAAGC AAGCCATAGC AGAATATGAA AAACGTTTAG 180

GCCCATACAC CAAGATAGAC ATCATAGAAG TTCCAGACGA AAAAGCACCA GAAAATATGA 240

GTGACAAAGA AATTGAGCAA GTAAAAGAaA AAGAAGGCCA ACGAATACTA GCCAAAATCa 300

AACCACAATC CACAGTCATT ACATTAGAAA TACAAGGAAA GATGCTATCT TCCGAAGrTT 360

gGcCCAAGAA TTGAACCAAC GCATGACCCA AGGGCAAAGC GACTTTGTTT TCGTCATTGG 420

CGGATCAAAC GGCCTGCACA AGGACgTCTT ACAACGCaTA AcTACGCACT ATCATTCAGC 480

AAAATGACAT TCCCACATCA AATGATGCGG GTTGTGTTAA TTGAACAAGT GTACAGAGCA 540

TTTAAGATTA TGCGAGGAGA GGCGTATCAT AAGTAAAACT AAAAAATTCT GTATGAGGAG 600

ATAATAATTT GGaGGGTGTT AAATGGkGGa CaTTAAATCC mCGTTCATTC mATATATAAG 660

ATATATCACG GTAATTGCGC ATATAACTT 689

(2) INFORMATION FOR SEQ ID NO: 684:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 858 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684:

TTATTAAATT GGTATGTGTT CATTATACAT ATGaCAAATA TGaATGTAAA CCGATAATTT 60

AGATTTTTTG GAATAACCTG AAAATTCAAG TTaTAGCGTT GCTTATATTT TAAAAGGTGG 120

TGATAATGAG ACTTTTTGAA AAATAAAATT CAAAATACTT ATAGCATAAT CAATATGCAC 180

ATTAAATAAA TGTACTCTTT TAATGCGTTG ATAACTGTAT TTGTAATTTA GAGAAGGGGT 240

GTTCACTATG CTGATGTGTT AAAAAATAAA ATAAAAAGGA CACCTCGATG CTATAAATAT 300

TAGCATCGAG ACGCCCAGTT AATGTCTATT AAATTGAATA TAGTCTCGGA CATGAATCAA 360

TGCCCTAGGC CCTGCAATGT TATATTGACA GTAGTTGACT GAATGAAAAT GACTTTGTAG 420

CTAGCTTTTT TCAATCCTTG TCGGTGCAAC ACATAGAGAA ATTGGATTCC TAATTTCTAC 480

AAACAATACA AGTTGCGGAA TAAGTCCCAA TATAGAAGGT GACAGTAAGC CAACTTACAA 540

TAATGTGCAA GTTGGTCGGG CCTCAATACA GAGATTTTCG AAAAGAAATT CTACATATTA 600

GCCACCTTGT TTATTTAAAT CGATAACACG GTTTGCGATT GTATTGATAA ATTCAAAGTC 720

ATATGAAGTA AAGATAATAG AACCTTTGAA TGATTTAAGT CCATCATTAA CAGCAGTAAT 780

ACTTTCTAAG TCTAAGGGTT GTGGGTCATC AAGTAAAAGA CGTTGCCCTG ATAACATCAT 840

TTACTAGCAn CACGACTT 858

(2) INFORMATION FOR SEQ ID NO: 685:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685:

TTAGTATTTT CAGGnTGGAA ATTGATGTTT GAAATTCACT GAAATGGGCC AGAACCTgAA 60

ATGaAACTTT ACCAACAATT TGGtCTTCAT CAATGAGGCC AAACGCACGG CTATCTTTAC 120

TTACTTCACG ATTATCTCCA AGCACTAAAT ATTTACCTTT TGGAATGACA TTTGATTTAG 180

GATTCGCATT CGGTAAATCT TTAACTTGGA AAGTCCCAGT AATGTAATCA CCTTGTTTAT 240

GTTTTAAATT GTAGTTTAAA TATGGTTCAT CTTGTTTTTT ACCATTGACA TATAATGTAT 300

CATTTTTGTA TTCTACTTTA TCACCAGGAA CACCGATGAC ACGTTTAACA TAGTCATCAT 360

TTTTGTTTGC ATGGAAGACA ACTACATTAC CTTTTTCCAA ACCACCTGTT TTATATCCAA 420

CAATGTTTAC AGCTACTCGC TCGCCATCTT TCAAAGTTGG ATCCATTGAT TCACCTTTAA 480

TTGTATATGG CGTAACAATA AATTTACCTA CTATAAATAA AATGACAAAA GCGACTGCAA 540

TTGAAATAAT CCATTCCAAT ATTTCTTTTT TCAATTTTGA CACCTCTTTT TAAGATTTGA 600

ACTGAACAGT CCATTTTGAA AAAGGATAGT ATCGTAAACt AACATTACCA ATAATAtCCT 660

TTTTATCGAT TAAACCAAAT TGTCTTGAAT CGTGCTTGTk ATTATCTTGA TCATTTAGCA 720

CAACAAAATT GTTTGGCGGA ATAATATCAC CATCTAATTC TTTAAAATTG CGCAAACTAA 780

AATCTTTAAT TTTTCTGTTC TTGGCATAAG ATGCGTCAAC CGGTCGGTCA TCACGGTATA 840

ATTGTCCCTG ACGAAACGCC ATTGATTGAC CAGGTTTGGC AATAATTCGA CTAGTATATA 900

TCTCGTTACC ACGCCTATAT GTAATGATAT CACCATTATT CAATTGATTA AATGTAACTT 960

TAATTTTATT TACAATAACA CGATCCCCTT TGTTAAGGGT TGGTGACATA TCATTATTCG 1020

GAATGACATG ACCAACTATT ACAAAAGTTT GTACGAACAG TACAATGATA ATAGCAAGTA 1080

TCAATGAAAT CAAATATTTT ACAACTTTTT TCACGATGTC ACTCCTTTTT CGATCCCATA 1140

ATCCCTCTTA AAGGATGCGT TAAAATTGTA GTAATTTCCT TACCTAAATA ACCTAAAATA 1260

ATTGTTGAAA CTAACTTTGA TGATGCCAAA ACAATGAAAT AATATTTAGG TCTAATATGA 1320

GATAGACTCG CTACAAAATT TATTAATGTA TTTGGCGTAA AAGGAAAACA AAGTAAAATA 1380

AACAATGGGA TTAATCCTTG GCGATCAATA AAACTAATCA AGCGTTGAAC AGCAGTACGT 1440

TGTTTAATTC GCTGCATCCT CTCAGTGTTC ACCAATCGTT TACAGATCAA ATAGACTGTA 1500

AATGTTCCAG AAATTAATCC AAGCCAACTA ATCAATATAC CTAAAATAGG TCCATAAGCT 1560

TGAATGTTAA TTAAAATATA GAGTGCTAAA GGAAATACTG GAATTATAGC TCTAATATAT 1620

AACAATATAA ATCCAGGTAA ATAACCAAAC TGTCGAAATA TCTCAAACCA TTCTTCTACT 1680

TGATGAAACG ACAAATCATC AATCCCTTTC TTTGGTTGAA GATAATTATT CTTACATTAT 1740

AAAGTTA 1747

(2) INFORMATION FOR SEQ ID NO: 686:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 645 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686:

CGTAAAGATT ACTATTTAGG AGGGTGACTA TGAAAAAGAA ATTAGGTATG TTACTTCTTG 60

TACCAGCCGT AACTTTATCA TTAGCCGCAT GTGGGAATGA TGATGGAAAA GATAaAGATG 120

GCAAGGTAAC AATTwAAcGa CaGTTaTCCm TTGCAATcAT TTgCAGAGCA AATTGGTGGA 180

AAACACGTGA AGGTATCATC AATCTATCCA GCAGGGACAG ATTTACATAG CTATGAACCA 240

ACACAAAAAG ATATATTAAG TGCAAGCAAG TCAGACTTGT TTATGTATAC AGGGGATAAT 300

TTAGATCCGG TTGCTAAGAA AGTTGCATCT ACTATCAAAG ATAAAGATAA AAAACTGTCT 360

TTAGAGGATA AATTAGATAA AGCAAAGCTT TTAACTGATC AACACGAGCA TGGTGAAGAG 420

CATGAACATG AGGGACATGA TCATGAGAAA GAAGAACATC ATCATCATCA TGGTGGATAT 480

GATCCACACG TATGGTTAGA TCCTAAAATT AACCAAACTT TCGCTAAAGA AATTAAAGAT 540

GAATTAGTGA AAAAAGATCC AaAACATAAA GATGACTATG AGAaAAACTA CnaAAATTAA 600

ACGACGATCT TAAGAAAATT GATAACGATA TGAAGCAAGT TACAA 645

(2) INFORMATION FOR SEQ ID NO: 687:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 956 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687:

TTTGTTACTG CTTCTAAAAT AATATCCTTT AATTGTTTAA CATGTTGGAT TGTCATATGA 60

GGTGATGGTA CATTAAAAGG ATTTAATTCA TCTATTTGTG CATATTGATT TATGACATCT 120

TGATGCATTG AAATAGGGTT GATATCATTT GTTACTACTT TATTAGATTG GTCTTGTGAC 180

ATACTAATGG TGCCACCAGT ATGAATAACA AGTAGATGTT TCATATATTT CCTCCTATAT 240

TTAATTTACC TAATTATGAT AAAATATTAT TCATAAAACG ACAAGGAAGG GAAATGACGC 300

ATGAAAGCCA TTAATATTGC ATTAGATGGT CCAGCTGCTG CCGGAAAAAG TACAATTGCG 360

AAACGTGTAG CCAGCGAACT ATCAATGATT TATGTCGATA CAGGAGCAAT GTATCGTGCA 420

TTAACATACA AATATTtAAA ATTAAACAAA ACTGAGGACT TTGCAAAACT AGTTGACCAA 480

ACAACATTAG ATTTAACTTA TAAAGCAGAT AAAGGTCAAT GTGTCATTTT AGATAACGAA 540

GATGTAACAG ACTTTTTAAG AAATAATGAT GTGACGCAAC ATGTTTCATA CGTTGCATCT 600

AAAGAGCCAG TACGTTCATT CGCCGTTAAA AAACAAAAAG AGTTAGCTGC AGAAAAAGGT 660

ATCGTAATGG ATGGTCGCGA TATCGGAACT GTAGTGCTAC CAGATGCAGA TTTAAAAGTA 720

TATATGATTG CATCAGTTGA AGAGCGAGCA GAAAGAAGAT ATAAAGATAA TCAATTAAGA 780

GGTATCGAAT CAAATTTTGA AGATTTAAAA CGTGATATTG AAGCTCGTGA TCAATATGAC 840

ATGAACCGTG AAATATCACC ATTAAGAAAA GCAGATGATG CAGTGACATT AGATACGACm 900

GGCmAGTCGA TTGAAGAAGT TACTGACGAn ATTTTAGCGA TGGTGAGTnC AATTnA 956

(2) INFORMATION FOR SEQ ID NO: 688:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688:

AAAAGGGAGG AAAGAGAACA GTTAAATATG AATACAAAAT AATTTTGTTT TCGGACAGCA 60

GGGGTATTAG ACGCGATTGA CAATGTCTGT TTAATTAAAC GTAATGTTTA TTTAAGCGAT 120

GAATATTAGG TGAAAAGTTT TTGAATTTGA ATGTAATTGA GGTTTATTGA TTAGACATTT 180

TATTGAATTG CGTGTTATTA TATAAATGTA AAAATAAGAC GACATGCGCG AACATGTCGT 240

TAATGCGGAA TGGTTTTTTT ATTTTCCGCT AATTGAAATA AAAATGACGT TTTAATATAT 360

TATGGGCTAG GTGGTTTGTA AGAAAGGGTT AGTTATTAAT GTTTTATGAA TTAAGGAAAT 420

TTGAGTTTAA GGTTTAATCA ATTGTGATTT TGTTGATGAA GCGTTTAGTT AGAGTATTTT 480

CGCCACCACT AGTTACTCCT TCTCCCACTT TACCCGAGAC TGGAGAAGAg CTATCTGAAG 540

AATAAATAGA TACTTTTTGG CCATTTTGTA GTAAACCAAG ACCTTTTAAC TkCTCGGTTA 600

GAGAATTCCA TGTATTTTTA GCATCTAGCT TTTTGTTAAA GTCAyCGTAG ACATTTTCCT 660

TAGTTAAATC AATTTGTTTT AATCCTTTAA AGTCTATAGA TTGTGTTAGA TGGCCTCCAT 720

CATCATTTCc AGGAGCAGAA ACGCTGCTAG AATATCCATT GCTTAATAAA TAAGTAACGT 780

TGATTGTTTC GTACTCGTTA CTTAAAATAA TATCAGAATC ATGTAAgAAT CTTTAACTTT 840

TTTCCATAAT TGACCATCTG TCATTTTTTC TTCTGCTTTA GCCGTTTTAA CAACTTTATT 900

TGTATCTAAT CCTAAGTATG AAGAATGTAA GCCTGTTCCT AATGTTGTTA ATACTAAAGC 960

ACTTGCTACT aATGTTTTAC CTAAAAAttT TGTATTCATT TTTATTGCTC CTTtTTTTAT 1020

ATTGTAAACG TTTACAATGA AAATATAATA ATAATTTTTT AAAAGAACAA TTAACTAAAT 1080

ATCAAAAATG TATTAACTAT CTATTAACTA AAAAATAGAA TAATTTTTTA ACATAGTTTT 1140

GTTGTTTTGA ATTATAAAAA CTAAAG 1166

(2) INFORMATION FOR SEQ ID NO: 689:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1083 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689:

AGCACTGAAG GATGGCTAGT TGTCATAGCA TATGCGGTCA TTGGTATAGT TATAACGAGC 60

GTTTCTTATA TGTTGTCTAT TAAAATTTTT AACAAACAAG AACTAkAATT GTCGATTTTG 120

GTGATGATAG TATTTGAAAT AATATTTAGA GCAGGTGATA AATCTTTACG ATTGTCATCT 180

GTTCTTTTkG GTGTGGAATG AAATGTGGGG GATAAGTATA GGTGACATAT CTATATTGAT 240

TTATTTGTTT TGAGGTGGTT ATGTTGTGTG GGAATTATTT CCTTTTAGAT AGCGGGGATT 300

AGAGGATATA TGTTATTTAT AAGTATCATT TGATGATTGT ATAGGCTAAC GATTTCCTCG 360

GAAATATTTA AAAACCTCGA TCATGTAGCA TAACTGAAGT TTGTCACAAA AGTATAATGT 420

GAAGTTCGAC ACTTTTGGaT TCAGTTCAAA TACTTTGACC GAGGTAAATA CTATTTATTC 480

TGATACTGAG ATAATCATTA CATGGTCGTG ACCTTTAAAT AAAAGGCTGA CAATATAAGA 600

CATAACGAGT ATACCTAGTG AATATGAAAT ATACTTCGCG TTTGTCAGTT CATTATGGAA 660

ATAAGGCGTG ATTAACCATA ATCCAATATA GAATATTAAA ACACTGATAT ACATCATATT 720

AATTTCAAAC AAGTCATTTA GTTTATTGTT ATTACTAAAA ACAATTGCAG CATTAATCAC 780

ACCTAAAGCG ATATTGATTA ATAGATGCGT ATACGATAAA CGGAAACCGA TAGATGTTAA 840

TTTATGATTA ATATAATTTT CAGTAATGAT CCAATATACA CCGAAAAGAC TAATTAAAAT 900

CATAAATTGG AATATATAAA TGTAACTAAA ATGATCAATG CTAAATGATG ACGAAGCTAA 960

ACCAACCAGT ACCTCGCCAr AGwTAtAATT GTTAGTAACG AAAAACGTCT ACTAAATGCA 1020

TCATATTAAC AGGTnTAATA CAAGTATTTC TGAAATGGAA TAAGnCTGTC GCTGCATGAT 1080

ACG 1083

(2) INFORMATION FOR SEQ ID NO: 690:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 627 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690:

TTAATCATCT GGATGTATTT AGTATTnAGA ATAATAAnAA AACGATCATG TTGTATTtTGA 60

GTAGCGATTG GTTTGCGGAA TTAGGCTTTA CTTTCTTTAA TTACCACTAT ACAGCAAAGT 120

TGATTAAATC ATCCTATAAT TTGAAATGTC TACTATTAAA ATTGACATAT CGATACCTTG 180

ATAATCAGCC TCTTAATGAC GCTGATAyTA GAAAATTACA GGATATTATT AAAATCATTG 240

CAAAAGAAGC AAGTATGGAT AAAAAGATTG CACAAAATCA ATATCGATAT GCGTATTATG 300

GTGATTTGCG TGATGAGCTC GAATATATTT ATCAAAATGT AAATCAACGA TTGACATTAA 360

AAAGTGTCGC TGATAAATTA TTTGTCTCAA AGTCAAATTT GTCATCACAA TTCCACTTAC 420

TTATGGGCAT GGGTTTTAAA AAATATATTG ATACTTTGAA AATnGGTAAA TCGATTGAAA 480

TTCTACTTAC TACTGATAGT ACTATTAGCA ACATAAGTGA nCATTTAGGT TTTAGTAGTA 540

GCTCCACTTA CTCTAAAATG TTTAAAAGTT ATATGGATAT CACACCGAAT GAATATCGTA 600

ATTTATCAAA ATATAATAAn TGTTTAC 627

(2) INFORMATION FOR SEQ ID NO: 691:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 641 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691:

TTGAACGTAA TGCTAGCAAA TGACTTTGTG CCATAAAATA TTCTTCCCAT TTGATTCTTT 60
CCAAGATGTT CACCTTCCAT ACTTAAAATT TAGTAACATT TTCTAATAAT ATAAGATTAA 120
TCACAAAAAA TAAAATTTGC AATTAAAATA ATCCATTATG TCGTGAAATA AGATTTCAGT 180
TTATCAAAAG TTTTACTTCC AAAACCTTTT ACTTTTTTCA AATCGTCAAT TTCTTGAAAT 240
GCACCTTGTT GGTTGCGATA TTCAACAATT GCATTAGCTT TAGCTTGCCC AACTCCAGGA 300
ACAGACATCA ATTCTGATAC AGATGCCGTA TTTAAATTTA CTTTAGTATT ATTTGTGTTC 360
CCaTTTTTTT CGTGCACACT GTTTACTTCA ATTTGTGGTT CAACATTCTT TTGTCCTTTA 420
TGAGGTATGA AAATCATTTT TTGATCTGTT AATTTTTCAG ACAAATTAAT TTGACTTACA 480
TCTGCATCCT CCAATAATTG TGCTTTATCA AGTAAATCAA CTACTCTATC CTTAGATGTC 540
ATTTTATAAA CATTAGGATG TTTAACAGCA CCTTTTACAT CGACATATAC AGGACCCTTA 600
TTTTTGGAAT TATCTCCATC TTTGACCTGG ACATCTTCTA C 641

(2) INFORMATION FOR SEQ ID NO: 692:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 631 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692:

TATTAAAGnA CTTGATGAAC CAAATCATAA AAAGCnATAT ATGTTATTTG CAGCTGGCAT 60
TGTGTTnGCA ACTATTTTAC TTATTTCGGC ACATTTATAC AGCAGAAAGA GAGGTAACCA 120
AGTTTGAGAA TCATAAAGTA TTTAACCATT TTAGTGATAA GCGTCGTTAT CTTAACCAGC 180
TGTCAATCTT CCAGTTCTCA AGAATCAACT AAATCCGGCG AATTCAGAAT CGTACCAACA 240
ACTGTTGCAT TGACAATGAC ATTGGACAAA TTGGATTTAC CAATTGTCGG CAAACCCACG 300
TCATATAAGA CATTGCCTAA TCGTTATAAA GATGTACCGG AAATTGGTCA ACCAATGGAG 360
CCGAATGTTG AAGCTGTTAA AAAGTTAAAA CCAACACATG TTTTGAGTGT GTCAACGATT 420
AAAGATGAAA TGCAACCATT TTACAAACAA TTAAATATGA AAGGCTACTT TTATGATTTT 480
GATAGTTTAA AAGGGATGCA AAAGTCGATT ACACAATTAG GTGaTCAATT TAATCGTAAA 540

GCAGCTAAAC AAAAGAAACA TCCCAAAGTA T 631

(2) INFORMATION FOR SEQ ID NO: 693:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693:

AATTTAACTA TGTTTTCCAC ATTGTTTCAT GTCACGAAAA GGACAACGCG CGACTATAAG 60

TATCAACTAT TTCCACAAGT TTTATTGGTG TTTTTATTAT TCATCGATAC GCTTCATTTT 120

CATCTCTCCA ACACAAAAAA GAAGCTAAGC AACTTATGTT GCCTAACTCC TCTATACTAT 180

CCATATTTTA CTATTATCCA TATTTCATTG AATTATCTAA TGTTGGcTTC TATTTTTTCA 240

ATATTTCTAC CGTCAATGAC GTCACTCATG CGATTTGTTT GTAATTTTTT ATTAAGTTCA 300

AACGTATAAT AGCCGCCATC TTTCATTATC ACTTTTATCT TACTATCTTT AGGAAACTTT 360

TTATACAGAT CAAAATTTTG AATTAAATAC TGTCTCAATT TAAAGTCGAG TTCTTTAAGT 420

GAAATCTCTT CTTTATAAAT GTAGTGTACT CTACCGTACG TAGCAATACC GTCACCTTCA 480

TCTCTCTTGA TTTGAAATCT TGGTGCGTTT ATATAATCAT AATAAGCGTC TTGATTTTTC 540

TTAGTGACAC CACCATATGA AAACACTGTG CCATTACGGT TTTCCGCTTC TTTAACAACA 600

AATATGTCTA ATCCCGGATT TTTACGTGCT TTAAATCTTT CAATATCTTT ACCAAATATC 660

TGTACTCTTG TGAATTTTCT ATTTTTATCA AAGATAAGGT AATGCTTGCC ACCTTTGCTA 720

TAACGATAAC CAGTAACATT TTTAAGTTCC TTACTTGCGC CACTATAGTA ATCTCTTAAG 780

TCAAAGATAT CTTTTGTCAC ATTTTCATAT TTTGCTTTAT GTTCACTCGC ATTTACAGTT 840

TGATGCAATG ACGTTATTGT TCCTGTTGCT AAAATACCTA ATGCTAAACT TGCTTTCGCA 900

ATTGCTGTCA TTTTCATAGT TGTATGCTCC ATTCGTAATT ATTAGATTTG TTCGCTTACG 960

TCTATTGAAT CATACAGCTT TATTATAGTT AGCGTATTTG ACCTTTCACA TTAAACCATG 1020

TTTAATAATC ATTGAATCAT TATTAAGTAA ATTAAGGAtC TATAATGTTC GTTAAATAAA 1080

CTGAnCCCGT TGTGCTTCAC ACCCGnTnGA T 1111

(2) INFORMATION FOR SEQ ID NO: 694:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694:

TTATGGATGG ATTAAGAGGT CGTGTTGAAA AAATCAACGA TAACTCTGTT ATTGTTGACT 60

TAACAATTAT GGAAAATTTT AATGACCTTG ATTTACCGGA AAAAACTGTT ATCAATCATA 120

AACGATATAA GATTGTTGAA TAAGAAGGTA AGTTATAATG AATAAAATCT CGAAGGCTTT 180

AACTTGGTTT ATTATAAGTT TCATTATATT TCATCTCATA TTATTTATTA TGTGGGGCGA 240

ACACCAAGAA TACTGGTATT TATATACAGG TATAATGCTA ATTGCTGGTA TCAGTTATGT 300

ATTTTATCAA AGAGATATTG AATCTAAGCG GTTGCTTACA TCAATTGGTG TTGGTATTAT 360

TACGGCAATT ATTTTAATTA TGCtTCAACT TTTATkCTCA CTTATAACTT CTAATTTAAG 420

TTATAG 426

(2) INFORMATION FOR SEQ ID NO: 695:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 737 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695:

AAAAGGGGnG TAAGGTTTAG CTCAAGTACG AGAAGTCTTT GGTGATGAAG CAATTGATGA 60

AAATGGTGAG ATGAATCGTC GTTATATGGG TGATCTAGTG TTTAATCATC CAGAAAAACG 120

CTTAGAATTA AATGCTATCA TACATCCTAT CGTGCGAGAT ATTATGGAAG AAGAAAAGCA 180

AGAATATTTA AAACAAGGAT ATAATGTAAT CATGGATATT CCATTATTAT TTGAAAATGA 240

ATTGGAAAAT GCAGTAGACG AaGTGTGGGT TGTATACACT TCTGAAAGTA TACAAATGGA 300

TCGTTTAATG CAACGTAATA ATTTGTCATT AGAAGATGCG AAAGCACGTG TCTATAGCCA 360

AATTTCTATT GATAAAAAAA GCCGAATGGC CGATCATGTT ATCGATAATT TAGGGGATAA 420

ACTTGAATTA AAACAAAACC TTGAGAGATT GTTAGAAGAA GAAGGTTATA TTGAAAaGCC 480

GAATTACGGA GAAGAAGATT AATATTACAC TATAAATAAG TCATTACTTT ACGTACGCGT 540

TGATGTATGT AAGTAATGAC TATTTTTTAT AAAAAAGATA AATAAATCAA CGGAAAACGC 600

TTTCAAATTT CATATAATAT GCTATACTAA TTCCATAAAG TATAACACAT AAAGATCAAG 660

GGGTGCTTTT AATGTCAACG AATATTGCAA TTAATGGTAT GGGTAGAATT GGAAGAATGG 720

TATTACGTAT TGCATTA 737

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696:

AACGATAAGA ACAAAAGATA TATTACAAAG CGTTTATTTA AAACGTTATT TATTACGCGC 60

GATGATGGCA GGATTTATTA TCGGGATTAT TACGGTCTTC GTATTATCAG TTAAAGCAAC 120

ACACGAACCA GATTTACCGC CAGgCATTGT GAATATGGCC AGTGCCATTA CATTCAGCTT 180

TGCGTTAGTA CTCATTTTAT TTACAAACTC CGAACTACTA ACCAGTAACT TCATGTACTT 240

TACTGTAGGC CTGTATTmTA AAGTAATTAA ACCAACTAGA GTATTGaAAA TATTTTTATT 300

ATGCTTTGCA GGAAATATTT TAGGTGCTGC TATTTyATTT AGTTTCATGC GTTTTTCAAA 360

TGTAATGACG CCAGATAwGt TAAAyCAGTT ATCAGCAGTT ATAGAGCATA AAACGTTGTC 420

TACTGGTTTT GT 432

(2) INFORMATION FOR SEQ ID NO: 697:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 782 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697:

CTTTTATACG AAAGTTAAnA TCAAATATAA CATTAATGTT TGATGGGGAT TTTGCGGGTA 60

GTGAmGCAAC ACTTAAAACA GGTCAAAATT TGTTACAGCA AGGGCTAAAT GTATTTGTTA 120

TACAATTGCC ATCAGGCATG GATCCGGATG AATACATTGG TAAGTATGGC AACGATGCAT 180

TTACTGCTTT TGTAAAAAAT GACAAAAAGT CATTTGCACA TTATAAAGTG AGTATATTAA 240

AAGATGAAAT TGCACATAAT GACCTTTCAT ATGAACGTTA TTTGAAAGAA CTAAGTCATG 300

ATATTTCGCT TATGAAATCA TCGATTTTGC AACAAAAGGC TTTAAATGAT GTTGCACCAT 360

TTTTCAATGT TAGTCCTGAG CAATTAGCTA ACGAAATACA ATTCAATCAA GCACCAGCCA 420

ATTATTATCC AGAAGATGAG TATGGCGGTT ACATTGAACC TGAGCCAATT GGTATGGCAC 480

AATTTGACAA TTTGAGCCGT CAAGAAAAAG CGGACnAGCA TTTTTAAAAC ATTTAATGAG 540

AGATAAAGAT ACATTTTTAA ATTATTATGA AAGTGTTGAT AAGGATAACT TCACAAATCA 600

TATCAGTGAT GCTGTGCAGT ATGTTAATTC AAATGAGTTG AGAGAAACAC TAATTAGCTT 720

AGAACAATAT AATTTGAATG ACGAACCATA TGAAAATGAA ATTGATGATT ATGTCAATGT 780

TA 782

(2) INFORMATION FOR SEQ ID NO: 698:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 714 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698:

AAATCATTGG CAAAATATAC GAATTGCATT TAAATCGTCA ATTTACATAT ATTTTTGCGT 60

AGTAATCAAT CGTTATCATT GTTATTTATC GTTACATTAT TTCGAGTATC AGTATGTATT 120

TCGGGCTTCG TTTGATAACG ACATTTCTTT GTGACATCGC TTCATCAGTG TAACAACAAA 180

TACAATGATT TCGTGATGTT AGTTACCCAT TTTATGTGTT GCATAAAATA TGTTGTTATA 240

AAACATTTTA AATCATTTTA TATAAACAAT CTATATATTT TTGGCATTTC CAAAATATCA 300

CTTGTTATAT TAAAAACCGA CAAGACATTT TATCTTATCG GTTGAAATTT GTTATTGTTA 360

TTTGTAATGT TTTTAGGTTT CTTTTTAATA TAATATATTT CAGTGAAAAT ACATGATTGA 420

TTGTGATTTC ACTGAAACAT GGTTAATTGC GTTGTTGATG AATAACTTTA GCATAAATAT 480

AGGAAGTTAT TTTGTACATC GCCATATATA GAAACGAAAT TATAATGACA GCTAGTACGT 540

AACTTGTTAA AAATATATGA TGGTTATTAA TACCTATCAT ATTTAGTAAC GTATATACAA 600

TGTTACTAGA AATTAATGTG TGAATCAGTG CTACTGTTAT TGGTATtGCG AACAAGAAAG 660

TCATTTGATT TCGTGTTATC TTTGCTATTC TTCCATTATC TAAACCAAGT TTTT 714

(2) INFORMATION FOR SEQ ID NO: 699:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699:

ACTGAGAGCA ATAATTTAGT AACTTCTACT CAAGGAATTA TTAAAGAAGC ATTGCATAAA 60

TTGGGATTTG nnTTTAATTA AAGAACCTTT AAGAATGTTA CAAGTGCGTA TCCCTGTACG 120

TGGACCAACA AAAGGGGGCG TGCGTTTCCA CCCAGATGTT GATGAAGAAG AAGTAAAAGC 240

ATTATCAATG TGGATGACTT TGAAATGTGG CATTGTGAAA CTTACCATAC GGTGGTGGTT 300

AAGGGTGGTG ATCGTTTGTG GATCCACGTC AAAnGAGCAT TCCATGAAGT TGGAACGTTT 360

A 361

(2) INFORMATION FOR SEQ ID NO: 700:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 943 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700:

GTCCTTAATT GGTATCCACC TTTAGCACCG CGTACACTTC GAATTAACCC CGCATTTCTT 60

AAAGGACCTA CAAGCTGTTC TAAATATAAA TCACTCAAAT TATTTTCTTC AGCAATTGAC 120

TTTAATGATA TACATCCTTG CCCCTCTTTT TTAGCAAGAG AAATCATCAA TGTAAGTCCA 180

TATCTCCCTT TAGTAGAAAT TTTCATTGTA TAACCTCACT TAATTCGAAT ATTGATATTC 240

CCATTTTAGC ATTTTTTGAG TTAAGATAGT ATAAGAAAGG TGTGACAAAT GTGAGTACAG 300

AACCATTAGC ATCGAGAATG CGCCCAAAAA ATATAGATGA AATCATTTCC CAACAACATT 360

TAGTTGGACC AAGAGGCATT ATCAGAAGAA TGGTTGATAC AAAAAAATTA ACTTCAATGA 420

TTTTTTATGG TCCACCTGGT ATAGGCAAAA CAAGTATTGC CAAAGCAATT TCGGGCAGTA 480

CGCAATATAA ATTCAGACAA TTGAATGCTG TAACTAACAC TAAAAAAGAT ATGCAACTTG 540

TTGTTGAAGA AGCTAAAATG TCTGGTCAAG TTATCTTGTT ATTAGATGAA ATACATCGAC 600

TAGATAAAGC TAAACAAGAC TTTTTATTAC CTCATTTAGA AAATGGCAAA ATCGTCTTGA 660

TCGGTGCTAC AACTTCAAAT CCTTATCATG CTATCAATCC AGCGATTCGT TCAAGAGCGC 720

AAATTTyCGA GTTATATCCT TTAAATGACG AaGATGTGCG CCAAGCGTTA ACTCGTGCAA 780

TAGAAGATGA TGAGAATGGT TTGAAAmCAT ATCaACCCAA AATTGATGAA GATGCCATGA 840

CCTACTTTTC TACACAAAGC CAAGGTGATG TTCGTAGTGC GTTAAATGCA TTGGAATTAG 900

CTGTATTAAG CGCAGATAAT GACAAAGACG GTTATCGACA TGT 943

(2) INFORMATION FOR SEQ ID NO: 701:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701:

CATTAAGTGA AGTTGTTGAT ACACCCATGC ATCAAGTCAA TTGTTCTGTT GATTTAGATA 60

CAGAAAGCTT ATTAGGCTTT AAAACAATTA AAACAAATGC GGAAGGTCAA CAAGAAATTG 120

TCTTTGTAGA TGGTCCAGTT ATTAAAGCTA TGAAAGAGGG GCATATTTTA TATATTGATG 180

AAATAAATAT GGCTAAACCT GAAACATTGC CTGTATTAAA TGGGGTCTTA GATTATCGTC 240

GTCAAATTAC GAATCCATAC ACTGGTGAAG TAATCAAAGC TGTACCAGGA TTTAACGTTA 300

TAGCAGCGAT AAATGAAGGT TATGTTGGtA CTTTGCCAAT GAATGAAGCA CTAAAAAAaT 360

CGCyTTGTTG TTaTTCACGT kGATTATaTT GATGGGGaCA TTTAAAAAAT GTGAnTAAGG 420

AGCAAGGTTT ATTACAAGAT GTTAA 445

(2) INFORMATION FOR SEQ ID NO: 702:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702:

TGCAAGATAA ACAAATTTGT CATTGTTTTG GTTGTAAAAA AGGTGGCAAT GTTTTTCAAT 60

TTACTCAAGA AATTAAAGAC ATATCATTTG TTGAAGCGGT TAAAGAATTA GGTGATAGas 120

TTAATGTTGC TGTAGATATT GAGGCAACAC AATCTAACTC AAATGTTCAA ATTGCTTCkG 180

AyGATTTACA AATGATTGAA ATGCATGAGT TAATACAAGA ATTTTATTAT TACGCTTTAA 240

CAAAGACAGT CGAAGGCGAA CAAGCATTAA CGTACTTACA AGAACGTGGT TTTACAGATG 300

CGCTTATTAA AGAGCGAGGC ATTGGCTTTG CACCCGATAG CTCACATTTT TGTCATGATT 360

TTCTTCAAAA AAAGGGTTAC GATATTGAAT TAGCATATGA AGCCGGATTA TTATCACGTA 420

ACGAAGAAAA TTTCAGTTAT TACGATAGAT TTCGAAATCG TATTATGTTT CCTTTGAAAA 480

ATGCGCAAGG AAGAATTGTT GGATATTCAG GTCGAACATA TACCGGTCAA GAACCAAAAT 540

ACTTAAATAG TCCTGAAACA CCTATCTTTC AAAAAAGAAA GTTGTTATAC AACTTAGATA 600

AAGCGCGTAA ATCAATTAGA AAATTAGATG AAATCGTaTT ACTAGAAGGT TTTATGGATG 660

TTATAAAATC TGATACTGCT GGCTTGAAAA ACGTTGTTGC AACAATGGGT ACACAGTTGT 720

CAGATGAACA TATTACTTTT ATACGAAAGT TA 752

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703:

nCGTTTTTGT nAAACnGCTT ATATGTATAA CTTTTCCCAA TTTATCATAA GTTTTGATAG 60

AAGGAGTTGG ATCGCTAAAG AAAATATCTC TAAAGATATC ATCTTCAATG ATAGGAATAT 120

TATGTCtTTC GCtATAAGTA ATTATATTTT TCTTTTGCTC ATTCGTTAAA GAACGACCTG 180

TCGGGTTATT AAACCTAGGT TCTATATAAA TCGCTTTATT TTTAAAATTA ATAAATCTAT 240

CAATGATGGT ATCAATTTCA TTAATTTGAT TATAAGGAAC ATCAATATGT CTAAAATTCA 300

ATTGCTCAAA AACATTTGTA GAGTGAATAT ATGATGGTGT ATTCGAAATT ATTATGGCAT 360

CTTGACCTAA AAACCCAATA GATAAAAGTT GAATGGCATG TAAAGCGCCT GAAGTGATCA 420

TTACATTTTC TCTACCTACA TTTATACCTT GCTTTGACAT TCGTTCAACG ATAATATCTC 480

TTAACTTGAT ATAACCATAG CCATTATTAT AACCAAAAGA TAAGTCTTCA ATATGACTGG 540

CTGTATTAGA CATGGCTTTT TTCAATTGAA TATGTGGCAT TAACGATATA CCCAATTCAC 600

CTTTACTTAT ATGTATATAC GAATCATCTG TCTCAATTTT ATTAATTAAT TGCACCGTAT 660

ACTGACTTCT TTGTTGAGAG GACCATAACA TCATTTCAGA CCACTTATTT GTAATATGTG 720

CTTCATTCAA ATAGTCATTA ACATATGkTC CACTACCTAC TTTAGTATAG ATAAATCCTT 780

CAGCTTCTAA TAACTCAATA CTTTTAATAA TCGTTACTCT ATTTACGTTG 830

(2) INFORMATION FOR SEQ ID NO: 704:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 659 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704:

AGTGGTGTTG GAAAAGCTAT TATGAAATTA TTACGTGAAC AACAAGTTTA ATAAAAAAAG 60

AGGGGTCAAA TATGAAAGGA TTAATTATTA TTGGCAGTGC ACAAGTGAAT TCACATACAA 120

GTGCACTAGC AAGATACTTA ACTGAGCATT TTAAAACACA TGATATTGAA GCGGAAATAT 180

TCGATTTAGC AGAAAAACCG TTAAATCAAT TAGATTTTTC AGGAACAACA CCGTCTATTG 240

TATTAGGAAC GCCAAACTAT CATGGTTCAT ATTCTGGAAT ATTGAAAAAT GCATTAGATC 360

ATCTAAATAT GGATTATTTT AAAATGAAAC CTGTAGGCTT AATAGGAAAT AGTGGTGGTA 420

TTGTTAGTTC AGAGCCATTG TCACATTTAA GAGTAATCGT CAGAAGTTTA CTAGGCATTG 480

CTGTACCAAC TCAAATAGCA ACACATGATT CTGATTTTGC TAAAAATGAA GATGGTTCAT 540

ATTACTTAAA TGATAGTGAA TTCCAATTAC GAGCAAGATT ATTTGTCGAT CAAATTGTAT 600

CTTTTGTGAA TAATAGTCCA TATGAACATT TAAAATAATA TTAAnAAATA TGTAAATnT 659

(2) INFORMATION FOR SEQ ID NO: 705:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705:

nCACCATATA GTAACTGGCA CCAACTACAT TACCGTCTTT TAAAAAGATT TTTTTATAGT 60

TATTATCAAC ACTATTAAAT ATTTCAATAC CTTTAATTTC TGCATTTTCT ACAATTTGAC 120

CAGCACTATA CAAGTCACAC CCAGAAACTT TTAATGACGT AAATGTTGTT GATCCCTTGT 180

ATCCGTTCGT TTCTTTATTT GTTAAATGAT CAGCTAATAC TTTACCTTGT TCATATAGTG 240

GTGCAACGAG TCCATAAACT TTGCCGTTAT GTCTGCACAT TCACCAACTG CATATACATT 300

GCTATCACTT GTTTGCATCA CATCATTGAC AACAATACCA CGATTACATC TAGACCTGAT 360

CTTGGCACTC CTGGGAAGGC GGAACCACTG CATACAACTA 400

(2) INFORMATION FOR SEQ ID NO: 706:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706:

TTAAAAATAC AGCTACAGGT AATTTTAATG ATTTTTCATC AATATCAAAT TTGGGATTAT 60

GGTGTGGCGC TGTAATACCT TTAACCAGTC AGAAAGAATG CACCTGGTCG TACTTTCAAA 120

TAATGTGAAA AATCTTCTCC AATCATCATT AAATCTGATT CATTAAAGCG TACATGTAAG 180

TCATTTGTTG CTTCTTTAAT AACTTGGATA TGCTTTCTCG TTTATTATGG ACAGGCAAAT 240

GCTTAATCCA TTTTGTCCAT ACATGATTCT GTATATCTGA AATCGAAAGT TCTnACTGTA 360

CCTTTACAAA ATGCCTTGnn 380

(2) INFORMATION FOR SEQ ID NO: 707:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707:

CAnAAAGGAT CAAAGTGATC GGTATAGTGA TAATTAGCTC CAAAGAAAGA ATATTCTAAA 60

TCAAATCCAT ACCAAGCAGA AAGTATTAGC GAATATCAAT TTAAATGGTA CCGATTCAAA 120

TAAAGAAACA CGACATATAG AATTTTTACT TGATGATTTT AGTGAATCAT ATGAACCAGG 180

AGATTGTATA GTAGCATTAC CGCAAAACGA CCCTGAATTG GTTGAAAAAC TAATATCCAT 240

GTTAGGTTGG GATCCGCAAT CTCCGGTGCC AATTAATGAT CATGGTGATA CAGTTCCTAT 300

TGTTGAAGCA CTAACATCAC ATTTTGAATT TACTAAATTA ACATTGCCAT TATTGAAAAA 360

TGCAGATATC TATTTTGACA ATGAAGAATT ATCTGAnCGT 400

(2) INFORMATION FOR SEQ ID NO: 708:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708:

TAATGCTGGT ACGGGTCATG CAGCATTATG TGAGTTGAAC TACACAGTTT TACAACCTGA 60

TGGTTCTATC GACATCGAAA AAGCGAAAGT GATTAACGAA GAGTTTGAGA TTTCAAAACA 120

ATTCTGGGGT CACTTAGTGA AAAGCGGTAG CATCGAGAAC CCAAGAGAAT TTATCAATCC 180

ATTACCACAC ATCAGTTATG TTAGAGGTAA AAACAATGTT AAATTCTTAA AAGATCGTTA 240

CGAAGCGATG AAAGCTTTCC CTATGTTCGA TAATATCGAA TATACTGAAG ACATCGAAGT 300

AATGAAAAAA TGGATTCCAT TGATGATGAA AGGCCGTGAA GATAACCCTG GTATCATGGc 360

GGCAAGTAAA ATTGACGArG GTmCAGATGt AAmCTyCGGT GAATTAACAC GTAAAATGGC 420

TAAAAGCATT GAAGCACATC CAAATGC 447

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: doubl
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709:

GTGTCTACCT GTTTTTGTTG TTCAATTGTT AACTTTTCTT TTTGAATAGT AGTATTCGAT 60

AATTCTTTAT CGCTTATAAA ATCATCTAGT GGATGGCTTT CTTTGAAACT TTTATTTTCA 120

GTCATCAATC ATCTCTCCAA TAGTTGCTAT TTTACATCAA TCTTGATGAT GTTTTTGATG 180

TAACTTATTT AATTCCATTT CAATATCTAA ACGTTCATAA TCATCTTCGT TGAGACGCTT 240

TAAATCAGCG ATTAATGTTC GTTTGACCTC ATCCAAAGTA ATTCGTGTTT GTTCTAACTT 300

TTGCTGTTCA TTAATTGATT TTTTGGGCAT TTTTGCTAGA CGTGTATATG CATCAACCAA 360

ATTTAAAGCA TTATCAATAT GAGAATAAAA AAAGCCTTCA ACTTTATAAA ATGATGCAGG 420

TCTCTGTCTA ACTGTCGTAT AAATAGAACG TGAAATTTGG TATATATCAT TAATCTGCCT 480

AAAATCTTTA ATTGATCTTA TATTGACATA CGTTTTTAAA ATACCTCTAA GTTTTTGGTG 540

TGTATGATTT AACTGATTTC GAATATAGCG ATAGTCTTTT CTAGTCAAAC CAATTTCGTT 600

TAAATATTTG CGTGAAGTGA GTTTTTGTAT CGGTAGGTAT GTCATTAAAA AGCCAACAAT 660

ACCAATAGAC ATATCAATTA AAAAAGATAC ATCAAGTGCA ATCATCCCAA ATATGCTTGT 720

TAAAAACGCT ACAGGAATTC CCACTAACAC CCCAAATATA TGAGAAATAT TATATCTCAC 780

TGTCATCTTC CTTTATTTAG CATTTTATAT TGATCGAAAA TCCGATAATT TTTGATTTAG 840

TTCTAACTCT TCAAGTTGAT GGCTTGTTAC ATTTGATGCT GGTGAGGCAC CTTCAATTAC 900

ACCTTGAATA AATCTCTCTA TATCTGCGTC ATCCCCTTGT GCATATATCT CTACATAGTC 960

ATCTACATTT TGAACAGTAC CGACAATGTT ATAGTTCATT GCAATGCGTT GTGTAAAATA 1020

TCTAAATCCG ACGCCTTGAA CGCGTCCGAA TACTTGTAAA TGTATATGtC TCaTTTTTAC 1080

CACCTCATAA TGTTATTATA CGTAGTTTTA CTTAAAAAAA CTAATAATTA CTATAGTTAC 1140

TACTTTGTTT GTTTCAAGTC GTCAAACTTG ATTTTCAGAG GATAAAGGTA TAAAAATAAG 1200

TATAGAGTTT TTGAAGTATG GAAGGGGTCT TTAATAATGT GGACAGTTAC CAAAATTAGA 1260

GCCGATTATG AGGGATGGTG GTTATTCAGT GACTGGCCAG AAAACATTGT TGAAAAATAT 1320

CAATATCAAG ATTTTGATGA CATGTTTAAG CACTATCAAC AATTGATTAA TCAATGTAAA 1380

GTTCAGTTCG ATAACTATGT CACAGGCAAA TATAATATTT ATGCATTTTA TAATAATTGT 1440

(2) INFORMATION FOR SEQ ID NO: 710:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710:

GCTGnAAAAT ATGTTAGAAG CAGATGCATG GGCAAAGCTG GGGTCCTTAT TTATTGTCAG 60

GTAAAGATGT CTTCAATTCA ACTATTGGAA TATATGGTAT GGGAGATATT GGTAAAGCTT 120

TTGCAAGAAG GTTGCAAGGG TTTAATACTA ATATTCTTTA TCATAATCGA TCAAGACATA 180

AAGATGCAGA GGCGGACTTT AATGCAACAT ATGTTTCTTT TGAAACGTTG TTAGCAGAAA 240

GTGATTTTAT CATCTGTACA GCGCCACTTA CAAAAGAAAC ACATCATAAA TTTAATGCTG 300

AAGCATTTGA ACAAATGAAA AATGATGCAA TTTTTATTAA TATCGGTAGA GGACAAATTG 360

TAGATGAAAC AGCATTAATC GATGCACTAG ACAATAAAGA AATTTTAGCA TGTGGTTTAG 420

ATGTATTAGC AAATGaACCG ATTGATCaTA CACATCCATT aATGGGaCGT GaTAATGtTC 480

TGaTTaCACC aCACATTGGG TAGGCGCATT CAGTTAACn 519

(2) INFORMATION FOR SEQ ID NO: 711:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711:

CTATTACAGG TGGCGAACCA ATGTTTTCTA AAAAGTCTAT TAGAAATGTT GTTAAACCTC 60

TATTAAAGTA TGCACATCAT CGAGGTATAT ATACACAAAT GAATTCAAAC CTAACATTGC 120

CTCAAGATCG TTATTTAGAT ATTGCTGAAT ATATCGATGT TATGCATATC TCACACAACT 180

GGGGAACAAC TGATGAATTC GCAAATGTTG GCTTTGGCGC AATGAAGAAG CAACCACCGT 240

TAAAAGCTAA GTTAAAATTA TATGAACAAA TGATTTCGAA TGCACGTACA TTATCAGAAC 300

AAGGAATGTT TGTATCTGCG GAAACAATGC TCAATCAAAG TACGCTACCA CATTTACGAA 360

AAATACATCA AGAAGTCGTT CATGATATGA AATGTAGCAG ACACGAGATT CACCCTATGT 420

ATCCAGCTGA CTTTGCAAGT CAATTAAATG TGTTAACTCT AGCGGAAATG AAAAAGACAA 480

TGTTTCCATG CTTAAAGGAT GATGAAGATC AAAAGTTACT ATCACGTTTA AGAAATGCTA 600

AAAATGTAAC GACTAGAAAT GACCCGGATG GCCGTAGTCG TTTAAATGTC AATGTATTTA 660

CAGGTAATGT AATCGTAACT GATTTCGGAG ATGAAACAGG TACAATTTCG AATATACAAA 720

AAGATAAATT AACAGATGTA TTTGATAAAT GGTTATCCTC TGATCTTGCT AAATCATTAA 780

ATTGTCATTG TTCCGAGTTT AGTTGTTTAG GGCCAAATGT TCTTGTTAAA AATATGTACT 840

ATCCGAATAT GGATTTTAAA GATAATGAGC GTCATATGCA CAAACAACCA CAAATTATAC 900

AATTTTAAAA ACTCTTAATT ATGCGGAGAA GCACTTTATC GATAAGTAGT CTCCGCATAT 960

TTTAATGCTA TTATAAAATA AAAAACAATT AATTGCTGGC AGTACTCTAC TTAAATAATA 1020

AAGGGCATTT AATAGGACTA ATAGTCTATA ATAAAAGGGG TAAATTTTAA CTAAAAGCAT 1080

AAACGTGCAT AATCAAAAAG ACAGaTTGTA GGTGGAATAT TCGAaCATAA CAGTTCAATT 1140

CATCCTTAAC AATCTGTCTT TATATTTTTA GTCTCTAATA TGTTGCACTT GAGCTAAATA 1200

TTCAATTGTT gTTTACTTtC AaTGCGaCGt GCTTttCTtC GTtCAaCaCG TgwGGTGCTG 1260

TATCATAAAA CCATTTTTCA ACATCATCTT CTGGATATAC ACCAGGTACA TGTTTAGGTT 1320

GCCTTCATCA TCTAACGCAA CAAATGTAA 1349

(2) INFORMATION FOR SEQ ID NO: 712:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712:

GAAATTAAAA AAGCAATTGG ACAAGATGCA ACAGTGTCAT TGTTTGATGA ATTTGATAAA 60

AAATTATACA CTTACGGCGA TAACTGGGGT CGTGGTGGAG AAGTATTATA TCAAGCATTT 120

GGTTTGAAAA TGCAACCAGA ACAACAAAAG TTAACTGCCA AAAnCAGGTn GGCCTGAATG 180

GAACCAGGAG GAAnTTGAAA ATATGCTGGG GATTACATTG TGAGTACAAG TGAAGGTAAA 240

CCTACACCAG GATACGAATC AACAAACATG TGGAAGAATT TGAAAGCTAC TAAAGAAGGA 300

CATATTGTTA AAGTTGATGC TGGTACATAC TGGTACAACG TCCTTATACA TTAGATTTCA 360

TGCGTAAAGA TTTAAAA 377

(2) INFORMATION FOR SEQ ID NO: 713:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 528 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713:

AATGAAnCGA AAAATGACTA TAAAAAGTTT AAAGTGTTTT CACTTATTTC AACACTTGTC 60

ATTGTCATTT TAGCAATTAT AAGATTTGTT CATAAAATGA TGTAATTAGA GTGAGACATT 120

GTTTTATGTC TCAGGATCCA GTTATTCATT ATATCTACAA TATTTACGAT TATATAAATA 180

ACCCGAGATT TTAGTATGAT TCATTtCACT AAAATCTCGG GTTTCTATTT GATAATTTTT 240

AATGGGATAT GGCATGTATA CGTTCTTGCC TTTTATCTCA TTTCCAATGA TTAATCTGGA 300

TATTGTTCTA AAAATGCTTT CGCTTCTTTA TTAACTGTTT TAAAATCAAT ACCTTGTTGC 360

ATCGCTGCAA AGACACATCC ACAATAACAC TGCCTAAAGA TATTATAGTC ATTACACATT 420

TCTATGGaAC GCTCATAACC TTTACTTTTC yTAAAATCAC TTGGcAAATA GTTCACaTCG 480

TATATTTTTT GGACATCCAT ACCAAGTTCA TTGATTAATT GTGCGTTC 528

(2) INFORMATION FOR SEQ ID NO: 714:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 731 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714:

TTTAATGGCA TGAAGTCACA GTATATAAAG AATCTGGTGT GACAATCAGT ATGACTAAGT 60

ATATAAAAAA AGAGCAGGTG cGAAATAATG GCGAAAGAGT CGAAATCAGC TAATGAAATT 120

TCACCTGAGC AAATTAACCA ATGGATTAAA GAACACCAAG AAAATAAGAA TACAGATGCA 180

CAGGATAAGT TAGTTAAACA TTACCAAAAA CTAATTGAGT CATTGGCATA TAAATATTCT 240

AAAGGACAAT CACATCACGA AGATTTAGTT CAAGTTGGTA TGGTTGGTTT AATAGGTGCC 300

ATAAATAGAT TCGATATGTC CTTTGAACGG AAGTTTGAAG CCTTTTTAGT ACCTACTGTA 360

ATCGGTGAAA TCAAAAGATA TCTACGAGAT AAAACTTGGA GTGTACATGT TCCGAGACGT 420

ATTAAAGAAA TTGGGCCAAG AATCAAAAAA GTGAGCGATG AACTAACCGC TGaATTaGaG 480

cGTTcACyTT CTATcAGTGA AATAGCTGAT CGATTAGAAG TCTCAGAAGA AGAAGTGTTA 540

GAAGCAATGG AAATGGGACA AAGTTATAAT GCGTTAAGTG TTGATCATTC CATTGAAGCT 600

GATAAAGATG GTTCAACTGT TACGCTATTA GATATTATGG GGCAACAAGA TGACCnTTAT 660

CGAGAAATCA T 731

(2) INFORMATION FOR SEQ ID NO: 715:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715:

TTTTAGrGGa AAGCGaATTA GtCaTATwCg CaGCAGATwG aATGATTGaA AAmGaAATTG 60

aTTCGATTCC AATTGTAAGA AAAAAAGATA ATCAAAAGTA TGAAGTAATT GGAAGAATTT 120

CCAAAACAAC AATAGCTAAG TTATTAGTAG CATTATATAA AGAATAGGTG AGAAGTAATG 180

GAAAAAATTA AAATTATCGT AGCTTCAGAT TCTATAGGTG AAACGGCAGA GTTAGTTGCT 240

AGGGCAGGTA TTTCACAATT CAATCCTAAG CAATGTAAAA ATGAATTATT AAGATATCCA 300

TATATTGAAT CTTTTGAAGA TGTTGATGAA GTGATTCAAG TTGCAAAAGA TACAAATGCT 360

ATCATTGTTT ATACACTTAT TAAACCTGAA ATGAAGCAAT ATATGAGTGA GAAAGTAGCA 420

GAATTCCAAT TGAAGTCTGT CGATATCATG GGGCCATTAA TGGATTTATT ATCTGCTTCG 480

GTTGAAGAAA AACCTTATAA TGAGCCAGGT ATCGTTCATA GATTAGATGA TGCATATTTC 540

AAGAAAATTG ATGCGATAGA GTTTGCAGTT AAATATGATG ATGGTAAAGA TCCTAAAGGA 600

TTACCTAAAG CTGATATTGT TTTACTTGGT ATTTCGAGAA CTTCAAAGAC ACCATTATCT 660

CAGTATTTAG CGCATAAGAG TTACAAAGTT ATGAATGTAC CGATTGTACC AGAAaGTGAC 720

ACCGCCAGAT GGCTTATATg GATATTAATC CAAAGAAATG TATCGCACTT AAAATAAGTG 780

AAGAnAAATT AAATCGCATT AGAnAAGAGC GACTAAAACA ATTAnGACTA 830

(2) INFORMATION FOR SEQ ID NO: 716:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716:

nGAAGAACAA GTTTAnCATC TAAATGCCCG TTTAAAACTA CAACTACTTG ACGATGTTAA 60

ATCAGTGTTT AAnTCTCAAA TGACGCAAAA TAGTGATTTT AATGAAGAAA AGAAAGTGTC 120

AGAACGTATA AAAAAATACT TTAATAAGCA ACTCACTGAG CAAATTGCAC CAATCGTTCA 240

ACAATTAGCA GATTTACATG TCATTATTAA TCCTCAGTTT AACTTTGAAT CAGCTAATAT 300

AGAGCAACCA TTATTGCACA TCGATTTCAA CGATATGCTA AATGCATTGC CTAAACAATT 360

AACAAAACGT AAAATTTTGA ATCCAAATGG GCAAAGAGAT ATACATGAAT CAATTTGTCA 420

AAGTACGTTA GGATTATTAC AACCACAAAT GGGATTATTG AGGCAACAGC TTGAATTATA 480

TGTAAAGCAA ATGGCTGTAG AAGCTGAATC GCAATTTGAA AGTTTTGAAG CTAATATTCA 540

AACGCAAATA AACGATTTAT TAGCATTTGA TTTAGATACA ACACTTATCA ATCAATTGAA 600

AGATAAACAT CAACAACTGA AAACTATTTT ATATTAAGAa AGAAGGAACG TTTTAAATGC 660

CTAATAAAAT ATTACTTGTA GATGGTATGG CGCTATTATT TAGACATTTC TATGCTACAA 720

GTCTTCATAA ACAATTTATG TACAATTCAC AAGGTGAACC TACAAATGGA ATACAAGGAT 780

TTGTGCGTCA TATCTTTTCG GCAATACATG AAATACGCCC TACACATGTA GCTGTATGTT 840

GGGATATGGG ACAATCAACT TTTAGAAATG ATATGTTTGA tGGTTATAAG CAAAAkCGTT 900

CTGCACCACC AGAAGAATTG ATACCACAAT TTGATTATGT TAAAGAAATT TCAGAGCAAT 960

TTGGCTTTGT AAATATTGGC GTTAAAAACT ATGAAGCGGA TGATGTTATA GGTACATTAG 1020

CACAACAATA TTCAACTGAT AACGATGTCT ATATTATTAC GGGCGACAAA GATTTACTGC 1080

AATGTATTAA TGACAATGTT GAAGTTGGCT AATTAAAAAA GGTTTAACAT TTATAATAGA 1140

TATnCATTAC ATCGTTTTn 1159

(2) INFORMATION FOR SEQ ID NO: 717:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 574 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717:

GATTTAATCA ATGCAGTTGC AGAGCAAGCT GATTTAACTA AAAAAGAAGC TGGTTCAGCA 60

GTAGATGCTG TATTCGAATC AATCCAAAAC TCACTTGCTA AAGGTGAAAA AGTACAATTA 120

ATTGGTTTCG GTAACTTTGA GGTACGTGAA CGTGCTGCAC GTAAAGGTCG TAACCCTCAA 180

ACTGGTAAAG AAATTGATAT CCCAGCAAGT AAAGTTCCAG CATTCAAAGC TGGTAAAGCA 240

TTAAAAGATG CTGTAAAATA ATTTTACTTA AAAAGCCCTG AATAAGGGCT TTTTATTTTG 300

CTTTTAATAC TTACAACCTG TACATAAATT GTAATGTTCT TCTAAGTTTT TAATCTTTGG 360

AACTACAAAA TATACATATG aATATTGaGa TTAATTGTTA GCGTTGaATT TACTTAAAAG 480

GTAACCATGT CTACTATAGT ATTTTACGTT ATTTAAAAAG ATGAATAATG TAAATGAAGT 540

AAAGGTTATT ATGAGAATTA CAAAAGCTAC ATAA 574

(2) INFORMATION FOR SEQ ID NO: 718:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 493 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718:

AAGaTATTGA AAmTGmAaTG GaGCACGCCC TTATTTGATA GAAGTAAAAG ACATTTAATT 60

CTTACCGATG CAGGTCAAAT TTTTTATGAG AAAAGTAAAG AAATTGTtGC ACTGTATGAT 120

TATTTACCAT CTGAAATGGA ACGCTTGAAT GGACTGGAAA CAGGACATAT AAACATGGGC 180

ATGTCGGCAG TCATGAATAT GAAGATTCTT ATCAATATTC TTGGTGCATT CCATCAACAA 240

TATCCAAATG TTACATATAA TTTGATAGAA AATGGCGGTA AAACAATTGA ACAGCAAATT 300

ATCAATGATG AAGTAGATAT AGGCGTGACC ACTTTGCCAG TCGATCATCA TATTTTCGAT 360

TATACTACCC TAGATAAGGA AGATTTGCGA CTTATCGTGA GCAGAGAGCA TCGACTCGCA 420

AAATATGAAA CTGTTAAACT CGAAGATTTA GCAGGTGAAG ACTTCATTTT ATTTAATAAA 480

GACTTTTACT TGA 493

(2) INFORMATION FOR SEQ ID NO: 719:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719:

GCATTGCCAA AACAATACGT TTATATTATT GAGGAACTAC TGTATAAAAG TAATGAATAT 60

CAAAATAAAA AATCATATTA CGAAACACTT GTTAACCAAG TAATTGAACT TAAACAGGCA 120

GATGATTTAA TTATTGGACT CGCTTATTCC GTACAACGCT TAGTCGTCGA TCATTTACAC 180

GTTGTCGGTG ATATTTATGA TCGTGGACCA CAACCAGATA AAATTATGGA TACACTGATT 240

AATTATCATT CCCTAGATAT TCAATGGGGT AATCATGATG TGCTTTGGGT TGGAGCCTAT 300

GATATTATCG AAGACGCTTA TGGCATTAAT TTAAGACCAC TGCTTACTTT AGCTGAAAAA 420

TACTATGACG CAGATAATCC TGCTTTTAAG CCTAAAAAAA GACCTGACAA ACACGAACGT 480

TTAACTCAAC GTGAAGAAAG TCAAATTACT AAAATTCATC AAGCTATTGC GATGATTCAA 540

TTCAAGTTAG AAATACCAAT TATTAAACGT CGTCCAAATT TCGAAATGGA AGAACGTCTT 600

GTGCTTGAAA AGGTTAATTA TGATACAAAT GAAATTACAG TTTATGGTAA TACATACCCA 660

TTGAAAGACA CATGTTTCCA AACTGTCAAT CGTGATAATC CAGCAGAATT ACTACCTGAA 720

GAAGAAGAAG TCATGAATAA ACTATTATTG TCATTCCAAC AATCTGAAAA ATTACGTCGT 780

CATATGTCTT TCTTGATGCG TAAAGGCTCT CTTTACTTAC CATATAATGG CAATTTACTC 840

ATTCATGGTT GTATTCCAGT TGATGAAAAT GGTGAGATGG AATCATTTGA AATTGATGGT 900

CATACTTACA GCGGCCAAGA ATTATTAGAT GTGTTTGAGT ATCATGTCCG TAAATCATTT 960

GATGAAAAAG AAAATACTGA TGACTTATCG ACGGATTTAG TTTGGTATTT ATGGACTGGG 1020

AAATATTCGT CACTATTTGG TAAACGTGCC ATGACTACGT TTGAGCGATA CTTTATTGCA 1080

GATAAAGCTT CTCATAAAGA AGAAAAGAAT CCGTACTATC aTCTTCGTGA AGATGTGaAT 1140

ATGGkTCGTA AAATGCTCaG TGaTTTCGGA TTAAATCCAG ATGAAGGACG CATTATTAAT 1200

GGTCACACAC CAGTGAAAGA AATCAATGGC GAGATCCTAT CAAGGCTGAT GGAAAGA 1257

(2) INFORMATION FOR SEQ ID NO: 720:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720:

TGAGCACATG ACAGTGGCTG AAAACATTAA ATTTTTTAAA TCACTTTGTA AAAATCCAAT 60

TAACGATACA ACTATCAACG AATATTTACA GCAATTAAAC TTTGATGATA CGTCTGCCAA 120

AGTATCTACA TTGTCCGGTG GGAATAAACG TAAAATTAAT ATATTAGTAG GTTTACTAGG 180

TCAACCTCGA ATTCTCATTT TAGATGAACC GACAGTTGGT ATTGATTTAA AATCTAGACA 240

TGACATCCAC CAACTACTTA ACATCATGAA ATCTAAATGT TTAATTATAT TAACTACCCA 300

TCATTTAGAT GAAGTTGAGG CACTTGCAGA TGGTTATCAA GTTAATTGGG CCAGGTnCCC 360

TTTTnTTCAA CAGTTTTTGG GGGCCAACCA TGGGCTTATA 400

(2) INFORMATION FOR SEQ ID NO: 721:

(A) LENGTH: 570 base pairs
(B) TYPE: nucl ic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721:

CTTATTTATA TTATAATATA AATATTTTAT TTTTCAATAC TTAATTTTAA AAATCCCCTA 60

TGAAAATGTT GATGAGCTAC ATCTTTAAAT CTTATTATAC ATTGTATAAA ATTATATTGC 120

GAGGTAGTAA ATTGATATTA TACACTTTTG GTTGTGTATG CATCTCACCT ATCTTTTTTG 180

CTTTTTTCAA ATAAGAAAGT ATTAAAAATy AATGCCTATA CAGGAACAGA CATGGCTAAA 240

CTTGATTTAA ATAGTCTTGA CGACGAGCAC GTAAAATTAT TAATAAATGA ATTAAAATAT 300

CCAGAAACTC ATATCGATGT AAATGAATTA AAAACAATAG TTGCTAGTCG AATAAATGAA 360

AGGCAAGAAA TAATAAGTTT TAAGTTAGGA ATAAAGTACT TATTAACAAT AAAAAGAGGG 420

AACATAGAAA AAGATAGGTT TTCAATTTCA ATCATTTTCA AAGATACCTA TCACACCCTA 480

GTTAGAATAG ATATTAACGG TGGTACTCAC GATAATCCAG ATGGAACAAT CGCTCCGAAA 540

AGTCATATTC ACATATATAA TGATAAGTAT 570

(2) INFORMATION FOR SEQ ID NO: 722:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722:

ATTTTAGTCT TAGGTGTTGA TTGCATGATG AATGCAGAAG TTATACCTGC AGCCATATTA 60

GCACCTTCAT TATTGTGTAT AATTTGAATA TTATTTGCTT TTAAAGTATG TCCAATTAAG 120

TTTGAAGTCG TTGTTTTACC ATTTGTTCCA CTGATAAATA CAATATCATC AACTTGCTCT 180

GCTAATTTTC TTAATATATC TGTATCCACT TTTCTAGCGA TTTGTCCAGG TAAATCTGTT 240

CCTCTTTTAC CTACTGCTCT ACTTGCTTTA CGCGCCAATT TCGCTAGATG GATTGCCGTC 300

CACTGTCTCA TGTGTTTCCT CCtCAAATTt CCACTCGCAT CATTATAACA TGACAAGGCA 360

ACTTCAAAAA AGTTTCTCAA TCACAAATnG ATACCAGTGT 400

(2) INFORMATION FOR SEQ ID NO: 723:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1113 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723:

GATTATATGC TGTTGGCAAA ACAATATACC CAGATGAATT TTTATTTTTA GTAATAGTAT 60

AACCATGCTT TGTCTTACTA ACTTTGACAG CTTCTAATGA ATTTGAAGCG TCTTTAAGCG 120

TGGTATAATC TTCGCCGTAT ATCCCTTTTA AATTTACTCG ATACTTACCT TTAGGCAATG 180

ATAATCTAAT TCTATCTGGA GCTTTAATGC GTATCGTTAC GGGTGTTACA ACGCGTCGAT 240

ATTTATAAGT GAGTTTATTT CTTTCTTGTG TATATTCATT CACTTTAACA TCATGAGCTT 300

TATCCGGCGA AAGTAATTCT AAATCCATTT CAAAATACAA ATCTTTAAAT TGATTAGAAA 360

CTGATTTTGG CAACTGTACA GTTAGACCAC CATTATTTTG TTTAACTTGT AATAAATGTT 420

TTGTAGGAGA TTGCCAGGCT GCACTATTTA ATTTAATTGT TGAATCTGAT AGTAAATTTT 480

TATTGGCTTT AAAATGTGTA TTAACATCTT TAATATTGTT AGAAACAATC CCTTGCAACA 540

TTGCTTGTTC TTTATCTAAT GGAGATTTTA ATTCTTTATT GGAAAAGACC TTATTTGTAA 600

TATGTGCACT TGGATAATGG ATGGTATTTT TAGAATGAAT CCAACGAACT TTATTGTCTT 660

TGTGTTCAGA CTTAATTTTA AATCCATATG GtAAGTTGTC ATCATGATtC ACTCTAATTC 720

GATCATTAAC ATTCCAAAGT GATAGTaAAT TTgACGATgC CAAGTAATCT ATAAGTGCTG 780

TTTTTATCGA TTGGCATATT AATTTGGAGT GTCTTGTCAT AATATTTTAA AATGTCTCCA 840

TTAAAAATAC TAGAATATAA TGAAATGCCA TTATAATGAT ATATAAATGG TGAATTTAAT 900

GCATAGTCTG ACATATAATC AATGCGATTA AATGAGCCTG TTGCATTTTG ATTTATCTTT 960

TTTATAAGCT GGTTTACATA GTTACTATGG TAATCATGTT GTTTCAACGT TGATAATGAT 1020

TGTTGATAAG GTTTGATTGC CATGTTTTTG TTGTTATCTA AAATGACGAT TTGTTGAATC 1080

ATaACGATTA ATACTAATAT TGCAACGGTT AAT 1113

(2) INFORMATION FOR SEQ ID NO: 724:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 464 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724:

TGCCGTTTAG CAAAATCTAG TATCGCTTGA TGATCAGATT CTGAAATTTC AGTGTGTACT 60

GATTGATTAA GTTTATATGC AAGTGCATGT TCTCGTCCAC CAGCACCAAT TACTAATACA 180

TTCATTTATG TTACGCCCCT TTAAAATTAG TGTTTAAAAT GTCGAGTGCC TGTGACTACC 240

ATTGCAATAC CATGTTTATT AGCCATATCA ATTGAATCTT GATCTTTAAT CGAACCACCC 300

GGTTGGATAA TTGCCTTTAT ACCATGTTGT GCTGCAAGTT CAACTGTATC TCCCATAGGG 360

AAAAATCCAT CAGATACTAA CGgCTACATG ATCATTGATT TCAATAGCTC TCTCTAACGC 420

AATTTTAGCA GCACCGACAC GATTCATTGG CCAGCAnCTA TACC 464

(2) INFORMATION FOR SEQ ID NO: 725:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725:

GTTAAATnCA nTATTTnAAA TaTATTACCT TATTAGAAAA AGTCGTAATA TGAGGTGTAC 60

AAATGACGCA AATTTTAATA GTAGAAGATG AACAAAACTT AGCAAGATTT CTTGAATTGG 120

AACTCACACA TGAAAATTAC AATGTGGACA CAGAGTATGA TGGACAAGAC GGTTTAGATA 180

AAGCGCTTAG CCATTACTAT GATTTAATCA TATTAGATTT AATGTTGCCG TCAATTAATG 240

GCTTAGAAAT TTGTCGCAAA ATTAGACAAC AACAATCTAC ACCTATCATT ATAATTACAG 300

CGAAAAGTGA TACGTATGAC AAAGTTGCTG GGCTTGATTA CGGTGCAGAC GATTATATAG 360

TTAAGCCGTT TGATATTGAA GAACTTTTAG CAAGAATTCG TGCAATTTTA CGTCGTCAGC 420

CACAAAAGGA TATTATCGAT GTCAACGGTA TTACAATTGA TAAGAACGCT TTTAAAGTGA 480

CGGTAAATGG CGCAGAAATT GAaTTAACAA AAACAGAGTA TGATTTACTA TATCTTCTAG 540

CTGAAAATAA AAACCATGTT ATGCAACGGG AACAAATTTT AAATCATGTA TGGGGTTATA 600

ATAGTGAAGT AGAAACAAAT GTCGTAGATG TTTATATAAG rTATTTACGA AACAAGTTAA 660

AACCATACGA TCGTGACAAA ATGATTGAAA CAGTTCGTGG CGTTGGGTAT GTGATACGAT 720

GACAAAACGT AAATTGCGCA ATAACTGGAT TATTGTTACC ACGATGATTA CGTTTGTCAC 780

GATATTTTTG TTTTGTTTAA TTATTATTTT TTTCTTGAAA GATACACTGC ATAATAGTGA 840

GCTTGATGAT GCaGAACGAA GCTCaAGCGA TATTAATAAt TTATTTCaTT CTAAgCCTGT 900

TAAAgATATA TCTGCaTTAG ACTTGAATGC aTCTTTAgGT AAtTTTCaAG AGATAATTAT 960

TTATGATGAG CATAATAATA AATTATTTGA GACATCGAAT GATAACACAG TGAGAGTTGA 1020

ATATTTAATT ATTAAAGAAC CAATTACAAC GCAAGATTTC AAAGGGTATA GCTTGTTAAT 1140

TCATTCACTA GAAAATTATG ATAACATCGT AAAATCATTG TATATCATTG CGCTGGCATT 1200

TGGAGTGATT GCAACAATTA TAACTGCCAC AATCAGTTAT GTATTTTCAA CACAAATTAC 1260

TAAACCGCTT GTCAGTTTAT CAAATAAAAT GATTGAGATT CGACGAGATG GTTTTCAAAA 1320

TAAATTGCAA TTAAATACAA ATTATGAAGA AATAGATAAT TTAGCAAATA CGTTTAATGA 1380

GATGATGAGC CAAATTGAAG AATCATTTAA TCAACAAAGA CAATTTGTTG AAGATGCGTC 1440

(2) INFORMATION FOR SEQ ID NO: 726:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726:

TGATATTCCG ACTTGCGAGG ATTATTGCGC ATTAAGGATT AACGCAGTAT GAGTCCAAAG 60

ACGCGCGACA CCTGGAAAAA GGATTACCTA ATGCCTTATT TACAGTAACC TTGTATGATA 120

AAGATCGGTT AATTGGTATG GGTAGAGTGA TTGGCGATGG CGGAACTGTT TTTCAAATTG 180

TTGATATTGC AGTTTTGAAA AGTTACCAAG GTCAAGGTTA CGGCATCTAA TTATGGAGCA 240

TATTATGCAA TATATTAAAG GTGTGGCTGT TGAGAGTACA TACGTTATCT GATTGGCAGA 300

CTACCCAGCG GGnTAAATTA TATACCAAAT TTGGGTTTnA TACCTACCGA ACCAGAnTCC 360

AGGCGGTGAT GTATG 375

(2) INFORMATION FOR SEQ ID NO: 727:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727:

TAAAAAACTT AGAGATGAAA ATCATATTAT TTATCTGTTT TTGGGACAAT TTTTTACTAA 60

AAATGAAGAT CCATGGCATC AAATACTTAA TGATTTAGAA GTTACAAATT CTGTTGATAA 120

TTTTTTAAGG TCAATAAGTA ATAAGGCCAA AGAAACAAAA AAAAGAGCTT TTATTATTAT 180

TGATGCGCTT AATGAAGGTG AAGGTAAAAG GTTATGGGGA AATTATTTTC AAAGCTTTAT 240

AGATGTTATA TTACCCAAAA ACGCAATACA AGATAACAAT ATTGTAGTAT TTCAGCATGA 360

AGGTTTTAGT AAGGAAGAAA ACTATAATCC AATTGTATCT TTTTGTGATT TTTATGGATT 420

AGAGCTACCT AAGTTACCTA TATTAAATCC AGAATTCAAC AATCCATTAT T 471

(2) INFORMATION FOR SEQ ID NO: 728:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1750 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728:

TAGGATGTTC CACCCTgGCA ATTGcTCTAA GACATCtACa GCAGTAGAAT ayCCTGTTTT 60

CGTCtTTTTA ATAACAGGTA ATTGTAATGT CTCAAACAAT ACAACACCTA ATTGCTTAGG 120

AGAATTTATA TTAAAATCTT CACCAGCTGC ATCATGGATA TTTCGAATCA AGACGTCTAA 180

TTTTTCTTGA ATTTCTTTTT CCATTTCTTC TAAATCATGA ACATCTGTAA ATATACCAAT 240

TTCTTCCATT TCACTTAAAA TCTTAGCTAG CGGTAGCTCT AAATCAGCCA AGAGTTCTAC 300

CTGATTGTAT TCTTCTAATT GTTTATCCAT ATTTGGTTTC GCAAAGTAAA TTGCATCAGT 360

AATAGAAGCA ACATATGGAT TTAAAACATC ATCTTCAGGT ACCTTAAATT TCTTACCTTT 420

TCCATATATA CTCACATCGT CTTTCACAAA ACTTTGACCG TACAATGAAA CAACTGATTG 480

AACATCACTA ATCGTACGAG ATGGATCAAT TATATAACTG GCCAACATAA TATCGAAAGA 540

AATATTTTGA ATATCAATCC CCAATCTATG TGATGCTACA TATGTTTTTT TAGCATCATA 600

TACGACTTTT TTCGAATTCG GATTTTCTAA CCATGAAACT AGTTCGACAT AATTATTTAT 660

GTCATCCGCA TTAATTACAA TATGTTTCTC ACCTGtAAAT aAAGAGAATT TTAAAAtATT 720

ATTtCGCAAA TAGtTACCAC CGtCTAATTC GAAATGGATG GCCGCTTCTT TcAATGAAGT 780

AAAATCcAAT ATTATCAAAA GACGTTTCcA ATTTCAAATG TCTTtTCTAT TGCATCTTCA 840

ACGcTtGCTG ATTGaTCAAT GTCAGCCAAC AATTGTTTGA ATTCTAACTT CTTAAACAAT 900

TCGATTTTTT CTTGTTGTTC ATCTtGAkGA GTCATTAACG TATCTTCaAG TTTTACTTCa 960

ATCGGACTAT CTACATTAAt CGTTGCTAAT TCTTTACTCA TTAATGCATC TTCTTTGCTA 1020

TTTTGAAGTT TTTCTTTTAA CTTTTTACCT GAAATTTCAT CTAAATGTTC ATAGACACCT 1080

TCTACTGTGT CAAATTGGTT TAGCAATTTT ATTGCTGTTT TCTCTCCAAC ACCTGCAACA 1140

CCTGGTATAT TATCAGAAGT ATCTCCCATT AATCCTTTCA TATCAATAAT TTGATTAGGT 1200

CCTTTTTTAG TGTAATAAAT GGTTACATTA TCCGTTGCAA GTTGTGTTAA ATCTCGGTCT 1320

CCCGTAATAA TAATTGTCTG AAAGCCCGCT TTATCTGCTT CTTTACTTAA AGTTCCGATA 1380

ATATCATCTG CCTCATAGTT ATCTAATTCA TAACGTTTAA TATGATAAGC ATCTAATAAT 1440

TGGCGAATAT AAGGAAATTG CTCACTTAGT TCAGGCGGCG TTTTCTGGCG TCCACCTTTA 1500

TATTCACTAT ATTTTTCATG TCTGAAAGTC GTTTTACCTG CATCAAACGC TACTAAAAAA 1560

TGATTTGGCT TTTCTTCTTT TAAAATCTTC TCTAGTAACA TTGCAAAACC ATATACTGCA 1620

TTGGTATGAA TGCCTGCTTT GTTTGATAAC AAAGGTAATG CATAAaAAGC TCTAAAACTT 1680

AAGCTATTAC CATCGaTTAA TACTAATTTA TTCACAATTT TAACCTCCAG AACTAATTTA 1740

TATATnTGTG 1750

(2) INFORMATION FOR SEQ ID NO: 729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729:

AAATTAATTT TAACATCCTT TCAAAATAGT TTTAACGGAT CcTCCcAAAA CGTAAACTCA 60

CATCAGTTAC TTGTAACATG CATTTTCTCC TTTTTTTCAT TCGATATTCT AACGGAAGAA 120

TTATATCATA TTATCGTCAC AGTTTCGACC TCATATAAGT TGTAATGATA GAATGACTCA 180

CACATGTTAT AATAATAAAG AATACAAGAA TCGAAGGAGA ATAAACATGG CATTAGACAA 240

AGATATAGTA GGGTCTATAG AATTCCTTGA AGTAGTAGGG TTACCAAGGT CAACTTACCT 300

TTTAAAGGAC CAACGGTGAA ACGTAAAGTT AAACCAATCA GAATGAACGT GATGATTGAA 360

TTAGAAGTAG GGGAGnATAT AGTTCCTCAT TTATCCAACC GGTCAGGTGG ATTATTGCAC 420

TCAAATATGC nGnTATACG 439

(2) INFORMATION FOR SEQ ID NO: 730:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730:

AGTTTAGGAT TGATGACAAA GCCATTACGA CCAACAAATC CTAAACCTGC ACGTTCTGCT 120

ACTGCCCTAT CTGATAATAC ACCCGTATCT ACCATAGATT TGATTTCAAC ATCTGGAACT 180

TTAGATTCAA TAAATGCAGC TAACATGTCT AATCGTTTAC GCATAATTGT ATGATAATCT 240

TGACCCCACG ATGCTCTAGC AAATAAGCCT CTGCGATCAC CTCTAACACT CTTAGGTGCA 300

CCTTTCAGTT TGTTAGGATA ACCAACTGCA ATTGCTATGA TTGACCTTGC TGTTGGTAAG 360

GATAATTTAG GCTCCGTTCG TAAAGCAATA TCAGATTCTT CAAaTCCTGA GGCATAACCA 420

TTTGCATGAT ATGCTTCTAG CTTTTGCTTC AATTCATCAA AGGGnTCGGC AGTAGTAAAT 480

C 481

(2) INFORMATION FOR SEQ ID NO: 731:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731:

GTGATGAAAA ATCTTTTTCT ATTGATTGAG AAAATAGTTA TTTATATAGT TTTTAAAGAA 60

AAAAAGTGAT AATATTTAGC TAATCTAATG AAAATTGATT TATTGGACAA AAAATACATT 120

TTAAATGAGT AGAGGAGGCT GCAAwTGGGT TACAGAACTT TAAAAAGTAT TTTTCATGAA 180

CACAATGAAA GTAAAATGAA GGAAGAGTAT ATTAAAAGAT TTAATTCTTT mGCTTCTTTC 240

AATACTAATA TTAATATCAT ACCTATGGAA AATGGAAAAA AAGTTAATGA TTTGGAATAT 300

CCTCTATTCT TTATGGTGAC TAAAAATCTA TCAAAAAAAC AAGAATTAAT ATCAATTAAT 360

AGTAGAAAAA TTGATAGAGC ACTTAATTCT TTACCATATG CAGCTAGAGA ACAATATTTT 420

AATGATTTAT TAATCGATGA ATTACAAAGT ACTAATGAAA TTGAAAATGT ATTTAGTACT 480

AAACAAGAGA TTGCACATGC GTTAAATAAC CAAGCATCAG AATTTCTTAA GTTCAGAGGC 540

CTCGTGGATC AATATAAAGA GATAGAACTT AATAAAAAAA TTAAAGTTGA TAATGTAAGA 600

GACATTAGAG CGATTTATGA TAAATTAGTT TCAAATGAAA TTAACGAACA AGATAAGTTA 660

GATGGAGAGC TATTTCGTAA AAATTTTGTC GGTGTGCATG ATGGGTCAAC GAATAAATAT 720

ATACATGTTG GGTTACAACC TGAAACCAAA ATTGTTGAAT TTATAGGTGA AATGCTAACA 780

TTTTTAAAAT ATTTTGATGC GCCTCAGCCG TTCAAAATCA TGGCTAGT 828

(2) INFORMATION FOR SEQ ID NO: 732:

(A) LENGTH: 1622 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732:

CGTATGTTTC GAATTTTATG nATTGCATTG GATAATAGTA CCAGTTAAAA GAACTAAGAT 60

TGTAATTATC CCCCCTTAAA ATTCAAGAAT ATATTTTCTT AATCTATCAG CAAGAGGTTA 120

TATTTCAAAG TGTTTATTTT TAAAACAACA TCTAAAAGCC ATTTcATAAt AAwGTTAAAT 180

CaTTAGaATG TATAAAGATT CCaATTAATA AAAATAGATA AAATGCAATA AAGTTCCAAA 240

TACTTATTAT TATTCATCAC AAATTACGTG ATGCCCTCTA CAACACTAAA TCAAGGATGA 300

TATTTATTTT ATATACATTA GCATTCATTG TTTGCTTACC CACATTATCC TGTTTAGTCT 360

TTTTTATAAC TCTAGTCTTG AATGTCATAT TTACAAAGAA AAAAACACTA AAATATTTAA 420

AACTAACACT ATTTATTCAC TTTGTTCTTT TATAGCACCT TTTATGTTTA TTTTCTTGTA 480

TTCAATAAAT AGTATGGAGA TGATAATTTA AAGTAGATAT ATTTGAAGTA TACTATAGAG 540

TAAATTATAT TGGGGAAATA TGTAAACGAA CCGGTTGATT TTATAGTGGA TTAACACTTC 600

ATAGAGAATA TAATCAAGAA CAAAAACAGT CAATAGGTGT GAATTTTTTT AAAGACGGAT 660

CTGTTGCTAC TAAAAAAAGA AGTATACAAT TCAATAGTTA AACCTTAAAA CAAGAAATAT 720

TATTCAAAAT CAATGAATTT CCTATCTTAT TAGTTTTAAC AATATTTATT CTCATAGAGT 780

TTGTCCAATT AAATATAGAT GATTCAAATA TTTATAAGCA TACAAAAGAG CAGTAAGACA 840

TTTTCTAATA GAAAATAACT TTACTGCTCT TTGTACATTA CTCATCAACT ATTGTAAATT 900

AAATAATAAA TAACTACCTA TTTTATTATT CAGCTAAAAA ATGCTCTGCT AAATATTTTG 960

CTGCGCCATC CTCTTCATTC GTGTATGCCG TTACATCTGA AGTTAATGCT TGGATTTCAG 1020

GGCGTGCATT TTTCATAGCA ACTGTATAAT GACCAAATTC AAACATTGCT CTATCATTGT 1080

CGCTATCTCC AATAACTAAC GTTTCTTCTT GATGAATACC AAAATGTGCA ATCATTTCTT 1140

TAATGCCTGT ACCTTTATCA GTTTGATAAG CCATTGTTTC CGCATTAAAT CTTGATGAAT 1200

TTGArACACT AATCTGTAGT TGCACATGAT TTTGCTTTAA TTCATCTCTA AATGCTGTTA 1260

TTTTTTCTAA ATTAGAACTG AATAGATAAA TTTTTGAATA TTCACCTTCA GGAAACTTAG 1320

TTACCCAATC TATCTTACCA GCAAGCGCAT CTTGTCTTGA AGACCATTCA CTATGACTTA 1380

CGCCATTAAT AGGATCTTGA CTACGAATCA TATCTCGCAT CCATGTTTCA TCTTCTTTTA 1440

AAGAAACTCT ATTACCTTCA AAAGGAAATA CCTCATAATA AATTTGTTGG CGCTTAGCTA 1500

CTACTTCTCC AATTGTTCCA TTTGAACTAA TGATGCCATT AACCGCAAAA TCTTGAGGTA 1620

CA 1622

(2) INFORMATION FOR SEQ ID NO: 733:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733:

AATGCCAnAT AAATCCAAAT TCTTTTAACG AACAAGAGTG CCCAAGTTAT TGCTGATCGT 60

TATGCCAGAT AnGCATATCA ATGATAATTA TGGTTTAGAA AGAATTTCTA AGACAAATCA 120

TGGATATAAT TATGTGTATT CCAATGATAA TTCAACTAGT AAGCAACATG TAAGTATTTC 180

AAATCAAGGC ATAATAACGA AATAATAGAT GGAACAGTGT ATTCTAATTG GATATACTGT 240

TTTTATTTTG CAATAATTTA ATTTAAAAAG GTGAATTCAA CTTATAAAAT GATGTAAATG 300

TTATGTCAAA ATCAACCAAT CCGTAATGTA TTTTAAAATG TTAATATAGT TCTGAAGAAG 360

TATAAATGAG GTGTTGAAAT GGCTAAAAAT AAGAAAACgA ACGCGATGCG TATGCTTGAT 420

CGTGCAAAAA TTAAATACGA AGTTCATAGC TTTGAGGTAC nTTAAGAACA TT 472

(2) INFORMATION FOR SEQ ID NO: 734:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734:

CATAGCCCCA AATTTTTTCT ATTATTTGTT CACGAGTAAA GATTTGCTTA GGACGTGCTG 60

CAAGCATAAA TAATAATTGA AATTCCTTGT TCGGTAACGT CATCGTTTTA TTAGATACTT 120

GGAGTTCCAA ATAGGATTGG TTTAGCGTTA AGTTGCCAAT AGTCATTTCT GAATTTGAAT 180

TGATATTATA TCGACGTAAT ACAGCACGAA TTCTAAAAAT AAGTTCCTTA ACCTCAAAGG 240

GTTTGGTTAC ATAATCGTCA GTACCGCTTA TAAACGCACG CTCTTTGTCA CTAAGTGCAT 300

CCCGCGCTGT TAACATAATA ACTGGTATAT CATAATCATT TTTTAATGTA TTACATAATT 360

GAAAGCCGTC CATACCATCC ATCATAATAT CTACCACTGc AATATCGaCA CGCTGTTTTT 420

GTTTTGTnAA ATGGGCTAGC TATAATAATT TAGGGGATT 519

(2) INFORMATION FOR SEQ ID NO: 735:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735:

ACTTGAAAAC GATAAACAGT ACTTTCCAGC TACACATTGG AAAGCTATAA ATGGGATACC 60

TTATGCAGGC AGTAGTGATA TTGATGGATT GCCTCAAGAC GGTATCATTT CGGTAAATGA 120

TAAAAATAAA TTAGATAATT TAAAAATAGG CGAACAGGAA TTATTCAAAA TAGCATTGTA 180

CAGAAATCCC CAAACGGTAA ATTGTGGAAA ATAACAGTTG ACGATAGTGG GAAACTTGGT 240

ACAGTGCTAT TTTATTAGAA AGGAAGGTGC ATTATGGAAA ATTTGTATTT AATAAAGGAT 300

TTGGGAGCTT TAGCAGGTCG AGATTATAGA GCTAAGGAAA TACAAAACTT ACAAGGAATA 360

GGCATTGCGC TGGGCTGACC ACCAGGGTTT AnGTGnCCnC 400

(2) INFORMATION FOR SEQ ID NO: 736:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736:

CTTTTTTATT GAAAAAGTGG TATTTGATTA TCTATTTACT ATTTATATTA GCGGCACTCC 60

TTATTACATT AACGACAATC CAACATGTAA CAGAAGATGA CAATCATnTT AATATAGGTG 120

TCGTAGATAA AGATCAATCA AGTGAAACGA AATTAATCTT AAACTCTATT GGTAAAGGGA 180

GTAACCTAGG AAAAAACGTG AGCATTAAAG CATATGATGA TAAGCAAGCA CATACTTTGT 240

TAAAAAAACA TAAACTTCAA GGCTATTTTG TTTTTGATAA AGGTATGACC AAGGCATTTT 300

ATAAACAAGG CGAACTACCA ATTTCAGTAT ATACATATGA TCAACAATCC ATGAAAAGTG 360

TCGTGCTATC TCAGCTAACA GATTCTGTTT ACCAACGTCT TATGCGATCA ATGGGTGGCA 420

TCTTAGCTTT TCAAGACTTA GCACCGAAAG CATCACATTC TGACAGTATC AATGTTATGA 480

CTGATTTGCT GATtACAGGA TTAAACCGTT CAGGTGCAtT TAACTTAGAA CCGATTCATT 540

CACTATCTTT ATTTACAGTT TTGAAAATGA ATCAAGATAC TGTATTGAAA GCGCGATTGA 660

AAATGTTTCA TTTTTCTAAA GAGCGTTTAT TAATCATTCG TACGTTGATT ACATGGTTTT 720

ATACTATGTT ATGGGnGTAT CGnTGGTGTA GTTTGGAATG TGGTTCAGTA TTCCGAATnA 780

(2) INFORMATION FOR SEQ ID NO: 737:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 946 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737:

TATTTAATTT CTTnATTnTG GTTTTTAATT nTAAGATGAC CATAAATGAA TTTCTTCTGC 60

TGTCATAGAA TTAGAGCAAA ATACGAGCAT AAATTTAACT AATTTCTTGC TTGTCTTATA 120

GTCTTGATTG CCTTGTAAAA ATGTTAGTAT TAATTGCTTC ATCGTTTCGA ATTGTTGTGT 180

TGATTTAATA GCGATTGCTA AACCTATATT TTTTTCGAAA AGCTTTTCAA AACATCTATT 240

TAACAGGTTG TAATTCGTTT GGCTAATCTC AATATCGTGA ATATCGTCAA TGAAAACGAC 300

AGGTTTTGGT AAGTGCTCAA AGTTAATATC GTAATATTCA TTGAAAAtAA ATTGAAATAG 360

TTCATTGAAA TTACTAAATC GAACAAATAC TTTGGCACGC TGACTTCGAT CTTTCGGATT 420

AAAATCATCT ATATGAATAT CTGTTGTATT TGTAGCCAGT TGAGCTGTTA AATCAATTGT 480

TGAAATTAAC TCAGTGAATT GTGATACGTT ATCTTGTTGG AAGTGTATTT GTGGTGGTTC 540

AGTAATCTTG GAAACGAGTG AACGGAACTG TTTAGGACTA AAATGCAAGT AATTCTTAAA 600

TTGATTTGCA AAATTTGTAT GACTGTTAAA ACCGGCCAAT TCAGAAACAG TTGTAATAGA 660

ATGTTTTGTA GAAAGTAATA AATTGATGGC GTTAACAAGT TTAATACTTG TAAAATAATC 720

TTTAAAATTC ATACTCAAAT ATCGAACAAA AAGATTAGAA CAATATGATT CAGAGATGTT 780

GCAATGCATC GCTATATCTT TTAAAGACAA GTGCGCATCA ATATkGTCAT GAATATAGTT 840

TACACAGTCT ATGAACACCG GATTGCTTAA AGCAATATTT GGTAAATATT CATGATCTAT 900

TCTTATAAAA GCTTCTTTAA GTAAAGTGTC TATnATACTT TGACCT 946

(2) INFORMATION FOR SEQ ID NO: 738:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738:

TTTATTTGAT GATGTACTAA AGCAAGATGA AAGATTTGTT ATTGTAGTTC AAGCATTAGA 60

AGAAAAGAAC GGACAATTAT TAAAGAGAAC TTTAAGGGAA TATCCCGGTT TAAACCATAA 120

ACAAATGAAT GATTTATTTA TGCACTTAAA GGAATTATTT TCCGAAGAAT CATTTGCTGA 180

AAACCAATCA GCGTTCAGTA TTACAGTTTA TACAAATTTA GATTATACTG CTGACCAAAT 240

ATATGCTCAT GTAAAACGTT TCAGAGGTAA GCATGACTGG ACACAAACAG CTAAATAAAA 300

TCAAGATGCT TGCAGTGgAT TkTAACmATT AATGtTAGaT gTCmCyGcAT TTTTaATGCC 360

ATTCGGTAAT TAATCCGGAT GGTCCAATTT AATTAAC 397

(2) INFORMATION FOR SEQ ID NO: 739:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739:

CAAGGTATTT CATTTGACCC ATTCACACCA TTAATAGTGG CAGCAGCATT ATACTTTGTC 60

TTAACATTTG TACTTACACG CATTATGAAC ATGATTGAAG GGAGATTGAA TGCCAGTGAT 120

TAAAATAAAC AATCTTAATA AAGTTTTTGG AGATAATGAA GTTTTAAAAs ATATCAATCT 180

TGAAATCAAT CAAGGGGAAG TAGTAGCAAT AATAGGTCCA TCTGGTAGTG GTAAAAGTAC 240

ATTGTTAAGA TGTATGAATT TATTAGAAGT ACCTACTAAA GGTCAAGTGA TTTTTGAAGG 300

CAATGACTTA ACGGAAAAAG GGACACAAGT AGATAAACTA CGTCAAAAAA TGGGTATGGT 360

ATTTCAAAAC TTCAACCTAT TTCCACATAA AAAAGTTGTC GATAATATTA TTTTAGCTCC 420

TAAATTATTA AAGAAAGATA ATAACGATGA ATTACATAAG GAAGCATTGT CGTTATTAGA 480

TAAAGTGGGA TTAAAAGAAA AAGCAGATGT ATATCCGAAT CAATTATCAG GTGGTCAAAA 540

ACAAAGGGTA GCAATTGCAA GAGCTTTAGC AATGCATCCA GATGTTATTT TATTCGATGA 600

ACCAACTTCA GCATTAGATC CTGAGGTAGT TGGTGATGTA TTAAAAGTAA TGAAAGACCT 660

AGCCAAAGAA GGTATGACCA TGGTGGTTGT GACACATGAA ATGGGATTTG CCAAAGATGT 720

AAGTGACAAA GTCATATTTA TGGCAGATGG CGTTGTCGTA GAGTCAGGCA CnCCAGTCGA 780

AATATTTGAA CAACCGCAAC ATGAAAGAAC ACAAAATTTC TTAGCAAGAG TATTATAACA 840

ACCTAACGAG GCTTGAATAT ATGATACGCA CCACAAAGTT ATATCATATA TTCAAGCTTT 900

(2) INFORMATION FOR SEQ ID NO: 740:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740:

AGTAAATGCG ATGTTGCATG GAGGCTATAG CAATGAGCAA TAAAGCTTGG GGCGGTAGAT 60

TTGAAGTACA ACCTGAAGAG TGGGTTGACG ACTTTAACGC ATCCATTACT TTTGATCAAA 120

CGCTCATAGA TCAAGATATC GAAGGCAGCA TTGCACATGC AACTATGCTT GCGAATCAAG 180

GCATTATTAG TCAACAAGAC AGCGAACAAA TTATACAAGG ACTAAAATCT ATTCAACATG 240

ATTATCATCA AGATCAAATT CAATTTAGTG CATCATTAGA AGATATTCAT TTAAATATTG 300

AACATGgAAT TAATTAAACG TATCGGTGgA TGCTGGTGGT AAGTTGCATA CTGGACGCgT 360

AGtAAACGAT CAAGTTGcAA CAGACATGCA CTTGTACACT GAAGAAACAA GTGCAAGnnn 420

TCATCGCATT GGATG 435

(2) INFORMATION FOR SEQ ID NO: 741:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741:

AATATCATAA CCAAAGCTTG TCATTACTTA TATGTAAAGA TTAGAGGCTA ATTACATAAT 60

CCTAACTTAT TTAACAGGAA GTCATGAAAA CTATATTACA ACTAAAAGTA TAACTTTCCA 120

TCACCAAAGT CAGAATTTAT TGAAACACTC AACTGATAAT ATAGAAGGCT AATTATAAAA 180

ATACCTGGCG ATTAATAAAC TGTTTCCGTT TTTTAGCACT TAATATATTT AAAAAGACAA 240

ATAGAGCCCT TTCAGGCTCT ATTTnCTGTA TCCTTAACAA CAGAAGCTGT TAAAACTACC 300

CGTCTTTTCa CAaCCAAaGc TaCAAAAaaG aTgGCTAGTT ATTCTTTCGT CACCCGCTGA 360

ATCATTAGTG TTGTTATTTC CTTTAACTTG CACGTCTAAA TCAAGAaCTT TTTCCAAaGA 420

TaAAACCCCC TATTTAAAAG TTGAAGTTAA GACCCcTTCA ATTGTCATAT TAATCATTAC 480

CACACAATAA ATCAATGAAT TTAATAATAA TTATTTGTTA TTAATTTGTA AATCGTCATT 540

TGAATATTTT TTGTTTAACT CTTAAATTTC GGGTTTAACT TCCTCTATTT CTAACAGTTA 660

TACTCCAGGA TTAGTTTCTT TAGAATCCGT ACCGATTAAT TTAACAGTAT GGTTTTGCCA 720

GTCAACTTCA TAAGTAGATG TAAACGTTAC TGTATTTTGA TnTTTGTAGT TATTTCCAAC 780

CCAGTGTAGT CGATTCCATT GATTAGTATA TCTATCCATT TCTCTTTGGT AAGTTACTTT 840

GATTTTAGAT TtTTTTGTAT CATTTTGTTT ATGAGAAAGT ACGCTTATAA ATTCTGGGTT 900

AAAGTTACCA CGCGCCAATA AAGGCATTTG ATGTGTTGGC AAGAAATTTT GACCAGCATT 960

TGAACTACTT TGTCTACCAC CTAAAAACAG TTCATTACCA TATGTTGGGT CATAACTATC 1020

TCTACCATAT GGTCCCCAAC CATTATTCAT AATTTTGTGC GCCTCAACAC CCCAGCCAAT 1080

TGATTTATGA TTTGTTTTTC TATCAATCGT AGTTCTGTAA CTTTCTTGTT TATAATTTAT 1140

CGTTTCTGAA AATGATTTTG ATCCATTTAA TCCACCTGAT AAGCCATTAG ATATATTA 1198

(2) INFORMATION FOR SEQ ID NO: 742:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742:

GTGGCATATn CAAACTACTA CTGAAAGATC AATTACATAC GTACAGATTT TGCAAAATGA 60

TCAAGATTAT CCAACAATTT TTAGATGAGa CAAAACGTAA ATCTGTAATT AATTcAGATG 120

TTAATGTAAC GGTAAAAGAT AGAATAATGA CTTTATcAAC GTGCGAAGAT GCATATAGTG 180

AAACGACGAA AAGAATTGtT GTTGTCGCAA AAATAATTAA GGTAAGTTAA ACAGAAAmGA 240

GGATAATTAT GAAATTTATG GCAGAAAATA GGCTGACGTT AACaAAAGGA ACAGCAAAAG 300

ATATTATAGA ACGATTTTAC ACGAGACATG GGATTGAAAC ATTAGAAGGC TTTGATGGCA 360

TGTTTGTTAC ACAAACTTTA GAACAAGAAG ATTTTGATGA AGTGAAAATT TTAACAGTTT 420

GGAAATCAAA GCAAGCTTTT ACGGATTGGT TAAAATCTGA TGTCTTTAAA GCAGCGCATA 480

AACATGTTAG AAGTAAAAAT GAAGATGAAA GTAGCCCGAT TATAAATAAC AAAGTAATTA 540

CATATGATAT AGGCTATAGT TACATGAAAT AATTGAATTT AAAGAGGTTG CAGTACTTGT 600

TATGACAATT GGTATTGTTA GCTTTTGTAA CGACCATACA TGATACCGAT GATGGTCGTT 660

TTTTTAATGa ACACAAACAT GCTAACAACA AATTGCTAAA ACATAGTTTG aTTTGAATGT 720

GgCTTTGGAA AATAATCATC CAtTATATCa TTtTGGATTn TATTTTGGAA GAAGAAAAGA 780

(2) INFORMATION FOR SEQ ID NO: 743:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743:

TGCTGGTAAA TCTTCCCTTA TCAAGTCTTT AATTGGTGAA TTTAATGCTA CCGGTACTAA 60

ATTGTTATAT AACAAACCTA TACAACAACA ACTGCAACAT ATTACATATA TTCCACAAAA 120

AGCACATATT GATTTAGATT TTCCTATAAG TGTGGAACAA GTGATTTTAT CAGGTTGCTA 180

CAAAGAAATT GGATGGTTTA GACGACCTAA TAAATCAGCA AGGGATAAAC TCAAACAGTT 240

ATTAAGCGAT TTAGAATTAG AATCTTTACG TCATCGACAA ATTTCAGAAT TAAGTGGTGG 300

ACAATTACAA CGTGTGCTAG TAGCAAGAGC ATTGATGTCC GnAAGTGAAG TTTATTTTCT 360

AGATGAGCCG TTTGTCGGAA TTGATTTTAG TAGCGAAAAA tTAATCATGA CAAAAATcGA 420

GAACTTAAaA CAACAAGGAA AACTTATTcT TATCATCCAC CATGATCTAT CAAAAGCAAA 480

GCAATACTTT GATCGCATTA TTCTATTAAA TCAAACATTA CGATACTTTG GTGATAGTGA 540

AGAGGCTATG AGTGTCACTC GCTTAAACGA AACATTTATG AGTAGCACTG ACTGTAGTGA 600

CCCTAGTCAA AGGAGCAATA TAACATGTTA GAGTTTGTCG AACATTTATT TACATATCAA 660

TTCTTGAATC GAGCATTGAT AACTTCAATT ATTGTAGGGA TAGTTTGTGG TACAGTTGGT 720

AGTTTAATTG TATTACGTGG TCTTTCATTA ATGGGAGATG CAATGAGTCA CGCAGTATTA 780

CCTGGTGTTG CCCTATCATT CTTATTTGGT ATTCCAATGT TTGTAGGCGC ACTTATAACT 840

GGTATGATCG CAAGTATTTT TATCGGTTAT ATCACATCTA GTAGTAAAAC GAAACCTGAC 900

GCCGCTATTG GAATTAGTTT TACCGCTTTC TTAGCTTCGG GGATTATTAT TATTAGCTTA 960

ATAAACACTA CGACAGATTT GTACCATATT CTGTTTGGTA ATTTACTGGC AATCACAAAT 1020

AGTGCATTTT TAACAACTAT TGTGATTGGT TCAATCGTCC TTATTCTAAT CATTATTTTC 1080

TATCGTCCAT TAATGATTTC TACATTCGAT CCAACGTTTA GTAGAATGAG TGGTCTAAAT 1140

ACGACGTTAT TACATTACTT TGTGATGTTG tTACTCTCAT TAGnAACAGT AGCAAGTAtT 1200

CmAACGGTA 1209

(2) INFORMATION FOR SEQ ID NO: 744:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 675 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744:

CCGCCTTTCG TAAACCTAAT ATAATACGAA ATTTTCGTAT TGTCAACATT AAATACGTTT 60
TTTTCGTAAA AAACTTTACT ATGATATGAA AATTTCGTAT AATAAGAAAA AAGGAGGTAA 120
GTAATATGAA CAAAGAmAGm AATATTATTA TAGCCAAAAm CATTAGAAAA TTTCTCAACG 180
ATTCAAATAT GTCTCAAAAG AAACTTGCTG AaCTCATTAA CATAAAACCA TCTACTTTAA 240
GCGATTATTT AAATTTACGT TCCAACCCCT CTCACGGCGT TATACAAAGG ATAGCTGATG 300
TTTTCGAGGT TGGTAAAAGC GACATAGATA CTACATACAA AGACGATAAC GACATCACTT 360
CCATATACAA CAAACTCACA CCTCCCCGCC AAGAAAACGT ACTTAACTAT GCAAATGAAC 420
AATTGGAAGA ACAGAATTCT AAAGGAGATA ACGTTGTAGA TATTAATTCA TATAAACAGG 480
AGAAAACTCC AGTTAACGTC AATGGTTGCG TCTCTGCTGG TGTAGGAGAA CGTTTACACG 540
ATGAAACGCT ATTTACTGAA ATGGTTAAAG GACCTATCCC CACACACGAT TTAGCGTTAA 600
AAGTAAATGG TGATTCTATG GrACCTATGT TTAAAGATGG CGAAATCATA TTTGTGGAGA 660
AAACTCACAA TnTGA 675

(2) INFORMATION FOR SEQ ID NO: 745:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 924 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745:

CAGGTGTCAT AGTTGAACTT GGtGGTTTTG GACTAATCGT TAAATCATCA ATTTGTGTCA 60
TCCAAGGTTG GAATTTACTG CCTTGTGTCT CCAGTGCGCT GAAAATACCT TTATCTTGAA 120
ATAAGTCAAC TAACTCTTGG ATACCTTTAA TTAATGCTGG GTTACCACCA GAAATTGTAA 180
CGTGGTTAAA TAAATCGCCA CCAATTCGTT TTAATTCATC ATAAATTTCT TCAGCGGTCA 240
TGAGTTTTAT ATCGCCTTTA GCACTACCAT CCCAAGTAAA TGCAGAATCA CACCAGCTAC 300
AGgATaATCA CATCCAGCTG TTCTCACAAA CATCGTTTTT CTACCGATTA CTCGACCTTC 360
ACCCTGAATG GTTGGACCGA ATATTTCGAG TACAGGAATT TTAGCCATTA GTTACACCTG 420
TTCCTTTGGT CTAAATACGA CATAACTTGT TGGTGTTTCT CTTACAAATA CTTGAATACA 480

TACGATTTCA GTTGAAGGGA TTTTGTTTTT AAAAGCAGGT AAGTTATTTA ACAGTTGATG 600

GTCAAATTTA CCGTGTATCA TCTTTTTCAA ATGGCTAAAG TTCACTAAGA AGCCAGTGTC 660

ATCTAGTTTA TCACCGACAA TTGTTAAaya cAAAGTAAGT ATGACCATGG ACATTTTGAC 720

AAATACCTGC TTCTTCACAT GGAATGTGAT GTGCAGCCGA AAAATTAAAA TCTTTATTTA 780

ATTCGAATTG ATATGGATGC GTTGTACTAG GATAGATTTG TTGTAACATT TTAAAGCGCT 840

CCTTTACTTT CAAGATATTG ATTTAGTCCA CGTTGACGTA AATGACAAGC TGGACATTCA 900

CCACAGCCAT CCCCAATGAT ACCG 924

(2) INFORMATION FOR SEQ ID NO: 746:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 971 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746:

ATCTTTTGGG TATTTTCTAT ATTAGCTGTT GTTTTCTTAG TATTATTTAG TTTTGCTGTT 60

GGTGCATCAA ATGTACCAAT GATGATTTTA ACATTTATAT TACTCGTTGC AACCTTTGGA 120

ATTGGATTTA CTACAAAGAA AAAATATCGA GAAAACGATT GGCTATAAGT TATATCGACA 180

ATAACACGCG TTGATTTAAG ACCACACATG TTCATGATGA ACATTTAACT GGTTTTATAT 240

TGGCGCGTGT TTTTATTATT TAAGGTATAA AAGCGTAATA TGTTACCTAA TTGTTAGGAC 300

TACATATTAC GCTTTTGGTA ATTATTTTGA TTTTCTTTTA AATCGTTGTT CATGTAATTG 360

TATTAACGCA TCATGGTGGG GCTCTAAaTA ATCATtGCTA ATTcTTGATG GAGACCmCGA 420

TTtCCAACTA rGATkGAATT kGGACCmCTA ATkGTTAATG GTcctCCTAG TAAATTGGAA 480

GCTTGTCCAT TaCTTCcATA TAAAtAACCA ATCCGCCAGC AAAtCCCcAT GGTkGAAGTC 540

TTGGCGTCAT ATATGCTTCT AAaTTACCTG TAGCAACTGA AACGATTTCA AGCGCTGCAC 600

TACCATATGC CCTTGCACTT CTAGAATCAT TAACAATTTC TTTAAAGATT TCTCCTAAAA 660

TTGGTTTAGT TAACCAGTTC GGATTGATCC CAATAATGCT TTGTCTTAGA TTAGAATCAT 720

TCAATGGTTT CAAGGGTTGG CTACCACGAT ATGCACCTTC CCCTACTTTA GCATGATATA 780

AGACATCAGC CATAACATCA TATACAAAAC CTGCATAAGG TTTACCATCG ATATAAATAC 840

CAATTGAAAT TGCGAAATTT TCTTGTTGAT GAACAAAATT CAATGTACCG TCTATTGGGT 900

CAACAATCCA TACCGTACCT TTGGAAGTAT CGATGTCATG ACCATGCCCT TCTTCACCTA 960

(2) INFORMATION FOR SEQ ID NO: 747:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 865 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747:

TTCTCGTCAC TGTACGTTGT ATTGCGGCAT CATCCATTAT GATACGTTCA GACATATTCT 60

CACCCTTTCA AAATTTAGAA ACAAAAAACC TCATGTCTTT AATATCGACA TGAGGTTTAG 120

TATATACAAT CAGCCTATTT ACATAGAAGA ATCGTAGTAT TACTACTTAT TCTTGCATAT 180

GTGAAAGTGT TATGATCATT TTAGTATATA TCTATATTTT CATGTCTTTG ACGTCTCTCT 240

GGACGCTCAA TTAAAGACTC TTTATGTTGT ACTTAAACTG TTATAAGGAT AATACTAATC 300

AGGCGCTTTG TCAATCTATA TTGAAAAATT AACCATACTC AGTAAAAATG TTAACCTTAA 360

TCTATTTTAT AATGTGTTTT CATTTAAAAA AAACGAAAAC GATAAACACT TATAGTTTAC 420

ATAATAATGT TATCGTAATT ATAGCACGAC ACAATTATGC ATCTCTTTTT CGAATTGTAT 480

CTAATAAATC TTCAAAGTCT TGTGGTAATT CAGCATGTCT TTCAATATAT TCACCTGTTA 540

CTGGATGTTC GAATCCAATA AGTCCAGCAT GTAGAGCTTG ACCACCAATA TCCAATGTCT 600

TTTTCGGTCC ATACTTTGGA TCACCAACTA ATGGGAAGCC AATATATTTC ATGTGAACAC 660

GGATTTGaTG CGTACGTCCT GTTTCAAGTT GACATTCAAC AAGCGTATAA TCTTTAAAAT 720

GTTCTAGTAC GTTAAAATGT GTCACTGCTT CCTTACCATC ATCAnCAACA GCCATAGATT 780

GACGATCATT TTTGTTTCTA CCAATTGGCG CATCGATTGT ACCGTAATCA TGAGGAATAT 840

TCCCGTGGAA CTAAAnCGAT ATAGT 865

(2) INFORMATION FOR SEQ ID NO: 748:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 818 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748:

ATAACATTGT GGAGCCTATG ACATTGATTT ATGTCTCGGT CTCAAATGTT CTTGTAAAAA 60

AACTAAGTAT AGTTGAATTT TAAGTTAAAA AAATTGTTTT TGCAAAAATA AAATAATCCA 120

TTTTAGGTTC TTCGCCTCTA AAAATCCTTG CGaTATTAGA GCGATGTCTA ATTATCAATA 240

TGATTGAAAC TAAGAAACTA ACGACTAATA AAATATAGTC TTGAATGATA AGCGAGCCAA 300

TCACACAGCA AATTGCTGCA ACGATACTTG CTAAAGAAAC ATATTTAAAA ATCTTCAATA 360

CAATAAAGAA GATAATTGCA AGTATTAGTA AAAGTATCGG ATTGACTCCC AAGACGACAC 420

CTGCACTAGT TGCAACAGCT TTGCCACCTT GGAATTTTAA ATAAACAGGA TAAACGTGTC 480

CAAGTATAGC GAATAAGCCA ACAATTAAAC CATTTGTAAA AAAAGTACTA ATAGGGCCAT 540

CTGCGTGAAC TTGTAACCAT AAAGGGAAGA AAACAGTTAT GAACCCTTTG AAAATATCTA 600

GAAATGTTAC CAAGAATCCT GCAGGACGAC CTAATACTCT AAAGCTATTA GTAGCGCCAG 660

TATTACCACT ACCAAATTGT CTAATATCTT TTTTGAAAAA TAATTTTCCA ATTACGAATC 720

CACTTGGGAA AGCGCCGATA AGATAACTTA GTAGTAACAT GACGATTATC ATCATAAATA 780

TTACACATCC TTTAATATCT TAGGACTATT TTATCATA 818

(2) INFORMATION FOR SEQ ID NO: 749:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 971 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749:

ATATCCAATa ACTGTTCATT GTCTTGATAT TCCTTAAATG TTTCATAATG CTCATTAGAA 60

ATGACAATTT CAAGCAACCA ACCCGTGCCA CTTTCCTCTT TATTAATTAT TACGCCATCT 120

TCTAATTCAT ATTCTATAAT TCTGCCGTGT TCATTCACAA TTTGAAACCT TACTGCTTTA 180

AAAGTTTTCA TATTCCCACA TCCCATTAGT TTAATATTTA TGATTTTTGA ATTATTTAGA 240

AGATTTAAGG TCATTTCATG ACTAATTTCT TTAAATATAA CAAATAACGA GATGCTATAG 300

CTATTAATTA TATAAAATTT GcCATTTTGa CCATTTTTAA GCTAGTAATT AAGATATAGG 360

cATAGGAGGT GAATCACACA CTACATGCTA AATAAAATCG TAATTGTCGG GAGcTGACGA 420

AAGACGCACA AATATTTGAA AAGGAGGATA GAAAAATTGC AACGTTTTGT GTTGCAACGC 480

ACCGAAATTA TAAAGATGAA AATGGAGAAA TCGTCTGTGA TTACTTATTC TGTAAAGCAT 540

TTGGCAAGTT AGCTTCTAAT ATAGAAAAAT ATACTAATCA AGGTACATTG GTTGGTATAA 600

CTGGTCAAAT GAGATCAAGA AAGTATGATA AAGACGGACA AACACACTTT GTCACTGAAT 660

TATATGTTGA AACAATAAAA TTTATGTCCC CTAAATCCCA AAATAATGAA ATTCTCTCAG 720

TCCAATTATC CTAAACATCC TTAATATACA TTTAATCCAT CCTAAATTTT TTATAGATCT 840

AATTAACTTG AAATATACTC ACTTAAAAAC GACTTACATG ACCTAGTACT GTTGGTAAGG 900

TCGnCTTTTG GTGTAGTTTT CCTAATAGAn AATAGACnTA GGTTGCCAAA CCGATTACAT 960

AAAAAATTGC C 971

(2) INFORMATION FOR SEQ ID NO: 750:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750:

ATAGATTACT CTTTTGATCT GTAGATCCTA CTGTAACGAC ATTGTCCATA GATGCAGGAA 60

CATCTTTCAC TTCGCCATTA CCTTGATATT CACGCTGTAA TTTTAGTTTC TGTTTGTCAT 120

TGACATCAAT ACCATCATTA CCAGCTGCAG CAACAACGAT AGATTTTTTC TTCTTGGCGT 180

AATTGATTGC TTTCTGTAAC GCATCGTATT CTACTTTTTC ATCTTTTCTA AATGTTTGAT 240

GGTCATTTTT GTCCAAAATA ATATAACTAC CAACACTAAT ATTAATGACT TGaTTTCCAT 300

CATTTGCAGC TTGAACAATC GCTTTTGATA CCCAAAGCAG TTCTGTTTTT TTACTACCAA 360

ACACGCGATA CATTGTAAAT TTGTTATTCG GTGCAACACC TATTAACTTA CCATTAGCAC 420

TCGTTTGACC CGACACCATC GTGCCATGTC CTTTCCTATC ATTGACATCG TGAACATCAC 480

CTGTTTCCTC CGGTTCAGTA CCTCTAAAAC CGTTTAAAGG TACTAAATTT TTAGAATCAG 540

TCGAGAAATT ATTTTTCAAA TCGTCATGGT TTTTCATCAC ACCTGTATCT ATGATTGCTA 600

TTTTGGTGTT AGCATGTTTT GGCAAATCAT CATACGATGC ACCATTATTG GTTATTTTAT 660

TCATATCCCA TTGTCTTGAA AATAATGACT CATTTGATGT TCTGTCTATT GTTTTCTCGC 720

TAGTAATACA AGTTGAACAT GTGGCATTGA TATATTTAAt ATCATTTTTA TAGTTTGCTA 780

AAGCATTAGC ATGCATTTTC GTCATTTTAA TCTGTGCCAC ATGGAATTCC GG 832

(2) INFORMATION FOR SEQ ID NO: 751:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GTAATATCAA TCTCTTCATA AGCTGAATTA TTTTCATGCA CTTCTTGATG TGATGATTTG 60

TCACGAACCG CTACAACTAA CATTTTATCG TCTAAAATAA GTTGTTTATA TTTTTCTAAT 120

TCATCAGGCG CTAAGTTGTA GCGTGATAAA ACTGCATGTT CACCATCTTC TCCTGTTAAC 180

AGTTTAGTCA TTCTATCACT AAATGTTCCA CTTGTTGAGA TAAGGGAGAT TTCAGAGTCG 240

TGTAAGTCAT TTAGGTGTAA TTTACTTTTA CTAATAATTG TTAGCTCTGA TTCTAAATAA 300

CCTTCAGATT TCTTTTGATT GATTACGTTG TATAATTCGC CAGTGTCATT TACTACAGTA 360

ATATCTGCCA TAGTTGTCGC CCCTTTAAAA ATTTGTTTAT tTAATCTTTT ACCCTTCTTA 420

TnATAAAGTA AAACCCTTAC ATTATTAAGT nATAAGTCTT CATTCGCATT AAACG 475

(2) INFORMATION FOR SEQ ID NO: 752:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1019 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752:

GCGACACTTG TGAGTTCTCC AGCAGCAAAC GCGTTATCTT CAAAGGCTAT GGACAATCAT 60

CCACAACAAA CGCAGTCAAG CAAACAGCAA ACACCTAAGA TTCAAAAAGG CGGTAACCTT 120

AAACCATTAG AACAACGTGA ACACGCAAAT GTTATATTAC CAAATAACGA TCGTCACCAA 180

ATCACAGATA CAACGAATGG TyATTATGCA CCCGTAACTT ATATTCAAGT TGAAGCACCT 240

ACTGGTACAT TTATTGCTTC CGGTGTAGTT GTAGGTAAAG ATACTCTTTT AACAAATAAA 300

CACGTCGTAG ATGCTACGCA CGGTGATCCT CATGCTTTAA AAGCATTCCC TTCTGCAATT 360

AACCAAGACA ATTATCCAAA TGGTGGTTTC ACTGCTGAAC AAATCACTAA ATATTCAGGC 420

GAAGGTGATT TAGCAATAGT TAAATTCTCC CCTAATGAGC AAAACAAACA TATTGGTGAA 480

GTAGTTAAAC CAGCAACAAT GAGTAATAAT GCTGAAACAC AAGTTAACCA AAATATTACT 540

GTAACAGGAT ATCCTGGTGA TAAACCTGTA GCAACAATGT GGGAAAGTAA AGGAAAAATC 600

ACTTACCTCA AAGGCGAACT ATGCAATATG ATTTAAGTAC AACTGGTGGT AATTCAGGTT 660

CACCTGTATT TAATGAAAAA AATGAAGTGA TCGGaATTCA TTGGGGCGGT GTACCAAATG 720

AATTTaATGG TGCGGTATTT ATTAATGAAA ATGTACGCAA CTTCTTAAAA CAAAATATTG 780

AAGATATCCA TTTTGCCAAC GATGACCAAC CTAATAACCC AGATAATCCT GATAACCCTA 840

ACAATCCTGA TAACCCTAAC AACCCAGATG AACCAAATAA CCCnGACAAC CCTAACAACC 900

CAATTAAGTT CGTCTAGATA AAATAGGAAG CAAAGTCTTA GCAACGTAAA ATATTTTGA 1019

(2) INFORMATION FOR SEQ ID NO: 753:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753:

ATTCTTATCC CAGGTAGGTG nTTTACTTCT TATATTAGGT GCAATAACTC ATGCCACTCA 60

TCTTGTGGCA CAACATGAaT CGCATTTTCA AAAATTGCAT GTCCTGCTTG ATCAGTCAAA 120

CCGGCAGCAT GATCAAAATG CATATGTGTC ATTAGCACAT AATCAATATC CTTTGGCGTT 180

AAATTATAAT TTGCCAAATC AGCAATTATA TGACTTTCTT CATCTACTCC AAAATTACGT 240

AATTGCTTTT CAGATAATTT ACCATTACCA ATACCTGCAT CTATAATCAA ATTATATTGA 300

GCCGTTTGAA TCAAAATTGG ATGTGTCGGT AAATTGATTT GATTTCGTTC ATTTGCATTG 360

TATTGCTTTG ACCACAACGG CTTCGGAACA ACACCAAACA TTGCACCGCC ATCCATTTTT 420

GTATTGCCAC CATTTAGaTA ATGAATAGaT ATATCCCCGA TTTTCATAAC ATCACCTATT 480

CTTTCTGTAT TCGTTATTAC AATTAGCATG TGTTTATTAC ATCATATCAC TAT 533

(2) INFORMATION FOR SEQ ID NO: 754:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754:

ATCCCCTGCA AGTGATAAAA TTATTGAAAA AGGCGACATG ATTACATTAG ATTTTGGCGC 60

GTATTATAAC GGCTATTGTT CAGATATTAC TAGAACATTT GCTATTGGAG AACCAGATCC 120

TAAACTGAAA GAnATATATC AnATAGTACT TGAATCTCAA ATGAAAGCAA TTAATGAGAt 180

TAGACCTGGC ATGACTGGTG CAGAAGCTGA TGCCATTTCA AGAAACTATt TAGAGTCAAA 240

AGGGTATGGA AAAGAATTTG GACATTCACT AGGACATGGT ATTGGTTTAG AAATCCATGA 300

AGGGCCAATG CTGGCTCGTA CGATACaAGA TAAACTTCaA GTTAACAACT GTGTTACAGT 360

AGAACCTGGT GTTTATATAG AAGGTTTGGG CGGTATAAGA ATAGAAGATG ATATTTTAAT 420

AGCGTGTAAA ATGAGGAGGA AACTGAATGA TTTCGGTTAA TGATTTTAAA ACAGGTTTAA 540

CAATTTCTGT TGATAACGCT ATTTGGAAAG TTATAGACTT CCAACATGTA AAGCCTGGTA 600

AAGGTTCAGC ATTCGTTCGT TCAAAATTAC GTAATTTAAG AACTGGTGCA ATTCAAGAGA 660

AAACGTTTAG AGCTGGTGAA AAAGTTGAAC CAGCAATGaT TGaAAATCGT cGCATGCAAT 720

ATTTATATGC TGACGGAGAT AATCATGTAT TTATGGATAA TGAAAGCTTT GAACAAACAG 780

AACTTTCAAG TGATTACTTA AAAGAAGAAT TGAATTACTT AAAAGAAGGT ATGGAAGTAC 840

AAATTCAAAC ATACGAAGGT GaAACTATCG GTGTTGAATT ACCTAAAACT GTTGAATTAA 900

CAGTAACTGA AACAGAACCT GGTATTAAAG GTGATACTGC AACTGGTGCC ACTaAATCGG 960

CAACTGTTGA AACTGGTTAT ACATTAAATG TACCTTTATT TGTAAACGAA GGTGACGTTT 1020

TAATTATCAA CACTGGTGAT GGAAGCTACA TTTCAAGAGG ATAATCTCTA ATTTGTTAAC 1080

AAATAGCTTG TATTCACTAT ACTGATTTAA CGTAAGAnAT TCTAAATAAG TCTCATAAAG 1140

CTATTGCCTA AAATGATTAT AGGTTATATG CTGATATGAG GCTTTTTATT TTTAAAATAA 1200

TTTTTAAAAT ATAAAACGAA TCGTC 1225

(2) INFORMATION FOR SEQ ID NO: 755:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755:

ACAAACAAAT CACTTAGTTA AAATTGACAG TGCATTATAT TCCGATAAAT TATTCAACAT 60

TGTAGAAAnn AGAATTGATA CACCAGATAT TGGCTATAAT ACAGTGGTTT TATCAGAAAA 120

ATGAGTGTAG AAATTAAAGG GATACCTGAn GTGTTGAATA AATTAGAATC GGTATACGGT 180

AAACAAGCAA TGCAGGCTAA GAGTGATAAA GCTTTAAATG AAGCATCTGA ATTTTTTATA 240

AAGGCTTTAA AGAAAGAGTT CGAGAGCTTT AAAGATACGG GTGCCAGTAT AGAAGAAATG 300

ACTAAATCTA AGCCTTATAC AAAAGTTGGT AGTCAAGAAA GGGCTGTTTT AATTGAATGG 360

GTAGGTCCTA TGAATCGCAA AAACATTATT CACTTGAATG AACATGGTTA TACAAGAGAT 420

GGAAAAAAAT ATACACCAAG AGGTTTTGGA GTTATTGCAA AAACATTAGC TGCTAGCGAA 480

CGTAAGTATA GAGAAATTAT AAAAAAGGAG TTGGCCAGAT AAATGAATAT ATTAAACACC 540

ATAAAAGGAA TTTTATTATC TGATGCAGAG CTCAAAACAC ATATAAATTC TAGAATATAC 600

TATGATTTGC CTTCAGACTT TATGTCTGAT AAATATCTCA GTGAAGAATA CTTAATTCAA 720

ATAGATGTAG AATCTTCAAA TAATCAGAAA ACAATTGATA TAACAAAACG AATAAGATAC 780

CTGTTATATC AACAAAATTT AATTCAAGCA TCTAGTCAGT TAGATGCTTA TTTTGAAGAA 840

ACTAAACGTT ATGTGATGTC GAGACGATAT CAAGGCATAC CCAAAAATAT ATATTATAAA 900

AATCAGCGCA TCGAATAGGT GTGCTTTTTA ATTTTTAAGG AGGAAATAAG CAATGGCAGA 960

AGGACAAGGT TCTTATAAAG TAGGTTTTAA AAGATTATAC GTTGGAGTTT TTAACCCAGA 1020

AGCAACAAAA GTAGTTAAAC GCATGACATG GGAAGATGAA AAAGGTGGTA CAGTTGACCT 1080

AAATATCACA GGTTTAGCAC CAGATTTAGT AGATATGTTT GCATCTAACA AACGTGTATG 1140

GATGaAAAAA CAAGGTACTA ATGAAaGTTA AGTCcTGaCA TGaGTaTTTT CaATATTCCa 1200

AGTGaTGaTT TAAaCACaGT TaTTGGaCGT ACTAAAGATA AAAATGGGTA CATCTTGGGT 1260

AGGAG 1265

(2) INFORMATION FOR SEQ ID NO: 756:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756:

CATATACCCG GGTTCCAAGA ATCCTCTATC CATATGGTCC CCCAATTTTG ATTCCACCAT 60

ATTGTTAAAT ATCACTTTCC CAGCCTACTT TTTTATnCAG TTGGGCTCTC TAAAATTGTT 120

TTGAAATCCA GGTTGAACAT ATTTCCAGTG TATGACCAAT CGAAACATTT GCACCAATAA 180

GGCCGCCAAT TTTTCCTGTA TCATCACCAG TAACATTACC GTTGAATCCA TAAGTTAAAG 240

TACTCATATA CTCTTTTGTA TCAATCGAAT TTCTTGGATA GTAATCAGAT ATTTGAGCTA 300

CTTCATTATC AGGTAGTTGC AACTGTACCT TAAAGGCTGA AGGCCAGGCT AAACCACTTT 360

TGTTAGCACC TTCTTCGCTA TAAACTCTAT ATTGACCAGC AATGGTACCT TTCGTTCTAA 420

TAACTAGCAG TTTTTTATTA TGATTTTTAT CATCGATAAA ACTATAAAAT ACTTTTTTGT 480

GCATGCCATT TTCTTTATCA TAAGTGACTA AATCACCTGT TTTTACTGTA GTATTGCTTC 540

CAATATCTGT AGTACCGGTT TTAATATTAA TATCAGAATC TGCGGCATTA GCGACAGGAT 600

TCATTAATAT GGAACCTAGC AATAGTGTTG TTGTTACTGA GCTGACTATA CGTGTTTTCA 660

TTTTCATCAT CCTTCTATTT TTTAAAACGA TTTGAGGAAA CAATAATCAA TATGTCAATT 720

GTAGCAACTG ATAAATTACT GAGTGATGAT GAGTGATTAT TTTAAGAATA TGTTTTTAAC 840

TTTTATTTAA AATTTGAAAG GAAGCATTTC AATTTCGAGG GTTAGTCAAA GTTGAATAAA 900

TTCTTTATGA AACAAGGAAA AGACATAGCT AATTTTtATTG ATTAATTTCT TTAAAACTAA 960

TGATTTGTTT GATTTAAAAA TGTAATCGAT TACAATATAA AAATACAAAT ATCTTAGAAT 1020

TAAATCAATT AATTAACTAT TAAATAAAAA TTAACTATAT ATTAACTAGT GTAAATTAAT 1080

AAATAGAAAT AGAGAAAAAG GGTATTAATT A 1111

(2) INFORMATION FOR SEQ ID NO: 757:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 466 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757:

TATCTATTGT ATGTAACAAT AGGTACATAA TATTTTTAGG GTGGGTTATA TGAGCATAAT 60

TACAAGATTG TTTAATAACA GTGATTTTGA AAAATTAAAT CAACTATGTA AATTATATGA 120

TGATCTAGGT TATCCAACAA ATGAGAATGA TTTAAAAAAG AGACTAAAGA AAATAACGAA 180

TCATGATGAT TACTTCCTAC TGCTTTTGAT AAAAGAAAAT AAAATAATTG GTTTAAGTGG 240

TATGTGTAAA ATGATGTTTT ACGAAAwAAA TGCAGAGTAT ATGAGAATCC TTGCGTTTGT 300

TATACATTCT GAATTTAGGA AAAAAGGTTA TGGAAAGAGA TTATTAGCTG ATTCTGAAGA 360

ATTTTCTAAA CGGTTGAATT GTAAAGCmAT AaCACTAAAT AGTGGTAATA GAGATGAnAG 420

ACATCTGCAC ATAAACTATA TAGTGATAnT GGGTATGTTA GCAATA 466

(2) INFORMATION FOR SEQ ID NO: 758:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758:

CGTACAGCAT AACCAAATAC ATATCTGCCA AAATCGCCAT ATGCCCCAGT TCCTCTTCCA 60

TATTCCGTTG TCATTGAGTT TTTAATTTTA TCGATAGAAA AATGTAAATG GCTATCTAAT 120

TTGTTTTTTA AAGATTTTAT GTAATCtCTA TATTTAAATT CGAATATTCT TTTTTATACC 180

AACTAATATA TwCAATTGTA TGCCTAGCAT AATCTCTCAT TAAAATATGA GGATATACCA 300

TTTCTTTATC AAATATtTCT TCATAAATAT AATTAGCAAT CTCTATATGT ATTtCACAAA 360

TGTCGATTCG AAGTGTCGCC CCTAAAACAG rAGCATATAA TC 402

(2) INFORMATION FOR SEQ ID NO: 759:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759:

AAGTTACTCA ACAGCCATTT GACACGTCTC GATTAGAGCG ATTAGGTATA ACCGAGCGCC 60

AAACTAAAGA CATGTATCGT TTATTAGGAC TAGCCAAATA TGAAGATCGA TTTGTTATTC 120

CAACATCACA CAAAGAAACC TATTTAGATA CGTATCACGC ACAAGGTAGT ACAGGATACA 180

ATTACGGCGG CGAGCATTTT GGAGATAACT GTGAAGGCTG TGGCGTTGCA GTAGGTTCAG 240

GGAAAACTGG TCAAGAAATT TATAATGGAG AATTCTATGG AGGGATTTCC GTGGTTAATT 300

TCGATAATTT AAAAAATATC CAAGAAAGTT TGGGTnnn 338

(2) INFORMATION FOR SEQ ID NO: 760:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760:

CTCTATTATA TTTAGAGTTA TAGCTATTGC aGTTGTTTAT TTATTGAAAA TAAATGTACT 60

ATCATTAGtT TTAGCAAGTG TATTAGGCAG TTTgGTATCt AGGCTACTAT TATCTATTAT 120

TTTAAATTTA CCTGTGTGGG TAGTGTTGTT AAaCGCGATT CCAGGCGTAA TATTCACTTT 180

AATTGTAGcT ATTCCTTTAT ATCTCACATT GAGAAAAAGA ATGGCAGTAT TACTAAGATA 240

ATAAATCAAA ACACGGTCGT CACAATTACT GTTGGCGACC GTGTTTTACT AGCTATTTAT 300

TGTTTTCAGT TTCTTTTGTA TCTAACAATT TCACTTTGTG ATTTTCCCAA TCAATTTCAT 360

ATGTTGaTTT AAATGTTCTA GTTTTAAAGT TTTTATAAT 399

(2) INFORMATION FOR SEQ ID NO: 761:

(A) LENGTH: 639 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761:

GCATATnCAA AACAATAGCT GCTTTAGGTG CGGGGGCTAT TAGCGTTATT TCTGCACTAA 60
CAGGAGGTTT AGTTGGCGCA GGTGTTGGTG GTTTCCTTGG ATCTATAGCT GCATCGAATA 120
TTGATACTAG TAAGGGAATA TATATAAAAT TAAAAACTAA AAAGTATGCA GCCGGGGAAT 180
ACGTTCTGAC AGGAGAAAAA TGGGGATATC AGTAAGGGTG ATTTTATGGA TAGATTAAAA 240
TATTCACTTA AAGTTGGAAT TTTAGCATTA TTATTATTTT GTACTTTAAA TTATTTAGTT 300
CCAATGCAAA GCAATGCTTT TTCAATAATT ATATATTCGG CAATTTTTGC TGTGTTACTT 360
ATGCTTTTAG TTTATATATT TTTAGGAATT TTAAAGAAAT GACATGAAAC AAATTAGCAT 420
TGGCTATGAA GAAATCTATG GGGATAGAAT TTTTCATAGC CATTTTTTAA AAGAGCATGA 480
AGTAAAAAAT TGGAAAACCG TCAATCAAAT AATTGAAAAA GAACACTTGG ACAAAAATGA 540
ATATGnAAGC GGAACCGCCG TTATTTTTCT TTTGCAGGAT CGTTAGATTA GATTnCGGTT 600
GTATAGTATA ATGAAAAATA TTATAATAAA TTTATAAAA 639

(2) INFORMATION FOR SEQ ID NO: 762:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 852 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762:

nTGTTCGTTG TCTGGATCCA ACGTAAACAG TCGCTTCATC TAATACAATG ATAGGCGCAT 60
CTTTTAATAT CATTCTTGCA ATAGTGACTC GTTGTTTTTC ACCACCAGAC AATTTATCTC 120
CCACTGTACC AACATTCGTA TCATATCCAT CTGGCAACTT TTCAATAAAT TCATGACATT 180
GTGCTAACTT GGcAGCTTTT TCAACTGCCT CATCCGTAGC TTCTGGATTG CCAAGTTTAA 240
TATTTTCTTT AAAAGTAAGA TTTAATAAAA AGTTATCTTG TCCAACAAAA CCAACTAAAT 300
CGTTAAGTTG TTTCGATTCA ATATCTTTTA TATTTATACC GCCAATCGTA ATTTCACCTG 360
AAGTCACATC CCAGTATCGT GATATAAGCT TGGCAATGGT TGACTTACCG CTACCAGaTG 420
CCCCGACGAT AGCTGTGAAA TTATTTTCTG GTACTGTAAA TGATAAATGC TTAAAGACCA 480

GAGGCTTCTT AAATTTTGTT GACAATACTA ACTCTTCTAG ACTTAATATT TGATTCACTT 600

CAGTTAATGC GTATTGTATA GACTTTAAAT GATTTACATA ATTAGTAAAA TTCTTAATCG 660

GTGCTACTAC ACCTAAAGAT AATACGATGC ATAGGAAAAA TTCCGCATAG TTTAATTGGT 720

TGATAGATAT CAAATACATG CCGACCGGTA AAATCCCTAA AAATGTTGAA GGTAATACAC 780

TAGCTCCTAA ATTCATATAC CCCCATGTAT TTTTAAACCA ATTCAAAGTG TGAATCTTAT 840

AATTATCTAC TG 852

(2) INFORMATION FOR SEQ ID NO: 763:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 852 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763:

CTCTTCATGC GTCATACGTT GTGTCGATTG ATCAGTTGTT TTGTCTAAAT CACTAGCTTT 60

AAATTTAGAT TGATTTGATT GACGTGTCGT AAATnGTTGT TCCTTTTGTT GGCGTTTGCC 120

TTTTTTTCTT GATCTTATTA AAAATAAATT GATAACCCCA ACAATAATGA GCGCTAAAAT 180

AATGTAGCTA ATAATGAAGG TCGTAGTCAT TTAATGACCC CCTTAATTTT TATGGATTTT 240

TACTTCAGCG TTCaTTCCaG GAACAACTTG TTTAGACGGT TcTGATTCTA GAGTGATTTT 300

AACAGGTATT ACTTGAGAAA CTTTAGTGTA GTTACCATCA CTATTTGATG ATGGCATTAA 360

TGAAAAgtTG CAGCAGTTGC TTTTCCAATA CTATCAACTT TACCTTTAAT AGAAGCTTTT 420

TGACCGTCAA TAGTCACATC AACATCTTTA CCTACTTCAA CATCTTTAAT ATCTTTTTCG 480

TCAATATTTG CTGTTACATA TAAATCATCT AAATTGTATG CATAAGCGAT TGGGTTACCA 540

GCTTGCACCA TTGAACCTTC CATACCATCT AATTTGGCAA TTGTACCTTT TTGAGGCATT 600

TTAAGATCCA TATCTTTCGT TTCGCCATCT TGACCTTGTA CAGTAACAAT TGCTACTTTG 660

TCACCTTTAT CGAGTTTGTC ACCTTGTTTA ACATTAAGTG ATTTAATTTG TCCAGATGCA 720

GGACTTGCTA TTTTAATTTG ATCGCCATTT ACTTTTGCAT TATCAGTTGT TACATAGCTT 780

GTTGTTTTAT TCCAAAAATA AAAGCCAGCA ATCCCAATGG CTAACnGTAC AACAACCGTA 840

ATGACATTnA AT 852

(2) INFORMATION FOR SEQ ID NO: 764:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764:

ACATATTCGA CATTCATTTT AAATTGCATA TAACTACATT AACCATTCAT TGTGCAGCGC 60

CTGTTGTTTA GATGATCATT TATTGACTTT TTGCTCTTAT nCCAnGCAAT TTTTTGATTT 120

ATTGCTTATA ATACATTTTA AGACAAATGT TTGTTTCAAC ATCGCATGCG ACATCATTAA 180

yTATTCATTT AAATTTATCC AGTTTCTATT TGTCTGCAAT TGCTGAAAAT TAAAGGAGCT 240

TATTTTTAAT AATGGAACAA ATTATCACTG AATTTATTAG CCGTTTTGGG TATGCAGCCA 300

TTTTTATATT AATTTkATkA GAAAATGTAC TACCTaTCGT aCCATCGGgA AATTATTCTG 360

ACATTTGCTG GTCTTATGTC TGTTAAATCA CATTTATCAA TTTTAACTTT ATTTATTATT 420

GCAACTATCG CATCGTTTAT AGGGCTGTTA ATTTTATATT ATATCTGCCG TTTGATTTCA 480

GAAGAACGTC TATATCGTTT TATTGATCGA CACGGTAAGT GGATTAAATT GAAAAGTAAG 540

GATTTAAAGC GAGCAAATGA TTGGTTTAAA AAGTATGGCG TATGGGCTGT ATTkATCTGT 600

CGTTTCATAC CTGTATTACG TGTAtTGATT ACCATTCCAG CTGGTGkaAA CCGCATGAAT 660

GTTGTGACaT TtACCGTTAT TTCATTAATA GGTACTACAA TCTGGAATTT CGGTTTAATT 720

TTACTAGGAC GCACTTTGAG CGATAGC 747

(2) INFORMATION FOR SEQ ID NO: 765:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 820 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765:

TTTACCTTTT AACCAATCAT GCATTAATGC AATGTGTACT GTCTTAACAA ATGTTGCATA 60

TtCATCTTCT GCACTCCACT TTTTCAATTC CTGTTGATTA ATGGCATGTT TTTCTCCATT 120

TTCCAACATA TTGACATACA ATTTATAATG TTTTTCAACT GCCTGAATAA AAGCGAGTTG 180

ATTTTTATTT AAATGTGATT TTAACTTTTC TAAATCTGAA TTAATAAAGT CTTCTATAGT 240

CGAATAAGAC ATATCTTGGT ATTCAACTAC TGCATTAATT TCATCTAATA ATTGCGATTG 300

TGATTTTAGC GTTATATAAC TCTCGTCTCC ATAAGATATT TCTGTAGTAG CTGCTGTAGT 360

AGGATTTGGA GAACTGACTA AAATATGCTC GCCTAATAAT GCATTTATCa AACTACTTTT 420

TGTTTCGTGG ATATCTTGCT TTGTACGCTT GAACAAAGGC ACATCCGAAA TTATATCAAG 540

CGCTTTTTGA ATATCTATAG ACATATTTGT TGTAGCTGTA TTTTGATTTA GCTGCTGATT 600

ATCACGATTA TCCTGAGCAT TATCAGTAGC CACTTGATAT GTTGTCTCTT GTCGACCTAT 660

TAATTTATCT AGAGATTCAT CTAAATGAAT ATAGTAGTGA CGATAATTCT TAGTCGTCAA 720

TGACTGACGC AGCTCATTTA ATTCTGTATA ACGTTGATAT TCTTTTAAAT CATCACTTTC 780

TTCTGTTGGn AATTCATCTG CCTGCACATT TTCTATnATT 820

(2) INFORMATION FOR SEQ ID NO: 766:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 672 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766:

TCAACATGAC ATTAATTTAA TAGCGATGCA TACAAATTTA GATGTAAATC CGTATGGTGT 60

CAATATGATG TTGGCGAAGG CGATGGGTTT GAAGAACATT TCAATAATAA ATAATCAACA 120

AGATGTATAC TATAAAGTTC AAACATATAT ACCTAAGGAT AATGTTGGAC CATTTAAAGA 180

TAAGCTTAGT GAAAATGGAT TAGCGCAAGA AGGTAATTAT GAATATTGTT TCTTTGAAAG 240

TGAAGGAAGA GGGCAATTCA AACCAGTTGG TGAAGCTAAT CCAACAATAG GACAAATTGA 300

TAAAATTGAA TATGTAGATG AAGTTAAAAT TGAATTTATG ATAGATGCAT ATCAAAAGTC 360

AAGGGcTGAG CaATTAATTA AACAATACCA TCCATATGAA ACACCGGTAT TTGATTTTAT 420

TGAGATAAAA CAAACATCCC TTTATGGACT TGGCGTTATG GCAGAAGTGG ATAATCAAAT 480

GACATTGGAA GATTTCGCAG CTGATATTAA ATCTAAATTA AATATCCCAA GTGTCCGTTT 540

TGTTGGTGAk TCTAATCAGA AAATTAAACG TATTGcAATT ATTGGTgGTT CAGGTATTGG 600

ATATGAAkAT CAAGCtGTCC AACAAGGcGC AGATGTCTgT TACGGTGATA TTAAACATCA 660

GATGCCTAGA TG 672

(2) INFORMATION FOR SEQ ID NO: 767:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GAAAAAGTTA AACCTACTGT AACTACAACA AGcmAAGTTG AAGACmATCa CTCTACTAAA 60

GTTGTmAGTA CTGaCACAAC AAAAGATCAA ACTAAAACaC AAACTGCTCA TACAGTTAAA 120

ACAGCACAAA CTGCTCAAGA ACAAAATAAA GTTCAAACAC CTGTTAAAGA TGTTGCAACA 180

GCGAAATCTG AAAGCAACAA TCAAGCTGTA AGTGATAATA AATCACAACA AACTAACAAA 240

GTTACAAAAC ATAACGAAAC GCCTAAACAA GCATCTAAAG CTAAAGAATT ACCAAAAACT 300

GGTTTAACTT CAGTTGATAA CTTTATTAGC AcAGTtGCcT TCGCAACACT TGCCCTTTTA 360

GGTTCATTAT CTTTATTACT TTTCAAAAGg AAGaaTCTAA ATA 403

(2) INFORMATION FOR SEQ ID NO: 768:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768:

TTCAATGCTC GTTTTGCTTG CGTTAGTAAT TTCTAACATA TTCATTCACA TTTTGGAGCC 60

TAAACTATCA ATCACCACTC AAATCATCAT CGTTTTGATT TTAATTGAAG CACTAATTGG 120

ACTGCGTTTC TTGAAAGCGT ACGATGTTAA GCGTGGCAAA GATAAAGAAA ATAAGAAAAA 180

TAGTAAGGAT TTCGTTAAAC TAAAATCAAT TTTAGTAGCA ATTTTATTTA CATCATTGGC 240

GCTGACAGCA GGTACTGTAG CTGATATATA CGGTTTCACT GACTTAGGAA ATACTAGAAG 300

TGATTTAATC GTTTGGAGCA TAGGTGGTAT TATATTTGGC CTCGTATGTT ACACAATGGA 360

AGATAAAAGA TAACGATAAG GAGCTGGCGA TTATAAAGCT AGCTCCTTTT TTAACTTaTA 420

TATGTAAAGA aCTaTCCTAA GGGkTTTTAA TCATATGTCA ATAATTTCTA TAATACATTA 480

TTA 483

(2) INFORMATION FOR SEQ ID NO: 769:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769:

ATTATATGTC TGATGTATTT CATGTCGTTA AAAATAAAGG TACGGAAGAT TTTAAAGAAG 60

GGATGATGCT TGAAGGTGAA AAAATCAAAG CTTTTTATGA AGATATGCCA CCGTATCAGA 180

CTGTCAAAAA AGGAACGATA CAAATTAAGC GTGATGGCAC ACCTATTATC CTATTAAATG 240

TCATTATACG CTnGTAGCTA CCCGCAAATC GGTACAATCG CAGTTATCAT TTACGAATTA 300

GCACAAAACC GCAGGATCAC GTTGAATTCC ATTATAGTAT TTACGGCTGA AGACTGTAAG 360

nTAnACTGGT AACCATATCA TGGATGATTG ATCATAGATG 400

(2) INFORMATION FOR SEQ ID NO: 770:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770:

ATCTCTTCTA CTTCTTTTAC AAATTGAGAA CGTCTTAAAA TGGCTTTCAC ACGGGCAACA 60

ACTTCTCTAG GTkAAAAAGG CTTAGTCATA TAGTCATCGG CACCTAATTC TAAACCTAAT 120

ACCCGATCAA ATTCATCATT TTTCGCCGTT AACATTAATA TAGGGACTAA ATTTTTATTT 180

GTTCTTACAG TCTTACATAC GTCAATGCCA TCTTTTTTAG GTAGCATAAC ATCTAAAATA 240

ATTAAATCTG GCTGTTCACT TTCTACCTTT TCTAAAGCCT CATCACCATC AAATGCGACA 300

ACAACTTCaT AACCAGCTGk TTCtArGyTA TATTTAAGTA ATGgTTaCGa TTGaATGtTC 360

GTCATCTACT wCCaACACTT TTTGCGACAT GGtATGCCTC CCTAACttAk AATTATATTT 420

cATTATAACC GAACTATTTA TAAAAATAmC ATCCTACACA TTATCTTTAC ACATTTTTTA 480

CATTACTTTA CATATAAATA AAATACTTCT TATATTTCCT TCTmTCATTT GCATGACTTA 540

CTCTGGGACA ACGAAATAAA TTTTGTAAAA ATAGCATTTC TATCCCACTA CCTATGCATG 600

AGTTTTACTC ATTTATTCCT AAGCTTATGT ACATATTCGC TTTGTCTAAT GTGTAAGAAA 660

CACTACATAA TCAATCATTG GTGACTCTTT ATTATTTCTA TCCTGTTGCC AaCTTCAATT 720

CATTTAAAAA GGCGAACCTA GCAATTAAAG 750

(2) INFORMATION FOR SEQ ID NO: 771:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATTTAATTAT TATTTTTCCA AATCAATACG ATATAATTTT ATGTTTTTAT CTTTTGGTGC 60

TGaGGCAAAT TGATAAGtCG TTTTGCCTTT TTCAATATAT CCAAAATTAC CAGCAACTTT 120

GCTATATTCC GTATGTGTTA CTGCTTTGCC AACATAATTT TTAACAGCTT GATATGTTGG 180

ACCATTAGCA TCATTATACA TCATTGAAAT ATGAGTTACT TTACCATTGT TTTTCTTACC 240

ATCAGTAGTT ACTAATAACA TACCTTTTTT AGTATGGAAT TCGTAATAAT GTTCAGTTCC 300

ATCTTCATTG TAAGAATACA TCGGATTTTT GTACTTAGTT AAAACATCTT TAATAGATTC 360

GCCAATTTTC ACATTTTCTA ATGACTGATC ACCCTTAATT AATTGTTTAA CAGTATCAAT 420

AGAGTTGCCA CTTGCTGCTT CGGCACTAGT GTTCACTAAG CCTACTCCCA TTACAACAGA 480

ACATGCAATT ATACTTGCCG TTAGTAGCTT TTTCATAAGC ACTCTCTCCT TTTATTTATA 540

TCGTCTTGTG CTCACAACCA TTATACAACA ATCATTTCTA AAACAACAGT CATATTACAA 600

TTATATTACA AATAATAATT ACTACTTTTA TATTTCACTT ATCACTAAAA ATTAAACATG 660

CTTTTCATCG TGATGTTTGT TGATAAATGC AGCTGTATCT TCGACGAATC TTTCTTGCTC 720

TTcAACAAAT GGGAATGCAC TTGATTCTTG ATATACTTCA AAGTCCGCAT TTTGGATTAA 780

ATCAGCTACT TCTTTAGCTT CTAATCTTGT TGTTCTTTCA CCGAATTCTC CTGCAATAAT 840

TTTTGTCGGT ACTACGACAT TTCTATAAGT TTGAGAAATA TCAGCGTTTT TGAATACCTC 900

TTTAACTGCT TGAATTTCTT CTTTAGTTGA TATTTCATTT GTATCTACGA CATGTTTGAG 960

GAATCGATTC ATTTTTCTCG GACGATAATA CTTACGCTTA TTTAAAAATT TAwCyTGtTT 1020

TTCaGGATCC CaGTTtCGAA TAATATGGGC ATaTTTTCTA AATAAACGTT CTTCCGGTAA 1080

TTCACCTTCA ATAGATGTTG GATTTACCAA CGTAAGTGAT GATGTAAATT CAGGATAACG 1140

TACTGAAATA TCCGCACCAA TGATTCCACC CATTkCATGG cATACAAATG CAACTTCTTC 1200

AATATATAAA TATTTAAGTA ATTCAACAAT GTCATCAGAA AAATCTTTTA TTTCAATGTG 1260

ACGAGGTTTA TCAGAATAGC CATGTCCACG TAAATCAATT AACACAACTT GAAATGATTT 1320

TGCTAATTCT GCTGCTAATT TATTAAACAC AGAATAATTA TCAAGTACAG TATGAATCAA 1380

TACGATAGGA TAGCCTTCAC CTAAnGTACT GTAATGTATC GATGTTCCAT CTTTTCTAGT 1440

AAATAGATCC ATAATTTTCT CC 1462

(2) INFORMATION FOR SEQ ID NO: 772:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 704 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772:

ATTATTATAA GGAGTTATCT TACATGTTAA ATCTTGAAAA CAAAACATAT GTCATCATGG 60

GAATCGCTAA TAAGCGTAGT ATTGCTTTTG GTGTCGCTAA AGTTTTAGAT CAATTmGGTG 120

CTAAATTAGT ATTTACTTAC CGTAAAGAAC GTAGCCGTAA AGAGCTTGAA AAATTATTAG 180

AACAATTAAA TCAACCAGAA GCGCACTTAT ATCAAATTGA TGTTCAAAGC GATGAAGAGG 240

TTATTAATGG TTTTGAGCAA ATTGGTAAAG ATGTTGGCAA TATTGATGGT GTATATCATT 300

CAATCGCATT TGCTAATATG GAAGACTTAC GCGGACGCTT TTCTGAAACT TCACGTGAAG 360

GCTTCTTGTT AGCTCAAGAC ATTAGTTCTT ACTCATTAAC AATTGTGGCT CATGAAGCTA 420

AAAAATTAAT GCCAGAAGGT GGTAGCATTG TTGCAACAAC ATATTTAGGT GGCGAATTCG 480

CAGTTCAAAA CTATAATGTG ATGGGTGTTG CTAAAGCGAG CTTAGAAGCA AATGTTAAAT 540

ATTTAGCATT AGACTTAGGT CCAGATAATA TTCGCGTTAA TGCAATTTCA GCTAGTCCAA 600

TCCGTACATT AAGTGCAAAA GGTGTGGGTG GTTTCAATAC AATTCTTAAA AGAAATCGAA 660

GAGCGTGCAC CTTTTAAAAC CGTAATGTTG ATCCAGTAGA AGTA 704

(2) INFORMATION FOR SEQ ID NO: 773:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 427 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773:

GACCACGACA CCACAAGCTA TGAAGAATGC CyTTGTTAAG CCGCcTTTGa ATtGCATAGA 60

GATGAAAATA CCAATATTAA TAAAGAAGTT ACAGAAAATA CCTTTTGTAA AAATATTCAA 120

CCATGTTGAA TCAACAGTCT TTTTCTGAAC TAAAGCTGTT AAAGCTTGTG TCATTTCAGG 180

TGTCATGACA TGCGCAAATT TCATTAAGAA AAATAACACA AACCCACCTA AAATATTTCC 240

TAAGAAACAA TATAATAAAA TCCAAGTCAT CTTCTTAACA GAAACGACTT TATAATACCA 300

GCCTACTGTA AAGTACATGA AGTTACTTGT TAATAATTCA GAGTTAGTTA ATACAACTAA 360

AATCAAACCT AAACTAAACG CAATGGCTCC CATTAAATTG ATAAGTCCAT CTACGTGAGT 420

ACtCGCA 427

(2) INFORMATION FOR SEQ ID NO: 774:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774:

AGGTGAGCAT TATTAAATAT TGCCAAGAAA TCAAAACTAA AAACTATGCA AAAGATGTAG 60

ATATATTATT TATTCTTGGC GGTGATGGCA CGGTTAACGA ACTTATAAAC GGTGTTATGA 120

CACATGACCT TCAACTCCCT ATTGGCATTT TACCAGGCGG TACTTTTAAT GATTTTACAA 180

AAACGCTAAA TATAGCACCT GAATCATAAA CAAGCTAGTG AACAAATGGA TTTCTGCACA 240

AGTTGGTACA TACGATGTAA TTGAAAATGA AATGAATCAA TATGCACTCA ACTTTGTGGG 300

CTTAGGTCTC ATGTTCAAAA CGCGGAAAAC GTACAAGAGG TTCAAAAGAT GTATTGGGTA 360

AATGGAGTTA TATTGGGTCC ACCGTCCAAA ACnCGGCnAA 400

(2) INFORMATION FOR SEQ ID NO: 775:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 484 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775:

AATTATTCCT CAATAGGAGC ATTACCCGCT CTCTCACCAA TTCCCAAAAA TGTAGTTTCT 60

ATTTGCTTTG CACCATTTAA AATTGCAGCT AATGTATTTG CAGTAGCCAA CCCTAGATCG 120

TTATGACAAT GAGCAGAAAa AATTATGTTA GAATATTTTT TTACAAAGTA ATTAAAAATA 180

TCTCCGTATT CTAATGGTGT CGAACATCCT ACAGTGTCCG CAAATGTAAC TGTTCTAACT 240

TGATATTTTG AAATAATTTC CATGTATTCT TTCAATTTTT CTCTAGAAGT CCTTGTTCCA 300

TCTTCAAAAC AAATATCTAC TCCTTTTTTA TCTTTCTTTA ATATATCCAA GCAGTCTTTG 360

ATTTTCTGAA TATAATATTT ATTTGAAAAA TTAAGCTTTT CTTTTATATG CAAGTCAGAT 420

ATTGGCAATA GTATTTtTAC CACTAAATTA TGAATTTtCA ATtTGACTAT TTTTgGTATG 480

TCnT 484

(2) INFORMATION FOR SEQ ID NO: 776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 788 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776:

CGCAAGATGA AGTTAAAGAA CTTAATCGCT TATTAGGTAA AGTCATTCAT GCATTTGATG 60

AAACAAAGGA AAAATAATTA ACTTTTGTCA TGACAATTAA AGTAATGTTT AGAATTTATT 120

AAGAATAGAA AAACAATTAG CACGCGTAAC TTGTTAGTnA AAAAACTGCT TGAAAGGTTT 180

CTTAGCCTAT CAAGCAGTTT TTTTATGCAT TATATTGAAT CATATTCCAT AAAGCACCTT 240

GATTAGCTAG TAATTGTTGA TAGTTTCCCT TTTCAACTAT TTTACCATTT ATCATCACAA 300

TGATGGTCTC AAAACGTGAC AATAAAGTTA AATCGTGTGT AGCAACAATT AATGTTTCTG 360

CATGTGCTTC AATTAAATCC ATAACTTTTA AACTATTTTG TTTATCTAAT GCAGTTGTTG 420

GTTCATCTAA AATCCATGTT GATGCAGTAT CTTTTAATAA CATCCTCGTA ATCGCTAAAC 480

GCTGAATTTC TCCGCCAGAT AATGTATGAC CATCTAAGTC AATTTGACGT tCTAGTGCCA 540

AATGTTCTAA ATCTAATTGC TTAAATATTG CTTGCACCGC TTCATCTTTT TCATCGGTAA 600

ATAAATTTTG ACGTATTGTA CCATCAAATA ATTGTTGAGA TTGTAGCAAG ACATTTAACG 660

ATTCAAACTT ATCTTTGTcA TCTATTTCAA ACATATCCAT ATTTTCGAAA CGAACAGAGC 720

CACTATCTAA TTGATATAAC CCTGCCATAA TTTGTAGTAA TGTACTTTTT CCTGAACCAG 780

AAGGACCC 788

(2) INFORMATION FOR SEQ ID NO: 777:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777:

TTACAAAAGA AATGCAACAA AATTTTTGAA TCATTACATT TTTTTATAAA AATTTCACTT 60

TAGATTCACA ATAATTACTT ATTTTGTCAA TTTATTTAAT GTCAATATGT TGATTAATTA 120

ATAGTGTTGT CTAATGTATA TAATATTTAG GTCATCGTTA TAGTCAACAA TAATAAGGTA 180

TTTCGAGTTG AAATTTATCT TATTATTTTT CCACTTTTAC GTGCTATCCC ATTACACAAA 240

AACAAATAAG TAAAGATATT AAGTACAAAA AAGTGGAACA CCTTGTAGAT GCTCCACCTC 300

AATTATATTA AGTTATATTA TTTTGCTGCT TGGTATAATT CATCAACTTT TTTCCAGTTA 360

ACAATGTTCC AAAATGCAGT CATATAGTCT GGACGTTTAT TTTGATATTT CAGATAGTAG 420

GCATGCTCCC AAACATCAAA TAGTAAGATT GGTGTTTTGC CTTCTGTTAA TGGATTATCT 480

GATCCAAATA ATGTTGTTGC TTTATTTGCA AATTCATTTT TAAATTCATC TAAAGTGCCC 600

CACTGCGcTT TGATGTCATC TATTACGCCA CCTTTTTCTT CAGAATTAGG TGATAGTATT 660

TCCCAGAATA ATGAATGGTT AAAATGACCA CCGCCATTAT TACGGACTGA CATCCTCATC 720

GCTTCCGGTA CCTTGTCTAA GTnAGCAATC ATATCCGCTA GTGATTGATG CTCTAACTCT 780

GTTCCTTCAA CTGTTGCGTT TAATTTCGTC ACGTACGTAT TGTGATGTTT GTCGTGATGA 840

AACTCCATTG TTCTTTGATC TATATATGGT TCCAATGCAT CATATGCATA TGGTAAATTT 900

GGTAATTTAA ATGCCATAAG TATATTCCTC CTTTTATGAA TATACTTTTA TAATAATTAA 960

TTTTGGGTGT GTTTTGCAAT AATTATTATT TATTTGTTAT ATCCAATTAT ATAAAATTTA 1020

AATATTCGAA ATTGATATAA TATTTAATAT TGAATGCAAA AAGGCATTTA ACTGCTTTTG 1080

TTTCCCGCTT TTAAAGAGAA TTAAAAAAGA CAACTTCCAT TTTTCAATAA GAAATTGCCT 1140

TTTCT 1145

(2) INFORMATION FOR SEQ ID NO: 778:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 902 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778:

AAAAGAGGnC CAATATTATC AATATACGGC CGGAAGATTC CCTTTTTCTT CTCCACTTAC 60

TAAGCCCATC AATGGTGTAT GTTATCaATT GGTGCTATCC GCATTAAATA ATTATCTTCA 120

ATTGTGGTAT CAAAGCTATT CGCTTTTTCT CCAATAATGT CTTTACCATA TTTATTGAAT 180

GCACCTACTA AAATCAACAT AAATGGAATT AACAAGGTTA CTACAATTGC CATTCTTATA 240

AATTGTGGTA TATAAGAAGG TCGCCAATTT AAAGCTTTAA TACCTTCTTw TCTAAATGGA 300

GTTTCTATAA AGCGATATGA TAGCTCTGCA AATATAATTG TTAAACTTAT ATCTATAAAG 360

TACACATATA CAGGTATCTG TCCGTCTACA TAGTAACTAT GTACGAAACT AATTACTGCA 420

AAATGCCATA AATATAAACT ATAAGACCTT TTCCCGATAA ATACTAACAC TGGATTTGAA 480

AATATCTTCG CtATCCATGT AGATGGATGA ACGACACTAG CAATAATAAA TAACGTTAAT 540

ATGGATATTA AATAGAAACC ACCATCATAT ATCCAATTCG TCTCATCATT AATAATGAAA 600

AATAATAATA TAAGTACTAT AAATGATAAA CTACCTATGC TATCAATAAC ATATTTTACA 660

ACTTTAGGTG GATCATTTTT CAATTTAAAC GGTGGCCATA AAAAAGCTAA AATAACACCC 720

ATACTATAGA TAAACATCAT TAACCCTAAA GAAATTATTG ATACTCCCCA AAAAATAAAT 840

CCTATTTTGT ATCGCTTTTT AATTGTTAAC AATAATGTAA CCAAAATAAC TGGGAAAAAT 900

AT 902

(2) INFORMATION FOR SEQ ID NO: 779:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779:

GGAATTAGTT TCCTAATGAT CAAACCATAA CCATTAGCTT TTAATGATGT TACGCCTTTA 60

AAGATTAGAG GATGATGACT AATAATAGTA TTATAACCTT TTTCGATTGC TTCATTTACT 120

ACTTCCAACG TACAGTCTAA TGCTGTTAAA ACACCAGTAA CTTCAACATC TTCATCACCT 180

ATTAACAATC CTACATTATC CCAAGATTCA GCAGTACTAA ATGGCACATG ATGATCTAAC 240

AATGTCATTA AATCAGCTAT TTTCATaCTA TAACACCCTT TCAATTACaG CAATTTCGTC 300

aTTAATTTGa GCTAAAcGTT GakGAkGTTG TTCAGTAwTG AGtTTCGaTT TAAtATGATA 360

AAgTGCyTCt AACTCtCTTT GcCATTTtTT TATAAAATAT 400

(2) INFORMATION FOR SEQ ID NO: 780:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780:

GTTCCTGTTT TAACATCAAT ATCTATCTTT TTAATATCTT GAACATAAAG CAGATTCAGT 60

TGGCTAATAT TTGAATTTAT GTTAATCACT TTTTTCGTTC CATTTTTAAA ATGTACTGTG 120

TAAGTnGCTT TTTTTGCATA TTTTAATTCA CGTTCCCCGA TACCTCTATC ATGCTTCAAT 180

ACTGaTTTAA CTTTTTTAGA GATATCTTTG TAGCCTACAC GTGGGTCACC TGTAAATTTT 240

AAATCTGaTA AAATTGGTGT TGATGTGCCA TTTACTGCAA TTGTGTATGG TACATATCTG 300

TCTGCTTTCG CTTTAGTTCC TGTTTTAACA GTAATTTCAA TTCTCTTAAC ATCTTTCGCA 360

TGAACTAAGT TTGCTGTGTA ATTTTTTGAA TTCAACTGTA AGATTCTTTT ACCACCATTT 420

CTATCATGCT TCAGTACTGA TTTTATTTGA CTAGTTAAAT TTTTGTAATT TGTCCAAGGT 540

TTATnTGAAA ATGAAAG 557

(2) INFORMATION FOR SEQ ID NO: 781:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781:

TTCTGATAAC ACAACTTTCT TGGACCAAGT GACAATGGTA AAGTTGATAT TCTCAAAAAA 60

TATATTTTAT TGAAAAGGTA ACTATATCGA CCGCTCTGTG CGACTTGCTG TGTAGAAACA 120

TCAAGCCCAG CTTGAAACTT CATATAAACT AATAACTTTT GATAAATGCT ATTCCCAATT 180

TGTTCATACT GCTCCAAGTT ATCATTAATT CTAAATTTAA TACTTACTTC ATTTTTAACT 240

GGAATAAAAT GTACATCACT CGCTTTCATT TCTATCGCTT TATTAATTAT TTCTTGAAAT 300

AGAATCTTCA AAAAAACACC TCCTACATAT AATCACGTAG GAGGTGTTTT TATTACTTCA 360

ATTTAACCGT GTAAAAATGG ATTTAATTGT TCATCATCAA CCGTCGTATA TGGACCATGT 420

CCAGGGAATA AAGGTAAATC GCCTTCTAAT TCAAATATTT TATCTTGAAT AGAAT 475

(2) INFORMATION FOR SEQ ID NO: 782:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782:

ATGAATATCG GTGCAGGACG TATCGTTTAT CAAAGTTTAA CTCGAATCAA TAAATCAATT 60

GAAGACGGTG ATTTCTTTGA AAATGATGTT TTAAATAATG CAATTGCACA CGTGAATTCA 120

CATGATTCAG CGTTACACAT CTTTGGTTTA TTGTCTGACG GTGGTGTACA CAGTCATTAC 180

AAACATTTAT TTGCTTTGTT AGAACTTGCT AAAAAACAAG GnGTTGAAAA AGTTTACGTA 240

CACGCATTTT TAGATGGCCG TGACGTAGAT CAAAAATCCG CTTTGAAATA CATCGAAGAG 300

ACTGAAGCTA AATCCATGAA TnAGGGCATn GGCCATTTGC ACCGGGGCCT GGCCGTAATA 360

AGCCAAnGGA CCGGGCCAAC CGTTGGGACC GGGAAGAAAA 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 810 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783:

GATTAATGTA CTCGTGTACA TAACGTTTGA AGTATGATAA ATAGATATAG AAATAAAGTC 60

ATATGTGACA TCAATTAAAT GATGTTCAAA TGACAAGATA CAATAGAGGA ATGTTTGTAA 120

TAnAAACGCT TCATATAAAG GTCGAGTCAA TATATGATAC GACTTTATAT GAAGCGTTTT 180

ATTTGCTATG AGCTAGTATA TTTTATAATA ATTTTTCTAT TTCTCTTTCG ATTTGAACAG 240

GTTTTTTTTG AGGTGCAAAT CGTTTAACAA CGTTACCyTC GCGATCCACT AAAAACTTAG 300

TGAAATTCCA TTTGATTTTC TCATTAAAGA ATCCGTGTTG TGCCGCAGTC AAATATCTAA 360

ATAAAGGTAA TTGATGTTCC CCTTTTACGT CTATTTTTTG ATGCATAGGG AAGGTAACAC 420

CATAGTTTAA TTTACAGTTT TGAGCTGCTT CTTCGCCTGA ACCAGGTTCT TGGCCACCAA 480

ATTGATTACA AGGGAAACCT AGAATTACAA ACCCTTGATC TTTGTATTTC TCGTATAATG 540

ATTGCAAACC TTCAAATTGT GAAGTAAAGC CACATTCGCT AGCTGTATTA ACAATTAGCA 600

TAACGTCACC CTTATATGCA TCTAATTTGT AAGTAACACC TTTATTTGTT TCTACTACAA 660

AATCATAAAT TGTCTCCATT GTATCATCCT TTCGATTTAC TTAAaATGTA CCAcAAAATC 720

GTGTAAtAGT CTkTACTArA ACTCTATGAT AGAATACTTT GAGTAGGATT TTATTAAGGA 780

GATGTATAAC ATGGnTCAGC AACAAATTCA 810

(2) INFORMATION FOR SEQ ID NO: 784:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 788 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784:

AAATTCATTG CAGAAAACAT AGATAAATAA ACAAATTGAC TTTAAACGAG CGTTGCAACA 60

TATCTCGAAT TGTAAAGGAG CTTGAAAATG AATAAAAATA TAGTCATTAA AAGCATGGCA 120

GCATTAGCCA TTCTAACCTC AGTAACTGGA ATAAATGCTG CAGTCGTTGA AGAGACACAA 180

CAAATAGCAA ATGCAGAGAA GAATGTTACG CAAGTTAAAG ATACAAATAT TTTTCCATAT 240

ACCAATAAAC ATGTATCAAA AGATTATAAA GTTGGCGATA GAATTACTGC CCATCCAAAC 360

GGTGACAAAG GAAATGGTGG TATATATAAA ATTAAAAGCA TTTCTGATTA TCCGGGTGAT 420

GAAGACATCT CTGTCATGAA TATTGAAGAA CAAGCAGTCG AACGTGGACC AAAAGGCTTT 480

AATTTTAATG AAAATGTCCA AGCATTCAAT TTTGCGAAAG ATGCTAAAGT TGATGACAAA 540

ATTAAAGTTA TTGGTTACCC ATTACCTGCT CAAAATAGTT TTAAACAGTT TGAATCTACA 600

GGAACTATAA AAAGAATsAA AGACAATATT TTAAATTTTG GATGCCATAC ATTGGAACCC 660

GGGGAATTCA GGGATCACCA GTTCTAAATT CTAACAATGA GGTCATAGGT GTGGTGGTAT 720

GGGCGGGTAT TGGGAAAAAT TGGGTTCTGG AATAATAATG GGTGGCCGTA TACTTTACGC 780

CTCCAnAT 788

(2) INFORMATION FOR SEQ ID NO: 785:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1023 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785:

CAATATTTTA GAAACAaTAA TTAACTTGCG ATGAACAAAC TATTAACAAT AATCTTGAGT 60

ATTATATTTA TCTTAATTAA TAATATATTT ATTTAAGATT ATGTTACTTC CAACTTTCAA 120

AGTAGAAAAA CGGTATAATT TGTTGATGGG TGTTTATTGA TAAACTGCAA AAAATACAGC 180

CTACAACCAC ATAGATTGTA GACTATATTT AAAATAATAG GTATTTATCA TATCTCGTAA 240

ACTTAGTGCC AATTTTTATA CTCGTGGTGC TGGTAAGCTA CCCTTAAATT CAGGAACGTA 300

GTGTGTaGGG CTATAACTTG GAACAGCATA TTGATAATTT ACATTTTTGA TATTTAATGA 360

TGGTTTCCCA ATTTTATAAC CATTTGATTG TGAAAATGAG AAATAkTTCT TCACACCTTT 420

AACTACTTTA TAAGAATAGA AGTATTTATA GTCATATGCT TTATTTACTT TAGCATTTTG 480

ATGTGTTGCT GTTGTGTTAT TTTGGAAACT TGGTACATGC ATACGATGTG AATTGTGACC 540

ATATGGTGGA ATTACCTTGA AACTATTTAT TTGTGGCACA ACACAAAAGT GATTAATTTT 600

AATGCTAGCA TGCCCTGGTG TAACAAATTT ATGCGCGTGA TATCCAGGAA CTGCAAAATG 660

ATGCTTGATA ATTAAAGATT gAGATGGATG TGTATATCTA GGCGATTCTG ATGGTTTAAC 720

AATAAAGTGT TTATTAATAG AATCCTTTGC ATGATTTACA TGTTTATGTA CATGTGTTGA 780

TTTGTATGAA GTAATAACTT TCTTGTAGTG GGTTTGCGTA GTAATGAAGT GGTGGTTTAC 840

TTGTTGTGAA GCTGGATTGT TTGTTGCTAC ATTCACGCGA TTATTGATTT CTTTGTACTC 960

TGGCACAATG TTTCCTAACT TTGATTCTGG nACGACAAAG TTTTTATCTA CAATTTTACT 1020

AGC 1023

(2) INFORMATION FOR SEQ ID NO: 786:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786:

TCAAGTTTAT TCGCTTGTTG GAAAGCTTTA ACTTGATTTT CTAAAGCTTT ATCAAATTGC 60

GTTGATTCAT TATCAACTTT ATAACCTAAA GCTGATAAAC CAATTTTAAT AGTTTTAATA 120

TTTTTATCAT CGTCTCCAAC TTTAAATGTT TTCGTATTAG GAATGACATT TAAAGATTGA 180

TATTTAGGTG TGTCAATAGT AACGTCTGGT TTAATGCCTT TACCGTGAAT ATAATGACCA 240

TCTGGCGTTA ACCATTTCAT TTCAGTATAT TTTAACAATG AACCATCCTT AAACTCTCTT 300

GTAGTTTGTA CGACACCTTT GCCGAATGTT TTTGACCCAT AAACTTTAGC TTTATTATAG 360

TCTTTTAGCG CACCAGTAAA CACTTCAGAA GCGCTAGcTG AACCTTCATT CACTAAGATG 420

GATATATCCA TGTCTTTCGC TTCTTTTAAC GCATCATTAG AAGTtGAATT GCTCAGTACT 480

TTACCTT 487

(2) INFORMATION FOR SEQ ID NO: 787:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787:

GnAAACnATA TTTAnAATTA AGTGTTCGAT TTGCAGTAAA TTCATACAGA AAAGCTAAAA 60

TTAAAATGAT ACaGTGGAAT AATGTCACAT TCTCCATAAA TAATTGACCG AAGAAGCATA 120

AAACATAGAA TAGTACAGTA ACACTTACCG GCTGCTTTTC TTTATATATA ATTGCATTAA 180

TACAATAATA AATAATAAAG AGTGAAATTA GTGTTGATGT CGCATAATTA TAAAATCCTG 240

CAAACCAGCC ATATGTATCT GCATAAATAG CACTTGGTAA AATTAACATT AAAGAAAATG 300

TGCCCATACT AATGAGGCCA TATGAAAGCC AACGTAACCA GCTTACATGT ACAGCTATAA 420

TTTCAAAGAT ATTTCCGATA TAGCGACCAT TAAGTGATGC AAATCCTACT TTTAAAATAT 480

CAGTATTATA ATTGCTAAAC CATTGTAAAT CATCGTGCAT GAGTGGTAGT AAGATACCCA 540

TAAAAGTATA AAACAATAAT ATCGCAATTA ATATCAAAGT TGTCTTGTGT AATTGAATTG 600

TTTTCACTTT GCTAATCCTC AAATCTAGTT AAATTTTCCT CAACTTGTAG GTCGAAAAAT 660

TAATTCAATA TTTTTAATGT ATTTCTAATT TTCACCTATG CATGTTTCCT CAATCAAATT 720

AGATAAACAA GGTATTTAAT ATTACTTTCA ACAATTTATC TAAATCGCCC CTCGTCTTTT 780

TCTATGaCGA ATGATTACAC TTG 803

(2) INFORMATION FOR SEQ ID NO: 788:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788:

GAAAAGTTGT ATTATGAATA AAGTTAATCA AGGTGCTCAG GAAGAGGCAA TGGAAGAGTT 60

ATTAGTGACT TTTCAAAAAT TGATTAAAGA CTAAAGGAGT TTAAGATGAT ACATCAAAAT 120

ACGATTTACA CAGCGGGAAT TGAAACAGAA GAACAAGTAA GTCAATTGAC AGAACGCATT 180

TCAAATATGA TAGGTGTTCA TCAAGTGAAT ATTAATATAA TAGATGGTCA AGTAACTGTA 240

TCGTATGAGA CACCAGCAAA TTTGAATAGT ATTGAAAAAG AAATCTATGA TGAAGGATAC 300

AAAATTGTAT TTTAGGGTAT AATGTAGAGT GCGCTATAGA TTTTAATTTT GAAAATAAAT 360

TAAAAATTTT GTAAATGATG TAGTAAAGGT ATGTCGAATA 400

(2) INFORMATION FOR SEQ ID NO: 789:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789:

GTTTAAAGAT GGAGAGATTA TTGATTTTTC AGCTGGAAAA GGTGAAGCGG TATTGAAAGA 60

TTTAATCAAT ACTGATGAAG GTTCAAGAAG ATTAGGTGAA GTAGCATTAG TACCTGATGA 120

ATGTCATTTA GCGATTGGAT CTGCTTACGC CTTTAATATT CAAGGTGGAA CGGAAATGAC 240

TGTTGAGGAA AAGATTGCAA GCGGATTAAA TGATTCAAAT GTACATGTCG ATTTCATGAT 300

TGGTAGTAGT GATTTGACTA TTTATGGCAT ATTCGAAGAT GGTTCAAAAG AACTAGTATT 360

TGAAAATGGA AATTGGGCAT CAACATTTTA ATAAATGTTA TTTTGAGGTG CTGAGTAGGA 420

AATGAAACAT GTATTTAAAG GTCAAATACG TGATTAAAGT ATAGATTGGG AGATAAAATA 480

ATGACAAATC AGGACAGACC AATGAAATCT ATGTCAGAAT CAAAATGTTA TAAAAATAGA 540

CAAGTTTTCC CTCAAGATAC GAATCACCAT CATACAATGT TTGGTGGTAC ATTGATGGCT 600

AATATTGATG AAATTGCAGC AATCACAGCT ATGAAACATG CTGGTGCGCA AGTAGTTACC 660

GCATCTACAG ACTCAGTAGA TTTCTTAAAG CCGATTAAAA CAGGGGACAT ATTACAATAC 720

GTAGCGATGG TTTCATACGC TGGGACTAGT TCAATGGAAG TG 762

(2) INFORMATION FOR SEQ ID NO: 790:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790:

TTTAATTTTA TCTTTTGGAT ATCACATAGA TGCTACTTTT CTATACTGTT CTAAATCTAT 60

TATTTCGTCA CATTGATTTG CAATAGCCAT ATCATGTGTT GCTAAAATCA GCACTTTATT 120

TTCATCGACC AAACCAAATA ATGATTGAAT AATCATCTGT CCTGTTTTAG GATCTAACGC 180

ACCCGTTGGT TCATCAGCTA ACATAACAAT CGGATCTTTT AACATCATTC TAATTAAAGC 240

GACACGTTGT TGTTCACCTC CACTTAGCGT ATGAACTTTT CTTTTTAAAC TGTTTGACAG 300

ACCAAACTGT TCtATATAAC GtATCTttAT TTGTnCTTTT TCTTTCTTAC TTATTTTTTT 360

ATATGCTAAT CCAATATCTA AATTTTCATT TACTGnCAAA 400

(2) INFORMATION FOR SEQ ID NO: 791:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791:

AACGTAAAGC GGAAGTTGGG ATGGTTGAAG ATGCTGAATT TCATGCGCAA CTACATCGTT 120

ATAATGCTTT TCTAGAGCAA CATCAAGATG ATAAAGTGTT GTATTTnGAA ATTGGAATTG 180

GTTATACTAC ACCACAATTT GTGAAGCATC CTTTTCAGCG TTGACACGTA AAAATGAAAA 240

TGCCCTTTAT ATGACGATGA ATAAAAAGGC TTCGCATTCC GAATTCAATT CAGGACGTAC 300

CATACTTTAA CTGAGATTCT CAACTTGTTC AGCAGACTCC GGACGCAGCA CACGAAATAC 360

ACATGGGGGC AGAGTnACTT ATGGACCGTT GAATGnGATA 400

(2) INFORMATION FOR SEQ ID NO: 792:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 678 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792:

GTTCCGTTTG ATACAGAGAA GCGAATGTAA GCATAATCTT TAACAGTATC GTATGATAtA 60

AtTTAATTGG CAACTTTTTG TCACCTTCAT AAACTTCAAA TTTTCTCCAA AATTGACCTG 120

ATTGTAATCC TAATTCAATT TCTGGTTTTG AATCAGTGAA AATAACTCTA GCAGGTTTAA 180

CAGAACTTGC ATAATGATAA AACTGTTGAG TTCCATCTTT CTTTTTCATT TCAAAATCAA 240

TTGGACGAGA GTTTGGTGCG CTATGATCTT TGTCTTTTAT TGCAGGGTTT TTAATCGCTT 300

CTCTAAGTTC CTGaTTCAAA ATAGGATATG TATTGTTAgT GGCyTTTGCT GCTGGTTTAA 360

CTTCTTTTGT TTCCTTAGGG GcTTTAACTT CTTTAACTTC TTTAGCTTCT TTTGTTTCAG 420

AAGTAGGGGC CTCAACTTCT TTATTAGATA CTGAGACAGC ATTAGCTACT GGTTTAGTTT 480

CTGGAGCTTT TTCAGATGTT GTTGTTGGAC TTGCAACTGC TTCAGTTTTT GGTTGTGCTT 540

CTGTATTTGT ACCACCTGTT TCTTCAGCTG CTGCTTGTGT TCGCCATTTG ACATTAATAA 600

TAAAAGTGTA CTAATTGCTA CAGATGCAAC GCCTAGTGAT GACTTTCTAA TTGAATAAAA 660

TGATTTAAAT TCTTTTTG 678

(2) INFORMATION FOR SEQ ID NO: 793:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ACTGGCGGAT CCACGATGGC ATGTGTTAGT GAAGCAATTC ATTTATTACC ATATAATGTA 60

TTCTTCGTAC CAGCCAGAGG TGGACTAGGC GAAAnTGTTG TCTTTCAGGC AAACACAATT 120

GCAGCCAGTA TGGCACAACA AGCTGGCGGT TATTATACGA CGATGTATGT ACCTGGATAA 180

TGTCAGTGAA ACAACATATA ATACATTGTT GTTAnGAGCC ATCAGTCATT AAACACTTTA 240

GGACAAAATT AAACCAAGCA AACGTTAATA TTACACGGGC CTTTGGTGAT GCGCTGGAAG 300

ATnGGCGCCT CGGACGTCCA ATCACCTGGA AAAGGTCCTT GGAACCACTT C 351

(2) INFORMATION FOR SEQ ID NO: 794:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794:

GGGCGAGGCG TTCGCGCACC GGCCGAGCAG CAAATAGGCC GGGATGTCGC GTCTTGCTGC 60

AGGTCCGAAA AATATCAACT TGAAGAGGTA ACACCGnTAG ATATGTTTCC ACAAACAACA 120

CATGTTGAGA CAGTGGCATT ATTCAATTTG AAATAGCGCA CATGATTTGA GATAAAATTT 180

CGCCTTAATA AGTGAAGAAA GAAGTCGTAT ATTAAAATTT TATTACAGCC AATTTACTTT 240

CTTGATATGA ACTTTTTAAA TTAAATGTGA CATTGTATAC TATATTTAAA GAAGAATAAG 300

AATGTCATGA TCGGGAGGGT TGGTAATGCA TAAAATTGAT TTAACGACAA ATAATTTTCA 360

AATGCGAGGT TTATTATCCT GGCAACCTGG TTATTGCGTT 400

(2) INFORMATION FOR SEQ ID NO: 795:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 407 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795:

ATGTTCCAGG AACGTATTTT TACAACCGAC AATTAGCATA TGTCATAATG AGTTTTATAA 60

TTGTATTTTT TATTGCATTT TTAATGAATG TTAAATTACT GAGTAATATT AAAGTGCAAA 120

AAGGTATGAT TATAACTATC GTCTCACTAT TATTACTGAC GTTAGTAATA GGTAAAGATA 180

TTAATGGTTC TAAAAGTTGG ATAAACTTAG GATTTATGAA CTTACAGGCA TCTGAGTTAT 240

TAAGTAAACC AAAATTAATt TTAAGTCCTA TTGTATTAGC ATTAGGTTGT ACGTTTTTAG 360

TTTTCCTACA AAAAGACGTG GGCAACATTA CTAATATTAA TnATnTT 407

(2) INFORMATION FOR SEQ ID NO: 796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1053 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796:

CAGTAGGTAC ACTTGCAGCA TTTGTTGGAT ACTTAGAGTT ATTGTTCGGG CCTTTACGTC 60

GTTTAGTCGC ATCATTTACA ACTTTAACGC AAAGTTTTGC TTCAATGGAC CGTGTATTCC 120

AATTAATTGA TGAAGATTAT GACATCAAAA ATGGTGTTGG TGCTCAACCT ATTGAAATTA 180

AACAAGGTCG TATTGATATT GATCATGTTA GTTTTCAATA TAACGATAAC GAAGCTCCAA 240

TTTTAAAAGA TATTAATTTG AGTATTGAAA AAGGAGAAAC AGTTGCTTTC GTAGGTATGA 300

GTGGTGGTGG TAAATCAACA TTAATTAACT TAATACCGAG ATTTTACGAT GTAACTTCTG 360

GGCAAATTTT AATAGaTGGT CACAACmTTA AAGaTTTTTT AACGGGAAGT TTAAGAAATC 420

AAATAGGATT GGTGCAaCAG GATAATATTT TATTCTCTGA TACAGTTAAG GAAAATATTT 480

TaCTTGGTCg TCCaACAGCa ACAGATGAAG AAGTAGTTGA AGCGGCgAAA ATGGCTAATG 540

CACATGACTT TATTATGAAC TTGCCACAGG GATATGACAC TGAAGTAGGT GAACGAGGTG 600

TTAAATTATC AGGTGGTCAA AAACAAAGAT TATCGATTGC TAGAATATTT TTAAATAATC 660

CGCCAATTCT TATCTTGGAT GAAGCAACAA GTGCACTTGA TTTAGAAAGT GAATCCATTA 720

TTCAAGAAGC ATTAGATGTG TTGAGTAAAG ATCGAACGAC ACTTATCGTA GCGCATCGCT 780

TGTCCACTAT TACACATGCT GACAAAATTG TCGTAATTGA AAATGGACAT ATTGTTGAAA 840

CAGGTACGCA TCGTGAATTG ATTGCAAAAC AAGGTGCTTA CGAGCATTTA TATAGCATTC 900

AAAACTTATA AAGTATTAGT TGTTTGACTT CAGTACAATC TTGAAGAGAA AATTTGTAAC 960

AGGATGGTGG GGTCATAACA TAGAAAAAGC AGTAAGAGAT TTTCTTAGTT GAAAATAATC 1020

TTnCTGCTTT TTTAAATTTA ATTTCGnGAT TCA 1053

(2) INFORMATION FOR SEQ ID NO: 797:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 544 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797:

AAGAGTGACT CCTGAAGTGA AAGAAGGGGA CCGTGTCGTG TTCCAACAAT ATGCTGGTAC 60

AGAAGTTAAA CGAGATAATG AAACATATCT GGTATTAAAT GAAGAAGATA TTTTAGCAGT 120

TATTGAATAA TACAGAACTT AATTCATAAA TAAATTAAAT AGAACGAAAA TGAAACACAA 180

CTAAACAAAT GGAGGTTTAT CATTTATGGT TAAACAATTG AAATTCTCTG AAGATGCACG 240

TCAAGCAATG TTACGTGGTG TTGACCAACT TGCAAATGCA GTTAAAGTAA CGATTGGTCC 300

TAAAGGACGT AATGTTGTAT TAGATAAAGA GTTTACAGCA CCTTTAATTA CGAATGATGG 360

TGTGACGATT GCyAAAGAAA TCGAATTAGA AGATCCATAT GAAAATATGG GGGCTAAACT 420

AGTTCAAGAA GTCGCAaATA AGACAAATGA AATTGCTGGT GACGGTACGA CAACTGCAAC 480

AGTATTAGCT CAAGCAATGA TTCAAGAAGG CTTGAAAAAT GTTACAAGTG GTGCGAACCC 540

AGTT 544

(2) INFORMATION FOR SEQ ID NO: 798:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798:

CAATTGCATA GATATTGCTG ATAGACGTAC GGCTTTGTTT ATCAACTTCT AATAATCCAC 60

GGTCAGCGAA TTTAACACCT AATTTCGTCT GTGTTTGGAC GACGACCTAC AGTTACTAAT 120

ACATAATCAG CTTCGATTGT TTTCTCTTCG CCTTTAGCTT CATAAGTAAC TTTAACTCCG 180

TTATCTGTTT CTTCAGCTGA TTTAGCCATA GCTTCAGTAA CGATTTCAAC ACCTTTTTCT 240

TTCATACCTT TTTTAACAGG TTGTGTGCAT TTGnTTTTTC GAGGCCACCT AAGATATCTT 300

TAGCACCTTC AAGGGATGGG GTACTTTCTG nAACCAAAGT TAGCAAATGC TGTACCTAAT 360

nCTGGTCCAA TG 372

(2) INFORMATION FOR SEQ ID NO: 799:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799:

AAACGACATT TGTTTAATTG GAAGAATTaG CACCATTTTT TGAGGCGGGT ATAGAtTCAT 60

TTAAAATCGA TGGTATTCTA CAAACGGAAG AATATATTAA TGTGGTAACG GAACAGTATC 120

GTCAAGCGAT AGATTTGTAC AATGAAGATC CTGAAATCTA TGAAGATGAG AAATTTATGT 180

TGATGGATCC AATTGAAGAA ATTCAACCTg ATCATCGACC ATTTGACGAA GGTTTCTTAT 240

ATAAACAAAC AGTATATTAA GGAGGTTAAT CATGAAGACA ATAGAAGAGA TTAAATCAAC 300

TCCTAAAACA GTTATGAAGA AACCAGAATT ATTAGCACCT GCTGGAAACT TAGAAAAGTT 360

AAAAATAGCA GTACATTATG GCGCTGATGC CGTATTTTTA GGTGGTCAAG AATATGGATT 420

ACgTTCaAAT GCTGaTaATT TCaCGATGGA AGAAATAGCT GAAGGTGTTG AATTTGCGAA 480

CCGTTACGGT GCCAAAATTT ATGTTACGAC AAATATTATT GCACATGATG AGAATATTGA 540

AGGTCTAGAA TCATATTTGC GTAATTTGGA AAAGACTGGT GCGACAGGTA TCATTGTTGC 600

AGATCCTTTA ATTATCGAAA CATGTAAAGA AGTTGCGCCA AAACTTGAAA TTCATTTATC 660

TACTCAACAA TCACTTTCTA ATTACAAAGC TGTAGAATAT TGGAAAGAAG AAGGATTGGA 720

TCGTGTTGTA TTAGCACGTG AGACCGGCGC GATGGAAATG CGTGAAATGA AGGAAAAAGT 780

AGATATTGAA ATCGAAGCAT TTATTCATGG TGCTATGTGT ATCGCCTATT CAGGTAGATG 840

TACATTAAGT AATCATATGA CTGCAAGGGA TTCCAACAGA GGCGGTTGCT GTCAAAGTTG 900

CCGTTGGGAT TATGAATTAT TAGAAGTTGA TGATAATGGT GAACTTGATG TTTTTTATAA 960

TCAAgGTGAA GTTACACCGT TTGCGATGAG TCCTAAAGAT TTAAAATTAA TCGAATCAAT 1020

TCCTCAAATG ATGGATATTG GTGTGGACTC ATTAAAAATT GAAGGACGTA TGAAGTCAAT 1080

TCATTATATT GCAACAGTTG TCTCAGTATA TCGTAAAGTC ATTGATGCGT ATGCGGCAGA 1140

TCCTGACACT TTAAGATTAA TCCGGAATGG TTAATAGAGT TA 1182

(2) INFORMATION FOR SEQ ID NO: 800:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 989 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800:

GTATTCTTCC AATAACACCT TTCATTTGGA AACCGTTTAG AAAGAATACA GTTACTTCAG 60

TTTGGTTTGC TTTAAAATTC TCTaGTGCTT TGTCTTGGAT GTTTTCGtTG cAATCATCTG 120

TTTTCTTTAT CTAACCAATG AACACTCATT TTATTCTTGA ACCATGTCAT TTGTCGTTTT 240

GCATATTGGC GTGAATGTTG CTTTAAATCA TTGACAGCAT CTTCATAAAT CATTTGTCCG 300

TTAATCACAG GTATTAATTC TTTATATCCA ATAGCTTGCA TACTTTGGCA AGATTCATAG 360

CCTTGTTCAA CAAGTTGTTG CACTTCTCTA AATAATCCGT GATCCAACAT AATATCAACA 420

CGTTTATTTA TTCTTGAATA TAATGTTTTA CGCGACATTT CAATCCCTAA TAATAATGTA 480

TCATAATTTT CAGTAAATTG TTGCACTTTC TTGCGATTAC TCAAAAGTTT TTTTGTTTTT 540

AAATAATATT CAATAGCGCG CAACACTCTT TGGcGGTTGT TAGGGTGAAT ATTTTCTGaC 600

AGAAACCGaC ATCAAATTGA GCTAAATAAT CGTGTAGTTG CTGATTATCT AAATGTTCTA 660

ATGCAGATAA CTTTTGTTTA ACTATGGATA ATTGTGCAGG TGTAcTGTTT CATCTTCTAA 720

TTCATAATTA TATATTAATG ATTGAATATA TAAGCCTGTT CCACCTGCTA TGATTGGaAC 780

TTTACCTCTA TTCGTtATAT CAGTAATTAA ATCTTCTGCT AATCGCTTGA ATTCATATGC 840

TGAAAATGTA TCATCAGGAT TCAAGATATC AATTAAATGA TGTGGAATAC CATCCATTTC 900

TTCAGGTGTn ACTTTTGCAG TTCCAATATT CATATGTCTG TAGACTTGCA TAGAGTCACC 960

GCTTATGATT TCACCATTGA TACGCTTCG 989

(2) INFORMATION FOR SEQ ID NO: 801:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 543 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801:

CGTTAGATAT AGAATTAAAA GATAATATTA AATTTCAAAA CGGTCAAAAA TTGACTGCAG 60

AAAAAGTGAA ATCTAGCCTT GAAAATAGCA TGAAAAAAAG CGACTTGGTC AAATATTCAT 120

TACCAATATC ATCAATTACC GCTAAAGGTC AAAAACTGAC AATTAAAACC AACTCCGCTT 180

ACCCTGaACT TGTATCTGAA TTAGCTAATC CTTTTATGGC AATTTATGAT ACAGATGCTA 240

AATCAGATGT TAATCAAACT CCTGTTGGTA CAGGCCCTTA CCAAATAAAA GATTATAAGC 300

AATCTCGAAA AATATCATTG TCGAATTTTA AGGACTATTG GCAAGGTAAA CCGAAACTTG 360

ATCATATTAC TGTGACGTAC CAAGAAGACG GCAATAATCG CGTCAGAAAT TTAGAATCTC 420

AAAAAGATGA TTTAATAACT GATGTCCCAG TTAATAAAGT TCAAGACATA GAAAATAATC 480

AAAATTTAAA AGTGTCAAAA GAATCTGGAT TTAGAACTTC TTTACTTATG TATAATCATA 540

(2) INFORMATION FOR SEQ ID NO: 802:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802:

GCGAATTCGT ACACACATAT ACACAAAGAT AATCATAGTT TTACATTGAA GCACATGAAA 60
GATAATTCAT TTAAAGGAAG GTATTATCAA TGACTAAAAA AATGGGATTA TTAGTTATGG 120
CTTATGGCAC ACCTTATAAA GAAAGTGACA TAGAGCCATA TTATACAGAT ATTAGACATG 180
GTAAACGTCC ATCTGAAGAA GAACTTCAAG ATTTGAAAGA TAGATATGAA TTTATAGGTG 240
GTTTATCACC ATTAGCAGGT ACAACAGATG ACCAGGCTGA TGCGCTAGTT TCAGCATTAA 300
ATAAAGCATA TGCAGATGTT GAATTTAAAC TATACTTAGG ATTAAAACAC ATTTCACCAT 360
TTATCGAAGA TGCGGTTGAA CAAATGCACA ATGATGGCAT TACTGAAGCA ATCACGGTAG 420
TACTAGCACC ACATTATTCT TCATTTTCAG TAGGATCATA TGACAAACGT GCTGATGAAG 480
AAGCTGCAAA ATATGGTATT CAACTTACAC ATGTGAAACA TTATTATGAA CAACCTAAAT 540
TTATTGAATA TTGGACGAAT AAAGTCAACG AAACATTAGC TCAAATACCG GAAGAGGAAC 600
ATAAAGACAC GGTATTAGTT GTTTCGGCAC ATAGTTTGCC AAAAGGTTTA ATCGAAAAGA 660
ATAATGATCC ATATCCACAA GAACTAGAAC ATACTGCGCT TTTAATTAAA GAACAATCTA 720
ATATTGAACA TATCGCGATT GGTTGGCAAT CTGAAGGTAA TACAGGTACA CCTTGGTTAG 780
GGCCAGATGT ACAAGATTTA ACACGTGATT TATATGAAAA ACATCAGTAT AAAAACTTTA 840
TATATACGCC AGTAGGTTTT GTATGTGAGC ATTTAGAGGT GCTTTATGAC AATGATTATG 900
AATGTAAAGT AGTTTGCGAT GATATTGGTG CGAATTATTA TCGTCCAAAA ATGCCGAATA 960
CACATCCATT ATTTATCGGT GCAATTATTG ATGAAATCAA GTCTATATTT TAATGACGAA 1020
AGAAGCGTGA AACGTTGTGA CTAAATCAGT GGCTATTATA GGAGCGGGGA TAACAGGTTT 1080
ATCAAGTGCA TATTTTTTAA AACAGCAAGA TCCTAATATT GATGTAACCA TCTTTGAAG 1139

(2) INFORMATION FOR SEQ ID NO: 803:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 989 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 803:

TATCCnAAAT AnAAATGTGC GCATTTATCA AAACCTTACA TACAATAGAG TTTTCCCTAA 60

CAGTAAATTA GATATTATTA CACCTGTTGA TATGTCTTCT AATGCCAAAC TGCCAGTTAT 120

TTTTTGGATG CACGGTGGTG GTTATATTGC GGGTGATAAG CAGTATAAAA ACCCATTATT 180

AGCGAAAATT GCTGAACAAG GGTACATTGT TGTGAATGTA AATTATGCAT TGGcGCCACA 240

ATATAAATAT CCCACACCAT TAATTCAAAT GAATCAAGcA ACTCAATTCA TTAAAGAAAA 300

TAAAATGAAT TTACCTATTG ATTTTAATCA AGTAATTATT GGCGGTGAyT CTGCAGGTGC 360

TCAATTAGCT AGCCAATTTA CGGCAATACA GACGAATGAT CGCTTAAGAG AAGCCATGAA 420

ATTTGATCAG TCATTCAAAC CATCGCAAAT TAAAGGTGCT ATACTATTTG GTGGTTTTTA 480

TAATATGCAA ACAGTTAGAG AAACTGAGTT TCCAAGAATA CAGTTATTTA TGAAAAGTTA 540

TACTGGCGAA GAAGATTGGG AAAAGAGTTT TAAAAACATT TCACAAATGT CGACAGTAAA 600

ACAATCGACA AAAAATTATC CaCCAACATT TTTATCTGTT GGAGATAGCG ATCCATTCGA 660

AAGTCAAAAT ATAGAATTCA GTAAGAAATT ACAAGAATTG AATGTACCAG TAGATACTTT 720

GTTTTATGAT GGTACGCATC ATTTACATCA TCAGTATCAA TTTCACCTTA ATAAACCTGA 780

ATCGATAGAT AATATCAAAA AAGTGTTACT TTTCTTAAGT CGTAATACAT CCTCTAGTGG 840

TATTCAAACT GAAGAGAAAC CACAAATAGA AAATCCGAGT AATGAATTAC CGTTAAATCC 900

TTTAAACTAA TGATAAACAG TAGTAATTTA TTACTTAAGC AACATTTAAG ATTTTCAAAT 960

TAAAAACGAG AATTTAAAAC ATGTGGTGC 989

(2) INFORMATION FOR SEQ ID NO: 804:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 711 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804:

TAAnCCCTGG TTTAATGATT TTGATTACGT GTTTTTATAA TAAAAACATA TCGAACATTG 60

ACTACGTTAT TAAGCTGCTT TTTTGTACAC TTTATAACCA ATAGCTTAAG ATTTAAAACT 120

AATCGGAAAG AACAATGATT CACCAnAAAA ATATTTATGT TGCTATTAAA AATCAGTTAA 180

TACGAATGTT AAAATACGTT TGATTTTCAT TAATAATGAT TCAAGTTTAT TTAAATGAGC 240

GTTAATGTCA GTCTGTTTTG ATGCACCTTA TAATAAAGAC AGATAGTTCA AATTACGTAA 300

AAAGCAACAT TAGCATTAGG AATATTAACT ACAGGTGTGT TTACAGCAGA AAGTCAAACT 420

GGTCACGCGA AAGTAGAACT TGATGAGACA CAACGCAAAT ATTATATCAA TATGCTACAT 480

CAATACTATT CTGAAGAAAG TTTTGAACCA ACAAACATTA GTGTTAAAAG TGAAGATTAC 540

TATGGCTCTA ACGTTTTAAA CTTTAAACAA CGAAATAAAG CTTTTAAAGT ATTTTTACTT 600

GGTGACGATA AAAATAAATA TAAAGAAAAA ACACATGGCC TTGATGTCTT TGCAGTACCT 660

GAATTAATAG ATATAAAAGG TGGCATATAT AGCGTTGGCG GTATAACAAA G 711

(2) INFORMATION FOR SEQ ID NO: 805:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 680 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805:

ATCAGGAAAA ACAGaATAAT GTAAATCAAG CTGTTCAGCC TCAAAATAAT ACTAATGAAA 60

CATCAAAAGT ACCGGCTAAT TTTGTCAAAT TGAATGATAT TAAACCAGGT GATACTTCTA 120

TACAAGGAAC AACTTTACCA AATCAATTTA TACTATTAAC TATTGATAAA AAAGATGTGA 180

GCTCAGTTGA AGATTCTGAC AGCAGCTTTG TTATGTCTGA TAAAGATGGG AATTTTAAGT 240

ATGACTTAAA TGGTCGCAAA ATTGTTCATA ATCAAGAAAT TGAAGTGTCT TCATCAGATC 300

CCTATTTAGG TGACGATGAA GAAGATGAAG AAGTAGAAGA AACTTCAACT GAAGAAGTTG 360

GTGCTGAGGA AGAAAGTACA GAAGCTAAAG CTACATATAC AACACCGCGA TATGAAAAAG 420

CGTATGAAAT ACCGAAAGAA CAGCTAAAAG AAAAAGATGG ACATCACCAA GTTTTTATCG 480

AACCTATTAC TGAAGGTTCA GGTATTATTA AAGGCCATAC CTCTGTAAAA GGTAAAGTTG 540

CTCTATCTAT TAATaATAAA TTwATTAACT TTGAGaCAAA TGCTAtGGTG GtCCaAATaA 600

AGAAGaAGCG AAATCTGGAT CAGAAGGAAT CTGGATGCCT ATTGATGACC AAGGATACTT 660

TAATTTTGAC TTCCAAACGA 680

(2) INFORMATION FOR SEQ ID NO: 806:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 950 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GTATTTCATT AGCCATTGGC AATTGACATC TGACAATGAG GAATGGCTTT TGCATTGGAA 60

TTCACAGTTG GAGTGCATTT ACTGGTTATT TTGGAGGTCA TTGTTGATAC ATTATTAATG 120

GAGAATAACC GAATTTGTTA TGTTATTTCC ATTTTTAATA TTTGCAATTG TATTAAATGC 180

TGCACTTGGA GATAAAATTA AAAATCCTTA TGGATCTGCC ATAATTCTTG TTCTAGTTAT 240

TATCGTATTA AGTTGGGGAG GTATTGACAA GACTTGTTCG TGGTAAAGTA CTTCAAGAAA 300

AAGAAAATGA ATACTTTTTG GCAGCAAAAT CAATTGGTAC ACCCACATAT AAAATTATTT 360

TGAAACATCT TTTGCCGAAT ATATTAAGTG TAGTTATCGT ACAAGCAACA TTGTTATTTG 420

CCGGTATGAT TGTAGTGGAA TCAGGrTTGA GCTTTTTAGG ATTCGGAATT AGTAAAGCAA 480

TACCATCTTG GGGTAATATG TTGAGTGATG CTCAAGAAGG GGATGTTATA AGTGGTAAAC 540

CGTGGATATG GATGCCACCT GCTATAATGA TTACATTAAC TATATTAAGT ATAAACTTTG 600

TAGGGGAAGG GATTAAAGAT GCTTTTAATC CTAGAGGTAG ACGTTAAATA ATAAAAGAGG 660

CACTAGTTAA TTCTAGTACC TCTTTATTTT ATCTCTTACG TCCTAAACCC ATCGCTTTTT 720

CCATTTTTTT GACAGTTTTA AATGAAACTT TGTGTGCTyT ATCTCTACCT TGATCTAAAA 780

TATCAyCAAG TTTATcTGAG TTATAGAAAC TTTCGTATTT TTCTTGGAAT TCTACTAAAA 840

ATGCTTTAAC TATTTCAGCA AGGTCACCTT TAAATTTACC ATAACCTTCG CCCTCATATT 900

TTGCCTCAAT ATCTTTAATT GGCATGTCTG TTAATCCAGC GTATATTGAA 950

(2) INFORMATION FOR SEQ ID NO: 807:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807:

GTTACCAGTC GAAGCTTTAC GACCTGTTAC GAAACATTGT TTACCCATAT GAGTACCTCC 60

TTTAATAAAT ATAAATACAC ATAACTACTT ATATACTTAA TTAAGATAGC ATAGTTTCAT 120

TTGAAAAACA ATGAATAATT TTCACATAAA AGTCAAAAAT ACTGAGTTTT GTGATATAAT 180

TGTAGACTGT GAAGTTATGT AGTATGATAT TTTAGAGAAA TAAGTGAATG AAACATTTAA 240

AATTTTTATT TrATGATACT ACATCTATTA AAAGAAAACG CCTATAGATA ATCGTCaTGA 300

GTGTAAATTC AGTTtACTCa AcAtATAaTA GGkGaTTTAA gCgTAAGtCa TTCTGATAAG 360

TTGTACCATT GATATTTTAT GAAATAnTCn ATGAACTTAA AGCGTTTATG CTACACTA 418

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 842 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808:

AATGGCnATT AATCTTTAAT ACGATGCTTG AGGATTTTTC CTAATAAAAC CTTGATTTCm 60

AAAAGGGTTT AAATCmAATG AAACAATAAT AAaAAAATGw CGCAATATAA TAATAAGTAC 120

AAATTTAATT AAGAAATTAA ATTGATTGTA TATGTATATT TTGGTAACGT AAAAGAGAnA 180

TATACAAAAT AATTAATTAT TTATATGAAA AGAGAATATA AATGAAGTAT AAAACAGAGA 240

GACGTGAAGC GATGGGATAT TTAAmAAGGT TTGCATTGTA CATAAGCGTT ATGAyTTTAA 300

TATTTGCGAT AGCAGGTTGT GGCAAAGGTA ATGAAACAAA AGAAGATTCA AAGGAAGAAC 360

AAATCAAAAA GAGCTTTGCG AAAACATTAG ATATGTATCC AATTAAGAAT CTCGAGGACT 420

TATACGACAA AGAAGGATAC CGAGATGGCG AATTTAAAAA GGGTGATAAA GGGATGTGGA 480

CGATATATAC AGATTTCGCC AAAAGTAATA AACAAGGTGG ATTGAGTAAT GAAGGTATGG 540

TCTTATACTT AGATAGAAAT ACACGGACTG CAAAGGGACA TTATTTTGTT AAGACATTCT 600

ATAATAAGGG CAAATTCCCA GATAGAAAAA ATTATAAAGT TGAAATGAAA AATAATAAAA 660

TTATCTTATT AGATAAAGTA GAAGATACAA ATCTAAAAAA GAGAATAGAA AACTTTAAAT 720

TTTTTGGACA ATATGCAAAC CTTAAAGAAT TGAAAAACTA CAACAATGGT GaTGTCyCAA 780

TTAATGAGAA TGTTCCAAGT TATGACGCAA AATTTAAAAT GAGCAATAAA GATGAAAATG 840

TT 842

(2) INFORMATION FOR SEQ ID NO: 809:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809:

TAAGACTATG CCATCTTGGC AACGCGTTGT CGCATATTCA TTATTAGTAA GTATATGCAA 60

GCATGATTTT GCCATAACtT TACCtCtTTC TATATTTAAG TACCACTTTT ATCATTCCCT 120

ATAATATTTA ACTTATTTAA TTAAACGTAA ATTTAACACA ATACGAATAC CAAATCAAAA 180

AAAAATAGAT GTAGTCAGTT TAATTAAACT ATCCAATTGA AAACACACTA CTTTTTAGTA 300

TTTTCAAAAT AATTTTAAAT GACCACATCT ACAACGTATT ACTATTATCT TTTGTTAGTT 360

ATATATTCAT TTTCAATTTA rAAATAAACA CTTAtTTAAA TCACATTCTA CTTTTGAGAT 420

GAGCTCAAAC TAACATTAAA TTGTTTATAT T 451

(2) INFORMATION FOR SEQ ID NO: 810:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1499 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810:

ACATTTTGTG CTTGTTGTCC AATCCAATTT CTACTTTGTT GAACAGTATG AGTTGCTTGA 60

CCACGCATGT TACTCAGCAT TTGTCCAACA TGAGTATTTT GAGCAAAGTT ACGAGATTGA 120

TTCAACACAC TGTTTTTCAT CATTnCCATT TTAGGTGAAA TACGACTAAC TGCTTGTTGC 180

ATTGTCTTTT GCAATCCTGT TTTAACTGCA AATTTTTCTC CGCCTTTGAA GCCTAATTTC 240

ATTAAACTTT TCCCAGCACC TTTGAGGAAG CCCATACCTG GCAATGGAAT AAGCGAAAGT 300

CCTTCCATGA TTCGTTCTTC TTTAGATAGC TTTCTTCCAG TTACAATATT TTTTCCTGTG 360

GCTGCATTTG CTGCTGAATA AGCGGAATAA GCACCAATAG CTACTGCTCC AGCAACAGGA 420

TTAATACAAG ATAAAACTAC CATACCAGCT AGTGCTGCAA TCTCTATAGC TTCTTCTTTT 480

TTCTTTTGCT CCTCTAGcTC TTCCGCTTCA GCTACTGTCA TGTAATCACA AGAAGCGCCC 540

TGAGTCATCA TTTTTTCAAA ATCACTTTTA GATAATTTCT TATCTTCTTT TTTCATTTCT 600

TTGTAATGCT GATCAATTAC TTTTACAAAT TCTTGATCCG ATTTTAATAT TTCATCGATG 660

CTATAAACAT CGCTGTCACT TTTCTTGGCA TCTCCCTTTG CAATTTTCCC AGAAGCCCCA 720

TAGGTATCTC TACCATGTCC ACCACCATTT TTAATTAGTA TATTTTCCAA TTTAACATTC 780

GTTATACCTT TGAATGCTTT ATCTATATCT TCTATAAATG GCGTGTCAAT AATTTCTTTC 840

ATTTTCGAAT CTAATTGAGA TGCATAATCA TATAACTCaT TTTGATAATA CCCCATTAAT 900

TTAGATCCTT GTGGAcCTAC TACACTACTT GTTAATGATA TTGCGCCATC TTCGTCTAAA 960

GAACTGACAT CGCTTACCGC ATCATCCATT GTTGTATCTA CATCTAAGAA GTCTTGACCC 1020

TcTATTGCAT CTATTACACT TTGGATAGAT GACTTTTCAT TGTCATAATC AGCTGTTAGA 1080

TATTCAATAT CTTTTGTCAT GTCATGCACC TATCCCTCAA TATTATAGTA AAGCTTGGCA 1140

CCACCGAGTG TACTCAATGG ACCTTTGAGA CCACTAATGA CTGTTGCAGC ACTACTATAG 1260

CCATTTTCCA TAGAATGTGC AGCTTTTTCA CTACTGTAGT AATTTAATTG CGCTATTTTT 1320

CCAAAGTTTT GAGCTATTTC ATCATACTTT TGACTTATGC TTTCCAATTC TTTTACAACA 1380

TGTGCAATCG TTTCAGCTTT AACACTAATT TTTCCACTCA ACGTCATTAC TCCTCtGcTt 1440

TATtAATATG ATTTTcATCA GTATCGAATC CAAATAATTC TCGTGATAAA nGTATTGAA 1499

(2) INFORMATION FOR SEQ ID NO: 811:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811:

CnCGCTGCAC CGAAGAATGC TTTTGGTTTG TGTAAAGATG CAGGATCTAA ACCACCTGAT 60

AATGTACGAC CACTTGGTGG AATAACyAAG TTATAAGCGC GTGCTAATCT CGTTATAGAA 120

TCCATTAAAA TAATGACATC TTCCCCAATT TCTACTAAAC GCTTTGCACG TTCAAGTAAT 180

AATTCAGCTA CTTTAACATG GTGTTCTGGT GGTTCGTCAA ACGTTGAATG AACGACTTCA 240

GCAGCTTCTA CTGAGCGTTC TAAATCTGTT ACCTCTTCAG GACGCTCGCC AACTAACAAA 300

ATAAATAGCT TTGCATCTGG TTTGTTCGTA CTGATTGCAT TCGCTATTTC TTTTAATAAC 360

GATGTTTTAC CTGCTTTAGG TGGCGCCACT ATTAAACCAC GTTGACCTAA ACCAATCGGT 420

GTTACTAAAT CCATGATGCG CGTTGAATAA TTTTGTATTT CTGTCTCTAA TTTAATACGC 480

TCATCTGGAT AAAGTGGTGT CAAAGCTTGG AAATGCGGAC GTTTCTTCAC TTCTTCTGCG 540

TTATGGTCAT GACAAAGTCA ACTTGTAATA AGCCATAATA TTTTTCGTTA TCTTTAGGTT 600

TTCTAACTTT CCCAGTTACT 620

(2) INFORMATION FOR SEQ ID NO: 812:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1094 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812:

CCGGCTGAAA TTAAGTTCTT GTTATATTTC GCAAAAATGA CAAAGAAAGA TAAAAATAAA 60

TGAACTATTT GCAATTAGAG AATTGTTAGA GAAAGGTTTG ATTGGTGATT GTATTCAACC 180

TATAATTGAA CCAATTAAAT ATACAACCAC ATTTAAAAAT ACTTTGCAAT ACTGTGGTGA 240

AAAAGCATTC TCTATAAATT TAGTAGTAAA TTCAAAGTTA ACTGAAGAAG AGATTAGTAA 300

CGAAaCTGTt GCACATTTAA CTGAAATAAT AACAAAAAAC AAAAGTGTTA TTCAAAAAGC 360

TTACTTGGGT CCTTCTGATG AAGGCAATGA TAGGTTGAAA CAGCAATTTT CAAGTAATAG 420

TTTAGCTATT TTAACAAGTG TAGATGATTG GGAAATGTTT GGAGATAAAA ATAAACTTGA 480

AATGGTTTTT GTACCAGATG ATAGACACAT TAAACGTAAA TTGCGTAATA TTCCAAACAA 540

AGGCATsATT ATGGATCCTT TTAATAAACT AAGTCGTAAT GTTGATTATT TAGATAATGA 600

TGACGAGTTT TATAGCGACG ATCACCTTTA TTATAAGGAA GATGGATACG TAGCATTTTC 660

AGACTATTCT GTTATAGGTG GAGAATATGT AGACGGTGGC TTTTCGCCAT TAGCtATTGc 720

GrTACATATT GTCTATTTTG ATGAGGCTAA TGAGCTAAGA GTTAAGCATT TtGTCTCTGa 780

TTCTAATAAT GATAGATCAA ATCCAGGTAA AAnGTTTTTT GAGGCTGTAG ATAAATTAGT 840

AACATGGTCA AAAAACTTAG ATATTAAAAA TAGATCTTAT GCGCTTGGAC AATTTGAAGA 900

ATTAAATGAA AATAATAAGT ATCCAGGATT AGGTTTAATT AAAnGTTATC TATCAGCATC 960

ACCTAGAAAT TATGAATAGA TACTGGGTCT CAAAGAAATA GGAAAAGTTT ATATCGAACT 1020

GAACTGCAAG AATGCATTGA CATGGATGAA CACACGGGTA AAATGATCGC AGCTGAAATG 1080

ACTATGGTAT TAGC 1094

(2) INFORMATION FOR SEQ ID NO: 813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 930 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813:

CACCTATCAT CGTCTCTTTA ATTCTATCTA TCTATTTACC CCAATCGTAA ATATGATGGA 60

CGTTATAGAA TACCAAGAGT TGCAGGTATn TCTATTATTT ATCTAGCTGT AGTAGGTGTT 120

ATTACGTTAA TTGTTAATTT ATTGATACCT ATTATTGGTT CGCAAGTAGA TAGTTTAGTT 180

AAAAATTCAC CGCAATATCT AGAAAAATTA ATTAATTCTA TTGATAAAAT AGCAAATAAT 240

ACGTTTTTCT CTTCGTATTA TAGTCAAATT AATGATTGGT TAAATTCTTT ACCTAAGAAA 300

ATACCATCTA TGTTAAGTGA ATTTACAGAT GGCTTTGGGT CTAAAATTGC AACGTTTGCA 360

CTTAAAGATG GACATCACTT CAAAGAATTT TCAACGAATA TTATGCCACC GAAATTCCGA 480

AAAGATTTTC ATGATCTACT TGAAAAAATG AGTGTTCAAG TTGGTTCATA CATTCAAGGA 540

CAAATTATCG TTTCATTCTG TATCGGTATA CTGTTGTTTA TCGGTTATTC GGTTATCGGG 600

TTGAAATATA GCTTAGTATT AGCTAGTATT GCGGCAGTTA CAAGTGTTGT ACCATATTTA 660

GGGCCTACTA TAGCGATTTC TcCAGCTATT GTAATnGCTG CTATAACAyC GCCGTGGATG 720

CTCTTAAAAT TAGCAGTAGT ATGGACTTTA GTACAATTTG TTGAAGGGCA CTTCATTTCA 780

CCAAATATCA TGGGTAAAAC ACTTAAGATT CATCCACTTA CAATCATTTT CATTTTACTG 840

TGTGCAGGCA AATTGCTTGG TATTGTAGGC GTTATTTTAG GTATTCCGGG ATATGCTATT 900

TTAAAAGTAT TtAGTTACTC ATTTATTCCA 930

(2) INFORMATION FOR SEQ ID NO: 814:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814:

GTATGATTGC TGTTTTAATA CCAGATGATG GCAGTGGCAA ATCTTATGAC TATATGCTTG 60

TGAACCCAAA AATTGTAAGT CATAGCGTTC AAGAAGCTTA TTTACCAACT GGTGAAGGTT 120

GCCTTAGTGT CGATGATAAT GTTGCTGGTC TAGTTCACCG TCATAATAGA ATTACAATTA 180

AAGCCAAAGA CATCGAAGGT AATGATATAC AATTACGACT AAmAGGATAT CCAGCAATTG 240

TTTTCCAACA TGAAATTGAC CATTTAAATG GTGTAATGTT CTATGATCAC ATTGACAAAG 300

ATCACCCATT ACAACCACAT ACAGATGCAG TAGAAGTTaA aACACATTTT cTAATTATCA 360

AAgCTTAGGA TAAtATGATG tCCTAAGCTT TcCTTTACAA CTTTTCGGAT AACCAACAGT 420

TAATATATCA CCTTCTAACC AAACTTTTAA TCCCTCATTA A 461

(2) INFORMATION FOR SEQ ID NO: 815:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815:

AACGATATAA TAGAATTGAA TAAAGTGGGT GATAATGTGA CTAAAAATGA GATTAGAAAA 120

TACATTTTAC ATAAAATGAA GAATTTTAAT AAAGCTGAAA AGCGAAAAGC AGACACATGG 180

TTAAGAAATC AATTTTTTGC AACTGAAGAA TACAAAGAAG CAAACGCAAT TGCGCTAGTT 240

CTTTCTTTTA ATCATGAAGT AGATACTTTT TCTATTATTG AACAAGCCTT AATGGATCAT 300

AAACGTATTT TTGTACCGAA AATGGATTAT TTAAATCATC AAATGACTTT TAAAGAGATA 360

TTTAATCTCA AAGATATTGA TGTCGATAAT AAGGGGATTT ACTATCCAAC TTCAAAAGGT 420

GAAACAACGA ATAACCTAGA TTTAATTGTT GTTCCTGGTG TTGGATTTCA AGACGATGGA 480

TATAGAATTG GGTATGGTGG TGGCTATTAC GACAGGTTTT TAGCTAATTA TCAGACAAAG 540

ACAATAAGCT TATTATACGA TTTTCAAATA ACA 573

(2) INFORMATION FOR SEQ ID NO: 816:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3989 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 816:

TAGTTTAACA ATGTCTATTC TCATAGAATT TGTCCAACTA AATGTAGACG ATTCACTAAA 60

CTTCTAAAAA AATAAACCCC AAATTATAAT AGTCTCAATA TTAATATATT ACAATTTATT 120

CATAGGATTT TTATCATTTC AATTAATAGG TTGTTATCAG GGTTAAATAA ACATTTTTTG 180

TAATAGTCCT TTTTTACGTT CTTTTAATAA CTCAATTCTA TTCATTTGAT TATTCATTTT 240

ATTGTCTATA GATTTTAACA ATGCACTTAC TTTATCyTGT TCAGTGAGAC AAGGTATTTT 300

AAGATTTATA TTGCATAAGT TCGCATGAGT TAATTTAGCT GGTGCATTAC CTGTGACAAA 360

TGCTCGTAGT TCTTTAAAAT TTAAATAATA ATTCATAAAA AACAAATTAT GATCATTACT 420

TTTAACTACA TGCGCATGAT TATTTACCCA GTATTGCCCA TTAGCAATAA AGCTACTCGT 480

CTCAAACTGC CCCCATTTTG CACCATCTTC TCCTATTAGT AATCGTTCTT CATTATTGAA 540

TAAATAATCT TTTACGTAAT CAATAATTCC AGTTGCACCA TAGTAAGGGT ATAACCCCTT 600

TTCTCTTAAT GAAGAAGTAA TTGGTTTTCT TCTATTATTT TCAAAGATAA AGATGTCTTT 660

TATGAATTTG TTTTCCCACT CTGGATATTC TTCACCATTC TCATCTTTGA ATCGCAATTC 720

TTGTGTGAAG ATTTTCTGCA TATAGCCTTT TTTCTGTTGT TGAAGCAATT CAAGTTTTTG 780

TTCTTCTAAT TCAATTTGTC GGTCGAGTTT GCTGAAGAAC TTGCCTATTT TTTGCTGTTC 840

TCGACTACCT CCACTTTGTG CAAGGAAAAT TTTCCTTTTA CCTTTTCTTG ATAATAGATA 960

CTGTCCAAAA AAATTATAAT AATACTCTTT TTTCAATCTA ATAATACATA CATGTTGATT 1020

TAAATTAGCA TGCGTTTCAA CTATCGAATT AATGGCTGTT CTACCTATTG ATGCTCCTGT 1080

AATATTTAAA AGAACATCAC CATAGTACGT TCTACTATTT TTCATCTCAT CATCTATATC 1140

TTTACTAATA TAAACTAAGT CATTAAGATT TAATTTACCA TTTCTAATAT TTTGACTCCT 1200

TAAAAATGGT ATGCCTTTGT TTGTATAGTT TTCACTTCCA CCTTTGGGAG TCTTTCCACT 1260

ACCTATTTTG GTAGTAAGAT TCCCTAACTT CTTCTCTTCC CATTCGCCTT CAAATCCTGG 1320

GAATCTCAAC TCTGGCACAT TTTTCGTTTG TGTATTACTC ATCTTTCAAC ACCCCAAGTT 1380

CTTTCAGGTA TGCATTGATT TCTTGTTCAA TTTCTGCGAT TTCTTTGTCG ATATTTTTCA 1440

AATCTTGTTG GACTTGATCT AAATCAATTG GTGCTTCTTC TTCGAATGTA TCAACATATC 1500

GCGGTATGTT TAAGTTGTAA TCGTTATCGG CGATCTCTTG TAATGTCGCG CTGTAGCTAT 1560

ATTTATCAAT CGTTGCTTTA CGCTTATATG TGTCTATAAT ACGTTCGACT TGGGCATCGC 1620

TTAAATGGTT TTGATTTTTT CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT 1680

TGTCGTCTTG TTGGCGACAT TTTTTAAATA CTAAAATACA TGTTGGAATA CTTGTCCCAT 1740

AGAAAATATT GGCTGGTAAC CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT 1800

AGCGACGAAT CACACCTTCT GCGGCACCAC GGAATAATAC ACCATGTGGG aGTACGACTG 1860

CCATGGTACC TTCATCGTCT AGGTAATGTA CCATGTGTTG AATAAAGGCA AAGTCTGCTT 1920

TGGaTTTTGG CGCAAgCTTG CCGTAACCAC TGAATCGTTC ATCATTTTCA AATTTTGAAT 1980

CTGCTGTCCA TTTCGCACTG TATGGTGGGT TCGCAATAAC CGCATCAAAT GTATTGCCTA 2040

AAAAGGCTGG ATTTTCCAAT GTGTCATCAT TACGGATCTC GAAGTTCTCA TAACGCACAT 2100

CATGTAATAA CATATTCATG CGTGCTAAGT TGTATGTAGT ATTGTTACGT TCTTGTCCGA 2160

AATAACGATA CACTTGCGTT TCTTTACCAA CACGTAACAA CAATGAACCG GAACCACATG 2220

TTGGGTCGTA CACGTGACGT AATTTATCTT TACCGTCTGT GACAATCTTC GCCAGTATCT 2280

TAGATACTTG TTGTGGTGTA TAGAACTCGC CTGCTTTTTT ACCCGcTGTC GCCGCAAAGC 2340

GCCCGATTAG GAATTCATAT GCATCACCTA ACATATCAAT TTCCATGTCA CTGTGAACGA 2400

ATGGTAAGTC GTCAAGATTA ACCATGACTT TAGAGATTAA AGCAGTACGT TCTTTGACAT 2460

TGTTACCTAG TCGCGTTGAA CTCAAATCCA TATCGCTGAA CAGCCCGATA AAGTCATTTT 2520

CACTTTCTTC ACCTAATGTA GATGTTTCAA CTTTGCGAAT CGCCGTCGCT AGATGTTCTA 2580

TATCGAAATC TTGCGTTTCA ATTTCACGAA TCATCGCACT GAATAAATCT TGTGGCTCAA 2640

CCCATGCTTC TTGATACGTG ATGTCTTCAC CTGACAAGGC ATCTGCATAT TCTTGTTCGG 2760

CTTTTTCAGA TAAGAAGCGA TAGAAAATCA AGCCTAAAAT GTAATTACGG AATTCACTCG 2820

CATCCATGTT CCCTCTTAAA TCATTCGCAA TCGACCATAA TTTTTTATGT AATTCAGCTT 2880

GTTGCTGACG TTGTTTTTCA GTAATAGACA TGTGATTCCT CCGCCTTTGC ATAAGTAATT 2940

TATCTCTTTG TGTAATAGAT TTATTATAAC ATTTGGTTAT GTTGCGATGT TGATAATTTG 3000

GATGTTGGTG GTGGAAATTT TGAGTTTTAG TGGCGCAATT GTTATTGAAA AATTTTATAG 3060

AAATGTTGTA GCTTTCAAAT GCTTTCAAAA TCATTTATAT TCTTAATGAT GTCAAAAAGT 3120

TGTTCATTCA TACATAAATA AAACCAATCA ACAATTGAGT TGGTGAAAAT CAATCGTTGA 3180

TTGGCTTTGA TGCATATTAA ATAATGCAAT ATATATTAAT AAATGTTAGT TATAGTATAT 3240

TTTGTCAGGA TTGGGTGAAT GTCTAAGTTT TAATTATTTA TCTAAATTAT CTGCAATGAA 3300

TTTCTTAATT TCAGGAGAGA AATAAACAGC AAATCCTCTT GTGCTTTCAC CTGATGGCTT 3360

ATTACCGGCA TAGATTACAC CAATAGCTTC GTGTTTACTA TTTAATATAG GTGAACCAGA 3420

GCTACCAGGC TGAATAATTG CATCCGATGA CACTATATTC CCATTCACTG ATAATACTTT 3480

ACCAGTTGAT TCATACATTT GTAGTTTATT TCCATTAGGA TTTGGATAAC CAATGACTGA 3540

TATAGGTTCA TTTTCTTTAG CTTCTGATGC TATATTAAAT TTACTAGTGA AATCTTTGAA 3600

TTTTCTACCT TTTGGTTGTG TTGATTTTTC TTCAACTTGT ACAACCGCAA TATCTTCTTT 3660

ACCAGGATAA TCTACAATCT TAGTAACTTT ATAAAGTCCA CCACCGTTAT TATAAAAACC 3720

ATTAGGATGT GCTTTGATTT CATCACCGAC TTTCATGTGA TAGGTAACAT GTTTATTGGT 3780

AATGATTGTA TGATTTCCAA CTACAAATCC TGTTCCAGCG CCCATCCATG TAACACCACT 3840

GTATGGTGCA ACATTTGTAT TTGTAATTTG TTTAACAGTA TTTTCGGCTT TGGCTGTTTG 3900

TTGAATACCT TCAACCATTG TTGTGCCGAC ACCAGTTATT GATGTTAAAA TCGTCAATGC 3960

TGCAATACTT TTGATGATTA TATTTTTAT 3989

(2) INFORMATION FOR SEQ ID NO: 817:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 904 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817:

CGTTGAGCAC AGTTTTAGAT AATAGATAAT CTTGCtCTAG TTGTTGCAAT GTCTGCGATT 60

TATGCGTGTA ACGTTCAGTT ATCGTTTCTA AGGTATACTG AGATGTATTT AATTGATATC 180

CTTTAGATTT AATACTTACG ATGATATCAT CCATAAAATT GCTATTGATA ACATGGATAT 240

CATTGCGAAC TGTGCGGTTT GAAACATTGA CATGTTTAGC AATTTCATTA GAACTAATGT 300

GCTTTGATGG ATTTTTAATA AAAAACTGGA GTAGTTTTAA GTGTCTATCA AGCATTTAAC 360

ATGTACCTCC TTTCTAAATT TTTCGTGTAA GCGTTTTTAA GGGTGTATTA ATATTATTAA 420

ACATGAGAGC TTATACATAC GTCAATGACA TTAAAGCGAA CTTTTATATG ATTTTAACAG 480

AGTGCGAATT ATGCAAATAA AGAACAGCAG TAAGATATTT CAAATAGAAA AATATCTCAC 540

TGCTGTTTTT CTGAATTTAT GCATCTGGTA CTTGTGGACG TATCAGGCAA ATGATTAATT 600

TTTAGGTGAT TGTGCTTGAG GTGTTTGTTT AGAAGGCGTA TTGGTATTAT TTGATTTATT 660

AGCAGGTGGT GTGTTCTGTT GTTGATTATT TTGGTTGTTT GTTGACGATT GACTGCCACC 720

ACCGTGAGTA TTATTTTTAT TTGAATTTGA GTCTTTTGGC TGAGCTGGTT GCGTATTCGA 780

TGGTACTGTT GAATGGTTGT TAGGAACATT TGACGGTGAA GATGGTTGAT TGTCATTAGT 840

AACGTTATTG CCATTATTTT GATTtTTATC TGTTTTGTCT GCACTATCAT CTTGTTGATC 900

ATTT 904

(2) INFORMATION FOR SEQ ID NO: 818:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818:

TTTAACAtGa TAATAAAAAA TCTTTTGTTA TATCATTAGG AATATTTGAT GAACTTGATA 60

TTAAGGTTAC ATTTTGAGAA ATGGACTTAG GGATATTTCC ACTATTATTT AGTAAGAAAT 120

CTTTAGCTAA TAAAGATTTT CCTACACCAT TTTTACCAAC AATGTGATTG ATCTGACCAA 180

GATAGAAATT TAAATCACAA TTGTCAACTA GTTGTTTGTT TTTAACTTTT AAAGAATAGT 240

TATTTAGTTT CATGTATACA ACTCCTATGT ATAAAGGGAT TTATTACACC GATATTTAAT 300

TGTATTTTTA AAAATTCtTT CACATTATGT ATAGAwGTTA TAAATTAGTA TATCaCACTA 360

TATTTtGkCT AAATGATAAA TATATCGTTA TATTTTTACA ATATTCTGAA ATTTATGTTC 420

GCCTCTGAAT GCTATATCCA GTGTAATGTG TTTTGCATAT ATGAAAGCAA TTTCAAAATG 480

TGAATATAGG TTCATTGTGG TATGACAAAC TTCATTGCTT GTCATGAGAT GGATATAATG 540

GACGGGACGT TTTTAGATTC AAAAAAGACA TATGATAAAC TTAGATTTGA AGCGATTTTT 660

ACTGAACTTA GAAATAGAGA TATTACATTT ATTGCTGCGA GTGGCAATCA ATATGCGAAG 720

TTGAAGTCTA TTTTCGGGGA TAGAGATATG TATTTTATTT CTGAAAATGG TGCAGTTATT 780

TATAATGGCA ATGAGTTATA TAATTATAAA AGCTTTAATC GTCAGGTGTT TCAACAGGTT 840

GTCGATTACT TAAATATGAA GCAAAGTATT GATCAACTCG TCATCTGTGG TTTGAAAAGC 900

GCGTATATTT TAAAACATAC TTCTGAAGCG TTTAAAGAAG ATACGAGATT TTATTATCAT 960

CAGTTAAAAG AAATTGACAG TCTACAGCAA TTACCTGAGG ATGATTATGT CAAAATAGCA 1020

TTTAATATTA ATCGTGAGAC GCATCCGAAT GTTGACGAAG AAGTAGCAAC GCAATTCAGC 1080

AATGATATTA AACTTGTCTC AAGT 1104

(2) INFORMATION FOR SEQ ID NO: 819:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819:

CCCnTTTTAC GGATTAAnGG CTTTTTCCTA TTTAAAACCT ACGGCATTTT CTTTTCAACC 60

ACGGCGGCTC CCATATGGAT GGTATnGGGA TTGGGGTTTA TAAAATGGGG ATTGGAAATG 120

GTCCATCCTA AATACTCAGT TTAGTGCTTA TTTCCTTTAG TGCTGACGAA TAAATATGAT 180

CTAACTCTAC GAAACCTAAT AACGTATCAA ATGCTTCATC ACCATTTTCA AATTTACTTA 240

AACTATTTTT AAAATCATGT CGCAAATCCT CTAAATATAG TGATGGTTTT CGATCTACAT 300

ACATTTTTAT ACTAACCTCC GATATATAAT CATCTTTATT GTACCTAACA TTTTATTAAG 360

ATAATACTAA TACACTATCG AACTTTGGGC TGATACTGAA ACAGCACAAA GAAACTCAAA 420

CAATTCGAAT TATGTATCAA AACCTTCAAT TACAGGAAGT GATTTTAAAA TGATTTAACG 480

CAAAAAAACA CCTGTTACCG TTATATAGGT ACAAGTGCTT AATTGATAGA GATGTTATAC 540

GTCTTTAAAT GATTCCACAA CTTTTGGATG TGGACCATCC ATAAGCGGTT CTCTTTGTCG 600

AACGCCACCA CTTTGGTTGC CAATTGATTC GCTATCAAAG TACGATTTAT CTTGATTTGA 660

TTGTTCTTGA ATATGTTCTT CATTATCAGT TGTTGCATAT TCACTATCCA CCTCTGTTTT 720

TTCCATTGTT GCTGTATGGA ATTGTACGAA GTTCTCTTCT TCTAATGCTT TGATTTCTTC 780

TTTCGATAAC GCTCGATACC AATCTTTCGC TTTTTTCGCC GCAaTAGGAa CAaCAtCTTT 840

TACTTCAAAT TCTTTCCATT TTTCGGGGTA ACCTTTCATT GTAAAGGGCA TTCCCTTAAC 960

CTCCAATATG TTATAATTCA TGTTATATAC CACCATAATT ATAAAATGAA ACATATTAAA 1020

CACAATTTTT TAGACTCCCG TCATAATAAC TTCAGACAAA CGTTAGTCTG ACCTGATAAA 1080

TATTTAATTT TAAACGTTCT TGTCTCTCTC ACGAAAACCA TTGTGTTGAA TATTCATCAT 1140

TGCTGATTGA ATATAATTAT ACTGTGGTAA ATCTGGTAAT ATCTTTATTT CTAATTCTGT 1200

ATTTAATTCG AAATGCTTAG CGATGTTTTC AAATATTGCT AAATACTCGC CCATTAATTG 1260

TTCATTTATT GTAAGTCTAT CTTCATTAGC CATGGCTCTA TTTAACATAA AGCTAATTTC 1320

TTCTAATGCG AATAAGCTAG GATAATAATT TTGAATCAAT GTCTTATCAC TAAATAATTC 1380

ACCATTAGCT GCATTATAAA CTTGCGTGCA TGTTATTTAA TTTGC 1425

(2) INFORMATION FOR SEQ ID NO: 820:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820:

nCGnCCTTAT ATATGTTTTT CATGTCCTAC AAAAAACGAA ATATTCCAAT TGCCTATATA 60

CAGATATTCA TTAATGACAC ACTCAATAGC AACCATnACA ATATTATGTT ACCTATTTAA 120

ATGAAATAGT TCTTTTAAAG AAATACATTT TTCACATATT AATCTATAAT CAAAATCAAC 180

TGACCGATAT TCTATAATTT ATGATTAAAA TAAGTTATAA TATAATAGTA AAGATAAAGA 240

TAGAGGTGGC TATAATGTGT GGACTTAGAA GTATAACATT AGGTACaACA AATATAGAAC 300

AGACaAAACa TTTCATGGTT GACATATTAG GATTAAATTA TGAAGAACTT CTTGAAAACT 360

CAATTCGTTT CGGCGATGCA GATATAAGCC CAGGAACAAG ACTTCAATTT ATACAAGTTC 420

CAAGTGAGCA ATTAGAAGAA TCTCACTTTG TGGGTATTGG ATTACGTACA CCAACTGACT 480

CAGGTTTAGA GGAGTATGCG GAAATATTAT CGAATAAGGA TATTCCATTT ACAACAGTTA 540

AAGAATTAAA TGGCAATAAA TATTTCAGTC TCGAAGATAA CAATGGTCAT ATTTTCTCAA 600

TATATTCAAA CGAGAATAAT TATGGCGTTG GTTTAGGTAT GCCTTCTTyT GAGAGTGCGG 660

TCAATCCGTT ACATCAAGTG CAAGGTTTAG GACCAGTGAT TCTTAAAGTG AATCATGTAG 720

ATATTACAGG TCAAATTTTA ACAAATATAT TCGGACTTGA AGTATTTGCA GAATACCAAC 780

CCTTCGACAA TGCTGACTAT CATGTCCAAG TATTCAAAGT TGGAACGGGT GGTCTAGGTG 840

ATCAAGTTGA GTTTGAAACG AAAGATGCAG ATTTCTTTAA TCAAGCGAAA TCGCGCTTAG 960

ATGAAGTGGA AATACCATAT CAAACGCTTG AGCAAGATGA TATTGAATCA ATTAGAaTTA 1020

CTGAAAACAG TGGATTATCG TTTATATTCA CTTTACAAAA ATAATTTTTT TACGATAGCG 1080

AGGACAAAAT TTATGTTACA TGAAACTTGG AAAGAACGTA CACCAATCAA GAAAGTAGAA 1140

GTCATTAATA CAGATGCAAA GAAAT 1165

(2) INFORMATION FOR SEQ ID NO: 821:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821:

TCGCCCAATT ATTATGAAAT ATTCAATACA GTTTATTGAT CAAAAAACAA AAATCCATTA 60

TGAACCTTGT CATCACGAAT ATTAACTGAC GTTAGATGGA CCTCTTTAAT GATAGAACAA 120

TTAATAAATA ATGCACTTAA GTATGCGAGA GGTAAAGATA TATGGATTGA ATTTGATGAG 180

CAATCCAATC AATTACACGT AAAAGATAAT GGTATCGGTA TTAGTGAAGG nACTTGCCTA 240

AAATATTTGA TAAGGGCTAT TCAGGTTATA ATGGCCAGCG CCAAAGTAAC TCAAGTGGGA 300

TTGGTTTATT TATCGTAAAA CCAATTTTCA ACACACACAA ACCATCCGTT TCCGTCGTAT 360

CTAAACAAAT GAGGGTACAA CCnTTACGAn TnCCATTTCC 400

(2) INFORMATION FOR SEQ ID NO: 822:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 760 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822:

TGATATAATA CTTTTGTAAA GAAAAGCATG TGTGGGAGGT ATGACCTGTA TGTCGAACGA 60

AATACTTATC GTAGATGATG AGGATAGAAT CAGAAGATTA CTTAAAATGT ATTTAGAAAG 120

AGAATCTTTT GAAATCCATG AAGCAAGTAA TGGCCAAGAG GCTTATGAAC TTGCAATGGA 180

GAATAATTAT GCTTGCATAC TACTAGATTT AATGTTGCCT GAAATGGATG GTATCCAGGT 240

GGCAACTAAA TTGCGTGAAC ATAAACAAAC ACCGATTATT ATGTTGACTG CTAAAGGTGA 300

TTCACCAAGA GAAGTAGTCT TAAGAGTTAA AGCACTTCTA AGAAGAACGC AATCTACAAC 420

TGTAGAACAA AGCGAACCTC ACGCACGTGA TGTGATTGAA TTTAAACATT TAGAAATAGA 480

TAATGATGCA CATCGCGTAC TTGCTGATAA TCAAGAAGTT AATTTGACTC CTAAAGAGTA 540

CGAATTATTA ATATATTTAG CTAAAACACC AAATAAAGTA TTTGACCGTG AACAATTATT 600

AAAAGAAGTT TGGCATTATG AATTCTATGG TGATTTAAGA ACAGTTGATA CTCATGTTAA 660

ACGcTTAGAG AAAAGTTAAA TCGTGTGTCT AGTGAAGCTG CGCATATGAT TCAAACAGTC 720

TGGGGCGTTG GGTATAAATT TGAGGTTAAA TCTAATGATG 760

(2) INFORMATION FOR SEQ ID NO: 823:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823:

CAAAGGAAAT TGCACAATTA GAAGACCGAT TACGTTCACG CTTTGAATGG GGGCTAATTG 60

TTGATATTAC GCCACCAGAT TATGAAACTC GAATGGCAAT TTTGCAGAAG AAAATTGAAG 120

AAGAAAAATT AGATATTCCA CCAGAAGCTT TAAATTATAT AGCAAATCAA ATTCAATCTA 180

ATATTCGTGA ATTAGAAGGT GCATTAACAC GTTTACTTGC ATATTCACAA TTATTAGGAA 240

AACCAATTAC AACTGAATTA ACTGCTGAAG CTTTAAAAGA TATCATTCAA GCACCAAAAT 300

CTAAAAAGAT TACCATCCAA GATATTcAAA AAATTGTAGG CCAGTACTAT aATGTTAGAA 360

TTGAAgATTT CAGTGcAAAA mAACGTACAA AGTCAATTGC ATATCCGCGT CAAATAGCTA 420

TGTcTTGTCy AGaGAGCTTA CAGATTTCTC ATTACCTAAA AATTG 465

(2) INFORMATION FOR SEQ ID NO: 824:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824:

CACCGCGGTG GCGGACGCTC TAGAACTAGT GGATCCCCCG GGCTGCAGGA ATTCGGCACG 60

AGGTAAGGAG GTCTCTGTAC CATGGCTCGT ACAAAGCAGA CTGCCCGCAA ATCGACCGGT 120

GGAGGGGTGA AGAAACCTCA TCGTTACAGG CCTGGTACTG TGGCGCTCCG TGAAATTAGA 240

CGTTATCAGA AGTCCACTGA ACTTCTGATT CGCAAACTTC CCTTCCArCG TCTnGTGCGA 300

GAAATTGCTC AgGACTTTaa AACAGATCTG CGCTTCCAnA GCGCACTATC GGTGG 355

(2) INFORMATION FOR SEQ ID NO: 825:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1099 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825:

TTCACTTGGC TTGTTGAcTG ACTTGTAtAT GATGATGTGC TTTGTGAATC GGATTCGCTC 60

GTGCTTGTAC TTGTTGAGTT TGAGGCACTT TGGCTTGCTG AGTTTGAGTC TACTCCGCTT 120

TGATTCATTG AGGCACTTAG TGACAATGAT GTACTCGTTG AGTCAGACAA ACTTGTACTC 180

GTTGACGTAC TTGTACTTCC TGATGTTGAT TGAGACATAC TTATGCTCAT TGATGTTGAA 240

TCGGATTTAC TTTCACTTGA TGATGTTGAG TCGGATTCAC TTTCACTTGT AGAACCACTT 300

AATGATGTGG ATGTACTAAT GGAATCAGAT TTACTTGTAC TGATTGAATC ACTTGTCGAC 360

ATTGATGTAC TTAATGAATC AGACTTACTA TCACTTGTGG AATCACTTAA TGATGTTGAC 420

AAACTTGTAG AGTCAGACAA ACTTGTACTC GTTGACATAC TCAGTGATGT TGAAACACTC 480

TCGCTCTTAA ACGTTGACGT TGATTCACTG ATACTTGTCG ATGTTGAAAT GGACGTACTA 540

CCACTTGTTG AATTACTTAA TGATGTTGAT GTGCTACCAG ATTCTGATGT ACTGTCTGAT 600

AATGACGTAC TCTCACTTGT CGAACTACTC ACTGACTCTG ATGTTGATTC AGACGTACTT 660

TCACTTAATG ATTCACTTAA AAAGGCAGAT GCACTTTGTG ATTCTGAATC GCTAGTACTA 720

TTTGATTCAC TTAATGATAT AAACGTGCTC TCTGAAGCAG ATATTGCTTC ACTTATAGAG 780

TCGCTCGTTG ACGTTGATTC ACTTATTGAA TCAGACTCTG ATGTACTTAA GCTTGTGGAA 840

TCACTCaTAG ATGTTGaTGT ACGTTCTGAA TTACTTGTAC TTAACGATGT CGAAGTACTT 900

ACCGAACCAG ATGTGCTCGT AGAAGCACTT TgTGATATTG ATTCACTTGA TGCAGTTGAT 960

GCTGATTTGC TATCACTCGT TGAATCACTA AACGACGTTG ATATGCTCAt TGAATCGGAT 1020

TGACTTGCAC TCAnTGAACC AGACGTACTT TGTGATTCCG AAGTACGTAC TGAAGCACTT 1080

GTCGACGTTG ATGTACTTG 1099

(2) INFORMATION FOR SEQ ID NO: 826:

(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826:

TATGCGTATC CTGATAGTCA CTTTGATTTT GATATGGAAT TAGCGAAAGA GCAATCTCAA 60

GACAATCCAG TTTACTATGC TCAATATGCA CATGCGCGTA TTTGTTCAAT TTTAAAACAA 120

GCGAAAGAGC AAGGTATTGA AGTGACTGCT GCGAATGATT TTACAACGAT TACTAATGAA 180

AAAGCGATTG AnTTGTTGAA AAAAGTAGCT GATTCGGAnC CTACAATTGA AAGTGCTGCT 240

GAGCATAGAT CGGCACATAG AATTACTAAT TATATCCAAG ATTTAGCCTT CTCATTCCAT 300

AAATTCnATA ATGCTGAAAA GTGTACCAGT TGGTATTG 338

(2) INFORMATION FOR SEQ ID NO: 827:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 838 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827:

GTATTTTCTT TCGCGAATGA TTTTATTACT TGAATACCAC GAATAACCTC CAATACCTTT 60

TCCACTAATT GGTTTTGTAC ATTATGATAC GcTGGCGCAT TTTGTCGACT CTTTCTTTCT 120

AATAATTGAA TCGCAAAAAA TGATAGTAAT ACGCCAATGC ATGCTAATAA TGATACTTGC 180

CACGAAACTA CAAGTAGAGA CAATATGAGT ACTGTAATTA ATATGTATCC ATTAACAACA 240

ACGTCCACCA TTTTCATAGC AAAGTTTTCT AAAAAGGTTA AATCTGTTGT TACTATTGTT 300

GTTAACTCAT TTGAATGATG CGAATTAAAA TAACCTAACC TTACATTTTT CAATTTATCC 360

CCTATATCTA AACGTTCTTT CGCACTCATT TCATAAGCGA TGCTCTCATG GCTTTTGCTT 420

TTGAAATATG CTGTAATAAA TCGTCCAATC ACTAATAAAA CCATGATAAT TACAACATTC 480

AATATATCTT TCATATAAAT AGGTTTATGA GATAGCACAT TATTAAATAT TTTTGCAGCT 540

AAAAAGATAG GTAACGCAAT AAAAATAGCA TTTAAAAATG ACATGCTAAA TCCTAAAATC 600

ATTCTTGCTT TATATGGTCT TATCCAGTTT AAAATTTTAA ATGTAATTTG AAACATATTT 660

GACCTCCTTT TCTCATTAGT TTAATTATGT CCAGTATTGA TTCCCCAATC TTTTGTATGC 720

ATGTGCGTAT CCCACATTTT CTTATAATTA CCGTTTAATT TTAGCAATAA GTGATGTGAC 780

(2) INFORMATION FOR SEQ ID NO: 828:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 898 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828:

TCCnAAAGAA GAAATAaCAT TATCATaAAA TCCATTGAAT ATAAATTCAG TCATCCCCTC 60

TGAACTtCTC CATAAATATA ATGGTGAATA AGTATTTGTA ATGCAATTAG TAGTTGTTTG 120

ACTTATTAAA TAAGCTTTTA TAATTAAATT TTTAAATCCA TCAGTCTTAT AACCATTTAA 180

TCGAACTCTA TCTCTAATTA TTTCCATATT GTAATCACTA GGCAACTTAA CATGATATTG 240

CATTGCATGC ATTTAGCATA CCCCCTTTTA TAAAAAGGAT AGCAATAATA AGTAAAATCT 300

CATATTATCC AATTGTGATA TAGTTATCAT AAAAAGTGAT AGGTGATTAA ATTGAACTTT 360

AATGATTTGG AAATTTTTAT AACTGTATGT GAAGAAGCAT CTATCAATAA AGCTGCAATT 420

AAACTTAGAT ATGCACAATC TAATATATCT CAAAGAATTA GCAAGCTTGA AAATGAATTA 480

GGTGTAGTTT TGCTTTTTAG AAATCAAAAA GGTGCTAAGG CAACTAAAGC AGGCGAAGAA 540

TTCTTAGCGT ATAGCAAAAA AGTATTAAGA GATACAGAGA CTATAAAAAA TAAAATGAAA 600

AATAATACTA TGTCTATTTT ATGCTCAGAA CTGTTATTTA ATTATTTATC TGAGAGCGAA 660

GAAATTATGA TGTCGAATAA CTCAATTAAT TTTATTTCTA GTGGAAATAT TAGAAAAGCT 720

ATAGAAAAAA ATAATTATGA TAAGGTTATT TCATTCATAA AAaTTAACGA CTCAAATTAT 780

AGACTTAGTA ATGTTGATAC TATGaaAGTA ACGCTTTACA GTAATGGAAG TAATTATGAT 840

AAAGAGGCTT TACTAATAAA TAAAGATGAG TTTGGTCCTT TAAGGnAAAT AACTTTAG 898

(2) INFORMATION FOR SEQ ID NO: 829:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 798 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829:

AGTAGGAGTC ATAAAATCGn ATTTCAAAAG CAATTAATGC AAAATACTGA GTCTACAGTG 60

CTATTTGCGA AAGCGTCcAT ACGAAgTTGA GcAATGCTAA TAATAATGGT CTATCAAAAA 120

AATATGTTGA TAGTTACACT GATTCTCTTA CTGGAGTAAC AACTTCTGCT TTTTTAAATA 240

AAGATACAGG CAAAGTAACT CTCGGGATGA CTGGGACTAA TTTACAAGAC GAAGCCTTTA 300

AAAAGTTAAA AGAAGGTGAA TTTTCAAGAC AAAATGTTAC CAATGCTTTG GAAACAGTTA 360

AAGATGGATA TGCAGATCTT AAAATATTAT ATTCTCCTGC ATCTGATCAA AACTATAGAT 420

ATGCGAATAC ACAAGAATTT ATAAATAAAA TAAAAAGTAA GTATGACATT GATTTTATTA 480

CTGGACATTC ACTAGGTGGA AGAGATGCGG TAGTTCTAGG AATGAGTAAT GGTATTCCGA 540

ACATTGTGGT TTATAATCCA GCTCCTATTT CTATAACTAG TTTGAATCCT AATTCCCCAG 600

ATGGAAAACG TTTATTAGAA TTATATAAAA ATTATAAAGG TAATATTACT AGGTTTGTTG 660

CAGAAAATGA TGCATTGACA GAAAATCTGA AGAAATATAA GCATTATGTT TTTTTCGGTA 720

ATGATAAAGT CTTTAAAAAT GGTAAAGGTC ATGAAATGkA AGGCtTTCTG ACCGAAGAAG 780

AACAAAAAGC tATAAAAn 798

(2) INFORMATION FOR SEQ ID NO: 830:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830:

AATATCAATC TCTTCATAAG CTGAATTATT TTCATGCACT TCTTGATGTG ATGATTTGTC 60

ACGAACnGCT ACAACTAACA TTTTATCGTC TAAAATAAGT TGTTTATATT TTTCTAATTC 120

ATCAGGCGCT AAGTTGTAGC GTGATAAAAC TGCATGTTCA CCATCTTCTC CTGTTAACAG 180

TTTAGTCATT CTATCACTAA ATGTTCCACT TGTTGAGATA AGGGGAGATT TCAGAGTCGT 240

GTAAGTCATT AGGTGTAATT TACTTTTACT AATAATTGTT AGCCTGATCT AAATAACTTC 300

AGATTCTTTG ATTGATAnGT GnATAATCGC AGTGCATTAC ACAGAATACT GCCAAGTGCG 360

CCCTTAAAAT TGTTATTAnC TTACCTCTAT ATAAGAACCC 400

(2) INFORMATION FOR SEQ ID NO: 831:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AAGTCTGCAT GACTTTTATT TGCAAGTTCG ACTGCTTGAT CAAAAGCGCG ATGATCTTCA 60

GGATtAGCAC TTTGAACTGA GCTGAAATTC GGATCAGGTT TACATTGTGC TTCTACAAGA 120

TTAAATTGAT TGAAATTCAA AGATTGTAAT AACTCAGGTA CAATCGGAAC ACTTGTACCA 180

TGCAAACTAG TGAACACAAC TTGTAAATCA GATTTAGGAA TATAGCCAAT CATATTTTGA 240

ATGTGTTTCA TATAGTCATC AGTTACAGAT TTCGGAAAAG GCTTGaTATA AGATGTATTT 300

TGTTTAGAAA tAGGTATATC AATCTGTAAT GGATCGCCAA CTTCTTCGAT ATAACGACTT 360

GCAAGCTCAG ATGCATCAGT CGATAATTGC GCACCATCAG AACCATATAC TTTGATGCCG 420

TTATAGTCTT TCGGATTATG ACTTGCtGTA ATCATAATGC CAGCAGTAGT ATTAA 475

(2) INFORMATION FOR SEQ ID NO: 832:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 724 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832:

CTTGAATTGA AGGATACGCA AATGATGCAT AATCAGCTTC TGTATAAAGC TGTAATGTAA 60

TGTCATCAAG GTCACCTTTT CTAACAAGCA CCTTATTAAT AGAAGTATGA TTCGCTTGCC 120

AAGTACCTTG ATTATTTTGT TCTAAATGAA TGACTTCGCC TAACGATTTC AACGTAATAT 180

CTGCACGCTC GTCTTCGCTA ATAGTATATG TCTTACCATC TCGCAAATTG AGCATCTTCA 240

ATTGTTTGTT ATATTTTATA ATCAATTTAT GCATTGTCTT TGCCTCAGTC CTATACTATT 300

TTTTTCTTTC AGCTTCTTGG CGTTTTTCTT TATCTTTTTG TGCTTGTTCT TTTTGTTTCT 360

TTTCGTTCTC TTCTTGTTGC TTTAATTTCT CATCTTTCGC TTTTGCTTTC TCTTCTTCAG 420

ATTTCGCTTT TTCATCTTTA ACTTGTTTTT CTTTGTCTAA AATATCTTGC AATTTATCGT 480

TATACTTTTT CGTTTCTTCA GAACGTTTAT CATTCGATAA ATCTCCGTTA TTTTTAATCT 540

CATTTAATTT ATTAATCAAC GCTAACTTTG TAATATCGTT ATCATCTAAA TAAGTGGCAA 600

TATTAATCGC TTCATCAAGA TGTCCTTGTC CTAATTCCAT CCAATATAAT AAGTAGTCTT 660

TGTTTGAATT TGGTGTCACA TTATTAAGTA AATTTTCTTT CGTATCTGTn TCTAAACCnT 720

GTTn 724

(2) INFORMATION FOR SEQ ID NO: 833:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 994 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833:

AGCAGTTTGG CTCGTAGAAA TCTCCCGTCT CTATTCTATG TATTAACTTT TATTATATTT 60

GTTATGATAC TATCGATATG AAAGCGTTGT CAATGGTTTT TGTAAAAATT TTGTCAAATT 120

TAATTTTTCA AGTCTTTATA AAAGTAGTTT AATTTGAAAA CTAGAAATAC CAATCCTAAC 180

TAATTTATTT ATGACGCTCT TTTGTTTAAT TGACATTCTT CAGCCATATT TTTTATGACT 240

AGTTGCATTT TTTACTAATA AACACCTCTA AAACTTTAAT GATTTTAATC GTTTTAGAGG 300

TGCTAATTAT TTTATTTGAT TATTTTTTGT TTGATACCTA CTGCATATCC CATATGAAAA 360

CGGCTTTTTT ATTATGTTAT ATGACTAAAT CTCGTGAAAA ATGAAATTTT TGCAGACTTA 420

TGATTTACCA AAGTTTATCA TAACTAGTAG TTACATATTT CGCTCCATTT TTAACAGCTT 480

CATTGACTTC ATCTATTGTA TTAATTAGGC CACCTGCAAT GACTTGTGTG TTTGTTTCTT 540

TCTGAATATG ATGAATCGCT TTACTCGCAA CACCTGGAAG TACTTCAACA AAATCAGGTT 600

CAACTTTTTT TATCAAATCT ATACTGCGTT TCAATGCTTG ACTATCAATA ATAAATACTC 660

TAAAAATCGT TAAAGTATTT AATGATTTAG CTTTTTTTAT TACTTTAGAT TTAGTCGATA 720

CGATACCTTT TGGCTTGTAT TGCTGAATAA TAAATTCACT TGCAAATTCA TCGTGGCTTA 780

AACCTTTTAT CAAATCTATA TGAATAAAAC ACTCTATATG ATTTTGCTTC AGCAATTCCA 840

TAATACTTTT TATATGTCCT ATATGCATAT CTAGAAGCAC ACACATTTTA TAGTCTGTnT 900

TAATCCAGTT TCTCTAAATC nTTAATGTTT CCTATAAGCA GGCAATATGT TGTTAATTCA 960

CTnGATCCAT CCTCTCTACA TCACACGCTT AAAT 994

(2) INFORMATION FOR SEQ ID NO: 834:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 783 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834:

TCnACAAAGT CGGTATTAGG CTATGGGCCA TTTnACTATT ATAACTAATC GGAAATATAC 60

CACATAACAT CATTATTGAG TTGATTCTAT CATTTGGCTT ATTAGGGTTT TTTATCATAA 120

TGATTTGCAT TTTGCTACTA GTTTATAAAA TGATTAGGAA CTATGATCCA AACACTATAG 180

ATTTAGTTGT AAGTGAATTT TGGTTTGTGT TGTTCTATTT TATTACAAAA GGACGGCGTC 300

ATCATGGCTA AGAAAGTTTT TATTATGGAT AGCGTAAAGA CAATAATTGG TACGTTGCTT 360

ATAGCTTTAG GATTACAATT TTTAGCTTAT CCAATTATTA ATCAACGAGT AGGTAATGAA 420

GCGTTCGGTT CTATTTTAAC GATTTATACA ATAATAACAA TCACGAGTGT TGTATTAGGC 480

AATACGCTTA ACAATATACG mTTGATTAAT ATGAATCTAT ACAAATCCAA TCATTACTAC 540

TGGAAATTTG CATCGATACT TTTAATCTCA ATTCTGATTG AGAGTATAGC TTTAATTATT 600

GTATTTCTTT ACTTTTTTAA TTTGAACATC ATCGATATTA TCTTTTTAAT TCTACTTAAT 660

ATTTTAATGT GTTTAAGGAT TTATCTGAAT GTATTTTTTA GGATGACTTT AAAATATAAT 720

CAGATTTTGT ATATTGCTCT TATTCAATTT TTAGGTTTGC TGATAGGACT ATTTCTATAT 780

nAT 783

(2) INFORMATION FOR SEQ ID NO: 835:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 794 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835:

TTACCTAATT TTTCAAtCaT AAGATTCCCC CTATTGTTTA AACaTAAAAA TATTATaCGA 60

TTAAGCACGA GmCACTTCAA TATATTTTTC AGAATATTCT TATAAATATT AATATGATCA 120

TTTCACTATT TAAACACGTT TAATATTAAA ATAAGTTATT CATATAAACT GGTGCTGTTT 180

GATCCAATTG CAGACTTACG AGTCATTGAA AAGTCTCACA AACTATTGmA AGTAAAtATC 240

TTAAAATAGA AAGTGAATGG TTAATTTAAG TATATTTmAA AAATATTAAC CTTTTTAAGC 300

ACTGCTATTT AGGATATACT AAATAATAAC TAAGTTTAGA AAAATAGGAG GAACATCGTT 360

TATGTTAAAC AAGGTTTGGT TCCGAACTGG CATCGCTCTG ATTATGCTGT TCATTCTCAT 420

CAAACTATTT ATGGAAGTGC ACGAAGTATT TACTCCAATA GCTACAATCA TCGGTTCTGT 480

ATTTCTTCCA TTTTTAATTA GTGGTTTTTT ATTTTATATC TGTCTACCTT TTCAAAACTT 540

ACTTGAAAAA GTCGGTTTTC CAAGATGGGC TAGTATAACA ACAATCATGT TAGCTTTGTT 600

TGCTATTATC GGCTTAATTG TTGCGTTTGT TGCACCAATC ATCATTTCAA ATATCAACAA 660

TTTAATTAGT CAGACACCTG gCCCTACAAA AAGGAAGCAG AGCAAATTAT TAAATTCGCA 720

CTGGCTCAAA TGGnTAAATT ACCTGGAGGA TGTAACCAnG TGGATTACCA ATATGGTAAA 780

(2) INFORMATION FOR SEQ ID NO: 836:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836:

TGTTTATACT GTGCCTGAAT TAGAAGAGGT TTTAACACCT ATGAGACAAG ATGGAACTCG 60

TGATATTTAT GTTAATTTAG AAAATGTGAG TtATATGGAT TCGACAGGTT TAGGTTTATT 120

CGTAGGTACA TTAAAAGCAT TAAACCAAAA TGATAAAGAA CTATACATTT TAGGTGTGTC 180

AGATCGTATC GGTAGACTAT TTGAAATTAC TGGTCTTAAG GATTTAATGC ATGTTAATGA 240

AGGAACGGAG GTCGAATAAC ATGCAATCTA AAGAAGATTT TATCGAAATG CGCGTGCCaG 300

CATCGGCAGA GTATGTAAGT TtAATTCsTT TAACACTTTC tGGCGTTTTT TCGAGACTGG 360

TGCCACATAT GATGATATTG AAGATGCCAA GATTGCAGnT 400

(2) INFORMATION FOR SEQ ID NO: 837:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837:

ATTGATCCAT TTTGCGGTTC GGGTACAATA GCTATAGAAG CTTGTTTAAT TGCTCAAAAT 60

ATCGCACCTG GTTTTAATCG CGAGTTCGTA TCAGAGCAAT GGAACATCAT GCCAGCAAAT 120

ATTTATGATG ATTACCGTGA TGAAGCGGAT AAGATGGCTG ATTATGATAA AGAAATCGAA 180

GTATATGCTT CTGATATCGA TCCAGAAATG GTAGAGATTG CTAAGCGTAA CGCTGAAGAA 240

GTTGGGTTGT CTGATATTAT TAAATTTAGT GTAAAAGATG TCAATACATT AACAATTGAT 300

ACAGAAGAAC CGGTGGCGTT AATTGGAAAT CCTCCATATG GTGAACGTAT TGGTGaTCGT 360

GAAGAaGTtG AAGAAaTGTA CCGTTATATT GGTAAACTAA TGAAACAACA TCCATTTTTA 420

TCTACATACA TTT 433

(2) INFORMATION FOR SEQ ID NO: 838:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 926 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838:

ATTGGGCCAA CTAATCCTGT ATATCCAAAT CCAGCAGACA ATGGTGTTCC TTTAACCTGA 60
AGAACGTAAG CAATGATTCC AGTAATTATT CCATTTATAG TCAATGGTAT CGAAATAATT 120
AAATTTTTCA AGTAAACTGG GATCATCATT TTTGCAGCTC CTATGAGTAA AACTGCATTT 180
ACACCAATAG AATTGACACG CAATGAGCCA AATAAGAAAG TAACACAGGC AGCCACTATA 240
CCTAGGTTTG CTGCTCCACT TCCTAGTCCG TTTAAACTAA TCGCAGTTGC AATCGCTACT 300
AACGATATTG GTGTTACCAT TAATAATGAA AATGCCACAC TAATAAGTAT AGACATTAAC 360
AACGGATTTA AGTCTGTAAA AGAATGAATT ACATTTCCAA TTGCTTGAGT AATTTTTCGA 420
ATGTAAGGTA ATGTGATTAG ACCGATACCC CCACTAACGA TAGGTACTAA AACTGGTAAT 480
ATAATTAATT CAAAAGATCC AAGTTTGTTT TGTAATACCA TATATATAAG ACATGCAATA 540
ATAACAACCA AACTCGTATT TATAATGtCa CCTATACCTT TTAACATAAA ACTATTATTG 600
CTATATACAA CAGCACCTGA ACCAATCATA GCTGATGTAC CTACTATAGC AGCACCTGCA 660
CCATTAAATT TAAATTGATG AGCAGCTAAA ACCCCAATAA TAAATGCCAT AAATGATTGA 720
ATTAGTATCA CTAACTGATA CGTTAATTCT AAAATTTCAT TACCACTTTT AAATATTTTt 780
AATACTTCAC CTAATAAAGC ATTCGGAACA AGTGCAATAA CAACACCAGC ACCAATAGAA 840
TTTAAAATCT TACTGAAAAA CTGTTTATTA TCAGCATTAT TTGCGTTACT CATAAACGAC 900
CTCCAATTTG AACATTAnAC TCATCA 926

(2) INFORMATION FOR SEQ ID NO: 839:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839:

CTTCGAAACG TACTTGGTCA TTCCCTTTAC CAGTACAACC ATGTGCAATA CCTACTGAAT 60
TTGTTTTCTC AGCAATCTCT ACTAATTTTT TAGCGATTAA TGGTCTTGAT AAAGCTGAAA 120
CTAATGGATA TGCATTTTCA TACATTAAAT TTCCTTTGAT TGCATAACTT ACATACTCAT 180
CACTAAATTC TTTTGTTGCA TCAATAATAT GACATTCAAC TGCTCCCATA TCTAAAGCTT 240

CGTATCCtTT GTCGATAAGC CATTGAACGG CCACACTTGT aTCTAGtCCt CCkGAATATG 360

CTAAAACAAT TTTCTCTTTC ATAAAATTCA CCTCATTGTA 400

(2) INFORMATION FOR SEQ ID NO: 840:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1043 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840:

GGATCGCGGT GTTGTGCTTG ATATACTTTG TAGCGATAAC GTTTACCTAC ACAATCATAA 60

CGACAATGAA AATCGTCATC GACTGTAACT ACATTGTTGA CATAAATATC ATCAGGTAAC 120

GTTCGGTTCA TTGCATATTG CCATTGTGAC ATAGGTATAT TCAGCTCTGT GTCGAAATGA 180

AAGTATTGCT GTATCGCATG TACACCTCTA TCAGTCCTAC TTGAAGGATG GATTCTCACA 240

TGTCTTTTAT GCATGCGTTG TAATAGCTTT TCAAATTGTT GCTGTACCGT TCGACCATTT 300

TGTTGAATTT GAAAACCTAG AAAATTATTT CCTTGATACG CAATTTCTAC TAATATACGC 360

ATGAATTTAC ACTCCTGAAT ATTTTAATAC GAATAAAATA ATTGCAATTG GGATAATCAT 420

GGTTAAAGAT ATCGTATCTC TCAATTGCCA TTTAAGCTGT CTGTAGCTCG TTCTCTTAAC 480

ATTGGCATCA TAACCCCTAA CTTCCATTGC GACCGCTAAT TCTTCGGCGC GTTGGAAAGC 540

TGAGATGAAT AGTGGCACTA GTAATGGAAT AAATGATTTA ATACGTGTTG CAATGTTCCC 600

TGAACTTATT TCAGAACCAC GCGACTTTTG CGCCAAAATG ATTTTATCTA ACTCATCCAT 660

TAACGTCGGG ATGAATCGTA ACGCAATGGA CATTATCATA CTTAATTGAT GAACTGGTAA 720

TTTAAACATC tTTAGTGGTG CAAGTAATCT TTCAAACGCA TCTGTTAAAT CAATTGGACT 780

TGTAGATaGT GTCaTAATTG TTGCAATCAT TAcAATCCCA ATTAAACGCA GTGrTATATA 840

TAGCCCTTCT AAAATACCAT TAGTTTCAAT CGTGATGCCA TGCCATTCAA CTAATACATA 900

TCCACCTTTA GTTAAAAATA TATGCATCAT TAATGTGAAG ATTAAAAAGA AAAATATTGG 960

TGTTAAACCT TTGATTAGGA ACCATAATTG AATTTTTGCT AATCTCATAA TGAAnAnGAT 1020

AAGTGCAAAC ACCCAAAGAT ATG 1043

(2) INFORMATION FOR SEQ ID NO: 841:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 841:

TCGAAATCAA ATTATAATAG ACAATTTTAG GAGGTGGACT TTCGATGACC AAAGGAATCT 60

TAGGAAGAAA AATTGGGATG ACACAAGTAT TCGGAGAAAA CGGTGAATTA ATCCCTGTAA 120

CAGTAGTAGA AGCTAAAGAA AATGTTGTAT TACAAAAGAA AACTGTAGAA GTTGATGGAT 180

ACAACGCAAT CCAAGTTGGA TTTGAAGACA AAAAAGCATA CAAAAAAGAT GCAAAATCTA 240

ATAAATATGC TAATAAACCA GCTGAAGGTC ACGCTAAAAA AGCTGACGCn GCACTGAGAG 300

nTCCCCTCAT AATTTCCCCA AnCGTAACCA TGTGTGAATA AAT 343

(2) INFORMATION FOR SEQ ID NO: 842:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 430 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842:

ATGAGTATTT TAATGATGCG CTACGAGCGT ATGGTCTTAC TGTGAnAACA GGTGAATTTG 60

GAACACACAT GAATGTTAGC ATAAATAATG wtGGwCagTC TCTGGTAGTT TAGAATTAGA 120

AGAATTAAAG CAATTTAGAC AATGGGGTTC TAAAACACCA GGTCATCCTG AATACAGACA 180

TACAGATGGT GTAGAAGTTA CTACCGGACC ACTTGGACAA GGTTTTGCTA TGTCmGTAGG 240

ATTmGCTTTA GCAGrAGATC ACCTAGCAGG GAAATTTAAT AAAGAAGGAT ATAATGTTGT 300

AGATCATTAC ACATATGTAT TAGCTTCTGA CGGTGATTTA ATGGAAGGTA TATCGCATGA 360

AGCAGCTTCA TTTGCTGGAC ATAATAAATT AAGTAAATTA GTTGTTTTAT ACGATTCAAA 420

TGGATATTTC 430

(2) INFORMATION FOR SEQ ID NO: 843:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843:

GGACTGCCCG ATGATTTGAC AAATGAATTG CTGATTTGAT TTATATATTA TCTGnAATTA 60

TCATCTATCC AACAATATGT CTTATCAATG GTATAGTCTT TGCACACCAA TGGAGGnAAA 180

TAAATCTCAA CCTTACTATA TTAATATATA ATCAAATCTT AGATTAACTA GTGTAATGAT 240

ACAGATGGAT AATTGAGTAC AAATTTAAAA CCCTGAGATT TTCGCTTTAA TTTGAAAACC 300

TCAGGGnTTA TTTGATTTTT ATATAATGA 329

(2) INFORMATION FOR SEQ ID NO: 844:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844:

AGATGAAGAA AGTGTTTCAT CGATTATCTT AACAGTTGTT GCTTTATATA CTACAnTTCT 60

TCCTAGATCT TGTACCGTTG AAAAGAGACC TGGTTGTAAA ATCTTAATTG ACATTTTCAA 120

TCACCACCCA GTCATCAACA TTAAAGTTGC CATCTGATAT ATCTCTTTCG ATTTGTATAA 180

ATTTCTGTTC ATCTATTGCA TAAAATTGTA TCCATTCTCC TGCTTCGTAC ATTGACATTG 240

GTTCACGCTC GCTGCTAAAT ACTTTTAACG GTGTGCGTCC AATAATTTGC CATCCGCCAG 300

GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG 360

AATTTTTTAA CCTTGGGCnG ATTACGTCTA nGGnGTATGT 400

(2) INFORMATION FOR SEQ ID NO: 845:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 535 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845:

CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT 60

TATTTCTTAA CTGATTAATG TTTCCCCAAC TCTCGGATCC AAACACTTGA ATATGACTAT 120

ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180

TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT 240

CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300

GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA 360

ACCGATTCGG AATTAAATAA AAGCTAAAAC TATGTTAAAT AAACTTAAAC AGTTAGTAGT 480

GTTATTTAAG CAAAACTTAT CATTTTTAAG TTGGACAGAA CAGATCAATA AGAGC 535

(2) INFORMATION FOR SEQ ID NO: 846:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 509 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846:

TCAATCGATC AAATGGTGAT TGACCTTTTA AATTTGTATG ATCAAAATAA TGATTGTTGG 60

CCATATCTTT ACTATGCTTA CGTGCAGTTT CAGAATTCTG TTTAGAATAC TTCAATGTAG 120

ATAATTGATG TTGTTTTCTT TCAGCATTAA CTAAATCAAA ATTTTGTAGT TCAAAACTAT 180

CTGCAAGCGA TTTCGATGGT GCTCCATATT GTTCTTTTAA TCTATTTTCC ATAGCATCAC 240

TTACTTGTAA AACAGCTGTT ACATTATTAC GTCGATGCTT ATCATAAAAT ACCGTCGTAT 300

AAATGTGATT TTTATGGAAA ACATCATATT CTTTATTATT TTGTTCGTAA CGCACTCTAC 360

CTTTAACAAT CTCTGTTTCT GGTTCGCCTA ATCTTTGCCT TACAACCGAT TTAGGTGTAT 420

TGTATTTAAT TTTTGATTTT GAAGTGATTA TATTTTGATT TGTATATAAC GCATTAACTT 480

TATCTTTCAT GTAACTTATC ATTATAAAA 509

(2) INFORMATION FOR SEQ ID NO: 847:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847:

CGTATTGATC TATAAATAGT GTTTAGATGC TATAGTCGGA TGCTTAAGTA ATTTAAAGAA 60

AGTATCTTTA ACATCGATGT GTGTATAATC ATTTTTAGAA GTATTATAAT CTTTTTCTTC 120

TCCCTTCTAA AATATATACA GGTGCTTCAT CAGCTAGTGG TTCAACTGGA ATGTCAGCAT 180

AAACTTCGCA TCATATGTTA AACAAAAACG ATTGTATCTG TACTTCACCT ATAACAGCAC 240

TATCCAATTC GTGCTTATCA AATAAACTAA GATTTTTGTC AGTACCTTTT CACAACTAGT 300

ACATACGTCT TGAGTTCTGA AGCATCATTT CATAAGGAGA ATACTGGCCA CGTGTGGACT 360

(2) INFORMATION FOR SEQ ID NO: 848:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848:

TACCACTTGA ATACATTGCA TATAAAATAC GACGTTGTAC TGGTTTTAAA CCATCACGAA 60

CATCTGGCAA TGCACGCTCT TGAATAATAT ATTTACTATA TCTTCCAAAG CGATCACCTA 120

AAACATCTTC AAGTGATAAA TCTTGAATTA TTTCACTCAC TAGATTTCCT CCTCATCAAA 180

TTGATCATTT TCAAGCACTT GTACTTCAGA ATTATCTAAA ATACTTTGGT CCTCTTGCAT 240

ACCAAACTCA ACATGCTTTT CAATCCATTC ACGTCTAGGT TGTACTTTGT GCACCCATTG 300

AATGTTGTTA CACGTTTAGA TGGAACGCAC TTGCATCTTG CAACTTGTGA CACGnATTGA 360

AAGTTnCGTG TTTGCGGGGG TTnCAGCGTC GTTTGCCCAT 400

(2) INFORMATION FOR SEQ ID NO: 849:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849:

TTTATATGAT TTATTTGAGG AGTTAAGAGA TTTATTTAAA GAAGAAGATT TAGAACCATG 60

GACATCATGC GAATTTGATT TTACAAGAGA AGGTGAATTA AAAGTTTCAT TTGATTATAT 120

TGATTGGATA AATTCAGAAT TTGGTCAAAT AGGTCGACAA AATTACTATA AGTATAGAAA 180

ATTTGGAATT TTACCAGAAA CGGAATATGA AATTAATAAA GTTAAAGAAA TCGAGCAATA 240

TATTAAAGAG CTAGAAGAAT AAACTATCTT AATGTAAGAC TAAACAATAA AGCTTTGTTT 300

AGTCTTTTTA GCGTTTAAGT AAAAAGCaAT AGATACCGTA AAGTTGATGC TCATCAAATA 360

ATAATATAaA GATAATTTTA GGTTTTTAAA CTTTTAATCG 400

(2) INFORMATION FOR SEQ ID NO: 850:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 923 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850:

CAGGCCATAC TTACAATTTT GGCCATCGTC CGGATGTATT nGGAATCGTT GGATAATAAG 60

CATCAAGGTC GTGACTATTT CGTAAAATTC CAACTGTCCC AGAATTTACA TCATTATGTC 120

CAATTACTGG GCAACCaGAT TTTGCCAACT ATCTATATtT CaTATATTCC aAATGTTAAA 180

ATGGTTGAAT CAAAATCTTT GAAATTATAC TTATTTAGTT TCAGAAATCa CGGTGATTTT 240

CACGAAGATT GTATGAATAT TATTATGAAT GATTTGATAG AGCTTATGGA CCCACATTAT 300

ATTGAAGTCT GGGGCAAGTT CACACACGTG GTGGAATTTC TATTGATCCT TATACAAACT 360

ATGGACGTCC AAATTCTAAA TATGAAAAAA TGGCTGAGCA TCGTTTGATG AATCATGATT 420

TATATCCCGA AAAAATAGAT AATCGTTAAA TGTATCATTT AATAAACACA CCAATAAGTT 480

GATTTTCCTA ACTTATTGGT GTGTTTTTCA TTTAGCATAC ATAATAGGTT ACATTAAAAT 540

AACATTTTAT ACCAAAGTAC ACCAAAAGAA TATTAGTACA CGAATTAAAC AACATTTTTA 600

TAGAAACCTA TTGCACTTTA ACGTCAATAA GTATATTTTT ATATTATCTC TAATTAATTG 660

TGCGCGCTTA ATAACAGAAT ATTCTCAATA TTTTTATTTT TTTGTGATTT GTTGGAATAT 720

TTAGTTGATA AGGCACAATC AAATTTACTT AAACTATTGT ATTAGGGGAA GAAAGGATGG 780

GATGTATACA TGACACAACA AAACTCCCAT GGAAATCAAA TTCAAGACAT ACCTCAAACA 840

GGATTTTTCG GGcATCCTCG AGGACTAGGC GTACTCTTCT TTGtAGAGTT CTGGGrAAGG 900

kTTAGTTATT ATGGGCATGC GTG 923

(2) INFORMATION FOR SEQ ID NO: 851:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1004 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851:

TTAnTTGCAT CTATTTCAGT TGGTGTAAAG AAAGCGGAAT TTGATTTTAT TGAAAAGTTA 60

GCtCAAGAAA AATTAATCCC CgAATATATT ACAATAGATA TTGCGCATGG TcACTcAGAT 120

TCaGTGATAA ACATGATTAA ACATATAAAA ACCCATATAC CTGATAGTTT TGTTATTGCT 180

GGTAATGTTG GTACGCCAGA AGGTGTTAGA GAATTAGAAA ATGCTGGTGC TGATGCTACC 240

AAAGTCGGTA TAGGTCCTGG TAGAGTTTGT ATTACAAAGA TTAAAACAGG TTTTGGTACT 300

GCCGATGGTG GTATAAGAAC GCATGGCGAC ATTGCTAAAT CAATTAGATT TGGTGCATCA 420

ATGGTCATGA TTGGTTCATt wTTTGCGGCA CACGAAGAAT CACCTGGTGA AACTGTAGAA 480

CTTGATGGTA AACAGTATAA AGAATATTTT GGTAGTGCAT CTGAATTTCA AAAAGGCGAA 540

CATAAAAATG TAGAAGGTAA AAAAATGTTT GTAGAACATA AGGGTTCATT AATGGATACC 600

TTAAAAGAAA TGCAACAAGA TTTACAAAGC TCAATTTCAT ATGCCGGTGG AAAAGACTTG 660

AAATCATTAC GTACTGTAGA TTATGTTATT GTTAGAAACT CTATTTTCAA CGGTGATAGA 720

GATTAATATT TATAGTAGGT GAkGTAAATT AAAAAATTCA TAGTAACTGT TGTTGCGTTT 780

TTATCAATTA TTATCATTGC GCCAnTAACA GAATTTAAAC CATTCATTCA TTTACAAAAT 840

GAAGTAAGAC AATATATTGA CATTCACATC AATAAAGAAA CAATTTCTGC GGAAAATAAA 900

TTGGATACAC CGAAGAAACA ACAATTTGCC TTTAATAATA TACAAATGAA CATGTCGAAA 960

TCAGATGTTG AGAAAACATT AAATAAACCA AAAAGAGTGA CATn 1004

(2) INFORMATION FOR SEQ ID NO: 852:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852:

GTTCGCTCCA ATGTACGCAG TTGTATATGC ATAGACACCA AAATCGAACC ATTCCATTGC 60

ATTACCGATA CCGGTTGCAA CAACGGTTTT TTTAGCTTTC TTTGCATCCA CCATGTTAAT 120

ATTCTCTTTA TTAAAATCCA TGAATTCATA CACTCCCTCT TGTATGTTTC ATAATTATAC 180

GGAGTTAATT AGTTTTGTCA AATTTATAAG AATTTAAACT TTTATATAAA TACCAAAGTA 240

TGTTTGTTCA AAAATTTCGC TTTATCGnAT TAAATTCATG GTTTTATACC TCATACATTG 300

ATTAGACATA ATAATCTAAA CACGACGTTA CTTTGGATAT ACTnAATGGT nnCACACTCA 360

GTAGGAAGCA CGCATTCGCT CGATAATGTA ACCATACTCA 400

(2) INFORMATION FOR SEQ ID NO: 853:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGTGAAATTG TAACTATATA ATCGATATTA CCTTCAGTGT TCAAAACTGG AAAATAATAA 60

TTACCATCAC TCTTTTTGTT GAATTTATAA ATTTTAAAAG GTTCACCAAG TGTATACGAG 120

GCTTTCTCTT TATTATAGAT TTTATCAAGT GAAGTAACAT AAGAAAGATA GTCTTTTTGC 180

GCTAAATTAC GTACGTCAGT AGGAAcACTC TTGTCCTCGA CATTAACTTG CACATGCTTC 240

TTATCTTTTG CTTTGATATT TGAATTGCTC TCAGCGTTTG CAATAGGGGT AACACTTAAA 300

GAaAATATTA AACTTAAAGC TATTAATTTT GGAAAGTTTC TTTTCATATA AAAACTCCTT 360

T 361

(2) INFORMATION FOR SEQ ID NO: 854:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 605 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854:

ACnTTATACT AGAnAAAGnT ATTAAAGTAT ATCTGCTTTA CACCATTAAA AAGCGGCAAA 60

TGCTATAGAT AATCTAAAGC ATCTGCCGTA TGAGnATTTA TTTATTTTTG ATTGTCATAA 120

TCGTGTGGTT TTAAATTAAT TGTTTCTAGC TTTACAAATT TTGTTTTGTG AATGATTTTA 180

TGAATAAAGT AAATCAACGC TAGAATGATT AAAGGTAAAA AGTTTTTAAA AGCATTTAAC 240

CATTGATCTT TTAAAATATA TTCAACTGAG CCACCAAATA GCAAGAATAA TAGTGTAGTG 300

ATGACAATGA TTGGTCCTAA TGGATAAAAA GGTGCTTTAT ATGGTAGGAC CTTATTAGGG 360

TCTTGACCTT GTTTTTTAAT AGCTTGTCGC AATCGTATTT GTGACCAAAT GCTTGATCCC 420

CAAACAACTA TAATCATTGA ACCAATAATT TCAAGTAAAT TAAAAACGGC ATTTGAATTA 480

AAGTTTGCAT AAATAATAAC AATAACAACG ACTGCATAAG TAGTTAATAA TGCTCTTAAA 540

GGTAACTTAG TTGTCTTGTT TAATTTACTT AAAAATTGGG GTGCTTTTTT GTCTGAACTT 600

AAGGA 605

(2) INFORMATION FOR SEQ ID NO: 855:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 515 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTGAACAAGC ATTTTTAAAT AGTCAACAAC ATCAmGCAAT TAGTGAAGAG GCACAACTTT 60

TAAATAATCC AGATGAATTA ATGGCATTTT TAAAGAATAA GCGTAAAAAT ATTTTAGAAA 120

ATGCATACAT TATGCCGCAT AATATGAGAG AAATGTTACG AAGTTATTTG GAAAGTATGT 180

CTCAAGACTT TAATGTTGGC GGATTTTTTA ATAAAAAGAA GAAAAAACTA CAAATTCAAC 240

AACAGCGATT ATTAACAGCG ACAGATGCGT TACAAGAACA TGTTAATCAA CAAATTCGTC 300

AACCAATGCG AGAAGATATG TCATTTGTTA CGCGTTTTAT CAATAAAAAA GmAGCTTCAG 360

aTAmAGTATT AAATCAGCAT TATGACGTTA AGCCAGAAAT GATTGAAGGT TTATATCAAC 420

CACAAACATC AATCAGCAAT ACTTATGTAC TTACATTTTC AGACGAAGTG GTTAAAGCCA 480

TTAAGAAATA TGTTGAACAA CAATCAACAC CAATT 515

(2) INFORMATION FOR SEQ ID NO: 856:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1607 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856:

GTCATTTTTA AAATTTCGCA TTCGCGTTTA ATTTTTTCTC TTTTTTCTTT TTCTTCTAGT 60

GACATACTTT CTTTAGGTGT TTCAACCAAT TCAGATGTAT CTACATCATC AATTTTAGTG 120

ATTTTGTCTA CATCTTTCTT TAAATCTTCT GGGACGTTCT CGAAACGCTT ATATTGCTCT 180

TTAGAGATAC TAGCAGCTAT TTCATTAGCT CCTAAAATTT CATCTATCAA GCCGAAAGAC 240

AAGGCTTCTT CTGCAGTAAG CCAAGTTTCT GCATCTAACA TCTGTTTTAA GTGTTCTTGA 300

TCTAAATCTT TTGCTTTATC TAAATAAGCT GAATTACTAA CAGCATCTGT TTTTTCAAGT 360

AAATCCGCTG TCTTTCTTAA TTCTTCTGCA TTACCTACAG TCATAACCCA TGAATTATGA 420

ATCATTAAAA AACTATTTTT GTGCATAAAA ATAGTGTCAC CACTCATAGC GATAACACTA 480

GCAATTGATG CCGCTAAGGC ATCGACATAG ATATTAATTT TTGCAGGATG CATTTTTAGC 540

ATATTGTATA TTGCATGTCC TTCAAATACA CTGCCTCCAG ATGAATTTAT ATGAACATCT 600

ATTTCACTGA TGTCTCCTAG TTCATCTAGT TTATTTTTGA AATCTGTAGC AGTTACATCA 660

CTTTCAAACC ATTTATCACT TACAATATCA CCATAAATGa ATATTTCACC TTTACTTTTT 720

GATTTTCTTT TCATTTGAAA ATACTTAGCT TTCATTGACA TTTTTATCAC CACCTTTCaA 780

AGATTTTCTT AATTCAAGTG GCGTGTCAAT TGGGTATAAA TCACCGCTTA ATTAGCGGCT 840

AACCACTACG AACTGCTTTA AAGTACACTT CTGCTTGTGT TGCACTATCA GCCCTTAAAT 960

AAGATTTAAC GTTAAATTTA AAATACCTAT TTTTTTCTCT GTCTGTTTTA GTAAGTAGTT 1020

TCCGATTAAn TTCTTCTTCA TACTGTTTGA CGATTGGCAA TAAGGTATGC TGCAAGTAAA 1080

ATCTGTTTAA CTCTTCATTT TTCGCGAAAT TTGTATTTGA TCTTGCATTT AAGAATATTG 1140

AGGGCAATTG AAAAACGTTA GCTACTCTTT CTCTTGTTAA ATTCTCGCTT GCCACTATAT 1200

CTTCAGAGAC ATATTTTTTA GGTAAAGGTT CGATTTCAAC ACCAGGCTCT TGGAATAATA 1260

TTCCACCGTT TTCTTCATAG TACTGTTTGA AATCTTCTAA CACTTGTTGC CTTTTTTCTG 1320

TACTTACATT GGAACCATAT TTAAGCATAA AAGAATCTGG TTTTTGCATT TCTGTAAGAT 1380

TAAAGGTTCT TACTGCATTG TCAAAATCAG TTGTATTCTT CAACACATCA ATCGGACTAA 1440

TACCTTGAAC CATATTAGAT GCCACGATGT GTTTAAAATG CAACATGTCC aTATTATGAA 1500

CAATCAATTT ATTTCCAGTT GCAGCATGAA TGGAATAATA AAGTTCACcG TGATTGGTTT 1560

TCAATTAACA TTTCAACAAC ATCTGGATTT AATAAGAAAA GCTTTGA 1607

(2) INFORMATION FOR SEQ ID NO: 857:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857:

ATGCGCATTT AACCGCATTT AGAGATGCTG AAGATCAGTA TAAAGCTTTG TTAGAAATTA 60

CAACATTACC AGAAGGTAGA ATTTATGTTG CTCGCCAAGA TCAACTCATT GTGGGTTATG 120

TCACTTTCCA CTATCCTGAT GAAATTGAGC GCTGGTCTAC AGGTAAGCTT CCATATTTAA 180

TCGAATTGGG GGCAATTGAA GTCAGCATCA ATTTTAGGCA ATTACAACTT GCAGAAAAGC 240

TGATACAACT TAGCCTTCTA CACCAGAATT CGAGAATTAT ATCGGnATAA CTACAGGATA 300

TTACCGGCAT TGGGGGTTTA AAAAATTCCC AGTnAGAGGT ATTnCC 346

(2) INFORMATION FOR SEQ ID NO: 858:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATTACTATAA TGAATCTTGC GAGATATTTA GAAGTAATGA TACAAnATAA TGGACTTTAG 60

AATTTmAATT TACAATAAAT AGTTCTATGA TTAAATGTCA GTTTTATGAC ATTTATTTAT 120

TGAAAATACG AACGAATGaG CGATaTGATA ATATAGATAA GAATGATTTT AATTTAGGAG 180

GCCTTTATGG TGCATAATAA AAACAATACA ATTTTAAAAA TGATCAAAGG TGAAGAAACA 240

TCACATACAC CTGTTTGGTT TATGCGACAA GCTGGCCGTT CGCAACCAGA ATATCGAAAA 300

TTGAAAGAAA AATATTCACT ATTCGATATT ACACATCAGC CGGAGTTGTG CGCTTATGTA 360

ACACATTTAC CAGTTGATAA TTATCATACA GATGCAGCAA TTTTATACAA AGATATTATG 420

ACACCATTAA AGCCAATTGG TGTCGATGTA GAAATTAAAT CGGGTATTGG TCCAGTGATT 480

CATAATCCAA TCAAAACAAT TCAAGATGTT GAGAAACTTT CTCAAATAGA CCCCGAACGA 540

GATGTACCAT ATGTATTAGA TACAATTAAA CTTTTAACAG AAGAAAAGTT AAATGTGCCG 600

CTAATAGGAT TTACTGGGGC ACCATTTACA TTAGCGTCAT ATATGATTGA aGGCGGACCA 660

TCGAAAAATT ACAATTTTAC AAAAGCGATG ATGTATAGAG ATGAAGCAAC ATGGTTTGCT 720

TTAATGAATC ATTTAGTTGA TGTATCTGTT AAATATGTAA CAGCTCAAGT CGAAGCAGGT 780

GCCGAATTGA TTCAAATTTT CGATTCATGG GTAGGTGCAT TAAATGTCGA GGATTACAGA 840

CGTTACATTA AACCACATAT GATTCGATTA ATCAGTGAGG TTAAAGAAAA ACATGATGTG 900

CCGGTAATTT TATTCGGTGT AGGTGCCAGT CATTTAATCA ATGAATGGAA TGATTTACCG 960

ATTGATGTAT TAGGCCTAGA TTGGAGAACG TCTATTAATC AGGCTCAACA ATTAGGCGTT 1020

ACTAAAACAT TACAAGGGAA TTTAGATCCA TCAATTTTAT TAGCACCATG GAATGTCATT 1080

GAAGAGAGAT TGAAACCAAT ATTAGATcAA GGTATGGAGA ACGGTAAACA CATCTTTAAT 1140

TTAGGACACG GTGTATTCCC AGAAGTGCAC CAGAGA 1176

(2) INFORMATION FOR SEQ ID NO: 859:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859:

ATTTGGTGCA TTGGTAnAAT TGACCTGAAA GnAAAAAGTG GTTTAGTTGC ACATTGAGTG 60

nAAGTGCGCA GATGAATTAT GTTGAAAACG TGAGGAAGAG CACCTTTGCT GTTGGTGATG 120

AAGTAGACGT AAAAGTATTA TCTATTGCTG ATGATGGAAA AATTAGTCTT TcAATTAAGA 180

AAAAAGCCGA AGATTTTGAA AAGAAATTAA GCAATTTCTT AAAAGATAGT GAAGATAAAT 300

TAACTTCAAT CAAACGTCAA ACAGAATCTA GACGCGGTGG CAAAGGTTCA AGACGTTAAT 360

TAAAATAAAT AAAGACTGTT TCGATAAGGA ATATATTTAG AATGATGCGT ATCGAATAAT 420

CGATTGCAGC GTTAGACAAT CTAAGACTGT TTCTTAAATA AGGAGCAGTC TCTTTTATTT 480

GTAATGATAT AACTAAGACT TATACCATTT TTGAAAATTG TAAAAGTGAG GTGATGTTAT 540

GCAGTTAAAT AGTAATGGTT GGCATGTTGA TGACCATATT GTTGTCGCTG TTTCTACAGG 600

TATTGATAGT ATGTGTTTnn T 621

(2) INFORMATION FOR SEQ ID NO: 860:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 544 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860:

TATATTAGGT ACTTGTGTTG GTATTGTGCC AGCTTTGCTG TCTACTATAA TTTCTAAAAG 60

GTTTGAACAT ATAAAAGGGA AAGTGCTAGG TGTATTTAAT TTTGTGAGAT ATATTGGAAT 120

GACTGTCGGT GCATTATTAA TTGGTATCAT TTCTCAGCCG TTGGTAGCCT TTTACTTCAC 180

AACTATAACT ATCATGTTAA TAGTAATATT TCTTTATATA AAGATAGTTG ACTTTCAGCT 240

AAAGTATGCC AAATAAACTT AAAAAAGCAG TGAATCATTT CAATAGATGG AATGATTCAC 300

TGCTTTTTGT TTATAGAAAT TTAAAATTCA TGCCTTTATG CTAACAACAA TATTATTTTA 360

CTCTCTTACG TTTGCCAATG TAACcGTATA GCAAAGTAAA TGACTGCGAT AATGATGACA 420

ACATACATAt ACGTGAATAG GAAGGAAGAC CAGTCATCAA CATACCAAAG CTATCGCTCA 480

AAGTGCGnCT GGTAAATTAA ACCGAATTCC AnGATTGTAG GAACCCnATT AATGGAAATA 540

ACGG 544

(2) INFORMATION FOR SEQ ID NO: 861:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 651 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861:

AATTTAAAAT ACATTTATGC TTTACCCATT CGAAAATACC TTAATCATTT TCATTTATAG 120

CATTGTTTGA TTGAAGGATA AAAAGTTGTT GTTTACAATA AAAATAATGA GTATCTGAAA 180

TGAGGGATTC AnTATGACAC ATGTGGAAGT AGTAGCGACT ATCGCGCCAC AATTATCTAT 240

CGAAGAAACT TTAATTCAnA AnATTAATCA TCGTATTGAT GCAATAGACG TATTAGAATT 300

ACGAATTGAT CAAATTGAAA ATGTCACAGT TGaTCAAGTG GCAGAAmTGA TTACAAAGCT 360

GaAGGTTATG CAAGATTCAT TCAAATTATT AGTTACGTAT CGTACAAAGT TACAAGGTGG 420

CTATGGGCAA TTTACAAATG ACTCGTATCT TAATTTAATA TCAGACTTAG CAAATATCAA 480

TGGCATAGAT ATGATTGATA TAGAATGGCA AGCAGATATT GACATTGAAA AACATCAACG 540

AATCATTACA CATTTGCAAC AGTATAATAA AGAGGTGGTT ATATCACATC ATAATtTCGA 600

AAGTACGCCT CCATTAGATG AATTGCaATT TATATTTTTn nAAATGCAAA A 651

(2) INFORMATION FOR SEQ ID NO: 862:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862:

TGTGAGTGGT AATGACACAC AAGCAGATTT AATAGGTTAT AGTTTTAAGT TTGACGGTGC 60

GATTTCAAGG CAAGAGGCTT CTAAAGATGT ACATGCAGTT ATATTATCGA ATAAAACACT 120

ATATTTATTA GATGTATTAC AAAAATTACC GATAGATAAA ATGAATTCAT TGAATATCCA 180

TCAAGAAATT ATTGATGAAA TGTCAGATAT CATTTTAATG TTATATCGTG AATATGCAGG 240

TATGTTTTTT AAAAGTCAGA AACTAATCAA CCAATTAAAA AGATTGGAmC AATAACaTAA 300

AATAATAAAa GGTATTCAAG TAGCCACATA GATGTGTTTA TTTGAATACC TTTTkGAATA 360

GaaAAGaGAT ACTGGcAATT TTACTAACCA GtATCTCTTT T 401

(2) INFORMATION FOR SEQ ID NO: 863:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863:

ACAAAGTAAT CAATATGTAA TATAAAATAC ACTGGTACTC AATATATAAT GATGATAAAA 120

TTAATTTTAA TTAGATAGAG TTGCTTTGTG TTTTTAACGC nGATGCTACT ACTTATCTTA 180

ACAGTTGATT AAGTAAATCA TTTAACAGCG AGATTATnCA ACCAGGGGGA TGACTTAATG 240

AATTTATTCA GACACCAAAA TTTAGTATCA GAAATTTAAT GTCGGTATTT TTTCAGCTTT 300

AATGCCAC 308

(2) INFORMATION FOR SEQ ID NO: 864:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1827 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864:

TTCTACATCT TAAACGATGA CCTAACTATG ACGTTAATCT GGAAAGATGG GGAGTTGCTA 60

GTATGATGTT GAAATTTAAA GCTTGGGATA AAGATAAAAA AGTTATGAGT ATTATTGACG 120

AAATCGATTT TAATAGTGGG TACATTTTGA TTTCAACAGG TTATAAAAGT TTCAATGAAG 180

TAAAACTATT ACAATACACA GGATTTAAAG ATGTGCACGG TGTGGAGATT TATGAAGGGG 240

ATATTGTTCA AGATTGTTAT TCGAGAGAAG TAAGTTTTAT CGAGTTTAAA GAAGGAGCCT 300

TTTATATAAC TTTTAGCAAT GTAACTGAAT TACTAAGTGA AAATGACGAT ATTATTGAAA 360

TTGTTGGAAA TATTTTTGAA AATGAGATGC TATTGGAGGT TATGAGATGA CGTTCACCTT 420

ATCAGATGAA CAATATAAAA ATCTTTGTAC TAACTCTAAC AAGTTATTAG ATAAACTTCA 480

CAAAGCATTA AAAGATCGTG AAGAGTACAA GAAGCAACGA GATGAGCTTA TTGGGGATAT 540

AGCGAAGTTA CGAGATTGTA ACAAAGAACT GGAGAAGAAA GCAAGCGCAT GGGATAGGTA 600

TTGCAAGAGC GTTGAAAAAG ATTTAATAAA CGAATTCGGT AACGATGATG AAAGAGTTAA 660

ATTCGGAATG GAATTAAACA ATAAAATTTT TATGGAGGAT GACACAAATG AATAATCGCG 720

AAAAAATCGA ACAGTCCGTT ATTAGTGCTA GTGCGTATAA CGGTAATGAC ACAGAGGGGT 780

TGCTAAAAGA GATTGAGGAC GTGTATAAGA AAGCGCAAgC GTTTGATGAA ATACTTGAGG 840

GAATGACAAA TGCTATTCAA CATTCAGTTA AAGAAGGTAT TGAACTTGAT GAAGCAGTAG 900

GGATTATGGC AGGTCAAGTT GTCTATAAAT ATGAGGAGGA ATAGGAAAAT GACTAACACA 960

TTACAAGTAA AACTATTATC aAAAAATGCT AGAATGCCCG AACGAAATCA TAAGACGGAT 1020

GCAGGTTATG ACATATTCTC AGCTGAAACT GTCGTACTCG AACCACAAGA AAAAGCAGTG 1080

AGTGGTGTAA GTAGTAAAAC GTATTTAGTG ATTGAAACAG GCAAGATAGA CGCGGGATAT 1200

CATGGCAATT TAGGGATTAA TATCAAGAAT GATGAAGAAC GTGATGGAAT ACCCTTTTTA 1260

TATGATGATA TAGACGCTGA ATTAGAAGAT GGATTAATAA GCATTTTAGA TATAAAAGGT 1320

AACTATGTAC AAGATGGAAG AGGCATAAGA AGAGTTTACC AAATCAACAA AGGCGATAAA 1380

CTAGCTCAAT TGGTTATCGT GCCTATATGG ACACCGGAAC TAAAGCAAGT GGAGGAATTC 1440

GAAAGTGTTT CAGAACGTGG AGCAAAAGGC TTCGGAAGTA GCGGAGTGTA AAGACATCTT 1500

AGATCGAGTT AAGGAGGTTT TGGGGAAGTG ACGCAATACT TAGTCACAAC ATTCAAAGAT 1560

TCAACAGGAC GACCACATGA ACATATTACT GTGGCTAGAG ATAATCAGAC GTTTACAGTT 1620

ATTGAGGCAG AGAGTAAAGA AGAAGCTGAG CGCAAATACG AGGCACAAGT TAAGATAAGG 1680

AGAGATGGAG ATGCCAAAGA AAACGGTAAC GATTGATGTA GATGAAAACT TATTAGTAGT 1740

AGCTAGTAAT GAAATATCAG AACTATTATA TGAaTATGAC AGTGAGTcAA TGTCAGCTGG 1800

ATGGAAGATG GCGATAATAG GGATATC 1827

(2) INFORMATION FOR SEQ ID NO: 865:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865:

TCAATTGCAT CATCATATGA AATTCTaGGG AATGGTGTCG CAACTTTTTC AAGTTTTGAT 60

GTATCACGCT CTAAAATTTT CAACTCTAGT TTACAATTTT CTAAAACTGA TTTTACAACA 120

TGTGTTACAT ATTGTTCTTG AATTTCTAAA CTTTCAGCAT GATTTGTGAA AGCCATTTCT 180

CCTTCAATCA TCCAGAACTC GATCAAGTGT CTACGTGTTT yTGATTTTTC AGCTCTGAAA 240

GTTGGACCAA ATGAAAATAC TTTTCCGTGT GCCATTGCTG CAGCTTCTAA GTATAACTGA 300

CCACTTTGAG ATAAAAACGC ATCTTGATCA AAGTATTTAG TATGGAATAA TTCACTTGTA 360

CCTTCTGGCG CACTTGCTGT CAAAATTGGT GGATCAACCT TTGTAAATCC ATCTTTGTTG 420

AAAAATTCAT ACGTTGCACG AATAACTTCA TTTCTAATTT TCATTACAGC ATGTTGTTTT 480

TTAGAACGTA ACCATAAATG ACGGTGATCC ATTAAGAATT CTGTACCATG ATTTTTAGGT 540

GTAATCGGAT AGTCATGCGC TTCTGAAATA ACTTCAATTG ATTTCACTTG CATTTCGTAT 600

CCTAAGTCAG AACGATTATC TTCTGTAATT GTGCCTGTAA CGTATAGAGA TGATTCTTGA 660

TGCATAAAGC CTGTTCCATC ACGTAATTGT AAAAAGGCGA TTTTACCACT TGAAcGTTTA 780

TTTGTTAACC AAGCACCAAT TGTAACGTCT TGGTTTAAAT GATCTTTCGC TTGTTTAATC 840

GTTGTTTTCA TAACCATTCT CCTATTTATT TTTTCGkTAT ACAATACTCA TTCATTTTAA 900

CAAAATCCGC TTTCAAGTTC TAGAACTAGA CTAAAAGATA ACGtGTAAAT GGTAATGATT 960

TACGCACAGA TTTGAACATT AATTTATATT AAGACAATAC AATCATCAGT TTCAGACAAA 1020

ATATATAATA AAGCCTCAAT ATTATTAGTA TGAAGGTCGT TTTTTGTnCT AACATTCAAG 1080

TTTAATTATA AAACTCAAAT TTTGACGACC AAACAAAAAT TCTTGTAACA GAACATAGCA 1140

CATGTCATGT CACAAGAATT TTACTTTGTA TTTCACTTTT TCTTTTTTTG AATTTGTCTT 1200

AATAATTTTC CAAACTGTTG AATGTCGCCT TTTTTCTGAC GATAATTTTC AAGTGTTTGT 1260

TCAAAAAAGT TTTTATAATT ACTGTTTATG AGTCGATCAT CAAATGAAAC TATTATGCCG 1320

CGATCATTTT CATTTCTAAT TAATCTTCCA AGTCCTTnGT CTAnAACGTG TAACTGCAT 1379

(2) INFORMATION FOR SEQ ID NO: 866:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866:

TTACAACGAA TAGTTCACCG TTCGAGTCTA ATCTATGTAA TGCTTGCTCG AATATACGAT 60

GCACGGTTTC TTTCCCTGCT CTTATTGGTG GATTGGTTAA AATAAAATCA AAACTTTTGT 120

CTTCCACAGC AGACAAAGCA TCACTTTCCT TTACGATCAC ATTATCAATA CCATTTAATT 180

TTTTGTTTTT TTCAACTAAG GCTAGCGCTC TGTGATTAAC ATCTAGCATT GTAATTGAAT 240

GATGTGGTGA TACTTTAGCA ATCATCAAAC CAATTGGTCC GTAACCACAA CCAACATCGG 300

CAATTCGCTT ACTTGGACCA GGTGGATGCG CTTTTAAAAA AGTTTGAACA AGAACATCTG 360

aACCATAATC TACTTTAtCt TTCGAAAACA CTCCtTATCA GTTATTAAAT CAATTTTATG 420

AnGGTTnTAA TTGGATATTG AGTACGTTGT 450

(2) INFORMATION FOR SEQ ID NO: 867:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867:

AATGTTAACA ATATAGCACC AATTAACCCC GACATGATAA TAACGTGTAA TGTTTTATTT 60

CCTATTAATT GTCTCGCAAT ATGAGGTGCA ATTAATCCTA AAAAGCTAAT ACCACCGACA 120

ACTGAAATTG CGGATCCTGC TAATATTACT GCTAAAATTA ACAATAGCAT TTTAATAGTT 180

TTAACTTTTA AACCGAGTGC GGTTGCAACA GCATCACCTA GATTCAATAC ATCTAATTGA 240

TAACTCCATA AAATGATGAT GGATCGTTAT TAAAACCAGG GAATATAGAT AATATCCGCA 300

TATCAGGCCA TATAGCTACC TGTCACCAAC AGGTTTnTGC TCCAnGGTTC TnTAATAAGA 360

CGCACACGCG ACAATGCGCT TGCTACCATT AGGCAGCTTG 400

(2) INFORMATION FOR SEQ ID NO: 868:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868:

AATCCnTnAA GTGCCATAAC ATCATCTCCT AACATCTTTA TTATACATCA ACATTTTATA 60

AAAATAACnT CTTATGATAA AAATGAAAAT ACTAATTTTA ATGAGAGCGT CTTAAGCCGC 120

AATTGATAAA ACATATGCTA CAATATTTTT AAACACTATA CAGGAGGTAC TCTATGACAA 180

AATATACATT TAAACCTAAA GATTTCAAAG CGTTCAACGT AGAAGGCTTA GACGCACGAA 240

TGGAAGCTTT AAACGAATAC ATACGaCCAC AACTCCGTGA ATTAGGAGAA TATTTTAGTG 300

ACTTCTTTAC AAGTCAAACT GGTGAAACAT TTTATCCTCA CGTAGCAAAG CATGCTAGAA 360

GAAGTGTGAA TCCTCCTAAA GATACATGGG TTGCTTTTGC AACAAACAAA AGAGGCTATA 420

AAATGTTACC TCATTTCCAA ATTGGTATGT TTGAAGATCA ACTGTTTGTT ATGTTTGGAA 480

TCATGCATGA AGCAAAAGAT AAAGCAACaC GTGCAAAAGT TTTTGAAAGA AAATTTAAAG 540

CTATTCAACA ATTACCTGAT GATTATCGTG TTTGCTTAGA TCATATGAAA CCTGATAAAC 600

CATTTATTAA AGATTTAACG GATGATGATT TAATAGAAGC GATACAAAGA GCCATCAATG 660

TGAAAAAAGG TGAATTCTTT ATAGCGCGTG CAATCACACC ACAAGATAAA AGATTAAAAA 720

GTGACAAAGC ATTTATTGCA TTTTTAGAAG AAACCTTCGA TCAGTTCTTA CCATTTTATT 780

CTGCATAAAT AACTTTGTTT AAATAATAGA GCACTTAATC ACATCCaTGA TTTCGTGCtC 840

TTtTTTCTTA ATATTAAATC GAACGTtCAA CATAaTAATT CATACTTTTA AAAAAATTAA 900

GGTGAGTCAA AATGAATAAT AAACGACATT CAACAAATGA ACAATTAAGT TTAGACGAAA 1020

TAAACAATAC AATTAAATTC GATCATCGCA GTTCAAATAA ACAGAAATTT TTATCATTTC 1080

TTGGACCTGG GTTATTAGTC GCTGTTGGTT ACATGGATCC CGGAAACTGG AT 1132

(2) INFORMATION FOR SEQ ID NO: 869:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869:

CTCAATGTAT TGACTGTGAT TTGGAGTGTA TAATGCTACT GTTTTGTCTA TAGCCATCGC 60

ATCAAATATT ATATTTGAGT AATCAGTGAT AACGACATCA GACATTAGAA TTAAGTCTTG 120

AGCACTAAGA TACTTTGGTG CAACAAGCGC CTCTTCTGGT AAGATCGCTT CATCAACACC 180

CTGAACCACA ACATGATAGG CTTTGAATAA AGCATCTGAT AGTGGTAATT GTTGCGCACT 240

CACTAATCCA ATAGGTGCGT ATAATAAAAC TGGTTTTTGA TCATTTATTT TAAACGATTT 300

CTTATACTGT TGTTGAGTAG TACTTTCGTT ACTCTTTTGT AGTAAATATT GGTGTTTAGG 360

ATTACCATAA GCCAATACAT TGCTTGGTGA CTAGGAAAAG nCGTTTGATA AAAGGGCT 418

(2) INFORMATION FOR SEQ ID NO: 870:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870:

GAGTnTGTTA CAGTAATTGA TTTTATTGGT AATTnTAAGA CAAATTATTT AATTCCGATT 60

GCGCTTTCTG GGGATCAATC GCAAnATAAA GATAATTATA AGAAGTTTTT AACGAATAAC 120

GATTCGATTA ATGGAGTATC TACAATTAAT TTTGAAGAAG TTGCTAAAAA ACAGATTTAC 180

AATTCATTGG ATGCAGTATC ATTAAATCAA AATAAATTAA TATTAAAAGC TTATGAAGAA 240

GTTGAAAATA GATTGGGACA CATGCCGTTA CTAATGGATT TCATACAACA ACATTCTATA 300

GATCCAAGCG TTATATTTTC TAAATTTAGT AATTATTACG AGTTCTTAGT GAGATATAAA 360

AAAATAGATA CATTATTGAC GGAAAATGAA TCTAAAAATC TGGTTTTCTT TTCAAGGCAA 420

TTAACATATG ATGAATTAAA AAATAAAATG TTGAACGAAG TTAAGGATAT AACAGAAGAT 540

GATATAGATA CTTCATTAAG AATTTTAGAT TTTTCATTTT ACAACGC 587

(2) INFORMATION FOR SEQ ID NO: 871:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 971 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 871:

CTACTAAACC AGGTAATCGG TAGAATCCAA GCAGGAATAA ATAAATTAAT GCnACACCAA 60

TAAACGATGC AAACACAGTn TTATCTAATG CATCTTGACC AAATTGGGCA CCTACTGAGT 120

TTGAATAAAT TTCTTTCAAG TCAACTGGTA AAGAACCTGC ATTTAACAAT kCGGCGATTT 180

GTTTTGCTTT TTTAACGCCT TCTTGTCCTT TAAATCCACC CGAGATTTCT ACGCTATCAG 240

AATTGATTGG TTGATCAACA CTTGCTGCAG AAATAAATTT AGGGTTTTTC TTTTGTGCTT 300

CTTTTTTATA GCTGTCACCT TTTTTGAAAT CTAACCAAAC AACCATGACA TTATCACGTT 360

TCTTAGAGAT TTCTTCCGTT ACTTTTTTAA ATTTGTTTTT GTCTTTTACT TTAAAAGTAA 420

CTGTAGGcTG GTTTGTTTCC tGtTTAAATT CTTGtTTGGC AGATCCCTGT TTaATATCAG 480

AACCGCTTAA TTTtACTTTA TCTTCTGCAT CGCGAATTGT TAAATTAGCT TGAGAAGATA 540

AAATTTTACG TGCTTCATTC TGGTCTGTTA CACCAGCAAG TTGTACTCTA ATTCTATTAG 600

GTTCTTCAAC TTGAATTTTA GGTTCCGAAA CACCTAAAAC GTTAACACGA TTTTCTAATG 660

TTTGCGCTGT TGATTGTAAG GCTTTTTTAT CTATTTTGTC GCCTTTATTT AAAGGATCGA 720

CTTGATAAAG CACCTCAAAT CCACCTTGCA AATCAAGTCC TAAATTGmCA TTCTTTATAA 780

CACTTTTATA AGTTGcAGCC ATTCCGGCAA ACAACAATAC GACTAAAAGC AAGAACGCAA 840

TTATTCTACT ACTTTTCTTC ACATGAACAC CTCATTATTT ACGTATGTAT TTAGAATACT 900

TGAATACTAT TTTATAACGC AAGTGAAATC TTTCTTACAA AATTTATTAG CCTTATACAT 960

ATTAACATAC T 971

(2) INFORMATION FOR SEQ ID NO: 872:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 636 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872:

CTGGTTAACA ACATCTGGTT CGGCATCTCC TTAGCTTCCA CTAAATCTTG GATGTCTTGG 60

nnATCTTGCG CAAGTnGTGC TTTGGCTTGT TCAATTtCTy CTTTAGTCAT CGCATTGTTA 120

ATGCCGTTAT GACCTTGTTG AAGTATTTGA TTAATACGAT CTTTAAGTGC TTGTTTTTCC 180

TTATCTGTTA GATTTGGATT TCGATCAATT TCGTCAATTA ATGCTTGaAC TTGcTTATCA 240

ACGTCTTTAT TGGCATCAAT TTTTGCTTTT GGTATTTCAT TGGCATGCAC TTGTTCAATC 300

GCGTGGTTGC CTGCTGTTTG AACTTGAGAT ACAGCCTGAT TACTTGTTGC TTTATTAATG 360

TTGTTGATGA TGCTGTTTGC CAATTCTTCT GCTTTATTTT TCGCAATAAG CTTGTCTTGA 420

TCCGTCGCAT TTGAAGCTTC GATTTCTTTT AGCTTATTAG CTAAAGCTTG ATTAATAGAT 480

TGAATTGCCT TGTCTTTAGC ATCTTGTAGT CGTTGATCAC CATTAAGATT ATGGATTGCA 540

TCATTGACtG CTTGGATTGC GCCATTGATA TCATTCACAT tTGTGTaTCA CTATTTAGCA 600

ATGTATTTGC TAGACGTTgG CATCATCGAA GTTTGT 636

(2) INFORMATION FOR SEQ ID NO: 873:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 659 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873:

CTCTGAATGC ATTCATTAAA CGCTGGGTCT CTTTATATGA AACGTATTTG TCATTTTTAG 60

AACTCAATCC GTAAAAATTG TCAACTTTCT TTTTAATATT ATCGTAATCA ATGGTTACAT 120

TACTTAAATC AATATCTAAA TCTATATTTT CTGCATCTTC TTTAAAGCCC GCTATACTGA 180

AAAAGCCTTC AATCGGCTGA TCAATCATTT CAATATATTT TAAAGCTGTG ATTGAACCTA 240

AACCATGTGT TACAAAATAT GTATCCTTTT TGCGTACATT AATTTGTTTC GTCATAGCTT 300

CAATCCACTG ATCCACTGTC TTCGCTtCAG GGGATTCAAA ATTAAATAAT GTTACGTCAT 360

ATCCTTCTAA AGTTAAGTTA TGCTCCAACC ACTGATACCA ATGATTTCTA CTATTTCCAT 420

GCATAGAATG TACAATAtTA CATCTGTCAT CTCATTCTCT CCTTTCAACT TACTACTTCT 480

TTTCTATTTT TAAAAAAATG ACTGATTACC TATAATTGTA AAATAAAAAC ACCTTAATTA 540

GAAATGTTAT ATCGCAAAGT GACATTTCTA ATTAAAGTGT ATTGTCATCA TTTCAATATC 600

ATTCAAAAAC AGCTAAACCT TTGTCTCTGC TTCAATTTCA CAAAAATAAT TCCCGCTGA 659

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874:

AAAATAAAAT CCATTTTAGT ATTCGTAGAA AATGAGAGCC CCCTTTACCA CAATATGTAA 60

ATGTATATTG TGAAAAGGGG GCTTTTATTT ATGACATAGT TGTTCAACTC ATACATTCAG 120

TTGATAATGC AGTGCGTTAT GCAGCTATCC ACTTCATATG TATGGCGCAT ACTTGATATA 180

TGAATATCAT CAAGATTTTA AAAGTATCGC TAATTTTAAA GTCTTAAAAC GCAGATTAAT 240

GGTCATGATG TGTTAnTGCG TTTTGGTTTT TAGAGCCACG TAATTCCCAn GGACATATAG 300

GAGGAACCAT TCCAC 315

(2) INFORMATION FOR SEQ ID NO: 875:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875:

TACACGACCT TGTAACTCAG CTGCTTTATA AGCTAGGGCG ATGTTATCAA AGTTGGATGT 60

ACTTTGAGCT TGGCATTTCG TTAATACTTT TAACGAAGGA TTTAATATAT GTCTGATACG 120

TATATATTGA TTATATTCAA TTCTTaATTt GGATAAGATT GCTGATAATT TGAAGCAATC 180

GGAGCTAAAT GGATCGAAAA ATGAATAAAT TTCGATTTTA CTTACAGGTG ATAGaTTGAT 240

ATCTTCACGA CTCTTATTTT CCATTAwTCG TAATTCTCCA GCCATGTTTA TTCACCTACA 300

ATTAATTTTA GGAATTCACC ATATGaTTAG CAGTTAATCT TaAGCGCTCA AATAAATAAT 360

CTCCAACACC TTGTGGAAAC caGCgCGaTT AATTGCTGTC TGCATATTTT CTAGCCATGC 420

ATCTCTTTCA AATTCAGTGA TTGTAAAATC TATATGTCTT TTTCTTAGCA TAGGATGTCC 480

GT 482

(2) INFORMATION FOR SEQ ID NO: 876:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 670 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876:

ATGCAATTGA ATTCTTAAAA GCAGAAGGCT TTGATGATAT TGAATGGGGC GAAGATTTTG 60

GTGCGCCACA TGAAACAGCC ATTGCTAATC ATTATGATTT ACCGGTGTTT ATTACTAATT 120

ATCCAACTAA AATTAAGCCT TTCTATATGC AACCAAATCC TGAAAATGAA GAAACTGTAT 180

TATGTGCAGA CTTAATTGCA CCTGAAGGAT ACGGTGAAAT TATTGGTGGA TCTGAACGTG 240

TGGATGACTT AGAATTGTTA GAACAACGCG TTAAAGAACA TGGATTAGAC GAAGAAGCAT 300

ATAGTTACTA CTTAGACTTA CGTCGTTATG GTAGTGTGCC ACACTGTGGA TTTGGTTTAG 360

GTTTAGAGCG TACAGTAGCA TGGATTTCTG GTGTTGAACA CGTTCGTGAA ACAGCGCCAT 420

TCCCAAGATT ATTAAACCGT TTATATCCAT AAGTTTTAGG GTCGTTACTT AAAATATATA 480

TTATGATAAT AAAAAGAATC GTCCAGCCTA TATTAATAGC TGGGCGATTT ATTCTTGGAA 540

AATGAAGATT GATAACGGCT TATATTAATC ATGAACAAAC TTTTGTTTAG TAACTATATT 600

TGGAAAATAA ATAGTTCATC TGATTATCCA TAAAGTTCAT TGTTAAAATC TAGTGTTAAA 660

AAATACTGTT 670

(2) INFORMATION FOR SEQ ID NO: 877:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877:

TGCAAAGTAA ACTGGATGGC TnTCTTGCCG CCAAGGATCT GATGGCGCAG GGGATCAAGA 60

TCTGATCAAG AGACAGATCC TAACCTCTCA TTTCCGATAA GTTTAGTATG TATTATAGGT 120

GATGATTnTC TTGTTTTCAA CCTTATACAC AATATTTTTG AnATTTATAT TATATTCATA 180

TAAGGAAGGC GATTAATTAC GATTCATCAT TATATCTCTA CGTGTTAATT TATTAACCtA 240

TACTATATTT ATCaACaCAA CAGTTTTTCC TTTCATTTTC AAACATAACA GAAAAAGCCT 300

GAGACATACT TAGTCCCAGA CTGTTCTATA ATTAATTAAA GATATAACAA GGTTAATCAT 360

TCAAAGCTAA CATCACATTT ATTCACTGTA ATTTTTCATA AAGAATAATA ATGACTGTAA 420

TTCTATACCT AAGTCAATTT GATGTACTTG CACATCTGAA GGCGTATTAA TTCTACCAGG 480

AGTGAAGTTT AAAATACCTT TCACACCAGC TTGGACGAGT TCATCTGCAA CTTTCTGTGC 540

TAATTCATCG TTATCTTTAA CAATAACGTT CCCTATTTTC TGGCCAATAA CATCTTCTTT 660

TACGTCAAAC GCTTCTGTAA TCGTCATATC GTCATGTATT GAAAAGTTAT ATGTGAGCAA 720

AGCTTTCCCT AGGTTCCCAA CTCCGACAAT TGCGATTTTG ATCATGTCAC TCTCGCTTAG 780

TTCAGATTTA AAGAAATCCA ATAAACTATC TATATTATAT CCGTaCCCTT TTTtACCTAA 840

TTCGCCAAAA TATGAAAAGT CACGACGAAT TGTtGCCGAG TCAATTTGTa ACGCATCGCT 900

AATCGCTTTT GAATTTACAC GATCTATACC TTTAGATTTT AATGAACTGA CAAATCTATA 960

ATATAACGGC AAACGTTTTA AAGTTGCTCG AGGAATTTTA ACTTGGTCAC TCATTCGCTA 1020

TTTCCTCCTT CGTGTTTGAA TGAATTATAT CTATGTATTC AAACGAGTTA GAGCGTAATT 1080

GTTAGATTAT TAAAArACAA ATAATTGaTT ACAATGAATA CCTAAATATT ATACATTAwT 1140

GAATTTTAAA AATAAATATC TTAGTTTCAA GACGGCGTTT TATACTGTAA AATGGTTATT 1200

AATGTAATAA TTACGCTTGT TTCATAAGTT AATAAAATTT GAGAAGACGA AGGTGAAG 1258

(2) INFORMATION FOR SEQ ID NO: 878:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 546 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878:

AAACAATCCC CnCCAAAGTA ATTCCACCAC TAATTGTAAA TAACTTTGGA AAGGATGTTG 60

TTTGTnATTC CCATGGACAC ATGCCATCTn ATTTAAGTTT TATACTCTAT TTTTCTGATG 120

TCTTGATTAA TTGCAAGCGG TCTTGCGAGC CTTGTTCAAG CTCATATTCT TTATCTACTT 180

GCTTACCGTT TTCryTTATT AATCTTACGG TTGCGGTAAT CTTATCACCA TGTTTTTCAG 240

CATCTATAAT TTGTGGTGAA CTAATCATCA TTAAACTTCC TTTAGATACA CGCTTCTTTA 300

CATCATCATA AAAAGATGAT CCTTTTTTTA TATATGATGA TACAAAATCA AAATCCGACT 360

GATTAAACGC AGCATTATTC GCTAAAGAAT ATCCAGCAAA GAATTCTATC AATTTGTTCT 420

TCAAGCTGTT TTCTTCTTTT TCTTTCTTTT CAACATAGTC TTCGATATCT TCACTGTCAA 480

AATTCAAAGT TATCTCTGTA TTGTATTTTA AATCGCTAAG CTTTAATCGT CTTCGTCTGT 540

GATGTA 546

(2) INFORMATION FOR SEQ ID NO: 879:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 870 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879:

TTTATGAATT TTTTATGTAA CATTAAATAT TCTTCTGGCA ATCTTCCtAC TATkTCTkTT 60
ATATATCCTT CTTCTCCTTC TTTAAATACT AAACCTGTGG GAGTTAGTGT GTTATACCTA 120
ATTTCTATCT CATTCAAATG ATCATTCAAA AGGTCAAAAA ATTCTCTATT AAAATAACCC 180
CATTTCCCAT TTTGTAATAA ATATTTCTTT CCATCTTCCA TTTCAACTTC TGCATGTAGT 240
ATCGTTTTTA GTaGCATATT ATTTGAATGC CCCAAATTAT CkATCACkTc AATTCTGACA 300
TCATTTATAG AATTAACGTC ATATTTTAAT AAGTAATCTC CTATTTCAGT GATGTAATCA 360
ACTTCAGGAT CAGTCGCATC AAATGTCTCT AATGTATTAT TTTTAAAAGA ATTTATATAT 420
ATATTGACGT CGAGCATATC ATCTAACAAG AGTATCATAT TACTTAGTTC TAAAAATCTT 480
GATATATCTA TAGATATATT TTCTGTAGTT GAAGAATTCG ATAGTTTTTT TAGCAATAAA 540
GTATCTAATA CTTCTATTTT ATTCAAGTCT TTTAAAGTTA CTATTCTAGG AAATTCACTA 600
ATTTTTTGAG GAAGATTAAT AATAGCGTTT ATTTCTTTGA TTATCACACT AATTTTATCT 660
ATGaATTGCT GcTTTCTATT CGGtACACGC AATGaAATAC TTGTACCACA AGTCCATTGt 720
TTTTCCaAAA ATTTGAGGaT TCTGTGGaTG tCCTTGGaCT GGaTATATAA GATTCTGAAG 780
GTCTAACGTA ATCTACACTA TTCCTTCTAT AATTAACAAT CTCTTTAAGC CTGTTTTGTT 840
GAAAAAAATT AACATTTTTA nTAACTAnGG 870

(2) INFORMATION FOR SEQ ID NO: 880:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880:

GGTTTACATC TTTATCAACT GTAATTTCAT TGACATCTTC ATTCATATTT AAAACACCAT 60
TAAATGTCCC TGAATATTCA CTTGTTTGTT TAACTGTGGC AGTGACTTGT CGTTACCATA 120
TGTCATCATA TATTGTGCAA ATGTTAAAGT CCCCATTGAG TTGACCGACA AAGTTGAATT 180
TATCGAATTG TATTCAGATT GTAAACTTAG CAGACATTTT TAACCACGAG CATTCTTATC 240
CAAATAGnCC TTGTCTGTTA TTTTCAAGTC AATTTTCACA ATAGGATCAC TGCATCTTTT 300

ACCCTCTTTT TCTGCTnCTC ACATAACTTT CAGATGGACT 400

(2) INFORMATION FOR SEQ ID NO: 881:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881:

AAGATATTGC GAAAAGAAGT GACAGTAACA GAGGAATTTC AAAATTTATT CAACCATATA 60

TTGAAAATTG ATGAAATGGT GCATGCAAAT GAAGCGCGTA TTGCGTATGA AGCAGACATG 120

CGAAAACCTT TATATAGTAA ACGCATTTAT CAAAATTTAA CATTAGACTC TATTGTTTTT 180

AGAAATACAT TGAGATATAC AGCGATTATG ATGATAGCGG ATATTTATTG CGTTAATGTT 240

TGATTTTGAA AAAGCATCCT GGATCCCGTT ATCTGCACAT CCAnTATTCC TAGGGCCATC 300

AnCCTATACC ATGCCATCCG AGAGAGGTAT GGn 333

(2) INFORMATION FOR SEQ ID NO: 882:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 617 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882:

ATTGAAAGAA AAACTGACGT ACTTATCCGA TGATAAAATG AAAGAAGTAG ATAATGCACT 60

AATGATTAGT TTAGGGCTGA ATGCAGTAGC TCACCAGAAA AATTAGGCGT CTATTATATG 120

TATTTTTCAG AGATAAATAA AATATTGATA TAAAAGACAA TAACTTTATA ATAATTATAA 180

CTATTTCTAA ATTCTGTACG AAGAATTTTC TTATAAACAA AGATTTTAGC AAATACCAGT 240

TATGATATTC ATATTTTTTA TTATAAAAGG ATGTCTTAAG TTTTTTAGGC TTTAGGTATT 300

CCATCCTAAA GTTTTTTTAG CTTAAAAGTA TCATCTACAG CAAAATTGCA AACGACAAAA 360

TTGATAAGTG CAATTAAATA AATGTTAGTA AGTGAATCAT AATTATCCTT GCTTAAGCAT 420

TTGCTTTGTA AGGGAAGTGA GGAGGCAACT AATCGTGGAA GAATTTAAGC AACATTATAA 480

GGGTTTAATT GATGAAAGTT TAACGTGCCA AGATAAAGTA GAATTGATAA AAAAGTGTGA 540

GAAATACACT GACGAAGTGA TTCGTAAGGA CGTCTTGCCT GAAGACATTG TCGATATTCA 600

(2) INFORMATION FOR SEQ ID NO: 883:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883:

GTTGTATTAA AATTTTTCAA TTTAACAACG AAACAATACG AAGAAAAACA TATTACTGAG 60

CCACTGGAAT TGACGAGCTT ATTAGGTAnT ATTTCTCGTC TAGACAATGG TCATTTTGCA 120

CATTTGCATG CTACTTTCGG TACTCAATCA TATGAAACTT TTAGCGGACA TCTCGCTAAA 180

GCAATTGTTT CTGCAACTGC TGAAATCATT CTTACTGTAA CTGATTTGGA CATTCAACGT 240

TCATTCAAAG ATGCAGTCGG TTTAAATTTA CTTGATCCTC AATAGCACTT TACTTTTTAG 300

TTGAATCAAA TTTTATTACA AGTTATCATA AGTGCTTAAT CATAAATGCA TTCTCGTTTA 360

TTAATATACT TCAACGAGTT AAATTAAATT TTTAATTAGG AATTGAATGC GTTTATAACT 420

ATCACATTTG aATGaATAAC TTTTTCATTA GAAAGTAGTG TkTATTATTG aTGCAATCTC 480

GaTACATCGC TAGAATTTAC TTTtaATTTT ATTTATCGTC TCCCTTnTTG AGACTAAAAT 540

TTTTCAATTT ATGACTTTAA ATTTGTTTTT AGCATATATA CCT 583

(2) INFORMATION FOR SEQ ID NO: 884:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 524 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884:

GCAGAGGGCT TACGATAAAA AGAAAAATCT CGCTCGCCCG CTTCAGTCAA ACTCACAAAA 60

GcTAACGCAt GwyTGCTyCA TTCGTGCGAT ACACTTTTGA TACATCTACA CCAATACTTG 120

ATATCGTTTC AATAATGCTA TCTCCAAATG CATCATTACC TAATTGTGTA ATCATAtACG 180

CTTGTTGTCC tAACTTTTGA ACTGTACAAG CTACATTGCA TGGCGCGCCA CCAATTTGCT 240

TCGTAAATGT TTGAACATCT TTTAAATTCG CATTTGTAAC ATTTGGAATA AAATCAATTA 300

ACGCTTCTCC TATTGAAAAT AGACGTCTCA TTTATGTTCA TCCTTTAAAT CATATTTAGT 360

AAATTGTAAA TATACTTGCC CTGATTCTGT TGATGTTTTA ATACCTAGTG CGTCTTCTGT 420

TGTATCAACA AAAATTTGTA ATTGCTTTAA TGGCGTGTCT AATA 524

(2) INFORMATION FOR SEQ ID NO: 885:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885:

TTAATGATTT CTTCGTATGA TTCACCAACA ATTTGCGCTA AAATATCATG CGCAAGTACT 60

TCACCTTCAA CCATAAATTC TATTTGCTCT ACTAAAAATT TTACGTCATT CATGCTATTC 120

ATTTTTGGAA TTAACAAAGC ATATAAGTTT GTAAATTCTT TTAAATACGC AGCATCAGCT 180

TTTAAGTAAT GGCGTAATGC GTCACTCCTA TATCTCCGGA TAACATCTTC TGAATAAAGT 240

CATCCTCATA AATATCATAA TGATGGCTTG CAGCTGGGTA CAATTTTGTG AAATTCCATG 300

TAAAAATCCT CCCTAAATAA AAAACTACTT CCAACATGAA GAGTTGAGGC ATGTGCAAAC 360

TAGCCCATCA CTCATAACAC TTCCACGTGG GACTACCAAC 400

(2) INFORMATION FOR SEQ ID NO: 886:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 857 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886:

AAGAATTTAA ACAAAATGAT ATTTGGAAAC ATTTTAAAGC TGTGAAAAAT AATCATGTTT 60

ATGACTTAGA GGAAGTGCCA TTCGGTATTA CAGCAAATGT TGATGCTGAT AAGGCAATGA 120

CTCAATTATA TGATTTATTT TATAAGGATA AAAAATAGTG AGTTGATATG ATGATAAAAA 180

ATAAAAAGAA ACTACTATTT TTATGTTTGT TAGTCATTTT AATCGCAACT GCTTATATTT 240

CGTTTGTAAC CGGTACAATT AAATTGTCAT TTAATGACCT ATTTACAAAA TTTACAACTG 300

GTAGCAATGA AGCAGTGGAT TCAATCATTG ATTTGCGATT GCCACGTATA TTAATTGCAT 360

TGATGGTTGG CGCAATGTTA GCAGTTTCTG GAGCATTATT ACAAGCAGCA CTACAAAATC 420

CTTTGGCAGG GCGAATATCA TTGGCGTTTC CTCAGGTGCA CTTATAATGA GAGCcTTTGt 480

ATGTTGTTtA TTCCACAATT GTACTTTTAC TTACCATTAT TAAGTTTTAT TGGAGGTTTA 540

ATATTAGTAG GTGTTGCGTT ATTCGTATTA TTAAATGGTG TTTTAGAAAT TTTAACTCAA 660

AACCCTTTAA TGAAAATTCC TCAAGGCTTA ACAATGAAAA TATGGAGCGA CGTATACATA 720

TTAGCAGTAT CAGCATTATT GGGATTAATA TTAACATTAC TATTGTCCCC TAAATTGAAT 780

TTACTAAATT TAGACGACAT ACAAGCGCGA AtATCGGTTT TAATATTGAT CGTTACAGAT 840

GGTTAACAGG GTTATTA 857

(2) INFORMATION FOR SEQ ID NO: 887:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 675 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887:

GATTTATTTT AATATTATTG TTAGAAGGAA TTTTTACAAA TTCAGCGAGT GCAATCGAAT 60

ATTCAGACTT ACATCATAAA AGTAAGTTTG ATTCAAAGCG TCTAAGTAAT GCTAAGATGT 120

CATTCATCAA TCCAACTCAG CTTGAAAATA AAAACACAAA CGATAGACTG TTGAAGCATG 180

ATTTGTTATT TCATGACATG TTCGTAAATG ATGATTGGAA AAAGGATTTT AAAGTTGAAT 240

TTGAAAATGA GGCACTTTCA AAGAAATTTA TAAATAAGGA TATCGATATA TTTGCTGGAA 300

ATTATGGATA CGGATGTCAT GGGGGAGCAA CCAATAAAAC GCAATGTAGT TATGGTGGTG 360

TTACTTTAAG TGACAATAAT AAATACGATG ATTATAAGAA TATACCTTGT AATTTATGGA 420

TTGACGGACA TCAAACAGAA ATAGAACTAA CTGCAGTAAA AACGAAAAAG AAAATTGTTA 480

CTATTCAAGA ATTAGAGGTT CAATTAAGAA ATTATTTGAA TGAGAAGTAT AAGTTGTACG 540

AACAAGGTGG CGACATTGTT AAAGGGTATG TTAAATATTA TAATGATGAT GAACAAAATG 600

TAGAATATGA TTTTTATAAT TTAAATGGTG AGTATGGTCG TGAGGTATTA AAAATGTATG 660

CnGATAATnA AACnA 675

(2) INFORMATION FOR SEQ ID NO: 888:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 851 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 888:

AATTCCTAAT TAACAATGCC TTCATTTAAA AACCTTCTTC CATCAATTTG ATGTTTTCAT 120

GATATTTAGG TTTTCTCTTT TCAAGATAAA CCATTAAGTy CTCAATAGAA GGTGTAGTGA 180

TATTCACTTT AkGACCTAAA ATTTCTTTAA ATACTTGCGC ATGTTCTGTT AATCCTATAA 240

ATCCCGTACG CTTATGTTCT TCATAAATAA GTAGAGATGC TAATTCATCA TCAAGGTCCT 300

CAATAGCACC ACTCACAACT TGATATCTTT GTAACAGTTG TTCTTTTGAA CCATTTAAGA 360

TAACTTCACC GTCACTTAAG TGAATGATAT AATCAGCTAT TTTTTCTAAA TCTGAGATAA 420

TGTGTGTCGA CATGAATATT GTTTTATTTT CATCAATTAA TTCTTGCTGA ATTATCTCCA 480

ATAGCTCATT TCTAGCTAAG GGATCGAGAC CTGAAGTAGG CTCATCAAAA ATATACAATT 540

CAGCATGATG TGAAAATGCA ACTGCTAGTG ATAATTTCAT TTTCATCCCA GTCGAAAATG 600

TTTTTATTGA TTTATTGATT GGTAAATCGA ACTTTTCAAG ATAAAATTCA AATACTTGAT 660

GGTCCCATTT ACGATAAAAA GGGGcAATCA TTTTTTCAAG TTGCTTCGTA GTCCATCTCT 720

CATTAAAATA ATTTTCAGAG TAAACnAACC CAATTCTATT CTTTAACTCT ATCGGATTGA 780

GAGCCATATC CTCTTCTAAT ACTCTAATAA CACCAGTTTG TGGGTGATAC AAATCCATAA 840

TTAACCTAAT n 851

(2) INFORMATION FOR SEQ ID NO: 889:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 889:

AATCACCTTC ACGCCAATAT TGATTTTCAT GCGTAAATAC TTGTGCCGTT TCATGATACT 60

TTGTCAATCG TGCGTGTTGC TGGGGGGAAT ATTTTTCAGT AGCCCAATTG GCTGCATGAC 120

CTTCAATGGC TAGTTCAATT GCAGGATTAA TTAAATCTTC CAATGACAAT TTAGCATAAC 180

GCTTGTGAAT ATAATCAAAC AGCTTTGGAA TTGCTGGCAC ACGACAGTTT TACCATGTGT 240

AGTCATATCA AAAAATGATT TATATTCGCC TGAATCAnCT AGATAAAATT GGTTGGCTAC 300

ATGGTCAGGG TGCTGGCTCA CGGTGCATCA AACGCnGnTA ATACTGCCCA GTACCTTTGC 360

TC 362

(2) INFORMATION FOR SEQ ID NO: 890:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890:

TTGGTTTATT CCCAAAAAGT ACGCGAAAAT TAGTAGAGAA GAATTTGAAA GTTTAAATAT 60
TGTCAAACCC GCTAAAAATA ATACTTTCTG GCCTGTTGCA GGATTTGCAG TGTTATTAAC 120
AACCTTAACA AGAAAATATA TCTATTTGCT TAACATCCAT TTAGAAAAAG AAATAGTTAT 180
ATTAACATGC TGTATGATAC TTCTAGGTGT TTTCGCATTG TTTATATATA TAAATACAAA 240
ATTGAAGTTA CATATTTTTG ATAAAAATAA AAGTAATAAC GAAAAGATCA TATTAATACC 300
TACATTTAAA AATATTTGTT TATCCTTATT TGCTTATATA TTATTTGGTG GATTGTCAAC 360
AATGGCTCTG AGTATGTTAG TAACTTCATC CCCTCAAAAT ATAATAGAAT TTCTTGCTTT 420
AATTGGCATG ACTGCATGCT TCTTTCTACT GAATATGTCA TCGGTTCTAG ATAAAAAAAT 480
TCATGTTATT TTAAAAACAA ATAAGTAGTA AAATTGATTA ACTTAGGTAG TATCGGATAC 540
TTAAATGTTG GTTCATAAAA AGCAATGATT TTAAATCGAG GAGCTATCTT AGAAcAGGGA 600
AATAAAACAG CCAAAGTTAT AAAAAGTGAA TTAATAACTA ATTATATTAT GTTAGCCACG 660
CTTCAAATAA AAnATAATTA GAATAAGGTG GGATTGATAA TCAAnGCTAn GCGAATCTAA 720
AATCATCAAT AAAAACCCCA AATATAG 747

(2) INFORMATION FOR SEQ ID NO: 891:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 526 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891:

ATTTTGAAAT TTTAGCAGAT ACTGATAATG GTCTCGATGC AATGAAACTT ATTGAAGAAT 60
ATAATCCTAA CGTTGTTATT TTAGATATAG AAATGCCAGG CATGACTGGA CTTGAAGTTT 120
TAGCGGAAAT TAGAAAAAAG CATTTGAATA TTAAAGTGAT TATTGTAACA ACTTTTAAAA 180
GACCGGGATA CTTTGAAAAA GCAGTTGTGA ATGAtGTGGA TGCATATGTT TTAAAAGAAC 240
GTTCTATAGA AGAATTGGTG GAAACCATTA ATAAAGTAAA TAACGGAGAG AAAGAATATA 300
GCGCCACATT GATGACTTCA TTTTTTGTAG ATAAAAACCC ATTAACGCCC AAAGAACAAA 360
TTGTATTAAG GGAAATTGGC AaTGGTTTAA GTAGTAAAGA AATAAGTGAA AAATTATTTT 420

ATCGTTTTGA TGCTTGGGAA AAGGCAAATG AAAAAGGCTG GACCTA 526

(2) INFORMATION FOR SEQ ID NO: 892:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 751 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892:

TATTTGATGT AAAAGCGAAn GAACCATACA ATGTAACAAT TACTAGTGAT AAATACATCC 60

CTAATACTGA TTTGAAACGT GGGCAAGCTG ATTTATTTGT AGCGGAAGGT TCTATCAAAG 120

ATTTAGTGAA ACATAAGAAG CATGGTAAGG CAATTATAGG AACGAAAAAA CATCATGTTA 180

ATATTAAGTT ACGTAAAGAT ATTAATAAAA TCTATTTTAT GACAGATGTT GATTTAGGTG 240

GACCAACGTT TGTCTTAAAT GACAAAGACT ATCAAGAAAT AAGAAAGTAT ACAAAGGCAA 300

AGCATATCGT CTCTCAATTT GGATTCGATT TGAAACATAA AAAAGATGCT TTAGCATTAG 360

AAAAAGCGAA AAATAAAGTT GATAAATCTA TTGAAACAAG AAGTGAAGCG ATAAGCTCAA 420

TATCAAGTTT AACCGGAATA TTATTATTTG TAACATCATT TTTAGGTATT ACATTCTTGA 480

TTGCTGTATG TTGCATTATA TACATAAAGC AAATAGATGA AACCGAAGAT GAGTTAGAGA 540

ATTATAGTAT TTTGAGAAAG CTTGGATTTA CACAAAAAGA TATGGCAAGG GGACTAAAGT 600

TTAAAATTAT GTTTAATTTT GGGTTACCTT TAGTTATTGC ACTATCACAT GCATATTTTA 660

CATCATTAGC ATATATGAAA TTAATGGGTA CAACGAATCA AATACCGGTT TTCATAGTAA 720

TGGGATTATA CATTTGTATG TATGCTGTTT T 751

(2) INFORMATION FOR SEQ ID NO: 893:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893:

GGATGTTGTA CATTATTCAG ATTACTTTGA AGGGGCACAA AAATATTTGA GCTATTTAAA 60

ATCAACAGTA GATGTTAACT TTGAAGGTTT GAAAATTGCT TTAGATGGTG CAAATGGTTC 120

AACATCATCA CTAGCGCCAT TCTTATTTGG TGACTTAGAA GCAGATACTG AAACAATTGG 180

TAGCTGAAAA AGTAGTTGAA ACTGAAATGA TTTTGGGGTT AGCATTTGGA CGGCGATGGG 300

AGACAGAnCC ATAGCAGTAA GATGGAGAnG GnCCAATCCG TTGACGGTGG ACCCAAT 357

(2) INFORMATION FOR SEQ ID NO: 894:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 464 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894:

GCTAACCTGC AAAATTCGAT AAGCGATTCA ATaCTGAcGC CTGcATTTCG CAAATTTTTC 60

ACTAAATAAA TCCAATTTAA ATCACTATCA TTATATATTC TATATCCATT TTCATCTCGA 120

TTAACTGGTG GAATCACACC AACCTTTTCA TAATATCTTA AAGTGTCTTG AGATATATTC 180

ATGAGCGCTA CGACTTCTTT AGTTTTCATT GCGACTATCC TTTCAGTTAT GTTTGGTCGT 240

CTAAAGTAAT GTTGCTTTAT ATATTGTCAT CTTCGTTTGA ATACTTCTTA TTTTATTACT 300

CAAATTTAAA TTTGTCTCTT TTTTAACATT TTACATTTCA TCGTTTTTAA TTACTTTAAA 360

AATTGTATAA CTkAAATATT TAAAATGATA TAAwCACTAA GATTGaTAAT AtTTAATTnT 420

TTGGAAAATT ATnTTAAGTT GCCAATTTTG GGGGGATGCG GAAA 464

(2) INFORMATION FOR SEQ ID NO: 895:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 599 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895:

AnAATGAAAG AGTTACAGGA CTTTATTGCT CGTTTCTCAG TAACGCTTCT AAATCTAAAC 60

AAGCAACAAG TCGTAAAAAA CAACTCGAGA AAATTGAATT AGATGATATT CAACCATCAT 120

CAAGAAGATA TCCTTTCGTT AAATTCACAC CTGAGCGCGA AATCGGTAAT GACTTACTAA 180

TCGTTCAAaA TCTATCTAAA aCGATTGACG GTGAAAAAGT ATTAGATAAT ATTTCATTCA 240

CAATGAATCC AAATGATAAA GCAATTTTAA TTGGGGATAG TGAAATTGCG AAAACCACAT 300

TGCTTAAAAT ATTAGCCGGT GAAATGGAAC CAGACGAAGG TTCATATAAA TGGGGTGTAA 360

CAACGTCATT AAGTTACTTC CCTAAAGATA ACTCAGAATT CTTTGAGGGC GTTAATATGA 420

GCGGCTTCTT AGGCCGTATG CTATTTAGTG GAGAAGAAGT TAAGAAAAAA GCTAGTGTAC 540

TTTCAGGTGG AGAAAAAGTA CGTTGTATGC TAAGTAAAAT GATGTTATCA AGTGCAAAC 599

(2) INFORMATION FOR SEQ ID NO: 896:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1057 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896:

TCATTAGTAG AAATCGTTAA AGATGCATCT TGCAATTTAA AATCCGAATC TTTGTATTGT 60

TTGTTCACAC TATCTACGTT TAACAATGTT GTCATATCCA TGCTCCTCTT TGTTTAATTT 120

TAATAAAAAC GTCTTCTCTT CAATAAATAA CTAAAGGCGT TATATATGAA AATAGCAATG 180

ATAAGTAGCA AACTAAAGCT TTGATTAATT CCAGTAGTAA TTGAATAAAG CCCAATTACT 240

ACAATGGCTA GTATCAATAT TGATAAGTTG ATCGCATATG TTTTAAATAA TGCAATTAAT 300

TCTATATGGC GTTCACCTTC ATCCAATATT TCCAATCGCT TTTCAGTGTA ATTCTTATCT 360

GCAATTTTTG GTATTCTGTC ATCAAACCTT CTATTAAACA GTGTAAATTG TGTATTGAAA 420

ATAGCACTAG CAAAAAATGG TATTAAAAAG AATAGTATTG CATTTGCTGC AGCGTGCCCT 480

ACCACAAAAA TAAGCAATAC TAAAAAAGCA ATAACTGTCT GCAGAATACT TAATATACTT 540

CCATTTAAAA CATAACGATT CGCAAGCAAC TCATATTGAT CTGTTGCATC GATATCTACC 600

TCTTTATCTA CAAGTTGCTT ATACTTCAAT GCACGTCTTT GATTCATCAA AACAATGGCT 660

TCTACCAATA TGATAATAAT CGTCGCAACA ATCGATATTA CAACGACATT GTTATATGTC 720

GCAAACGTCA AGTTCTCAAT ACCAAATCCA TCAAAATTAC CTAAAATTCC ACCTATGATA 780

CCCCCTACAA GTCCACCCAG TAAAAGATAT CCGATATATC TTAGTATTTT CATGCCTCAT 840

CCTCCTCAAT AATAAAAACA GTTyCCACCG TTTCATTGAA AATGCGAGCA ATTTTTATTG 900

CCGTTAATAC TGATGGCATA AAATTGTTTC GCTCAATTAG CGATATGGTT TGTCTTGAAA 960

CGCCCGCTTG TTTAGCAAGT TGCGTTTGGT TTAAGCCATC TCGTGCTCGT AATTCTTTCA 1020

ATCGATTACG CACATCGCAT CAACTCCnTA ATTACAC 1057

(2) INFORMATION FOR SEQ ID NO: 897:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897:

AAATTATTGA GTTAACAAAT CATTACGGAG CACATAATTA TTTACCATTG nCAATTGTCA 60

TTTCAGAAGC CGAnGGGGTA TGGGTTAAAG ATCCTGAAGG CAATAAATAT ATGGATATGT 120

GAnCTGCATA TTCCGCTGTT AACCAAGGTC ATAGACATCC GAAAGGTATT CAAGCATTAA 180

AAGATCAAGC TGATAAAGTG ACTTTACTCT CACGTGCTTT TCATAGTGAT AACTTAGGTG 240

AATGGTACGA AAAAATTTGT AAACTGGCAG GTAAAGATAA AGCTTTACCA ATGTAATACA 300

GGTGCTGTAA GCAGTAGAAA CAGCTTTGAA AGCAGC 336

(2) INFORMATION FOR SEQ ID NO: 898:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898:

TGnTGnTTTC TTATTGTTGA CCAATTATTT TGCATACCAA ATCCAAATCA TGTATTTATC 60

AATCACATCC TAATGCTAAA TCCAATGTAT TACATTGTTT AATGGTATAG CACAATCTAT 120

CATATTTGGT ATATCAAGTA TGGAAAACAT TCCATATCAT TTTTACTTTA TTTTATTCTT 180

ATGTTTAATA GCTGCAGTAA ATTTCGTATT AGCAGGTATA CGACACACGG CAATTTATAA 240

TAAAACATCT AAAGTGACAC AAACTGATAA TCAACAGGGA GTTTCAAAGA TAGTCAGACG 300

GG 302

(2) INFORMATION FOR SEQ ID NO: 899:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899:

CCACTAGCTG ATACAGTAGG TATACCAAGA TTCGTCATCG TTACGACATA TCAATTTGGT 60

CAATATGCGA TGTTATTCTT AGCGCCGACT GGAcTTGTTA TGGCCACACT ACAAATGTTA 120

AACATGCGAT ATTCACATTG GTTCCGATTT GTATGGCCGG TAGTTGCTTT TGTATTGATT 180

TATAAAAAAT ACTAATGGGG TTTTATGCAT CTCGTAGGTT TGTAGAAATA CTAAACTAAG 300

CGAGGTGCAT TATTATTTTT GATTAAGAAA ATAATGACGG TAATGATAAC ACTAGTAAGT 360

AATTGATACA ATGCTCTATT TAATAATGAT ATTTTTAAAA TTTGTTTTTA ATGTAATGTT 420

AGATCTATGG TATATTATAT TTAACGTGGT AAATATGTAT TTGCTGTAA 469

(2) INFORMATION FOR SEQ ID NO: 900:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 821 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900:

CTTTATTGGT AACTCTCTAT aATATtTTaA CATTTTTACG CTATCGTGCA AACGCAAcCa 60

CTTTGAATTy TCTGATATTT TTAGCATATA ATTTACACCC TGCACGATGA ATTGTTAATC 120

CAGTTGTATA AATATCGTCA ACGAGTAATA TTTCCTTACC ATTTAAATCT AATTCCGTAT 180

CAATAATAAA TGGATTTTCA TCTGCCAGAC GCTCTTTCTT AGTTAAATGA GACTGTTTTG 240

GTCTATTTGA CATCTTTAAA ATCTTATCaA AGCGAATCCC TTTAGCTTTT AGTACTGCTT 300

CTACCGGGTT AAATGTTCTA GATAAATCAT GTGCCGGCGA AGAAGGAATT GGCACAATAT 360

AGTCATAAGA TGTTTGTGGT ATTTCAATCA AATGTGCCAA TAATTCACAT AAATAATAGT 420

CTTTCAAAAA TTTATACTGA TGTATCATCT CTTTCATTAA ACCGTCATAT TGAAATTGAC 480

AATATAATTG TTCCATTAAA TTAAAGTGTG CCGATAGAAA CTTGCAGTCT AAACAATACG 540

CTTCATCTTG ATTTAAGTGT TTTAAGCACC TTGAACATCG CCTTGCTTTA ATATCAAGTT 600

TAATATTGTC CCAATTCTCT TTGCATCTGT CACATAATCT ATTAGGTTTC TTGAACAAAT 660

TATAAATGGT TATATTTTCA TATAACTTAG CACCACAACT CAAACAATTA TTCATCAATC 720

CAACCTCTTT TTAATGCTAA TTTGTTCATC CTTTGAATCT CTTTTTTAGC TTGAATCATA 780

TTCATACTTA CCCCTTnCAT GAAAAAACAA TACTTTTTCC A 821

(2) INFORMATION FOR SEQ ID NO: 901:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TGATGCTATT AAAAAGTTAA TTGTGCGGTC TGTTTTGATA ATTTTAATAA TAACTTCAGG 60

TAACTAAAAA TCCTAATATT GAAAAAACAA AGCCATTTAA AACATAACCT AGTATATTCC 120

ATGTATGATT GTAACTCATT TGCCAGTTnT GTACTGACTT GCATAATTCT GTCACGTnCG 180

AACCATGTAC AAGCCTGCAA CTACTGCTGA ATGATTCCTG ATGCGTGAAC AATTCAGCAA 240

TTAAATACGT AACAAATGGT GTTACAATTG AATAATTGAA ACATATTAAT GTTTCATATC 300

CTCGACGnCA TCAATGTTAA TCCGGACCTT ACTAATGCAT ACCTATAAG 349

(2) INFORMATION FOR SEQ ID NO: 902:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902:

CAAGTGGTAT AAATTTACCT GGTGAAATGT AGGTCGTGGT GGCGATGATA CATTATTCGC 60

TAAAATCGAC GGCGTTGTTA AATTCGAACG TAAAGGTCGC GACAAAAAAC AAGTTTCTGT 120

ATATGCAGTT AGCTGAATAA TTTTGTCTAG TTAACACCAG AAAGTGAATC TTCTGGTGTT 180

TTTTACTTTT TATAAAATGT TTTTCATTAT TATTTTCATT ATGnTATTTA AAAATGGGGA 240

TTTTAGACGT TATACTAAAT GTGCACTGTA TAGGGGCCCT AATCACTAAC TATAGGGGGA 300

CAAGGATACA GTGCAGCGTT AAGGATAACT GnCCACATTG GTCTGGGAAT ATAGGATTTA 360

AGCAAGGTTA TAAAGTACTC nTAGGCCCTA 390

(2) INFORMATION FOR SEQ ID NO: 903:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903:

GGAATAGACG TATATGCGCG TTGAATTTAA TCCTAATAAG CTTTCGCATG ATGAAGTGCT 60

TTGGTTAAAA CAAAATATCA TCAGTTATTT GGACGATGTT AGTTTTACGA GATTAGATTT 120

GGCTTTTGAT TTTGAATTTG ATTTAAAATG ACTATTATGC ATTGTCAGAT AAGnCGGTAA 180

AAGAAACTAT ATTTTATGGC CGAATGTAAA ACCAGAACAA AATATTTTGG TGTnCGAATA 240

GATTCACATT CTATGCGGTG GAATTGATTA AACG 334

(2) INFORMATION FOR SEQ ID NO: 904:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904:

CAAGTTGGGG ACACTGTTTC AAATGAAACA ACAGTGTGTA TTTTAGAGGC AATGAAACTA 60

TTTAATGAAA TTCAAGCAGA AATTTCAGGT GAAATTGTTG AAATCTTAGT AGAAGACGGA 120

CAAATGGTAG AGTATGGCCA ACCGTTATTT AAGGTGAAAT AATGAAAAAG GTTTAATTGC 180

AAACCGCGGT GAnTCGCAGT TAGGATTATT CGCGCTTGTC GTGATTTAGG CATCCAAACT 240

GTTGCATCTT TCTGAGGGGA TAAAGATCGC TACATCTCAA ATGCTGATGA GGCATATnCG 300

TGGGCCnCTT GTCTAAGGTC ATATTTAATA TCCG 334

(2) INFORMATION FOR SEQ ID NO: 905:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905:

TTCACCCTGT AATTCTTaAC CGTCAATTGA CCTTTATGCA GATTTAATAT TCCTAAAACG 60

TATAACTCTT CTAATGATAA TTGACACATA TTTAAATAAC ACTTTAGATT CCGCAATAAT 120

TCTTGTGACG ACAATAAATA CGATACATAG TCACAACTAA AATCAAATGT ATATTGACCA 180

AAATAACGTT CAATATAGTC ACTAAGCTCA TTATTCATAT ATTCTATTTn ATCTATATGC 240

ATTTTATTAA TCGAAATAGT CAATTTACGT TGATCCCTTT GATCTCTTCC TTTCAATAGC 300

CATTGATGAT TGTnTAAATA ACTTAACATT TGAAGAAGGG CCATCTTAGA TTGGATTTCT 360

TTCATTnTTA ATAAACTATC TATTGAAGCG CTATTGGAA 399

(2) INFORMATION FOR SEQ ID NO: 906:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1478 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906:

TACATTTTTC AATTTATGGC AAAATnCACA ATTTTCATCG AAATATTTTG TAnAnAATCA 60

TTGCTAGGTG ATGAGTTATC TCGGTTAATT ACAAAACGAT ATCTAAGTTT AAATATTAGA 120

TCATAAAAAA ACTATCTACT GAATATCCCT CCATAGCATC ATTTTTCTAA GCAAAAGTTA 180

AACTTAGTTA GATAAAATGC AAATGAGATT ATTGTAGATA GTCTCTTTTT AATGTTTAAA 240

AATGATTAAT GCCaTAAACA TAAATAATTC CaAAGAATGC CGCGCCACTA AGCACTGTTA 300

ATATAAGACT TAGTAACAAT GTGCGTTTAT AATGTTTaAC AAATGCtATG AACAAAATGA 360

CTACATTATA CGCAAAGAAA AGTCCGAATA ATGTCATTGT TATTTTCAAA TCAGAATAGA 420

AAATATTTAA TAGTAATACA ATGACTGCAT AAATTAAATA CGGAATAACT ATAAATTTGC 480

GTTCAAATCT TAATTGTTCG AAaCGtTTAT CTTCGTTTGT CATGATATGC TCCTTTATGA 540

TTTAAAAGTA AATAAGTTTA CGGAAtATCT TGTCCGaTAA TAGCGGTGTA AAtGTCAAAC 600

CACGACTGAT CATCtAAATT AAGTkGTAGC CCtTCGATTG CTTGATCAAT ACGCTTTAAC 660

TGACTTGTTC CAAGTATCCG GCATGATACG ATGCGGTATT TTTACTAACC ACGCTATCAT 720

CACAGCTGTG TCACTyACAC mATATTTGTC AGCTATTGAT TGAACAACTT TCATAATACG 780

TTGCGCTTTA ATATCTTCCT TGTCGAAAAT TTTACCGCCT GCAAAAGGAC TCCAAGCCAT 840

GATTTGAACA TGGTTTTGAT ACATTGAATC CATTGTTCCA TCTTGTAAAC TATCAACGTG 900

ATATGGCGAT AATTCTAATT GATTGATGCT AATATGTAGT CTTTCTTTCA TAATATATTG 960

ATTTAACAAT TGGTATTGTG AATGATTAAA ATTCGACACC CCGAATGACT TCAACTTACC 1020

TTGTTTAACA AGTTTAGTTA ATGCATCAGC AACTTGTTCT GGaTCCATCA ATGGTGaAgG 1080

ACGATGAATG AGTAGACTAT CTAAATAATC TACATTCAAA TTGATTAATG ACTGTTCAAC 1140

AGATTTCACG ATGTGCTTAC TACTCAAATC ATAACGATGT CCATTTGTAA AATCAAATTG 1200

CTTAGAAGGC AAAATGATAC CACATTTCGT AACAATTTGA ATTTTATTTC TTAATTCGGG 1260

TGATAAATCC AAAGCATTAC CAAACAGTGA TTCACATTGA TAATCTCCAT AAATATCAGC 1320

ATGATCCATC GTTGTAATTC CACGTTCAAC TAATTCATTT ATAAAATAAT TTAACTCTTT 1380

CGCAGTCATC TTCCATTCAT TTGCACGCCA AAAACCTTGT ACAAGCCTAG AAAAATGAAC 1440

ATAGTGATTA ATCATTATTT GTTCCATATn TCATCCAC 1478

(2) INFORMATION FOR SEQ ID NO: 907:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 543 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907:

TTCTATGAGA ATAGATATTG TTAAATTAAG AAAGTAGTCA ATTTTATTAT GACAAAAGAA 60

AGAAGAACAT TTAGTTCAGA GTTTAAGTTA CAAATGGTTA GATTATATAA AAATGGTAAG 120

CTTAAGAATG AaATTATACG AAAGTATGAT TTAAAACCCT CAATTATCTC AAATTCGATA 180

AAACAACACC AAAATACTGG ACCCTTCAAT CATCAAGATA ATTTAAAAAG TGATGAAAAA 240

GAGTTAATAA AATTACGCAA AGAAGTTCAA CATTTAAAAA TGGAACATGA TGTTTTAAAG 300

CAAATTTTAA AGTTGATTTA GAAACTGAAC TTTTTAAAGA TACATTACTT GAAGATTCTA 360

ATTTATCTGA TTATATAAAG AACCAACTTC CAACGATATG GAGAGACTAA GAAATAGTTT 420

AAATTTATTT AATTTCAATA AAAACTCATA ATAATATTTA AGTAAGTTAG ATTGCTTTTA 480

GCATTAGGAA TTCGCTTATA ATTAGATGTT CAATATAGAC TTTTTTACAC ATACATGAAC 540

TAT 543

(2) INFORMATION FOR SEQ ID NO: 908:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 751 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908:

TTTnCGGTnG AACATGATTn CGATATTACT TCTAAAACGA TTCAACCAAA ACCAGGAGAA 60

AGTGTTGGAC GTTTAGTTAA TGTCGATTGT AAAGATACAG TACTGGAGTA TTCAGAATTA 120

GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAAACTT 180

GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTTG 240

AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCAA CTTTAAAATT CGAATTGTTC 300

TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTCACGT TACAAGTTCC TAGAGAAGAA 360

GAATTTTCAC CTCTTAAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGAT 420

TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAAA 480

AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAA 540

GAAATTGGTA ATGCGGCATC TCATGGTGTT GCAGCTTTGT TAACATTATT AGTGTTACCC 600

TATGTTATTT CTATCTTTAT GATGTTTATT TCATCTACTA TTTATCATTC TATGCAAAAT 720

GAAACACCTC ATAAATATAT TTTAAGGATT A 751

(2) INFORMATION FOR SEQ ID NO: 909:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 909:

AAATTGTCAC AATTCAGTCT AATTTAAAAG GAAGTTAATT ACAAAATTAA AAAATCATGC 60

ATCGTGTCAT TTAGATATTG AAAAAGATGA GTCAAATTTG TTTCATATAT TTTCCAATAA 120

CAAATTATTA TATCTAAATA TACAATCAGA AATATATGAA TAGAAATATC AATAAGAAAA 180

ATAATATGAT TAAAAATGAT GAATGGCATA CTTATAAAGT GTCTAAATAT TGGCGGTCAA 240

TATTACTTAC AAACACGAAT GTTAAGTAAT GTAGACAATG cTGaAAAAAC AATaAGTAGa 300

AACTCTATAT AGAATGTTCG TTTTTATTTT TaATAATTGa ATAATCaTTA TTGGGTGGAT 360

TTTAATATGG nATTCCGGTC GGCACACGGA TTAC 394

(2) INFORMATION FOR SEQ ID NO: 910:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1022 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 910:

TAAAGCTAAG AAAAAAGAAA AACGTAAAGC TTATAACCAA CGAATGAAAG AACGTAGGAA 60

AAATCAACCT AGCGCAGTTA GTCAACGTCG AATGAATTTT GAAGAGCGAC GTCAAATTTA 120

CAACAATGAT ATTTCTGAAG AACGCAATTC AAGTGAAGTT AAGGACAAAA AAGAGCAAGA 180

ATAAATATTG ATGATACCCA GATTAGTAAG CAGAGGTCTT TTGCTTATTA ATCTGGGTTT 240

TTATATGAGG TTAATTATCG ATAACGTTTA ATTAAAGTGT TTAGGTGTCA TAATTTTAAA 300

TGACGATTTC CCCATTACkA TACACCTAAA TtATCATCAA TCTGaATTCA GATGTTTATk 360

ATAAAAATTA GATGAAAAAT ATGTTAATAT ACAAGkAaTT TAATGTGcGk ATATCTATAG 420

GCTCGTAGTA TACTTATTAA AATATTAAAC AAAGAAAGGA TTTTAAGATG AATAGAAAAC 480

GGCTATCCTA TTTTTCTTTA AAAAGTGGTA ATGCATCACA ACGTGAAGAA TTAGCGAAGC 600

AATTATCTCA GAACGGTGGC AAGGTTTCTT TAGATATGCT TCAGACAACA ATGGGTGCAT 660

TAGCAATTAT TTTATTAATT TCAACACTTT ATGGTATATT TGCGACAATT TGTATTAAAG 720

GACGTAGAAA ATTATCGATT ATACTTTTTG TTATCGCGAT AATTGTAAGT TTGATGGCTC 780

TTAATTTAAT TGCAATTGTC TTATGGGTTA TCGTGATGAT TATGTTGATT TCTAAAAAAG 840

AATCAAAAGA AACAACACAT AAGGACGATG AGTATATTTA TCATTAATAT GTTCATAGCA 900

AAAGAAAAAC CATTAAAATG TTAAGTTGTT AATTATTAGA TACAACCAAC ATTTTAATGG 960

TTTTATTTTT AACTTTGTAG TTCTTGGAAT GTTTGAACGA TTAAATAGAC ATTTAAAATA 1020

CT 1022

(2) INFORMATION FOR SEQ ID NO: 911:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 911:

GGTACTTTAT TTTTATTTTT GGTCTTAGTG ATTTTTACAT TATTTACATA TAAAGCGCCT 60

AATGGTATGC GTGCCATGGG TAGCATTAGC TAATGCAGCA ATCGCAACAT TTTTAGTGGA 120

AGCATTTAAT AAATATGTnG GTGGCGAGTA TTCGGTATTA AATTTTTAGA AGAGCTAGGA 180

GACGCTGCGG AGGTCTAGGT GGTGTCGCTG CCGCTGGATT AACAGCATTA GCTATCGGTG 240

TGTCACCAGT ATATGCATTA GTTATAGCAG CCGC 274

(2) INFORMATION FOR SEQ ID NO: 912:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 679 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 912:

CTTTAATTGT TCACTTTATC ATTATTATCA ATCAACTCTA TGATATGAAA TTGTGTTAGA 60

GATAAATCTA GTTCCTCATT TTCCTTTTTA TACTGTCTTC TTTTATCGGC ATTTTCTCTT 120

TCTATAATAA ATTGTTGTAA TTTTAAAATA ACTTCTCTCT TCATATCCAC TATTATTCCT 180

TTGTTGTAAT TAACATATAT TTACTTAGTT ATGCACCATT TATTCCGCAT TTCACAAATC 300

CACCTATAAT ACAAACTATC ATTTTAAATA AGCAGAATTT ACCCTGTCTT CCACACAAAT 360

TGTTTTCGAC ACTTTAATGT GCCTACTATC CAAAAAAGTT ACTCATAACA AATTGCGCAT 420

TTTAATAAAT GTAGCAATGC CATTTGCATG CTGCAAAAAT ACTCGTATTC ATATTTATGT 480

TTTATATTAT TAAAGTTTTT TAAATCCATA TTTTTATAAC ACTTGCTATG TGATAAAATT 540

AATnTTATAT ATAAAATCTT AAGATTCAGA TTATTTAATA GCAAAGGAGA TAGTGATATG 600

GATGTTTTAA CAATAGAACA TTTAACAAAG AAGATAGGCA ACAAAACGAT TCTCGAAGAT 660

GTATCATTTA AGCTGAAAC 679

(2) INFORMATION FOR SEQ ID NO: 913:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 913:

GCCATCCTTC AGTGCTAATT TTTTCAAATT CTAATGCAGA TGCACCACTA ACCATACCAT 60

ATATAAAGAA AAAGACCACG AAAGnAATAA GTAGTAGTAT AGATGCACAT ATCATAATGA 120

CATTGGAGTT TTCAGCGCCA AATTTAAATG TCAATGsGAA AATGATAGAG TATGCCCCTA 180

TGATACCAAA ACTCATTAAA CCTGACATAA TACCAATCAT CACACTTTGG GTCACAATCG 240

TAGTCACAAC TAATCCAATC ATTAAACTTG CACCGAATAA GATTAAATAA AAGGCAAAGT 300

ATGACTTAAT ATAATCACTA CGTTTAACCG GTAAAGTAGA TACATAATAC ATCCATCTTG 360

AGTCTTTTTC aTGTTTAATA TTATCAGTAA TAGGTGTGAT TAACATAACC CCAGCCATkG 420

CCGAACTCAT CAACGGATTA AATACTGCAA AGTATCCTGC AGCTATAATA GCGACTATAA 480

AATAAATATA TGTTTGCnTT CTCGTTGCAT AAAAACTACT TAGGAACATA CCTTTCATTA 540

TACTTCACCT CGCATTATGA TTTT 564

(2) INFORMATION FOR SEQ ID NO: 914:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 643 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AAAGAAGAAG CAAGTGCAAA TAATTTAAGT GATATATCAC AAGAGGCACA AGAGGTTCAA 60

GAAGCTAAAA AAGAAGCACA AGCAGAGAAA GACAGTGACA CATTAACTAA AGATGCAAGT 120

GCAGCAAAGG TAGAAGTATC AAAACCAGAG TCACAAGCTG AAAGATTAGC AAACGCTGCA 180

AAACAGAAGC AAGCTAAATT AACACCAGGT TCAAAAGAGA GTCAATTAAC TGAAGCGTTA 240

TTTGCAGAAA AACCAGTTGC TAAAAATGAC TTGAAAGAAA TTCCTCAATT AGTTACTAAA 300

AAGAATGATG TATCAGAGAC AGAGACGGTT AATATAGATA ATAAAGACAC TGTTAAACAA 360

AAAGAAGCTA AATTTGAAAA TGGTGTTATT ACACGTAAAG CTGATGAAAA AACAACTAAT 420

AATACAGCTG TTGACAAGAA ATCAGGTAAA CAATCTAAAA AAACAACACC TTCAAATAAA 480

CGAAATGCAT CAAAAGCATC TACAAATAAA ACTTCAGGTC AGAAAAAGCA ACATAATaAG 540

AgATCATCAC mAGGTGcAAA GaAACAAAGT AGTTcmAGta AGTCaACTCA AAAGAATAAT 600

CAAACTAGTA ATTAAGAnTT CAAAAACAAC AAATGCTAAn TCC 643

(2) INFORMATION FOR SEQ ID NO: 915:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 915:

AGGTTTAAGG GAAAAATCCT ACCTGGAGAG ATTCAAAAAC TAAATGGACT ATTTCCAAAA 60

ATAAAGGGCA ATCACATGGT GGTTCTTATT GGAAGTTAAT AAATAACAAA GGAAAAAGAA 120

TAGCTTCTTT AACTAAAGAA GGAAAAATCT TAAGGGAATA AGGTGTTGTA AATTATGTGC 180

TTTGATATAA ATAATTTGGA TATAAAAAAG TTGAATTTTA GAAAGGTAAA AAACGCAATT 240

CATTTAAGTT TAAGTGGCGA TAAATACCAG TTTTTGGAGG ACGGTAAAAC TATCAATAAT 300

ACTTATTTTT TAGCTGTATA TGATAATGCA ATAAACATTT TTGAAGATTT GTTTtCGCCT 360

tCTGATTCTA TAAATTTGGn TCATGTAGTA TATGTTTATA 400

(2) INFORMATION FOR SEQ ID NO: 916:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CCCAAAGTTC GATAGTGTAT TAGTATTATC TTAATAAAAT GTTAGGTACA ATAAAGATGA 60

TTATATATCG GAGGTTAGTA TAAAAATGTA TGTAGATCGA AAACCATCAC TATATTTAGA 120

GGATTTGCGA CATGATTTTA AAAATAGTTT AAGTAAATTT GAAAATGGTG ATGAAGCATT 180

TGATACGTTA TTAGGTTTCG TAGAGTTAGA TCATATTTAT TCGTCAGCAC TAAAGGAAAT 240

AAGCACTAAA CTGAGTATTT TAGATGACAA TTTCAATCAC ATTTATAwAC ACAATCCTAT 300

ACATCATATG GAGCGACGTG TGAAAGAAAT GCGTAGTTTA ATAGAAAAGC TTAATCGTAA 360

AGGATTACAG ATTAGCGCAG AAACTGCCAA AGAACATATA 400

(2) INFORMATION FOR SEQ ID NO: 917:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 917:

GAAAATTACT ATGAAGATTG CATTAGGATG CGACCATATT GTTACAGATA CAAAAATGCG 60

TGTATCTGAA TTTTTAAAAT CAAAAGGACA TGATGTCATT GACGTAGGAA CATACGATTT 120

CACAAGAACA CATTATCCAA TTTTTGGTAA AAAAGTTGGC GAACAAGTTG TTAGCGGTAA 180

TGCAGACTTA GGTGTTTGTA TTTGTGGAAC AGGTGTTGGT ATTAACAATG CTGTAAATAA 240

AGTACCGGCG TTCGTTCAGC ACTAGTACGT GATATGACAT CAGCGTTATA CGTAAAAGAG 300

GAATTAAATG CGAACGTTAT TGGCTTCGGT GGACGTATTA TAGGTGAGTT ATTAATGTGC 360

GATATTATCG ATGCCATTAT TAATGCTGGA TTATAAACCC 400

(2) INFORMATION FOR SEQ ID NO: 918:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1220 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 918:

GTCTCCAGCC ATTwCACCAC ACATACCTGT CCATTTACCT TCTTTATGTG ACGCTTCAAT 60

AACTTGTTTA ACTAAACGTA AGATTGAAGG GTTATATGGT TGGTATAGAT ATGATACACG 120

CTCTGACATA CGGTCAGCAG CTAATGTGTA TTGAATTAAA TCATTTGTAC CGATACTGAA 180

GATTCCTAAT TCTATATCAT CCGAAATGTC ATGACCTTCA TTTTTAAGGT TTTCTTTTTC 300

TTCTAATAAT ATAGCTTTAG CTTCTCTAAA TTCGTTAATT GTTGCAACCA TTGGGAACAT 360

GATATTTAAC TTACCATAAA CTGATGCACG TAATAATGCA CGTAGCTGTG GTCTGAAAAT 420

ATCTTGTTGC GCAAGGCATA AACGAATCGC ACGGTAACCT AAGAATGGAT TCATTTCTTC 480

AGGCAAGTTT AAGTATGATA ATTCTTTATC TCCACCTATA TCTAAAGTAC GTACAACAAC 540

ACGTTTACCG CCCATTGCTT CTAATACTTC TTTATAAGCT TCAAATTGTT CTTCTTCTGT 600

AGGCATTTGG TCACGACCCA TATATAAAAA CTCAGTTCTA TATAAGCCGA TACCTTGTGC 660

ACCATTTTCa ATAACACCTG GCAAATCATT AGGTGTACCA ATATTTGCAG CAAGCTCTGC 720

GTGAACACCA TCAACTGTAA CAGTATCAGC ATCACGTAGw TTTTGTAATT CTTTCTTGTC 780

AGCAAAATAA CGCTCACGTT TATCTTGATA AGCGATTAAC TCATCTTCAG TTGGATTAAC 840

GATTACATCA CCATTTAATC CATCTACGAT AATCATGTCG CCTTGTTTAA CTTCTTGAGT 900

AATTGATTTT GTACCAACAA TTGCTGGaAT TTCTAAAGAA CGACTCATAA TTGCAGAGTG 960

aCTTGTTCTT CCGCCAATGT TTGTAGCAAA ACCTTGTACG AATTCTTTAT TTAATTGAGC 1020

AGTATCAGAT GGCGTTAAGT CATTCCCTAC AATAACAACG CTTTCATCAA TCATACTCGG 1080

ATTCGGTAAT TCTACACCTA AAATATGTGA TAACACACGT TTAGAAACGT CGCGAATATC 1140

AGCCGCACGT TCTTTCATGT ATTCGTTATC CATAGATTCA AAAATTGTAA CAAATTGTGT 1200

TGTTnACATCC GCTTAATGTG 1220

(2) INFORMATION FOR SEQ ID NO: 919:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 919:

TTAGATTGAC TGCAAATGCC GACTCAAAAG AACAAGCACA ATCATTGATT CAACCTGTTA 60

AACAAGAAAT TCTTGATCGT ATTGGAGAAT ATTATTATGG TTCAGATGAC ACATTAATTG 120

AGCAAGCTGT AATAAAGAAA ATTCATGAAC CTTTTGTAAT ATATGATGGT ATTACTAATG 180

GTGCTTTATA TCATCGATTG AAAGAAGTGG ATTTAAACGA TGTTCTAAAG GGTATGATTA 240

ATCACAATGA AAACTTTGTt GATATTAATa AACCTATTGA GCaGCAATTA AAAGATGCAG 300

TGCAATTTGT TAATA 315

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 920:

ACTTTGTAAA CCTACAAATG TAATGAATAA TCCTATACCT GCTGAAACAG CCATCTTCAT 60

TTGATAAGGA ATTGCATTAA TAATAACTTC CCTAAACCCT GTGACGGTTA ATATCGCAAA 120

GAATATACCT GAGAATAAAA CGCCTGTTAA ACCAACTTGC CAAGGAATAC CCATGGTTAA 180

CACAACAGTA AATGCAAAGA ATGCATTTAA TCCCATACCT GGTGcTAACG CAATTGGATA 240

TTTAGCTATT AGCCCCATGA ATAGCGAGCC TACAAATGCT GCTAATGCAG TCGCTACAAA 300

AATGGCACCT TGGTCCATTT TCATATCTTC TGATACGCCT TTAACACCTG CTAAACTTAA 360

AACTTGCGGG TTAACTGCTA AAATATAGGC CATAGATAAG AAAGTTGTGA TACCGCCTAA 420

GATTTCTCTT TTA 433

(2) INFORMATION FOR SEQ ID NO: 921:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 921:

CTATTTTATT TGTATAGCGC TTGATGTAAA GTTATTTTAG CTGTCATACT ATGTGCTAAA 60

CCAAATTCAG TTGTGTCATA TCTTCGCTTT TTTGTCACTG TTATAATAGG TATAATCGGA 120

TATAATGAAA AGGkGAGGGA GGATTCAAAA TGCGTAGGTT ATTATATTCA TTTCTTTTTT 180

ATATGATCAT AGGTTTATTT AGTGGCTTTT TCTATAGAGA GCTAACAAAA GCATATGATT 240

TTACTGGTAC AACACAATTA TCACTTGTAC ACACACATAC ACTTATTTTA GGTATGTTTA 300

TGkkTTTAAT ATTATTACCA TTGGaGAmGT TATTTAAATT ATCAAGTTAC TACTTATTTA 360

ACTGGtCTTC TATGTATATA ACATAGGTGT TATCGTTACT ATAGGTATGA TGGTGACAAA 420

AGGATTCTTC CAAGTCACT 439

(2) INFORMATION FOR SEQ ID NO: 922:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 474 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 922:

GTAATATCTA TATACGTATA TTTAAATGAT ATATCTGGGT ATTTTCTTTT TAATAGCGGC 60

TGTAGCCAGT CATAAATATC TtTCGaTGTT GGCGCATTAA CGCAACTTGC ACATATAACA 120

TCTGCCCCAT AAACTACCAC ACTCACGTGC TCCATATATT TATCCCCCAT TGGTTTGATA 180

GATTTTTATT ACACTATCTA TTATAATATA sTmATAAAGA TTATCAAATT CATCTCTCGA 240

AAGGAGACTT GCCTGATGCC TACTGAAGAT ACAACGATGT TTGATCAAGT AGCAGAAGTT 300

ATTGAACGTC TTCGTCCATT TTTATTACGT GATGGTGGCG ACTGmTCATT GATTGACGTG 360

GAAGACGGTA TTGTAAATTA CAATTACATG GTGCATGGTG GnACATGCCC CAAGTTCTAC 420

AATCACTCTT AAAAGCTGGG TATTGAGCCG TGCATTACAC GAAGAAGTGC CTGG 474

(2) INFORMATION FOR SEQ ID NO: 923:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 554 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 923:

TCAACTTGTG AAGAAAATTT ATTAACTTTA GTAACTCTTC CAACAAAACC TTGTGATGTC 60

ATCACAGCCA TATTTGAAGT TATACCTGAT TTAGATCCCT TATCAATTAC AATTGTATTC 120

ATCCACTGAT CCGGATTTCT TGCCAAAACC GTAGTAGAAA TAGGATCAAA TTTTGAAATA 180

TCTTTTAAAT CAAGCTCTTT TTTTAATTTT TCATTTTCCG CTTCTAATTG TTGGTTCTTA 240

GATTCTAACT GGCTAATCTT ATTTTTAGAT TCTTTAGAAT CTCCTTTTTT AAAAAAGTCC 300

CCAATCGTAC CAGCAACAAA ATTAACTGGA TAACTCACAA CTCGTTGTCC AAAAGACACA 360

GAATCACCTA TATATTGTTC AGGAGGTGAT TGAGATTGTG AACGTATGGA CAGCCCAATT 420

AATGCAATAA AAACGATAAT TGCACATAAA ACAACAATTA ATTTGGTATT TTTAAAAAAC 480

TTAAGCACCC AGAACACCTC TATTATGTCA nAATATTGTA TATCCTTTTC TAATTnATAT 540

TACTCCCATT ATGA 554

(2) INFORMATION FOR SEQ ID NO: 924:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 575 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 924:

ATCTTTAGGC ATTAAGCAAG TTTATGTAGA AGACTTTGAA CATAAATCCT TTAGCAAAGC 60

TAAAAAAGCC TTAGAAGAAA AAGGGTTTAA AGTTGAAAGT AAGGAAGAGT ATAGTGACnA 120

TATTGATGAG GGTGATGTGA TTTCTCAATC TCCTAAAGGA AAATCAGTAG ATGAGGGGTC 180

AACGATTTCA TTTGTTGTTT CTAAAGGTAA AAAAAGTGAC TCATCAGATG TCAAAACGAC 240

AACTGAATCG GTAGATGTAC CATACACTGG TAAAAATGAT AAGTCACAAA AAGTTAAAGT 300

TTATATTAAA GATAAAGATA ATGACGGTTC AACTGAAAAA GGTAGTTTCG ATATTACTAG 360

TGATCAACGT ATAGACATTC CTTTAAGAAT TGAAAAAGGA AAAACAGCAA GTTATATTGT 420

TAAAGTTGAC GGTAAAACTG TAGCTGAAAA AGAAGTCAGC TATGATGATG TATAAATATA 480

ATTGAAGTAA ATGTACCGAG GTTTCTATTT GGAAGTCTCG GTATTTTTAT GTTGGAGATT 540

GCGGTAGTTT TAAAATGCnT CnTGTCnTCA TATAC 575

(2) INFORMATION FOR SEQ ID NO: 925:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 925:

AAAAACGCTG CTGAGTTTAA AAAGCAACAA TTAAATGAAC AAGGTATTTT CAAGAAACCA 60

GTGATTACAC CTATTAAACC ATATAAAAAT TTCTATCCAG CTGAAGACTA CCATCAAGAT 120

TATnACAAAA AGAACCCCGG TACATTATTA CCAATATCAC CGTGGGTCAG GTAGAAAAnC 180

GTTTATAGAT CnCATTGGGG GGATCCAAAG CTTAAAAAGA TAAAAGTGAC TACCAGATAT 240

AGATATATTG TTACACAAGA AACGGCACTG GACCACCATT TATGAATGAT ATTGGACCAT 300

TTGCTAA 307

(2) INFORMATION FOR SEQ ID NO: 926:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 926:

CTCTACGCAC TCATTCAGAT ACACACATTG CGCATTGCTC ATAGAATCAG GTGTACACAT 60

TAAAGAAATA CAAGAAcGAT TACGGCATAA AGATATCAAT ACCACTATGA ATATCTATGC 120

TAAAATCACA AATTCATACA AAAAAGACGC CTCCCATAAG TTTAGTCACC AAATGGAAGA 180

CGTCTCGTAA TTAAAATATA TTTGCGTGCA TTCTAATTTA TACTTAGAAT GAATCATACT 240

CGTGCATAAT GTAATTTTCT AGTTAGTCAA AACTATAAAC AGTTTTACAT CATTCCTGGC 300

ATGCCACCCA TGTTAGGTTG GTCATTATTT TTTTCTGGAA TTGATGCTAC AACCGCTTCA 360

GTCGTTAAGG ACATTGCTGC AACACTTGCA GCAGTTGnAA 400

(2) INFORMATION FOR SEQ ID NO: 927:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 809 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 927:

TTTAGGTGGT TTTAATnGTT ATGGTCATTC TGGACACCTA CTTATAATAA AATTTCAAAT 60

CAAACTGAAC nTTTTGTACC GTTTGATTAA ACTCAAATTT ATTAGCTCCG TATTTAAATT 120

TTGGTTGGGC TATATTCGTT TCGGTACTTA TTTCAACACC GTTTTTATAA ACTCGGAAGC 180

TATCATAAAC AATTcTGTCT CCAGCTTTTA GTTTGATCCC TTCGATTTTC ATTATTTCAG 240

CATGCGTTAA ATTCCATACA AACGATTCTG TATCTTCGCC TAAAATAATT GTTATCTTTT 300

TATACATGTT GAATTGGTCG TTAGGAGCAC TACCATGATA GTAAACTGTA CCTTTGCTCA 360

AATTTTCAAA TGTATACTTT CTTTTGTCTC CGCCTGCATG CCAATCAATA TTAAAATCAA 420

ACGACCACAA TCCAACCTTT TTGTTTTCTT CTAACTCTAG GCTTGTTCCA ATACTTTCAC 480

CGTATGGTAA TTCTGTAGTT TCGAATTTTA GTTCAAAAGA AACTTTATTA CCTTTTTGTT 540

TAGGGTTTAT AACTCCGTTA AAAATAACTT TATACTGTTT ACCATTTACA TAAATTTGTT 600

GATCGTGTCT TGAATATTCG TAATCCGGGA AGTTGTTTTT ATCTAATTTC ACGTAATCAT 660

CAGAAGTTGG TTGAGTAAAC CTGTAATTCA ACTCTTCTTT TCTTCTGATn TCTCGCAAAT 720

ACATAGGTTC TATGTCTGTC GTTAACGAAT ACAACATATC TCGCATATAA GCAATGTCTG 780

AACGATTTTT AACTTTACAA AAACAAGGA 809

(2) INFORMATION FOR SEQ ID NO: 928:

(A) LENGTH: 1016 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 928:

nAAAACTATT ATCGCATCTA CaGTaATCGC TGCAGGTCTT TTAACTCAAA CTAATGATGC 60

TAAAGCTTTC TTTAGTTATG AATGGAAAGG TTTAGAAATC GCAAAAAATT TAGCAGATCA 120

AGCTAAAAAG GACGATGAAC GTATTGATAA GTTAATGAAA GAGTCTGATA AAAATCTAAC 180

TCCTTACAAA GCTGAAACTG TTAATGATCT GTACCTTATT GTTAAAAAAT TAAGcCAAGG 240

TGATGTGAAG AAAGCAGTTG TCAGAATTAA AGATGGTGGT CCTAGAGATT ACTATACTTT 300

TGACTTAACT CGTCCTTTAG AAGAGAACAG AAAAAATATT AAAGTTGTTA AAAACGGTGA 360

AATCGACTCG ATTACTTGGT ATTAAAAAAC ATACTGAATT AAATAGTTGT ACGCCAAACG 420

TTAGAAAACA ATGCTAACGT ATTGGCGTGC TTTTTTATTT TAAGTAACTT CCAATTTATT 480

TAGCATCTTT ACGACTGTTT AATAAAGCAC GTATGATTAA CACGGTTGCC ACTATATCCG 540

TTACAATTTT TATGATTGTT AATACATTCG ATTTCCTTTT CACAATAGCC ACCTCGCTTG 600

TTCAAAACAT AAACAACTAT TGCATTCACT TTTAAGTAAT TATTTATATT ATTTATCCCA 660

ATAAGCTCAC CATTCAAATA AACACAATAT TATAAAATAA TTATACCTTT GGATATAGCA 720

AAAAGCCACA CTCTATAGCA TGGCTTCTAT CAATTATTTT AAAGTATTAT ATTTTAAAAC 780

TAGATCGATT TGTCTTTGTA ATTTTTTCTT TTCATAACTG TGTTGGAAAT GAATTAAATT 840

AACAGCTCTT TGTGCTTTAC GGTGTGTTGC AACAGTTCTT GTACGTTTGA AAAAGTTTAC 900

AGCTTTTTGT GCATCCACAA CTTTTttATT TACTTGwTTT kTAAAGTTTG TTGATACTGA 960

TCATATTTTT TAGCAGCTTC ACCGTTnTTA GTTGTGCATG AGATCACCGG CAACCG 1016

(2) INFORMATION FOR SEQ ID NO: 929:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 929:

AAATGAAATC ATACCTAAAA GAGATATTAT TACAGAATCA ATGATTTGTG ACTGTATTCA 60

AAATGCAGGT ATTGATTTAG AAGTATTTAA AGACGACTTA CAAAAAAGTA AACTAACCGA 120

CGTTTTCTTT AGTGAAGATG TTCATGAAGA AGGTTTAAAA GTCGAAGGAT TATACCCATA 240

TCACATCTAT ACTTATATAA TTAATGAATT GATGGGTAAA CCTATCGAAA AGAATCTTCC 300

TCCTAAATTA GAAACTTATA TACAGCAACA ACAACTTGTA ACGATGGAAG AATTACTTAC 360

TATTTATGAA TGGCCAGAAA AACTTTTAAA CAAAGAGTTA 400

(2) INFORMATION FOR SEQ ID NO: 930:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 930:

TATTTCTGAC ATGTATCATG CTCCTTCGTG CTTTATTCTA ATGTAATATA CACAATTATA 60

CATTGAAATT CAAATTTGTG AACACATTGT GAACTGACAT AAATTATACA CAATTTCATA 120

GCGCATAATG TTTTAAAAAT ACACATTATA GCAATTATAA TTAAGTTCAT TGTGTTGTCA 180

TCAAAAAAAG AAAAAGGTGA TGTTTTAAAT GGATACAGTT GAATCAGTCG GTTTTTGACA 240

GCATGACTTA GCAGTTCATA TCATTTTGCA ACGATGGTGT GGTATGCTTA ATGTCGCAAT 300

TCAGATTTTA GGATCGCAAA ATGACTCATA TATAGCATGC CAAGTGGCAA GTATCATACG 360

ACATGGnGTG TCAGGCATAn GGCTCATACT GTGCAATATG 400

(2) INFORMATION FOR SEQ ID NO: 931:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 543 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 931:

CCAATCAATG TTGCCAATGG ATCACCTAAT GACAACCAAG TAATTGCTAC CATAGTAACT 60

GCTGTTTTAA TTTTACCTAA TTGACCAGCT GCACTTACGA ATCCTTGTTC AATTTGTAGT 120

AAACGTAAAC CAGTTACGGC AAATTcTCTG GCAATaATAA TGATTGCTAC TACAGAATTT 180

GTTAGTCCTA GTTGCACAAG TACAATTAAA GCACTTGCAA CTAATAATTT ATCCGCTAAT 240

GGATCCAAAA ATTTCCCCAT ATTTGTAACT AAATTCCATT TTCTAGCTAA ATAACCATCA 300

ACAAAATCGC TAAGGGAAGC CAATATAAAA ATAAAACCAC TGATTAATAA CTCAATTCTT 360

ATAAAAACTG GTATTAACAC TACTCTAAAA ACCGTAATCT GGTTCGGAAT ATTCATTATA 480

CATCCTCATT TCTCACTAAT TTATTTCTGT TAAAAATATT AAAACTAACC ATGATCCATA 540

ACC 543

(2) INFORMATION FOR SEQ ID NO: 932:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 932:

GATTGCGAAT GAGATTAGTG GGATGATACC GGTAGAATGG GAGCAAGTAT TTACAATAGC 60

TTATGTAACT GATCAAGCTG GAGAAGTCAT CTTTAATTAT ACTAAACCAG ATAGTGATGA 120

ATTAAATTAT TATTCAGmCA TACCTAAAGA TTGCAATGTC TCAAAAGATA TTTTTAAGAA 180

TTCATGGTTT AAAGTTTATC GAATGTTTGA TGAGTTAAGA GAAACTTTTA AAGAAGAAGG 240

GCTTGAACCA TGGACATCAT GCGAATTTGA CTTTACAAGA GATGGCAAAT TGAATGTATC 300

TTTTGATTAT ATAGATTGGA TAAATACAGA GTTTGATCAA TTGGGCCGTC AAAATTATTA 360

TATGTACAAA AAATTTGGGG TTATACCAGA AATGGAATAT 400

(2) INFORMATION FOR SEQ ID NO: 933:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 759 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 933:

ATTTTTACAA AGAAATAGTA GTCTTATATA TCTTAACATT TAATAACTAA ATCAAACATA 60

TTTTGAGCCT TTTTTTGAAA ATTAACATTT TAACCTTTTT GATTTTACAA CAAATTATAG 120

CTACGTATTG AAAATTAAAG CmTTGGtTTA AGTGTTGTGT TAAAAgyTTT TATGTTTAGA 180

TTGTTATATT ACTATGTATT CTTAAATTTG TTTAAAAAAT TAATGCTTTA AATTGATGTA 240

TAATGGGAAT AAGAAATAAA TAAAAACGAC CCGCACGATT AACGTACGGG TCCACTACTA 300

AAGGGAGTCA AATTTTTACC TcGTTTGTAT CATGCAGCGT TTTACACATA CTTTTAAGAG 360

ATGTTTATTC GTTATCGAAG GTACACCTTT ATTATAACTT ATATCATTTT TATTAAAATA 420

ATAATGATTA TTAAATAGTA ACTAAATACA AAATTACATG GGGTGAATGA TAATGAAACA 540

ATACTTAATT ACTGGTGGGA CTGGTATGGT TGGATCTCAA TTAGTTAATG AAATTAAAAA 600

ATCAGATTCA CATATCACGA TATTAACGCG ACACGACCAA ATTTCAAATG ATAAGAAAAT 660

TTCATATGTC AACTGGGCTA AATCTGGGTG GGAACACAAA GTTCCTCAAA ATATCGATGT 720

GGTCATCAAC TTAGCAGGTG CTACATTGAA TAAACGATG 759

(2) INFORMATION FOR SEQ ID NO: 934:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 934:

GATCAAGCTG GGGAAGTCAT TTTTAATTAT ACTAAACCAG GTAGTGATGA ATTAAATTAT 60

TATTCAGACA TACCTAAAGA TTGCAATGTC TCAAAAGATA TTTTTAAGAA TTCATGGTTT 120

AAAGTTTATC GAATGTTTGA TGAGTTAAGA GAAACTTTTA AAGAAGAAGA GCTTGAACCA 180

TGGACATCAT GCGAATTTGA CTTTACAAGA GATGGCAAAT TGAATGTATC TTTTGATTAT 240

ATTGATTGGG TGAATTCAGA ATTTGGACCA ATGGGAAGAG ACCATTATTA TATGTATAAA 300

AAATTTGGnA TTTGGCCTGA AAAAGAATAT GCCATAAATT GGGTTGnAAA AATAAAGnTT 360

ATGTTAAGAG CAAGnTTGAG CTGAACTATA GGGGAGATAA 400

(2) INFORMATION FOR SEQ ID NO: 935:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 935:

CTGAATATAA TTTTTnCAAC TACATCTCGT TTATTAGACA CCGTGCACTG ACTAAGAAAA 60

TTTCTCTTGA CTCCATTAGT CCTGACGAAT ACTAACATTT AACTACCTTG CTCATCGATA 120

GAAACAACTT GTAATGTTAA TTTCCCTTAT TTTCTTAGTT TTAATCTATC AGCGATTAAT 180

TCGATTGCAT CTTTTTCATA AGCAATTGGA TAAACTTGAC CGCGGTACAC CTAACGCTCG 240

AAATATGATT TTnTATCGTC ATAATCTAAA ATATTATnGG CAAAATCACA GCAGTTTTCA 300

(2) INFORMATION FOR SEQ ID NO: 936:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 619 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 936:

GTTATCATCA TCTTCTGAAG TATCATCTTG CCCATCGACT TGACTTGCAT CAGTTCTCTT 60

TAAATCATCA AACTCTGGAC TAGCTAATGT ATTATATAGT GTTTTAGGTA AGTAATAATA 120

TTCGTTTAGC ATATCTTCTT TTAAAATATC ATCTACTTGA TACATAATTC TTTGAGCCAG 180

ATACATATTA TCTTCAGAAT TTTGATTTTG GAAAAAATTA GGTAAATATA AGAACATATT 240

TACTAAAATA TCATCTAAAT CTGAATGTAT AGATGGTATA TCAAAGAAAT CTTGGCTTAA 300

AAATGCATGT TCTAAATACA AAAATAATAA ATCTGTATAT TGTGTTTTAG TACGATACAC 360

TTTAATTTGA GATTCCGTAT ATGATATACG TGTATCTAAG CGAAGATCAA TTAATTTAGC 420

AGTACTTGGG CGCTCAACTT TAATAGAATT TAATACGCGC ATATCTTCTA ATAATTTAAA 480

AAGTTGTTGG ATAAAATTTA GGGtGTTTAA AAGTTTTATC TTGtACTACT TCATTTACAA 540

TTTGtACATC CaTCATATGA TAACCGTAAG CAGCTAACAT AACATCTGTT TTTAAACCAG 600

CCATTTCGAT ATGGCTTGG 619

(2) INFORMATION FOR SEQ ID NO: 937:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 937:

TAATCCCTTT CATAATGGGC ATCAATATCA TATTAATCAA TCTAAAAAAC TTACAAATGC 60

TGACGTTACT ATTGCAATAA TGAGTGGTAA CTTTGTCATG CGTGGCGAAC CAGCAATCTA 120

TAATAAGTTT ACTCGTGCAA AAATGGCATT ATCAACAGCT GATTTAGTTA TCGAACTACC 180

AGCAACTGCC AGTTTATCAT CTGGcGATCA TTTTGCCGAA CTAGCAGTTA AAGTCGCnGA 240

TTATATGAGT GTCGATACAA TTGCATTTGG TAGTGAAAAT AATGAtATCA AAACATTAAA 300

rCmATTAgCA CACAGCATTA ATGaAATTGA mCAATCTGaA TCCTTTTCAC aAAAAGTrAA 360

AAGTCCTAAC AACATACTTG GTATTAGTTA CCTGAAAGCA ATTGCTAAAA ATGCTAAAAA 480

CATCAATGCA ATTTCTATCA AACGAGAAAA TGCTCAACAT CATGATTCAT TAATTCAACA 540

CCATCAGTTT GCAAGTGGTA CATCTATTAG AACATCAATC ATTAGTCAAG ATGATCATTG 600

GCATCATGTG GTACC 615

(2) INFORMATION FOR SEQ ID NO: 938:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 938:

AGAATTGAAG ATGGTAAAGT TTCAAAATAT CATTCGGTTA TCATAAAAGA CGCACAAGCA 60

ACTTCACCAT ATTCAATTTT TATCAGAGGT GCTATTTATC GCTTTGAACC ATTAGTATAA 120

ATATACGTAA GTGCTATGAG CGAGAATGCC CATATGAATA ATGACAAGCA CAATGGAAAG 180

AATCGTAATA TATTATTTAA TCGTGATGCT TAATTAAAAT GAAAAAGATT GATAATATAA 240

ATGTGAAAAA GTAAGTATAC CCGTAAACTA AAGTATTCAC GGTGAGAGGT GCTCATGTCA 300

TAATGATGCA CGTGTCATAA TTATAATAGC TTAnATATGT CCATACAACA CCATGTAGAT 360

ATGCATATAC AGGGTATGAT AGACATAGnG TCTGnGAAAT 400

(2) INFORMATION FOR SEQ ID NO: 939:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 466 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 939:

GTACAGGTAT GATTGGTGAT CCCATCAGGT AAATCAGAAG AACGTGTGCT ACAAACAGAA 60

GAACAAGTAG ATAAAAATAT CGAAGGTATT AGTAAGCAAA TGCACAATAT TTTTGAATTT 120

GGAACAGACC ATGGTGCAGT GCTTGTTAAT AATAGAGACT GGTTAGGACA AATCTCATTA 180

ATTAGTTTTT TACGTGACTA TGGTAAACAC GTCGGCGTTA ATTACATGTT AGGTAAAGAT 240

TCAATCCAAA GTCGTTTAGA ACATGGTATT TCATATACAG AATTCACATA CACGATTTTA 300

CAAGCTATTG ATCTCGGTCA TTTGAATAGA GAATTGAATT GTAAGATTCA AGTAGGTGGA 360

GTAGATAAGC AAATGATTAA TAGTTGAGGG GTATGTCGAT GAAGCG 466

(2) INFORMATION FOR SEQ ID NO: 940:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 940:

ATGAATCACC CATTGATACC AATCATTTAC ATCACTGTCA TACGAACATA TATTTAAATA 60

GAAAAAAATT ATTTTAAAGA TTATAACTAC TCTTAATCAT TTTAGTGAAT TAAAAAAAGT 120

AGTGCAAAAA GCAAAATATA CTTTATACAC TACAAATCAT TTATTTATAA TAAAGTTTCA 180

CCAAAAAATG TTCCAACTAA TGAAACCGCT TGTTCAGCAG TATGATTATn ACTGTCAATC 240

AATGGATTTA CTTCAACTAA ATCCATTGAG GAAATTAAAT GTGATTGATG CAGTAATTCC 300

AATGCnAAAT GGCTTTCTCT ATnACTAAG 329

(2) INFORMATION FOR SEQ ID NO: 941:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 941:

CGATATAGTA CCAATTTATT TGAAGAAAAA TCCGAACTTC AAATTTCCGA TGAAGCAAGA 60

TATACCGGTT ATTATGATTG GACCAGGTAC TGGAATTGCT CCTTTTAGAG CATATTTACA 120

AGAACGTGAA GAACTTGGTA TGACTGGAAA AACATGGTTG TTCTTTGGTG ATCAACACCG 180

TAGTTCTGAC TTTTTATATG AAGAAGAAAT AGAAGAATGG CnTGAAAATG GAAACTAACA 240

CGCGTAGATT AGCATTTCCA AGAGnCCAGA CACAAGATAT GACAGCCnCG ATATGGAGAA 300

GTAACGTTCC ATGAT 315

(2) INFORMATION FOR SEQ ID NO: 942:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 699 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 942:

TACCAATAAT CAACTTGTTT TACATCATCG TGTGTTTCAA TCACTTTCCT TTTTATACCT 60

TTCTTACCTT TAAAGAATGC ATCAACATCT TTTATTGAAG ATCCTTTTGA ATCTTTAGTA 120

AATCTATAAT CTGCAAGTTC CACTTTACCC ATTAATTCTT TGTAATCTTT CCATCCTTGA 180

ATCCCTTTAC TATTCGTAAA CGACTTTTCT GTCATTAATG GATCCAACTT ATCAAGAGAT 240

GGCGCATCTT TAATTCCTTT CATTTTCTTC TCTATTTCTT CATATTTCTC TAAATCTGGA 300

TCTTTCTCTT CTTCCGATTC TTTTTTTACA GTTTCTTGTT TTGATTCTTC TGATTTCTTT 360

GATGATAATT TATGATTCCC ACCAAAAGAA CAACCTGCTA CGACTAAAAG CATAATTAAA 420

AGTAAACATC CCAGTGTCTT TTTCATAAAC TTTCTCCTCT TAAGTTATTT TGTTTGAATC 480

AAATAAACAT ACATAAATTT AAAAAACTTA TTTATATTGa TATTTTACAT TAACCATCAA 540

TATTTTTAAA TACTTTAAwT GaTAATTTAA GAAAATTGTT TTGTCTAATA ATTTAAGTAG 600

TTAAAACATA GATAGATATA AAATAGTTTA TAGCCATTAA TTTATAAGTT TAAAATTCGC 660

ACTATTTCAA TTTGCCATTT AAAAATAGTT TGTTTAATC 699

(2) INFORMATION FOR SEQ ID NO: 943:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 943:

CGCTCCATAA ATCAACAATG TTCGAGTCTG TAATCTAGAT GATAAAACGC CAAGAATGAT 60

CATAAATGGC ACTTCTAAAc CAGCACATAA ACTAGCTAAA TAACCGACAT GTTGTTCATT 120

TTCTTTTAAA TAATCAGTAA CAAATAAAGG CATATTCATC GTATACATCC ATTGTCCAAT 180

GTGTAATAAA ATAAATGCAA TAAATGGTAA TAAAAGCGTT TTGTCTTTAA ACATATTAGG 240

AGCAATTTTT TCAACATGTT GTTGCGTACT AATAGGGTGT TTAATGTTTA AATCCTTATA 300

GAnAAACACT TGAAGTACTA AAGTAAATAA AATGATACTT ATTGGGCCAC CAAACAATCC 360

AGCATAGCCT TTTAATCCGA TTAATTGGGC ACCAATAAAT 400

(2) INFORMATION FOR SEQ ID NO: 944:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 570 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 944:

AAGATGACAA TACTTTGTTT CAAGAATTGA AAAAAGAATT AGAACAATGG GATTTTAATG 60

TTGCTGGTAT TGAAGATTTC GGCAAAGTAA TGGATACATT TGAAAGTTTT AATCCTGAAA 120

TTGTTATATT GGATGTTCAA TTACCTAmAT ATGATGGGTT TTATTGGTGC AGAAAAATGA 180

GAGAAGTTTC CAACGTACCA ATATTATTTT TATCATCTCG TGATAATCCA ATGGATCAAG 240

TGATGAGTAT GGAACTTGGC GCAGATGATT ATATGCAAAA ACCGTTCTAT ACCAATGTAT 300

TAATTGCTAA ATTACAAGCG ATTTATCGTC GTGTCTATGA GTTTACAGCT GAAGAAAAAC 360

GTACATTGAC TTGGCAAGAT GCTGTCGTTG ATCTATCAAA AGATAGTATA CAAAAAGGTG 420

ATCAGACGAT TTTCCTGTCC AAAACAGAAA TGATTATATT AGAAATTCTT ATTACCAAAA 480

AAAATCAAAT CGTTTCGAGA GATACAATTA TCACTGCATT ATGGGATGAT GAAGCATTTG 540

TTAGTGATAA TACGTTAACA GTAAATGTGA 570

(2) INFORMATION FOR SEQ ID NO: 945:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 945:

CCGAGnCCAC CGTTCCAAAG TCCATTTTTA TCCCCATCCC TCTCTGAATT GAACTATAAT 60

TTTTGAATTT ATTAATAATG CTATTTTTnT TATTTTATCA AAAACTGATT ACAAATACAC 120

ATAGAAAATG AAATATATTT TTCTTTGACT ATACATAACT GTTATTTCTT TGGATATTTA 180

TATTAAATGC ATTGGTAGTA GTTGTAGCGC ATTAATGTTT GACGGTGTAT AGTATTAATT 240

ATATTGAAAG TTAGTTGGAA GTTGATAGTA GGAGTGGGAG CATTGAAGCG ATTTGTGGCG 300

ACGGTATTAT TATTACTAGT CTTTATATCA GGaTGtGGTA ATGrTaAATA TGTGAAAGAA 360

ATaGATGAAG CAGTTAAAaT TCAAAATCaA AAACAAGAAC ACTTGCCCAA AAAAGGCAAC 420

GGTGATCGTG TTGATCATTT TGAACGCAAA GATGCTAATA TTTATGTCTA TGATAAGGAT 480

AAAATTATCA TTTTAGCTTA TAAACCTTTG AGTAATGATG ATGAAGTGCA TTATTATGCA 540

TATGATTTTA GTGATAAACG TGTATCATAT AAGCAAGATT TTGATTCGAG ACGATATTAT 600

CAACAACATG ATGCGGATTA TCATGAAGAA AATATGACGA ACTAGATATG AATAGGAGTT 660

GGTAAAAAAG AATCAGCAAC GACATCTTCG AAAAACGGCA AACCATTAGT TGTCGTATAT 780

GGCGACTATA AATGTCCTTA TTGTAAAGAA TTAGATGAAA AAGTCATGCC AAAGTTGCGT 840

AAAAATTATA TAGATAATCA CAAAGTGGAA TACCAATTTG TCAATTTAGC TTTCTTAGGT 900

AAAGACTCAA TTGTTGGTTC GCGTGCGAGT CATGCAGTAT TGATGTATGC ACCTAAATCA 960

TTTTTAGATT TTCAAAAGCA ATTATTTGCT GCCCAGCAAG ATGAAAATAA AGAATGGTTA 1020

ACAAAAGAAC TATTAGATAA ACATATTAAA CAACTGCATT TAGATAAAGA GACGGAAAAT 1080

AAAATTATAA AAGATTACAA GACAAAAGAT AGCAAGTCTT GGAAAGCTGC AGAGAAAGAT 1140

AAAAAAATAG CGAAAGATAA TCATATAAaA aCGACACCAA CTGCATTTAT TAATGGCGAG 1200

AAAGTTGAGA TCCATATGAT TATGAAAGTT ATGAGAAGTT A 1241

(2) INFORMATION FOR SEQ ID NO: 946:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1057 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 946:

TAATACAATG ACACCATTTA GCATGACCGT TATCCCTGTA ATTCAGCTGA TATTATCTGT 60

TGCAATTTTA TGTGACGAAC TGTTGCACTT AATTTGATAA ATCnACAAAT ACAAAAAATC 120

TAAGTTGAAC AATTATGATA CAACCGTGCA AACGATATGT AGTATAACTT GTCAACTTAG 180

ACTTATTGAT AAATATATTA ATAGTGGTTT ACCATAGCAG GAGATTTCAC aTCaAAATTT 240

TGAAGTAGCG TATCaATCTT TGaATCaTCa ATATATACCt TATGTAAATT TTTCaTATAC 300

ATCGAATGAG AAAGTGCTTC aTAATTTAAT GAAAAAGATA TATGATCTCC AACTTGATAG 360

TGTCCTTGAC CATTTAAATC AAGCATTAAA TGATCACTCG AAGCGCCTAA AATATTGATA 420

TGCTGATCCA TAGGTGAAAT ATTATCGACT TTTGTAyCTA AATAACCAAT ATCTACAATA 480

GCTTGTAAGA ATGATTCATG CGTTTGTGTA TTAACTCGAG GTTTAATTTC TAAAATCTCA 540

GCCTCCAATG TAATCGCATC TTGATATAAC ATAGCGATCG CTTGATTTGT CGTTGTATCA 600

ACACCTCTAA ACAACGTTTC ACCTATTCGC AATTCATTTA TTTTACCCAA ATCATTATAT 660

AAAAGTTGTG GTAACATGCT CGAATTACCA CCTGAAATAA TTTTCAATCG ATATCCTATT 720

TCTCTTTCAA CAGCTGAGAC GAATCGATTA ATCATAAAGA TATCATCATC ACTTGGCGCA 780

TCAGATTTAA AACACATAAA ATTGAATGCT AAACCTACAA AATGGATATT TTTCAAGTGA 840

CAATCTACCA TTAATAAAAT CTTATGTTTT TTTCCTAAAA CTTCTGgCTA CTTCATTTAT 960

TTGATGTATG GGTAGATAAT TCCGGTTTGG GATACCTCCA TATCnAACCT TTTTTCCTAA 1020

TCAATATCCT GGAAAAnCCC TTTTTTTGGG CAGGGCG 1057

(2) INFORMATION FOR SEQ ID NO: 947:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 649 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 947:

GATATCCGCT CGATGAATAT ACCTTTAAAG GTGTTGGTGC AAATTCTGAA CAATTAAGTG 60

CTATGAATCA TGATTCTTTA AAAAAGGAGT ACATTTCAAA TGACTGTTAA ATATAATCAA 120

AATGGCGAAT TAACAATGGA TGGTATTAGT TTAAAAACGA TTGCACAAAG CTTTGGTACA 180

CCTACCATTG TTTATGATGA ACTACAAATT aGAGAACAGA TGCGCCGTTA CCATCGCGCA 240

TTTAAAGATA GTGGATTAAA ATACAATATT TCATACGCCT CAAAGGCATT TACTTGCATT 300

CAAATGGTCA AACTTGTAGC TGAGGAAGAT TTACAGTTAG ATGTTGTTTC TGAAGGTGAA 360

TTATATACAG CTTTAGAAGC AGGTTTTGAA CCGAGTCGCA TCCATTTCCA TGGTAACAAT 420

AAAACGAAAC ATGAAATTAG GTATGCTTTA GAArATAATA TCGGTTATTT TGTTATAGAT 480

TCATTAGAAG AAATTGAATT rATAGACCGC TATGCTrATG ATACGGTTCA AGTTGTATtA 540

CcGAGTTAAT CCcAGGTGgT TGrAAGCcAC mTrCaCaCgA aTTTATTCaA ACyGGGcaaG 600

AAgGATAGGT TAAAGTTTTG GGATTAAnCC nnTTTCCCAT TAATGGGCC 649

(2) INFORMATION FOR SEQ ID NO: 948:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 948:

TACAAAGCTT AAAAACAGAG CTTAGTyTCG TTGAACCATT AATTAGCCGC TTAGAATTAG 60

AAGAAGCTAA TGATAAACTA GCTAATATCA ATGATAAGTT AGATGACATG TATGATTTAA 120

TTGAACATGA AGTTAAAGCT AAAAATGATG TCGAAGAAAC AAAAGATATC aTTACGGATA 180

AAAACTACTA TATAAATGAA TCTGATGCTC AGAGTGTTCG TCAATTTGaA AATGrAATTC 300

aAAGTTTAAT TTCTGTATAT GATGATATTT TAAAAGAnAT GTCTAAATCT GCTGTGCGAT 360

ATAGCGAGGT TCAGGATAAT TTACAATATT TAGAAGATCA TGTCACAGTT ATTAATGACC 420

AACAAGAAAA GCTACAAAAT CATCTGATTC AATTGCGTGA AGATGnGCAG AA 472

(2) INFORMATION FOR SEQ ID NO: 949:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 949:

AGAGGATCCC AGGCGTTTGT TGATCCAGCA GCCGATnCAG AATACATCTT CTATGCATAT 60

AAACGTTTCA ATTTCGAATT GAAAGATCCA AACTTCACTA GTGAAGAAAA TATGTTTAAA 120

GATGTATCAG ACAAACCATT AATACCTGCT CGTAAAGCTC AAATTACAAA TGCGAACTAT 180

AAACGACATG GTATGAAGTT GATGATTCTT GGGAATGACG AACCATATAA CAATGAGTTC 240

AAGAAAGATG ATCGAAAATG CGAAGAATGA GAAATTTCAA AGGTGCGCAn GTCAAGCCAT 300

GTGTCAGGGG GGCATATGAT TTCnGGTCAT CAGTAAGGAC TGTGTCATGC CATGGCCATC 360

TGTTGTACnG ATCTCTAATA GAATCTCAGA TGCCCGGCAA 400

(2) INFORMATION FOR SEQ ID NO: 950:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 556 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 950:

AAAATCTTCG ATGACAAAGA AATCTAATGA TGTTTCTTTA AAATGACCAA ACTGCAACGG 60

AATGATATAA CCACACTTGA GATATGGCGC TTCTTTTTTC AACTTAGTCA TCACATCATA 120

ATCCAAAGAC ATCACACGAT ATTGATGTTC AACACCATGC TTTTTCAAAA TATCAATAAC 180

ACGTTGTGTA TAATCTGCTG GTTCTTTACC ATGTGGCTTT AACTCTACTA GTAGCTTCAC 240

ATTTGATTGT TTAGCCGTTT CAATAAATTC GTCTAAGGAT ACAAATTTTG CTTCATGTCC 300

ATTTTGACGC ATTTTCAAAC CGACGATATC TTTGAAATTA GATTCAGAAA TATTTTTATT 360

CATAATTGTA TCTAACTCAA CGTATTCGAC ATTCGCTTTT GCAGCAGCTT TCAATGACGG 480

AATAGAATTT TCAACACCTT TATCTTCGAA ACCACGTGGC CAATAATGGA GATATTGTAA 540

TTGATAGTAT TATTGG 556

(2) INFORMATION FOR SEQ ID NO: 951:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 951:

TTGTGGTAAT GATGTTAATC AGTATATTTC TACTTTTGAC AATGACATCT AAAGGATTAA 60

GCAATCTTAG AGTAATAGAT GATGAGGCAA ATATCATTTC TTTTATTACT GAATTGAATT 120

ATATTAAGTC GCAAGCTATA GCAAATCAAG GATATATCAA TGTTAGATTT TATGAAAACA 180

GTGACACTAT TAAAGTAATA GAGAATAATA AAATACGATT TCTAAAATTA AAAGTAGGCA 240

AAATAATTAA TGTTGCAAAA GTTGATATTA TTGCCTTTGA TAAAAAAGGG AATATCAATA 300

AATTTGGTAG CATAACAATT TACAATAACA ATTCAATTTA TAGgAATAAT ATTCCATATT 360

GaAAAAGGcA AGAATTCGTT ATGAAAAGCT ATAAGTGTAA AGGTTCATTC TTAATAGATA 420

GTATGGCTGG nTTTTTGCCA ATTGGGATTG nATTACATTA CTATTGATT 469

(2) INFORMATION FOR SEQ ID NO: 952:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 730 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 952:

ACATnTATAA TnCTTATTTG CTTGCTCCTT TCACTTTTTA AGAGTAAAAn ATAACCTGAA 60

ACATAACTTT AACATCCAAG TTTCAGGTTA GTGTAATGTA AATGATTTAC TTTGTTnTAT 120

TATGATTAAA CATCTAATTC TCTGCTTGTA AGTGCTTTAA TCATCTCTGG ATCAGCATGT 180

GAGAAAAATT GGCTATTACT TTCTTCTAAT GTCGCAATTT GTTGTTTATC TTCTTCTGTA 240

AGTTCAAAAT CAAATATATC TAAGTTTTGA GCCATACGTT CTGGATTTAC TGATTTTGCG 300

AGTACAACAA TGTCACGTTC TACTAACCAG CGTAAAATAA CTTGTGCAAT TGATTTGTTG 360

AATGGTGCCC AAGCTTCTAC CACAACATTT TCTTGTTGAA GTGCTGCAAC TTGTTCTTCT 480

TGTTGATGGA ATGGATTAAT TTCTATTTGG TTCACTTGTG GTTGAATTTG ATTGTGAATA 540

CCTAAATCTA CAATTCGATC AACGCCGAAG TTAGATACAC CGATTGCTTT AAaTTTTACC 600

ATTTTCtTTT AACTCCTCCA ATGCACGCCC ATGGAGCCAT ATACnGCCAT TGGTAAAGGT 660

TGGGTGGAAT nAAGCACCTA GGATCCAGGA TAGGTCCCAA ATTTTAATCC GGTGGGnAAT 720

GGATCGGTTC 730

(2) INFORMATION FOR SEQ ID NO: 953:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 953:

ACAAATGACA ACGTACAATG ACGTCTTCAC AAACATGCAT TTTAGGAGAT TGATTATTAC 60

AAATATCCAG TTTTTTGTTA CATCTATTTG CAAATCTGCA CTTATTAACG TGAAATGCTT 120

GGATTGATGG CACAATTCCT TCTATCGTTT CAAGTCGTTT CTGCTCTTCT TTAAGTTTTG 180

GAATTGTTGA TAATAATTTT TGGGTATAAG GATGTTTCGG ATTGTGTAGT ATTTCTTTTA 240

TGCCTCCAAA TTCTACAATT TGACCTGCAT ACATAACTAA GACTTTATCG CAAAACTCAG 300

CAACTACACT CAAATCATGT GTAATCATCA TAATTGCCAT TTGCGTTTCC TTTTGCAATT 360

CTTTTAATAA GTCTAATATT TGCGCTTGAA TCGTGACATC 400

(2) INFORMATION FOR SEQ ID NO: 954:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 954:

TAAATCTTGA GGACGTTTGG TCTGAAAGCG ATGCTCAACT GTTGATAAAT CCAATTCGAT 60

AACATCTGTA TAATTAGGAT CTTCTTTCTC AACATCAAAn ACATATGGTT TTGTTTCAAA 120

TATTCTTTTA CTAGCGCGAT ATGTTCGTCT GATCTACCAG TTAACTTCAT ATATTTAAGA 180

ATTCTCATCA ACTGGGGAAG AATCCGCAAG TTGCTCCATA CTCTGGTGCC ATGTTTnCAA 240

(2) INFORMATION FOR SEQ ID NO: 955:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 514 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 955:

AAACATTTAC ACAAGTAGTA GAAGCAATTT ATGATGAAGA AGGTAACAGC TTaGamgCGG 60

CGCGCCATCC aTTACAAATC GTTCAAATTA AAGTGGATCG CCCGATATAT CCAAACAACA 120

TGATGAGAAA GGAAATTGGC TAATGAAAGC TACTACAATC ATTGGCATAG CTGGTGGATC 180

TGGCTCAGGA AAAACAACTG TAACTAACGA AATTATGAAA AACTTAGAAG GTCATAGTGT 240

CGCTTTACTT GcTCAAGATT ACTATTATAA AGATCAAAAG CACTTGACTT TCGACGAGCG 300

CCTAGAAACC AATTATGACC ATCCATTTGC ATTCGATAAT GATTTATTAA TTGAAAATCT 360

TAAAGACTTG AAAAATGGTA AAGCAGTAGA AGTACCGACA TATGATTATG CtAGTCATAC 420

AAGAAGTGgA CATTACCATT GGATTTTtAA ACCTAAAGAT GtTTATTTAT CGTAGAAGGG 480

CCTTTTTCGC CTTTAGGAAA ATAAGGGTAT TTAC 514

(2) INFORMATION FOR SEQ ID NO: 956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 388 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 956:

ATTTTAACGA ATATCTTGCC GTACGATGCC CAAGCTGCAT CTGAAAAGGA TACTGAAATT 60

ACAAAAGAGA TATTATCTAA GCAAGATTTA TTAGACAAAG TTGACAAGGC AATTCGTCAA 120

ATTGAGCAAT TAAAACAGTT ATCGGCTTCA TCTAAAGAAC ATTATAAAGC ACAACTAAAT 180

GAAGCGAAAA CAGCATCGCA AATAGATGAA ATCATAAAAC GAGCTAATGA GTTGGATAGC 240

AAGCCATAAA GTCTCACCTG AATGACGGTC AAGTGTATAG CATAATAGTC ATGCTAAGTT 300

AATGAGTCTC AATGTGTAGG GCACAAGTGC GGGCGTCTAT GCATGAATGT TGCCACGCTC 360

ACAACTGGGA AGTGTAAATG TGACTGTA 388

(2) INFORMATION FOR SEQ ID NO: 957:

(A) LENGTH: 394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 957:

AACAAAGTAC ATCGCAGTTA CGAGAAGAAA TAAATGCATT GTATAATCAA GTTATAGAGG 60

TTGGACAAGC GTTATCAAAG CAGCGTCGTA TAGTCGCTAG GGAGTTAAGw GACCACATTG 120

TATCGGAAAT TCAAAACTTA CAAATGAAAG ACGCAAATCT TGAGATTTCA TTTAAAAAAT 180

TAGAAGAACC GAATATTGAT GGAATCGAAT TTGTAGAATT TTTAATCAGT CCAAATAAAG 240

GGGAACCATT AAAAAGTTTA AATAAAATTG CGTCAGGTGG AGAACTTTCT AGAATTATGT 300

TAGCGTTAAA AAGTATTTTT GTTAAAtCGa GAGGTCAAAC TGCAATTtTr TTcGATGAGG 360

TTGaCTCAGG TGTATCtGGr caAGCTGcAC CAnA 394

(2) INFORMATION FOR SEQ ID NO: 958:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 958:

CCGCCATTTT TTTCGATTTC TTTTTCAAGT TTTTCACGGT CTTTTGAAGA TAGACTATTG 60

AAATCTTTTG CACCACTATC ATCAAAATCA ATATCTGCTT TCAATTTTGT GCTAGATTTT 120

AAAATGAAAT TAATTGGTTC TTCAGcATAt TTGATGCCGA TATyTAACGT AGATTTCTGA 180

GTGTTATTyT TTACGTCAGA ATCTATATTA TTTTCAAAAG TGAATTCATT TTCGTCGCTA 240

TATTTATCTA ATGCGACAGT GATTTTACCT TTATCTTGAC GTTTTGTGCC ATCTACTTTT 300

TCTTGGTTAT CTAATTTGAT TTTTGATTCA TCATATTCTG TCTTTTTACC AAATTCGTAT 360

TTATCATTAT ATTTATTtATC TTTwTCTTTA GAAGATACGC CTTTAATTGT ATATTTCGCT 420

TCAGCATACG TGTATTTATC TTGATCGAAA TCAAGTGCGT AATCTAGTTT TAACTTATCG 480

TCTTCTAAAG TATTAGTACC TTT 503

(2) INFORMATION FOR SEQ ID NO: 959:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 959:

TCAAACGTAC AGAGCTTGTT AAGTGTTTAG ATTATTTACG AGAGAGCGAC ACATTAGTTG 60

TCTATCAACT TGATCGGTTA GGTAGAACGA CAAAACTATT AATTGAATTA TCACAATGAT 120

TCGATGATAA CGGAATTGAC TTACCAnATT AGTAACCTGA ACATTTCCAC GAAAGACCCC 180

ATGGGGCCAA AATGTTTTTA CCGATGATGA GTGCCTTTTT CCGGGTTAGA AGTTAATTTA 240

CTATGTGAGT GTATAAAATA GACTnAGCAG CCACAAGnCG AGAGGCCGAA AAAAGCGGGC 300

GCCCTCT 307

(2) INFORMATION FOR SEQ ID NO: 960:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 960:

ATAAGGACAT TTATAGTCGC CATATACGAC AACTAATGGT TTGCCGTTTT TCGAAGATGT 60

CGTTGCTGAT TCTTTTTTAC CGCAAGCTGT TAAAATTAAC ATGCTCACTA TAAATAATGT 120

TAGTAATTTT TAGTCCATAA TTACTCCTAA TCCTAACCAn GTCnGCnAAA TTTCCTCCAT 180

GATAATCCGC ATCATGTTGT TGATAATATC GTCTCGAATC AAAATCTTGC TTATATGATA 240

CACGTTTATC ACTAAAATCA TATGCATAAT AATGCACTTC ATCATCATTA CTCAAAGGTT 300

TATAAGCTAA AATGATAATT TTATCCTTAT CATAGACATA AATATTAGCA TCTTTGCGTT 360

CAAAATGATC AACACGATCA CCGTGCCTTT TTTGGCAAGT 400

(2) INFORMATION FOR SEQ ID NO: 961:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 961:

ACAATTAGTT ATACCCAAAA GAGTTATGTC AGTGAAGTAG ACAAGCAAAA CTCAAAATCT 60

GTTAAATGGG GTGTTAAAGC AAACGAATTT GTTACGCCTG ATGGAAAAAA ATCTGCGCAT 120

GCTCCTGATA ATCAATTGCC ACCTTTAGTT CAAAGTGGCT TTAATCCATC GTTTATCACT 240

ACACTATCAC ATGAAAAAGG TyCAgTGATA CGAGTGaATT TGaAATTTCa TATGGTAAGA 300

ACTTAGATAT TACCTATGCG ACTTTATTCC CTAGAACTGG TATTTACGCn GGAAGGAAGC 360

ATAATGCATT TGGAAATAGG AACCTTGTAn TTAnGTATGG 400

(2) INFORMATION FOR SEQ ID NO: 962:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 962:

CTTTTACAAA GACAAATTAG CGGTAATCGG TAAnGATCGT TGTTGATCCA GTTGCACTAT 60

TGAAAGAATT AGACGGATTA AATGAACGTG GCATTCCTAC AAGTAATTTA CGTATATCTA 120

ATCGTGCGCA AGTGATTTTA CCATATCACT TAGCACAAGA TGAATATGAA GAACGTTTAC 180

TGGTGACAAT AAGATTGGTA CACTAAAAAA GGTATCGGTC CAGCATATGT AGCCAAGTCA 240

CGTATCGGTA TCGTATGCAG ATTACTTGAA AAGAACATCG AAGATATTAA ATCAACATGA 300

TATAACCAGC TATTCAAGGA TGTTACGAAC ATGnCACATT GATGAAnCTT GAGATATA 358

(2) INFORMATION FOR SEQ ID NO: 963:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 963:

AGTGAGCAGG TTGAAGTAGT AGGGCCGATT CAAATGGAAA GAGATACACA TAAAGATGGT 60

AAGGTAAAGT GGCAATTGCT TTATATAATG AATCAGGATG ATGATGAAAT TAAGCCACCA 120

TTTTTTATTC AATGGGAGGA AAGTGATTCC ATTGCGTACT AAAAAATTGC AAAAATATTT 180

TCAAAACCAT TTTCAATTGA AACTGTATTG TGAAAGTAAA ACCGTCACAA CAGTATCGAT 240

TGGTTGAAnT GGTTGnAT 258

(2) INFORMATION FOR SEQ ID NO: 964:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 388 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 964:

TTATCAAACC GCCATAGCCA CATCTCGATT CAAGGATAAA TTTGTTTTCT CATATCTTAT 60

CTCTCATGAC AGTGCACGAT ATATATCTTT TCCAAATATT CATCACTTTT TTCCTGTTAA 120

AATCATTTCT ATTATTAATG CTTTAATGAC AACTTATTTA ATTTATTGCA TTTAATGCCC 180

TGCTTCATTT TCAAATATTA ACTTTAATCG ACTAGCTCAT CACACTATTT ACCCTTTCCA 240

CCTATCACTA CTGAATTCAA AACGATTTGT TTACAAATCC CCTTATGCCA ACGGTCGAAT 300

TTCATCATGT TTACATTTAA TTGCAAATGC CCTCTTGAAA TATTTTAAAA TTAATATTAT 360

TCTTAGCATA CTAGTCGGAA TTATATTC 388

(2) INFORMATION FOR SEQ ID NO: 965:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 965:

AAAGTGAGGT ATAGTCCGAC CATACTCTAA AAACGTAGCG AGATAAATAT ATTTCAATCC 60

TAACTTTTAT GTTTTGAGGC ACTTGCCATT TAGGATATTG TCGTTCGTAA TACGACACTT 120

GTTGTATAAA TACACCTAGT CCAAATGGCA GCATCATGAG TAAGATACTT CTTAAATAAC 180

TTAAACCAAT ATCATGCCAT ATGTGTCCAA TAATCAATTG AAAGACAATG ATAGATACTA 240

TTAAAACGAT TATATTTATT GTCACTTGTT CAAACGCACT CCTTTTCCAA ATAATAGAAT 300

TGCTGCTTGC ATGACAACCA TAAAACATAC AAACATAGCA GTTTTAAGCG TTAGACTTTC 360

TAGAATGTGa TTTAGAACAT GTAAGGGCTC ATTAAAGAAA TAAACGGaAT GTAAGCGTAA 420

GAAACGACCA ATATAAATTC CGAATCCATT TAAAAACATT AGcACGaCAA CrATTAATCT 480

ATTaAGCCAA CGGTGaGaAG TCAATGtTAG TATTTCAAAA TAGATTnAAA TCATCACATA 540

AACCGCTAAG AAGACACCAA GCAGTAAATA GGTAAAGTAT TTCCACTCAC TTAAATTTAG 600

TC 602

(2) INFORMATION FOR SEQ ID NO: 966:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 744 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 966:

GTCCTAAGGT AGATTTATCT ACAACTGTTG TTATTTTAnC AATTATTGGA GCGATTTTAT 60

TAATGTTTGC TAGCATATAT TTTATnAAAA TTGTGACATC ATACTTTACT AAGAAACTTT 120

TAGAAATTAA ATTTAATTCG AAATAGTATT TTCAATGAAG TGCTTCAAAG CTAAACTTTC 180

ATGACATTTT TTTGAAACTA GAGAAAATGG CTCATCAACT TCTAGCtGAA TGCCTTCTTG 240

AAAATGTATT AATGTTGAAT TCTCTATGGC AGTCATACCA ACAATATAAT GTGCATTGAT 300

ATAAATTTGT ATCGGTGCAC GTTTATGTTT TAACGGAAAA AGTATAGTTT TTGGGTTGAT 360

GTAAATAGGA ACCAGTTTAT TAATATTTAG TATGTTTTTT GCAGTCTCAA TTAGCACACT 420

TTGTGATGAT AAATGCAATT TCGCATAATA TGrAACGAGT TTGTTAATTG GAACTTTAAG 480

AATGTAATCG CAATGTAAAA AGACACAATT TGTTTCGAGA TGGTTTGAAG TAGCAGTTTG 540

GATATAAAGT AGATATTTAG TAGAATTGTC TTGCAAATAT AGTACTCCTC GTTTAATAAG 600

TTGTTAATTT AATGGTTAAA ATAAATTTAT ATGAAGATGT TAGGGTGTTT CAACATCATT 660

AACACATCGA CCGAAATTTC ACAATAAACT AATTAAAATT ATGTTGGCAT TTACGCTTAA 720

CGGACATCTT AATTAATTTA ATCG 744

(2) INFORMATION FOR SEQ ID NO: 967:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 967:

TACTTTGCAG GAGCATTAGG TATTCTAGCA TTTATAATGT CAATTGTATT GATTCACGAT 60

CCGAAAAAGT CTACGACAAG TGGTTTCCAA AAGTTAGAGC CACAATTGCT AACGAAAATT 120

AACTGGAAAG TGTTTATTAC ACCAGTTATT TTAACACTTG TATTATCGTT TGGTTTATCT 180

GCATTTGAAA CATTGTATTC ACTATACACA GCTGACAAGG TAAATTATTC ACCTAAAGAT 240

ATTTCGATTG CTATTACGGG TGGCGGTATA TTTGGGGCAC TTTTCCmAAT CTATTTCTTC 300

GATAAATTTA TGAAGTATTT CTCAGAGTTA ACaTTTATAG CyTGGkCaTT AwTATATTCA 360

GTTGTTGTCy TAAwAwTAwT AgTTTTtGCT AATGGACTAT TGGGTCAATA ATGGTTAATC 420

TTTTCCnAAn ATTGCnGGGG AAG 503

(2) INFORMATION FOR SEQ ID NO: 968:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 968:

TACAGGTAAA AAAGGTGGTC CGTTTATCGA TTCATTAAAC CATCGTAGTT ACACGAAAGC 60

ATATGTTTCA TCAGAAACCG ATATTCCATT TTATGCTGAA GCATTTGGAA TTAGAGAAGA 120

AAATGTTGTA CCAACAGGTG TACCACGTAC TGaTGTACTA TTTGATGAAG CTTATGCAAC 180

ACAAATTAAA CAAGAGATGG AAGATGAATT GCCAATTATA AAAGGTAAGA AAGTTATTCT 240

ATTCGCACCG ACATTTAGAG GTAATGGTCA CGGTACGGCA CATTATCCAT TTTTTAAAAT 300

TGATTTTGAA CGTTTAGCAA GATACTGCGA GAAGCATAAT GCAGTTGTGT TATTCmAAAT 360

GCATCCGTTC GTAAAAAATa GmCTTAATAT TcaCgTGaAC CATAGACCAT ACCTTAATCC 420

GATGTGGTCC AGATCCATCC GTGGAAAGTT AAACGGATAT TCCnC 465

(2) INFORMATION FOR SEQ ID NO: 969:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 969:

AATTCGGAAC AACGAGCTGG CAACAACATA AGATGACAGA GGCGAATGGT CAATCAATTC 60

AAGTTAACTT AAATAATGCG CAAnGCGATT TGGGATATTT AACTGCTGGT AATTACTATG 120

CAACAAGAGT GCCGGATTTA CCAGTAGCGT TGAAAGTTAT GAGGGTATTT ATCGGTATTC 180

GTAAAGATGA TACAACAACn ATTTACTCAC ACCTATACTC TAAAAGATTn CACACGTCAT 240

CACAACGGCG ACTTGAGCAA CATGGACAGT TCCTAATGAA CATAATCAAC GGTATTGTTC 300

(2) INFORMATION FOR SEQ ID NO: 970:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 970:

ATACGCGAGC GAACGGTGAA GCGACTTGCT GCTGCAAAAC GTCTGCGACC TTGAGCAACA 60

ACATGAATGG TCTTCGGTTT CCGTGTTTCG TAAAGTCTGG AAACGCGGAA GTCAGCGCCC 120

TGCACCATTA TGTTCCGGAT CTGCATCGCA GGnATGCTGC TGGATTATCA TCCGATTTTT 180

AAAACGTTAT TAGGCGTTGT CGTTGCAATT CAATTTACAG TACCTGCTTT GATTGGTGCA 240

TTGGTTGCCA TGAAATTTGA CCTATCGCCA TTAGCAATTG CTGTTGTGGC AAGTGCAGCA 300

TATGTAGGAA GCGGTGCAGC GCAGTTTAAA AATGGTGCTT GGATGATTAC GGGTATTGGT 360

GATTTAATnA ATACAATGAT TACAGCAGCG ATTGCAGTTG 400

(2) INFORMATION FOR SEQ ID NO: 971:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 971:

AAGTGTAAGA TTAGAATAAA AAATTTATAA ACGAATTGAG AAAGACCAAA GCTAGCAATT 60

ATTCAGAAAT TAAATCGAAG AGTCCTACAG TTAATGACTT ACCTGAACGA GATTTATCnA 120

ACAAATCTCA GTATGACCAA TATGGCAAAT GCCGTGTCCA TGTTAACTGA TGAAAAGTAC 180

TTTGGTGGTA GTTTTGAAAG ATTACAAGCA TTGACGACAA AAACAACATT ACCCGTATTA 240

TGCAAAGnCT T 251

(2) INFORMATION FOR SEQ ID NO: 972:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 972:

TGAAGCTCTT aATAAATCTT TTCTTGAACA CACACCAACA AAATCGTTAT CTTCATTAAT 60

AATAAATAAT GTACTTACAT CTTCTAAAAA AATTGTACAA ATAGCGTCAT AAACTGTTGT 120

ATTCTCTCTT AGCACAACAG GTTGAGACAT ATAGTCCTTA ACCTCAAATT GTCGAAGTTT 180

TTCTAAAAAA CCTGACATTG TTAATATCGC TAAATCTGGT CTAAGCGTTG CTCTTGTTAA 300

ATTCAACTTA TCTGCTATTT GTTCACCAGw AATGGGTCCT TTAGTTTTAA CAATTTCGAT 360

GATTCGTTCT TGTCTTTGAC TGAGTTCTrw AGGkCTTCAc CCCTTTtTAT GCnC 414

(2) INFORMATION FOR SEQ ID NO: 973:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 973:

GAAATCGATA CTAATATCTT CTTTATTTAC ACCTGCTAGT TCAGCTTCTA AGTAATATAA 60

TTCGTCTGTt CATAtATATt CGTtACAAaT GAAGGTGTtG AAAaGTAaTT AAaTaCTTGT 120

TTaCCTAAAT CTTTAAaTGT ATCACTTGGA TTACCGTTAA AAAAGTTTTG ATTCTCGAAT 180

TGATTGAAGT TCAtATCATC ACTTCCATTA TAGAAATTTG TATTACAAAG CCATTATATG 240

AGTAGTATTA AAAAAGTTAA AGTAAAAGGG GAGATAAAAA AGTAATAAAT GGGTAGATTT 300

GTGCCTGATA AGGAATCAGG GCAAAAGAAC TGAGCATCGA GATTTATACA AGCAATAAAG 360

ATAATGAATA AACATATCGA TGCATACTTC TGCCCATCAC CTTATGATAG GGAGTTATTT 420

TTTGTCGGAA TAGTCAAAAT TTTTAGAAAC AAAATTCCGC AAATTATTAA TTATATCTGA 480

TGCTTCTCGT TCTGAAATGT TGAATTCATT AAAGACcTTA ACAGAAATTT CAGCAAGAGG 540

GCTTTTTATT GCTTTACCTT GTTCTGTTAG AGAAATTTGT AGGTTTCTTT CATCTTTCTC 600

TTCACGTGTT CGAACAACGT AATCTTTCTT TTCTAATTTC TTTAGTAATG GkGTCAGTGT 660

TCCAGAATCT AAGAACACAC GTTCACCTAA TTTTTTGATG TTAAGTTTTT CATCATTTTC 720

AATCGCCAAT TAAACCAnGG TAnCnGG 747

(2) INFORMATION FOR SEQ ID NO: 974:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 974:

TGCTTCCAAG TAATGTGGAC ATTTAATACG AGCTGGGATT GAGATACACC TTGCAATGCT 60

TCTTGGnCAT TTGCATTGCT TCTCCCAAGT GAATGCCTTT AACAGCTTGT GTCATCATCG 180

ATGACTTGCC ATTGAAATCG ACAACCTTCA CCTTCAAACT TAGCATCTTT TATAATGCCG 240

nCTTCTATAT CAAATGT 257

(2) INFORMATION FOR SEQ ID NO: 975:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 975:

CAATGGAGCA TATTTTACGT TCGGCAATGG ACATTGATCA nACAACAAAA CATTATATAA 60

mTAATAAAGT AGAAGTTATC AAAGAAATTA TTAAAAAAGT AAGAGGGGGA AATCACGTGA 120

CATCACAAAA TCCAGAAGTT AATTACGAAG CATTAGCTAA ATATGGCCGC GACTTAGTAG 180

AAGAAGTTAG ACAAGGTAAA ATGGATCCTG TTATAGGAAG AGATGAAGAA ATTCGAAATA 240

CGATTCGTAT TTTAAGTCGT AAAACTAAAA ACAACCCTGT GCTCATTGGT GAACCAGGTG 300

TTGGTAAAAC TGCAATTGTT GAAGGATTAG CGCAACGTAT AGTTAAGAAA GATGTGCCAG 360

AATCATTATT AGATAAAACT GTTTTTGAGT TAGATTTAAG CGCATTAGTA GCGGGCGCTA 420

AATATCGTGG TGAATTTGAA GAGAGATTAA A 451

(2) INFORMATION FOR SEQ ID NO: 976:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 976:

AACTATTAAT AATATTAAGT TCACTACAGA TGTTGCTAAT GGACCATAAG TTTTAAAGAC 60

ATCTTCACTT TTATAACCAA CAATCGCATC TAAAAATTGA ACTAAGATCA TTGCAATGGA 120

TATAGTTATC AAAAATATAG CACTATGAAT GACTAAAGAA AnAATAGCTA ATAAaAATAA 180

AGGTAAGCTT CGACTAAGTG cATAATATGC ATTTATATTA TGGCTAGATG CACATGCTTG 240

AATTGAATAA CCTAAACTTA CACTGGCACT GATTATTGTA AATATTGCTA AAACAAAATA 300

CATGTTAATC CTTCTTTCTA TATTTGGATA TAAACAAGTA CTTGTCTAAA GTTATTTAAA 360

TATAACTATG TCATAAACTG AATTTGTTGA AATTTTTCAT TATGCAAATT TATTAATAAC 480

AAACAGCTCG AACTATAGCA TCATTTTACT AATGAATGCA TTAAAGTAAC TATGACTAAA 540

AATGCATATT AATTATCATT ATTAAGACTA T 571

(2) INFORMATION FOR SEQ ID NO: 977:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 977:

CCCGAAAAAA TTTAGACATT TTCAAACAGT AACATTTGAA GATTTGTCTA AGCTGGAAAA 60

GAGTAGTATG CCATCAGGGG TCGGTATATT AGGCTATGCT GTTGACAAAG GTGTTGCTTT 120

AAACAAGGGG CGCATTGGTG CAAAAGAAGG ACCAGATGCG ATTAAACAAG CATTTGCAGG 180

TTTGCCGGAT TTGAATCCAT GTGnACTTTA GTCnGATTAC CGGAATGTTT ATCCTGGTCA 240

TGGGGGAATT AATTGGATAC CCCAAAAAGG AATT 274

(2) INFORMATION FOR SEQ ID NO: 978:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 877 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 978:

nTnTTACTTC TTCTTTTAAT ATTTCTCGTA TAGCTTCAAA TTTTTCACTG TCAAACAGTG 60

TTCTTAATAT CCCTTGCTTT TCACGACTGT TTGATATTAA AAAGCGTTTG AATTCACCTT 120

GAGGCAAAAT AAACAATTGT CGGAATTGAT CTGCATTTAC TCCTAATAAT TCAATAATGA 180

ATTGGGTACC TGAAATTACT TTACTTTCTC TAATTTCATA CTTGCCATCC ACCATCTCAA 240

ATaCATCAAA TTTAGCGTTC GTTTTTGTTG TATTACCTTC TTTGATATAA GGGCCTTGTC 300

TATGCACTTT ATAAATTCGA TGATTTAATT GAAATTCAAA TGTTACTGAC ATCGGCTGTT 360

TACCATCAGC GAAATGACTT CTCAAATCAT TTTCTTCTCT TTGTTCAGTT GATGCTTTAC 420

CAAACAAGGC ATAAGTCATT GCATCAAAAA TCATTGTTTT ACCCGATCCA GTCTTACCAC 480

TTATTAAAAA CAATTCATTA TTATCAATTT TAGAAAAATC AATTTCTTCT TTTAAAAAGG 540

CGTTTTCTAA AATATTTTTT ATCTTTTTAG ATTGGATATC CgATAATTCT TTATCAGTTA 660

TATGTTTATA AAACATTTCg ATAATTGACA TGTCaTCTTT TTCACTTATT TCyATAGCAT 720

TATTTTCTTC ATnGTAATTA AAAGTTTCAT TCGTCAGCGC TAAAGTATTA GGATAAATTn 780

GTTTTAAACT CATCATTGGA TCAGTAATAT GAGACATATT TTTAAGTTTA AAATGTAAAA 840

TAATTATCGT TATnTTTCAC ATGAACTTnT TCATTAA 877

(2) INFORMATION FOR SEQ ID NO: 979:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 624 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 979:

ATTGGTACTA TACCATTTGT CCATTTTAGC GAAGACGTTA AACTATCGAT TAGCTAGTGA 60

AGAAATTAAT CTCACTATAC CTTCTATACA TAAGCAAATT AAAAATTTAG AACAGCATCT 120

CAATGTGAAA CTATTTGAAA CTTATAAAAA TCAAATTATC TTGACTGAAG ATGGTCATAC 180

ATTTCTTCCA ATTGCGCAAA GTTTTATTGA ACAATATGAA AGTGGCATCA AACATATCCA 240

ACTTAAAAAA ACGATGTTTC AATCGAAATT AAATGTTGTC GTGTCTTCAT ATATCGCGAC 300

ATTCATTATG CCCAAATTTT TAAAATCTTT CTTTAACGAG CATCCTTTTA TCGATGTTTC 360

TCTTCATGTC AAAAATGAAA ATATTGAAAA AGATATTAAT AATCATACGT ATGACATCGG 420

GATTAGCAGA AATCAACCTA AACTAAGAGA AGTTCATTCT GAAAAAGTAT GCGAAGGTAA 480

AATTGTATTG ATTGCTCCCA ATAAAGAGAA TAATCATCTT CTAACTGAGG CATCTTTATT 540

TGAAAAATAC AAAATAATAA GTGATAACCA TCCAGAATAT TGGGTCATCA CTTAAAAATA 600

ATATTTTAAA TATTTATGAA AAAG 624

(2) INFORMATION FOR SEQ ID NO: 980:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 457 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 980:

TTTGTCCTGT TGCATAAACT GCAGCTAGCA TAATGTTAAT TGTTGCACCT ACGCTAACCA 60

TkGATTCATC AATTTCAGCA CCTAAAGCTT TAAATCCTTT AATATGTTGA TCAATTGGAC 180

GTGGCCCAAG TGGACATCCT CCCGGTAAAC CAATCACACA TTTTTTAAAT CTACCTAACA 240

TGGCACCCAT CATATAGTAT GAAGCACGTA ATGATTCAAC TTTATTATTT GGtAATGCAG 300

CATTTTGtAT TTCAGTTGTA TCAACTTCTA AwTCCGTACC ATTTaGTGaw GcCTTAAtAt 360

TTAAAtCtkC tAAtAAACTC aCTAAAGTTT TAACATCAGA GATTTnGCGG TAACCCTTCT 420

AATTTCACAT GTCCTTGAGC TAATAATGTT GCAGGAA 457

(2) INFORMATION FOR SEQ ID NO: 981:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 997 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 981:

ATTGCAGCAA CGCCCCCTGT AAAACTACGT ACTCTTACAT TTATGAAACC TGCTTCTTCA 60

AACATGCGCT TCAACTCTTC TTTTCCAGGA AAATTAAACG TAGATTGCTG TAACCATTCA 120

TATTCTTCTT TTGATTTTGC AAATAATTTT CCAAAAATAG GCATAACAAA TTTAAAGTAT 180

AGTGCATACA TTTGTTTAAA GACTGGCAAA GTTGGTTGGC TCGTTTCAAG ACATACCACC 240

ATACCACCTG GTTTAAGTAC TCTATTCATT TyTTTTAaCG CGACTAAATA GTCTGGCACA 300

TTTCTTAATC CAAACCCAAT TGTTACATAA TCAAAAGAAT TGTCTTCAAA CGGCAATTCC 360

ATTGCATCAC CATGAACAAG TTTAACATTT TCCATTGAAG CAGTTTTTTC TTTTCCTACT 420

TCTAACATAT TCTCACTAAA GTCAATACCA GTAACTTCAC CTGTTGGTCC TACAGCTTTG 480

CTTAATGCGA TTGTCCAATC ACCAGTACCA CAACAAACAT CTAATGCTTT CGTCCCTTTT 540

CTAACACCCA TGTCTTTCAT GACGCGTTTT CTCCATACTT TATGCTGCTC AAAACTAATA 600

ATATTATTTA ATCTATCATA TTTTTTTGAA ATATTTTGAA AAACGCGATG TACTTGCTCT 660

TTATTTGCTT TATTGTCAGC CATGCTTAAT TACCTCTACT TTTTAAATAA CTTTTTTGGA 720

TATCGTGTAA GTAATGCTTT ACTTCACTTT GATTATATTT CTTGAAGTAT GATGGATAGT 780

AATCAGACAT ATCTTCAAAT AAATAATTAT ATATTTCCGA CTCATCAATA TTGATACCGA 840

AATGAGATAA CGTAAtATAT GGgAAAAGTG tTTCAATTTT TACTATTGCT TGAGAAATTT 900

CATAATCATT TAAAGCTTGA TGATGTAATG AAGATTTCAA TTCATTAATT TCAACAATTG 960

CTTTACTAAT TTCATTTTGA AATGATAAAT CATTGAT 997

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 982:

CATTCCCTTT ATCGGnACAA TTATTTTAAA TAATTGGTTA ATAAGTTTTT CTATTAATTG 60

CTGTTTTACT TTCTAGAGCA ACAATAAATG TTTTCAGTTT AAAATAATTA AGATTGTCAT 120

TTACTAATTT GCTTTTTCCA TTCTTTAACC ATAAATCAAC TTGTAATTGC CACTCAATAG 180

GATGATTTTT AATATAAATT TGCTCTGGAA AAATATAACC ATAATTGTGC ACTACTTCTT 240

GATCAGTTAA CTGTAATTGA TACATTGCAC TTAAAGTGGG TTCTAAAACA GAATTTTGCC 300

AGCGACAATA TTTGATATAT TGATTAATTG CGAACTTTGA TAATTTATAA ACAGCATGAT 360

AATCACAAGG CGCCTCATTA AACAACTCAC TAATTTTGGC ATTTCTTTTT TCAGCGACAT 420

ATTTGTGCCC GCCTAAATAT TGTATTTGTT GAAACATCAT TATTTGTTTT TTCTCTAAAT 480

TGAACGTATG AAGTTTTCGA GTGAATGGAT TAATAAACAT ACTTTGAAAA TGATTGAACT 540

TCACTTTATT ATGACAATAA TCAACATCAT TTAmTAACCA ACTTACTTTA TATCCCATTT 600

TCTTkAAACC TTCCGTTCGT TGAAGAATCT GTTTATAAGG AATTGGCGAA TACTGTAGCT 660

CAATAACATA TTTATTATTA ATCAAAATAT CCGGAATTTG TTTTATTTCT TTTAAAAATG 720

GCTCTATCTC TACTTTACAT CCTTGTTGCT GTATCATCTG TGCTAAAATC AATTTACTTT 780

TATAATGTTT AATCGTTTCA TTATTAAAAC ATTTTTGTTC CGCTAAATGT TTATGTGCAA 840

AATGACTAAT TACTTTGAGC CCACGCTTTA AAATAACTTG CTTGCCACAC ACCGGACAAA 900

AATATTGTGT CTTTCTCAAT GCAGTAGTTG CTAATACGCG TTCCTTTTCT TCATTTAAAG 960

CTACTAACAT ATCTTCACCT CAAAATATTA CACGTAAGTT TAACTACTAT TACTTTTTCA 1020

GCTTTGGAAA TCCATTAAAA AAAAGGGACC CCCAAAGGAG GCCTCCTTTC ATAnGTGCGG 1080

TGGCCTAATT AAATAATCCG TTAATTCCAG GTGGnCnC 1118

(2) INFORMATION FOR SEQ ID NO: 983:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CATCCCCTGT TAAAAATTGn TATTTGTGTA TTGATGCTTC TCAGnCATTA TTACGAGTCC 60

ATATTCATTG CTTCAGTGAA ATATCAGTAG CAATAACATT TAAATCCGGC TTTTCACATT 120

TCAAGGTAAT TGCAGTACAC CACTACCCGT TTCCGATATC TACGGATTGT TGCATCATCT 180

TCTAACTGTT GGTAAGAAAT GCAACCATTA CTGCTTCAGT TTCAGGTCTG GTATCAAACA 240

ATTTGAGTTT ACATCAAACG GTCTACCTT 269

(2) INFORMATION FOR SEQ ID NO: 984:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 984:

AACCCAAGTG GAAnnGGTTT TGGTGGAAAA ATTTTAGGTC CTTTATCTGT CGTGCGAATC 60

ATTGTATTTT TTAAACTTTC CGCATAATCT TGATGGTCGA TTAACTTTTC GCGATAACAA 120

TATTCAATCA CTTCAGAAAT CGCTTGCTCT GATATCTCTT CTTTTTGTAA ATATTGTATA 180

ACTTCTTTTT CAGTTCTCTT TTTATATGAT AAATATTGGA TTGCTTTATT TAAACCTATG 240

CGATAATGAT CATACTTTTG AATCTCTGCC ATGTCAGCAG CnTCAAGTTG TnGCCCTT 298

(2) INFORMATION FOR SEQ ID NO: 985:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 985:

CCATGCGATT CCACCTATTA ATAGTAAGAC AATAATAATA GGAATTATAA TTTTTAACTT 60

TTTAGACATT TTGCTTCCTC CCAATTATTT ATGAGTTAAT CATATCAGAA CAATACATTT 120

TATTAAATGG TTTATTTTAA ATTTTGTTTA AATTAATAGA ATTTTAGTTA TAATAATGTT 180

TAATAAGTTA TTGGrAATCy AATAAACTAC mAAAAATAGT TTGATTACaT AATGATTCtT 240

GAAAAATGkT GGkTAACyTA ATAATATGCA TTTTTTkGGC GArGArGATT tATTtAACyT 300

ATAAAAATAT kGAaGTAAGA TtGGGGAGAT tATGAATTtA TGGrATtGAA AGTCGATGAT 360

TTTGTAAAGA ATATAAAAAG ACCATACTTG ACTGTATTGG GAGTATTTGT AGTTGCAGTT 420

(2) INFORMATION FOR SEQ ID NO: 986:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 986:

AAGGTTAGGn TGGAGTACCC AAAGTAGGTT TTAAAGGTTG GAAATACnAG GAGGATGAAT 60

AACATGAATC AGTCAGTCAA ATTACTTAAA CATTTAACAG ATGTAAACGG CATTGCTGGT 120

TATGAAATGC AAGTTAAAGA AGCAATGCGT AACTATATAG AGCCTGTCAG TGATCAAATT 180

ATTGAAGATA ACTTGGTGGC ATTTTTGGAA AGAAAAATGC TGAGAATGGT CAATACTCAT 240

TATGATTTCT GGTCTATGGA TGAAGTGGTT ATGGTAACAA GATGTAAACT GTTATTCATT 300

ACGCGTGGTG TGTGATCAGC nGCACTCAA 329

(2) INFORMATION FOR SEQ ID NO: 987:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 545 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 987:

CATATTATTT nTATATGAGT TTACCAGTGT CAAAAAAACA ATTGCTTAAT GCCAACTATA 60

TTACATGCAT TGTTTTAACA TTAATTGGAA CGCTTGTTAT TAGTTTATAT GCTTATGAAG 120

CAGATGTGAT TGAACCAAAT TCAATCTATT TTTCAACTGC ATATGCATTT GTCATATCTA 180

ACTTCTTGTC TATACCAATT GCATTTAGTC AATTTACAGA ATTGCGTAGA GTCAAAGTGC 240

CATATGGTAT ATACGTGTTT ACTATTATCA TTTTAGTTCC ATTTTTATTT TCAATTGCAA 300

TAGTATTGGT GAATTATTTT GTTCTAAGTC AATCATCATT CCCAGATTTA TATTCATATA 360

TTTTAAATAT TGGTTTTCTA ATTATAAGCA TTGTTATACT TATTGTTAAT TATTTTAAAC 420

AGCTCAATAA AATAAATACT AGAAAATTTA AAGGAGGCAG TCGATGAAAT TAGAACATAT 480

TACAAAAAAA TACGGCTCAA ATGTCGTTTT AAATGATATT GATTTTGACT TTGGCGAnAG 540

TAGAA 545

(2) INFORMATION FOR SEQ ID NO: 988:

(A) LENGTH: 607 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 988:

ACCTAGCATG ACATAATCAA ATATATCAAA AACACCTTTC TGAACTGATT CAACCGTTCC 60

AATAGTTAAT GGTCTTTCAG AATCAGATGT CTTTCCACCT TGAACAGTCA GATGACTAAT 120

TAAAATATTG ACGGCATCTT CATCAATTTC CGGTGCTATT GTTTCAATAC AGCGCGTAAT 180

TCCCTGTTGA TGTGTTTCAA TGGTGTCATC TTCAAAGTAG TGTTTCATTT CGCTCACAGT 240

AGCATAAGGG AGTGTATAAA AATTAACCCC ATTTATCTCT ATTGGTGAAT TAATCGATGT 300

AAAATCTGTT CTTATAAATA ACTGATTATG TTCAAACCAA CTCGCCCCAT AGTTTAACCT 360

CTCTTTACCA TCGTGATTTC CACTAATAAT AATTATTGGT ATACGCAGTT CTAAATTTAA 420

CTTTCCAATC GCTTGTTCTA ATAACATGAT TGCATCTTTA CTTGGATATG TTGTGTCATA 480

TAAAcTCCAG CTATCACAAT GrTATCAGGT TCTTCTTCTT TCATTTTTTC TACGAACATA 540

TCTAAAATAT ACGCTTGaTC TTCTAAAAGC TGTTTGCCAT CTAATATTTT CCCTAAGTGC 600

CAGTCTG 607

(2) INFORMATION FOR SEQ ID NO: 989:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 722 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 989:

ATCGCGTTAA GCAACAATTA CAACAATCAT CATATAAGCT AACGCCACAA CGCGAACTAC 60

TGTTAGAGTT CTAATTGAAA ATGAAAAAGA TCATCTAAGT GCTGAAGACG TATATCTGAA 120

AGTAAAAGAT AAAGCGCCTG AAATTGGCTT GGCGACAGTA TACAGAACGT TAGAGTTGTT 180

AGCTGAACTA AAAGTTGTCG ACAAAATTAA CTTTGGTGAT GGCGTCGCTC GTTTTGATTT 240

AAGAAAAGAA GGCGCAAAAC ATTTCCACCA TCATTTAGTA TGTATGGAAT GTGGTCGTGT 300

AGATGAAATC GATGAAGATT TGTTACCAGA AGTTGAAAAT CGAGTTGAAA ATGAGTTCAA 360

TTTTAAAATT TTAGATcATC GTTTAACTTT CCATGGTGTG TGTGAAACGT GCCAAGCTAA 420

AGGTAAAGGA TAGTAAATTG CGTAGGTTAA ATTAACCTTC GCTTTTTTTA GAGGTGTGGT 480

TAACACAATT GGTGCTTATA GACGTGATTT GAAAAAGTAT CAAGATTATA TGACTGAACA 600

TCATATCTCG CATATTGATT TTATAGATCG ACAATTAATT CAAGAGTGTn TGGGGCATTT 660

AATAGACCAA GGGCAATCTG CTAAATCTAT TGCGCGATTT ATTTCAACAA TCCGTAGTTT 720

TC 722

(2) INFORMATION FOR SEQ ID NO: 990:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 990:

ATCCAAAAAA TACGAAAGCG CTTTCTATAT TGGTATGCAA GTATTTCAAA AAGAATAAAT 60

TTAATTTTCC TACTTTTCTA AACATTTATC TTTATGTATA ATGTTTTCAA GTAACTAAAT 120

TATAAATTAA ATAAAGGGAG TGTTTATCAT GCTTACAATG GGGACAGCAT TAAGTCAACA 180

AGTAGATGCC AATTGGCAAA CTTATATTAT GATTGCCGTC TACTTCTTGG GTnATGACTC 240

CAACTTATTG ATAGTGTTnT TATGTTTCAG ATAATGCCCG ATGACTTTGT CATGCCAGCT 300

CCACCGATTT TGAGnAACGA CAGCGACTTC CGTCCCCAGC CGTGCCAGGT GCTGCCTCCA 360

GTATTC 366

(2) INFORMATION FOR SEQ ID NO: 991:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 991:

TGACTACAGT AACATTACCT GTAAATAATG ATTGAATGGC TTCATTTTCA TCATGAATAC 60

CTGTAATAAA TTCTAATTCT TCATCTGAAA CTTTTACAAT ATGCGCCAAT GGCAAAAAGG 120

TATGAATAGT TTGTCTTAAA TCTTCAGCGT TATCCCATAA TGGCAATCTT ACATTAGGAT 180

CAAATACGAC AGTACCATTT GCATTTAATG TTTTGGTAAT CAATTGATAA TGTGCATCTC 240

TCATCGGACT ATCGACCAAA TCAACAGAAC AAAAATGTAC TACATCATTT TCATTCACAT 300

CaATATCATT CACAAAACTk GGkTCaAaTA aCATATCn 338

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 992:

AGTTCATCGT ATTCTTAATA CCTATATGCT ATCGTTCACA AACTTTTGTT CTTTTCTTCC 60

AACATACCGC CTATAATGCT CAAAAAGAAA TCAGCAGTGG AACCACTACG TTCCCTACCG 120

CTTTATCATT TTCAGGCTTA AATATTTTTA AAATTTTGTG AGGAATCCGC TTAAAAAAAC 180

TCATATCTTC AAAAAAAATG ACAAAATTTA AATTTTTGAA TAACATCATT TTTTAGTAAA 240

TGTTATAATT TCTTTATAAT ACAAATATCG AAAGAAGGCG ACTGACTTTG AAAAAATTAT 300

GTTCATTAAT TGTAGGTAGC ATTAGTTTGT ATCCTTGCCA TTATCAGCTT GTGGnAAAGA 360

ACnAACCnAA A 371

(2) INFORMATION FOR SEQ ID NO: 993:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 530 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 993:

ATAATGATTT ATCAATCGAT GTTAGATGCG GTTCAATTAT ATCCTAAGTC TATCGTGGTT 60

GATTATACTG TGGATGGACA ATACaAAAAT GATTGTCACT ATTTCGGTCA ATCATCGATC 120

AACATTGCCG ATTGGGCTCA AAACAATAAT TATTATCCTA ACCTGATATA TGCGATTCAA 180

CAGACTCTTG ATTTAATACA TTATTACTCT GTAGAAACGA TTTTCGATTT AGCTTTATTG 240

ACACTTCTGA AAGGTGATTT ATCAATCGAT GGTCATGTCG TTTTTGATTT TAAAGCCCCT 300

ATAGCAACAA GTGCTTCAAT ATGGGAAACT ATTAAAACTA TTGAAGATTT TGATATGATG 360

TCcAGTTTTt TTGAtAAAtG GCTTATATtG ATCATCATCC TATACCTTTT CGCAACCTTT 420

TTATCGAGGA TTCAGAACAA CTTAATTCGC CAGATAATTG GTTGTATTCT ACCAAGTTTA 480

TGCTACCTAA ATGGGnTATA TAAAATAAGC AAAGCAACGT GCTGATAACA 530

(2) INFORMATION FOR SEQ ID NO: 994:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 551 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 994:

TATTGGATTn TTnCCACCAA AGGCAACGGT TCCTTTTCTA ATTCTAATAA TCAAATCCCC 60
ATTAATATCA ATCCCACTCA AATTCTTTCA CATCATTGAG TATAAAATAA TATGGTGATA 120
TACGTTGAAG TTGATTnTCT TATTTAAGTA TACTCCAACA GTATTTTATA AAATTATTTA 180
GTCATCATCT TCAGTGTTTA ATTCAAAAAT ATAGAATCTA CTGTATTGCA TAATAAATTG 240
AAATGCCACA AATTGTGTAC AAGCAATAAT AATGATACTT ACCATTATGA CAAACTTGGA 300
TTCTACGACA TTGGGCACCA ATATATATTC GATAATTCTT TCAATATATA TAAATGCGCT 360
CAACGCGGTT AATAATAAAC CGAAATGTGT TTTaGTTTTA CCACCCCAAC GTTTTGTyAC 420
TTTAGGTAAT TTTAATAACG TGAACATTCC GCCAATTACT AATAACAAAT AACTAATTAT 480
GATTGAAATC GTACCCATCA ACCAATAATT GAATAGGTCA TAATGATTTT GTACAGCAAC 540
AAAATAATAA A 551

(2) INFORMATION FOR SEQ ID NO: 995:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 995:

ATTCGCCACC ATTAGGTAGT GGAACACGAA CTTCATCATC TAAACCTTTA CCAATTAACG 60
CTTTAGCCAT TGGTGATTCA TTTGAAATCT TACCATTAAA TGCATCTGAT TCAGCTGAAC 120
CAACGATTTG ATAACTTTCC TCTTCATCAC CTGGTAATTC TACAAACGTT ACTGTTTTAC 180
CAATTTTAAC AACGTTGTTA TCTCCAGTAT CTTCAATGAT TAATGCATTT CTTAACATAT 240
GCTCAATTCT TTGAATATCT TGTTCGATGA ATCCTTGTTC ATCTTTTGCT GCATCATACT 300
CAGAGTTCTC TGATAAGTCA CCAAATGAAC GTGCAACTTT AATTTTCTCT ACAACTTCAG 360
GACGCTTAAC TGTTTTTAAT TCTTCAAGTT CACGCTCTAA TTTTTCAAAA CCTTCTTGAG 420
TCATTGGATA TTGCTTTTGA TTTTCCATAT TGTCATCTTC CTTTACTGAA TTATACTATT 480
GCTTGCTAAC TAAAGACTGA ATTTTTGTTG TCATAATATC TATTGCAACT TTATTGCTCC 540
CACCTTCAGG AATAATTATA TCAGCATATT TCTTAGTCGG TTCAATAAAT TGGTCATGCA 600

TTAGTATCTC GTGTTGAAAC GGCGTAATAT nCTCAAGTCT GGCATCTGTA TCAACATATA 720

TnTTnAACA 729

(2) INFORMATION FOR SEQ ID NO: 996:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 996:

GACAAATATA CTGCTTCTAC TCAAATATTA GTGAACATGA AAAAGTCCTC AAGTGATTTA 60

GCTTTCCCAA AATGTTCAAA GTAGTTTGCA GTCTGTTAAT ACATATACGG AnATTATCAA 120

AAGTCCTAGA TTCTAGATAA AGTATCTAGA GAATTGATGG TCAGTATTCA ACAGCTGAGT 180

GAAATCATTT TAAAAGTAAC CATCCAACCA ACTCTCAAAT TATTACTGTA CAGTTACACT 240

GGGATAATCT GATCTGACAA ATGTATAAAT ACTAAGTTTT GCCAGCAGCT AAATAGAGGT 300

GTATGTACGA CTTCCAnCTG TAGnG 325

(2) INFORMATION FOR SEQ ID NO: 997:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 997:

CTTCAGTTGT CGGCAAATCT TCTATATTGG AAATACCAmA TACATTTAAA AATAAATCAG 60

TAGTAATTAA CTGTTGGCTA CGCTGTTCAT TAACCACTTT AGCCTCAACT AGTCCTTTGG 120

CAATCAATGT CTTAACTGCA CCATCTGAAT TGAtACTACG AATTAATTCA ATATCACTTC 180

TTGATAATGG CTGGTTATAA GCAATAATTG gATAGTACTT CCATTGCTGC TTGTGAtAAT 240

TTCATTTGTG aCTTTTGTTC AATTGAATTG T 271

(2) INFORMATION FOR SEQ ID NO: 998:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 498 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 998:

TTTATGTGCT AATTTGTAAT TGAGATTCAT AATGGTATTT AAATCATTAT GGTGCGGGAG 60

TTATGGTATT GCCATAATAT GAGAGTGCAT CCACTTCTAT AAGTAATGCA TATTGCGAGT 120

GCAGGaATGA ATGAGTGCTT GATTAAAATC CTTATGGGTG GTTGACATAA TTAAAAGAAA 180

CCACATTTAA AATTTCTTAA TCACAAGCGG TTAACTAGGT ATAGTTTAGT TTTGAGTAAA 240

TCTTTTTAAA GGTGTACTTG TGCATTTTAC TTAATTAAAG ACATAAGACA TTTAATCGGC 300

CTAAAATAAA TAAAAAACTA CCTGTTTAGG TAGTTTTTTT AATGTAATAG ATTAAAACAC 360

TAGTTCATTT CTTATTAAAG ATGGATAGTT ATTTTATAGA TAAATTTGTC CTTTAGTGTA 420

GCGGTAATTT TTAGGACTTT TTGGTGGnAA AAATGTTCTT AATAAAAGTA ATAGTCCTAC 480

TTTACCGCCA AAGCCATA 498

(2) INFORMATION FOR SEQ ID NO: 999:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 568 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 999:

TGAGCTGGTT GTTTATTATC ATCAGTTTTC TTCTGATTAT CATCTGATTT ATCTTGAGAT 60

GCTTTGTCAT CCTTATCTTT CGACTCATCC TTTGATGCTT TATCATCATT CTCTTCTTTA 120

GCAGGACGTT GCTTTGTAGG TGCTTGTTGC TGAGGTGGCA CATATTGATA TTGATTCTGC 180

TGTGGCAATT GCTGATATTG GTTTGCTTGT GAATCTAGCT CATTCTGCTC TTTTTCCTCT 240

TGTTGCTTTT TCTTTCTCTC TTTTTCTGCA TTTTCTTTTT GACGCTTTTC TTTTTGTTCC 300

TGCTTTTGTT CGTTCAACAT ACGTTCTTTA GCTTTATTCG AATGATCTAC ATATGCAAAA 360

ATTGCAAATA CTAATCCTCC GAGTAATAGC AATACCGTCG CAATGCTAAC TACTTTCGCT 420

GTTGTACTCA TTTTCTTCTT ACTTCCATCT TCATTTTTAT TGTAGTCGTA ATTTTGATTC 480

GACATACTCT CCCTCACTTC AAACTAATTT AAATATAGAA ATTATCACGC AAcCATTAAC 540

ATTTTCACAA CTAATTTGCG ACCnAGTA 568

(2) INFORMATION FOR SEQ ID NO: 1000:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1000:

AGTGTTTCTA ATTGCAAAAT TCCAAATACA GTGTCGTTAT TTACTTTTTT CATGCTAAAC 60

ATCTCCCAAT TAATAATCAC ATATTTAGCT ACTATACAAG TATTAACAAA CATCCCAACA 120

ATCCCAAAAC TTGTATGTGC TAACTTATGC ATAAAACTAC AAGTGTAAAT AAACTTGCTT 180

TCTATTCAAT TGTCAAAGTT GAATAAAATT AAATAAGTAT AAAAACCAAT AATCAATAGA 240

GTTAATATTT AGAAATAAGA TAATAGTACA TAAAACAAAT CACTCTATTA CATATTAATT 300

TTATAATTTA TATACAAAGA AAATATATCA ATATTACCAT TAAATTGCAA CAATTCTACA 360

TATATTTCTT CAAAAAAGAT ACGCATTGAA TTTTTATTAC ATATAACTCT CATGAAAATT 420

GATTAAACTA AATTAATTAG TTAGCCTTAA ATTTAACAAA TTAAATCAAA CCGAATGAGG 480

CTAAATTGGT TATTTTTCAA GATATGaTTT GTATAAATCA AAACATTTCT TACAAATCAA 540

ATGTGTATAA AATGTGATAT ACATTTTCAA CCTTAAAAAA GTTCTAAAAA AAGATGAGCA 600

TCTACTGTCT CATCTTTCAG TTCTTTTTTA CGGGTCTGTT TTCTAATTTG AGCACAATCT 660

TCGATTTCTT TATCTAAATG ACTACCAATT AAATCTATTT CTTCTATTGT TAAATCGCTA 720

TCTCCATCTT CTTTTATCTC TGGTATTATT TTTTCTTCAA CTAAGTCACG ATATAGTGTT 780

TTTGAATTCT CGTTCAATTT CGATTCGTGA TTTTGAATAC TTTCTTCCGC ACCAATGTAT 840

ATCTATTGGC ACTAGCTTCT ACTTTTGTAC CATCAATAAA AATTGAATTA TCATCAATAA 900

GATTTTGCTT TAAACATTGA CTATAGAACT GAATAAATAA AGATTCAATT AACGCATCAG 960

TATTAGGATT CACTCTAAAA CGATTAATAG TTTTATAAGA AAGTGTTTGA TCTTGGGCTA 1020

ACCACATCAT TCGAATACTG TCATGAAGTA ATTTCTCTAT TCTACGACCA GAAAATACAG 1080

ATTGAGTATA TGCATATAAG ATGATTTTTA ACATCATTTT TGGaTGATAG GATGTTGCAC 1140

CACGATGATG TCTGAATTCA TCGAATTCGC TATCAGGTAT CGTTTCAACA ATTTCATTAA 1200

CATATCGCGA AATATCATTT TGAGGAATTC TAACGAAGTT TCTATTGGTA GTGTAAGTTG 1260

GGGTCATGTT ATAATTTTTA TACATAAGGC ACCTCTTTAA TTTAGTTTAG TAGTATTTAT 1320

TAAATTATAC GaAGGGACCC AACACAGAAA ATTCATTTTA TTGAATTTTA CATTTATGTG 1380

CAAGTTGGGG AAAAATGTCT TATTTTTTCA AAGTATTTAA AAGTAAAATT ACATGTTAAT 1440

A 1441

(2) INFORMATION FOR SEQ ID NO: 1001:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 587 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1001:

TAATAATATC TGTCATATTA AGTCTCCCTC ATTAGAACTC ATTATAAATG AAGTTATTGT 60

GTGTGTCGCC ACTGCCATAA ATTAAATATA AAGTAATAAA TATTGCCAAA TACAATAGTG 120

TTAATAAATA TGGTTTGAAT GCTTCAACAT ATTTATTAGG TGGCTGTTTA CTTTTAGATT 180

TCATATTGCA CCTCTTAAAG TTCTTAGTAA AAACGCCTTT ATAAAGACCG TTCAATATAA 240

AATACGTTTT AAAATTTGTT TTTTACAATT CATTATATCG ATATTCATAA TGAAATTCAA 300

TTTTAATTTT ATAGATTCAA CATAGTAATT GGTTGTCATC ACTCAAkTAT TGTAAATGAT 360

ACACTTTGTT GAGrACATCA TTCATTTTAA AGGTTATTTA AACAATAAAC AATTACAGTC 420

TATATAACAA TTTTGTTATA TACGTCAAAA TCAAATAAAC TCATCACATT AATATGACGA 480

GTTTATAATG TTATTGAATT ATCATCAGCG CAAATATATA CATTCGCAAG TCAAGCATAA 540

CATATTTAAC AATTGCTTTG CTTGGTTTTA CCAATGGATT AAAAACC 587

(2) INFORMATION FOR SEQ ID NO: 1002:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1002:

CAATTGTGTC ATAATTTTGC TGATGATAAC TAATCGTTTT GGAGTAGCTA TTTGATGAAG 60

TTCGTCCAAT ACCTTTTGTT GAATCGAATT TACCACCTGA GCGTATATGA AAATGTACTG 120

TCTACTTTTG CAGTTGAAAT TTTATTTTTC GGCAATTGGT CTAATATTTC AGTTTTACGA 180

TTTCTTTTTA CTTGAAAATC TACATGGTAC TCACTTGGAT ACTTTAACCA ATTTGAATTT 240

TTTTCTTCTT TATGAGATTC AAACTTTAAA TTTGAATGAA TTGAGCCTTG TTTTTTAACA 300

AGTAATACAT TCTTGTCATA AGTTGGATCA TCGATAAAGT CGAATTGTAA ATTTTGGAGT 360

ATATTtGTwT TCTCATCATA TACTGTTTCA GTTCGTTTTG TGATTTTACC GTTTTTCCCA 420

ATATCATCCG GTGCTGTTGA ATTTTTATCT TTATTAGTAA CATTACGTTG CTTTTGTGAn 480

CTTATCAACA TGTCTTCTAT TTGGCTGAnG CTTATGGnGA TT 522

(2) INFORMATION FOR SEQ ID NO: 1003:

(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1003:

TCTTTGTTTG AGACATAATG TCATGTAAAG TTTTCACAAT GCGTTCTTCA ACTTGTTGCC 60

TTGCCTCTCC TTTGAAAGGA ACAATTCGAT CTCCGAATAA GTCCTCAGGC TTGTATAGAT 120

TATCAAATAG ATAGACTGAC TCACCTTCAA ATATTCCAAA ATGCCATTCC TTCAGTCCCT 180

TAAAACGTTG ATACGATTGG wTAGGTGCAA CATTTTCAAG TGTGTCACTT GCGCGTTCTT 240

GCGTTGATGA TGCATATAAA TCGAAGTTTA TCCCCTTAGT TTCATAATAA CTACGTGCCT 300

TTnGAGCTTG AGCAATTCCA AGT 323

(2) INFORMATION FOR SEQ ID NO: 1004:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1004:

TTCTAACTTG ACGTGACTGG GCATTTCTGT GnAAATnTTC TGACATTCTT TTTAATATCC 60

GCAACGCAAT TGCTTCAGTT AAAGATTGnA ACTTGCAACA TTATTTGGTA CGAAAAAGTC 120

AGTTTTAATG TCGATATAAG ATTTATTTTT TTTGTTATAT AGTTTCGCAA CTACATTTGG 180

TTGTCTTACT TGATCATATT TTGCAACCGT ATCGAATGCC GTCTTTTCAA ACAGCTTTAC 240

GAGATACGTA AACCATGACC CATCCATCGA AGTCCTTGGT AAAAACCCAG GGTTTCCGAA 300

GCCGTAGGGT TTGAAAGATA 320

(2) INFORMATION FOR SEQ ID NO: 1005:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1005:

nATTAATGCT AGCCAAAACA GAnTTGCAAn ATGTAAAGAC ATGTGAAACC CTCCTTATAT 60

CGATATTTAT AAAAAATAAT ATTTCACTTA ACCAGTTTTT AGTTATCATT GCAATGGTAA 180

AGGATACGAT GAGTATCACA CCACAAATGA TAATACCAGG CAGGAGCCAA CATAAATCAT 240

CTAAATCTTT ATTATATGTG ATTAAAATAT TAAAGATAAC AAAAGTGGTA GTAATAACTA 300

TATTG 305

(2) INFORMATION FOR SEQ ID NO: 1006:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1006:

TTCAAGATAT CAGTATAAAT AAAAACTTAA TATGCTCATT ATAGACAGCT ATAACTATAT 60

TTTCTCGTCC CACTCTATAG AAATCAATTT CATTTATTAC CATTTTCTCT ATTTAAAAAC 120

ATATTTTTGG TATTAACAAT TAAAAGTGGG TATATATATT TAATGAACCA ATTTTTTAGG 180

AAAGTAGGGC TAAACCTATG GAAAATAAAT TATACCACAT GGTGTCCTCT TTTACCATGA 240

ACACAGTGAA TTAAAAAATA TTAAnCAAGG TATTGGGGAA GTAnCACCAG CATTAGGTCC 300

AATTGGTAGC CACCTTCCAA TCCATTGGGG GnAA 334

(2) INFORMATION FOR SEQ ID NO: 1007:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 565 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1007:

AGAAAATTTG TTATATTAGA AGCGAATAAT TTTAAAACAT ATTATGAAAT GTAAGAAGAA 60

ATATTATGAA ACTAGGAAAA GTAGATTGTT GAAAATTCCA TACAATAGGn GAnGTAAAGT 120

GAATAAATTC TGGTATTACT AAAGCTATTG ATTGTCCTAA TTGTAATAAA AAGTTGGATA 180

GTGTAGTTGA GGGGAGAAAA ACTAAAATGC AAAAATATAT TCTCAATGGA TCATTATAAA 240

TACCAATTAG aTTAAAGTAT TGCGaACATT TACAATTAGa AATCAGTATT AATCTGCCAT 300

AGATAATTGT ATTAATGTAA AAmATAAAAT AGAATGAGAA TATACGGAAA TTTTTTATAC 360

ATTTATAACC AATTCTGTTA AACTGTGAAG AGTAGAGTTA AAAACGAACT TTTTGTTTAT 420

AATGATTGAA CGCTATTCTA GAGAAGAAAT GTCTAATATT TGGACTGATC AAAATCGCTA 540

TGAAGCCATG GTTAGAAGTG GAAAT 565

(2) INFORMATION FOR SEQ ID NO: 1008:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1008:

CAACATTAGC GTCTAAACAA ATCTTTGACT AAACGTTCAC TTGAGCGACC ATCTTGATAT 60

TTAAAATGTT TATCTAAGAA TGGCACAACT TTTTCAACCT CATAATCTTC ATTGTCCAAA 120

GCATCCATTA ATGCATCAAA GGACTGTACA ATTTTACCTG GAACAAATGA TTCAAATGGT 180

TCATAGAAAT CACGCGTCGT AATGTAATCT TCTAAGTCAA ATGCATAGAA AATCATCGGC 240

TTTTTAAATA CTGCATATTC ATATATTAAA GATGAATAAT CACTAATCAA CAAGTCTGTA 300

ACAAAGAGAA TATCGTTAAC TTCACGATGA TCTGACACAT CGATAAAGTA TyGTsTATGT 360

TCACGTGAAA TAyyAAGTCy ATTtTTTACG AaCGGATGCA 400

(2) INFORMATION FOR SEQ ID NO: 1009:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1009:

TATTGTAAAA ACTGTGGTTC TTACAATGGC GAAGAAGTAG CAGCTAAATA ATTTTAGTTA 60

CTCAATATAA AAaGTCCCGC TTAAAATGAT TGTTTTAAGT GGGACTTTTT ATATTGCGAA 120

AAATAATTGG cGAACGAGGT AACTGGATAC CTCATCCGCC AATTAAAATT TGTTAATTTA 180

ATAATTAAAT ATAAAGACGA TTTATTAGTT TTTACGTTTT CTAGGTAATA CGAATGCAAC 240

GATGCTACTT AAAGCTAATA ATGCCATTAA TGGTAATGTC ATATCTnTAT TTGATTCTTC 300

ACCAGTTTGT GGTAATGATT TTGCTTTATT TTCTTGTGTA TTTGTATTGT TTTGGCTTTG 360

GAGTGTGTCC ATCATTTGTG TTTTTAATGT TTGCTTnTnG TAATGGAGCA CTAATCTTTT 420

GCCTCGCTAG AACCTGCCGG AGGTTTGGAA CCAC 454

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1010:

GGTACAACAA CTTTAGACAA TGAAATATTA AAAGATACGG ATGATAAAAA GTCGAGTAAA 60

ACTTTTGTTG GCGGAACAAA AGTTGATGAC CAACATGCTA GTATCGGAAT GGATTTTGAA 120

AATCAGGACA AAACTTTAAC TGCCAAAAAA TCATATTTCA TATTAAACGA TAAAATTGTC 180

TTCTTAGGAA CTGGCATTAA AAGTACTGAT TCATCAAAGG ATCCCAGTTA CCAACCGATG 240

AAAATCCGCA AGCCGATGGG GAATACGGTA TTTTCCGGCC GTTAACCAAC CACCCATTCC 300

GGTTATCCGG GAAACCATTC CATCCTTTTA GGAGnCnCCG GTnCCnAAAA GGACCTCGGG 360

TATCCTTTTT TTAACCAACC CGAAATTACT GGTAAAAAAG 400

(2) INFORMATION FOR SEQ ID NO: 1011:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1011:

TTAGGTATTC GCAAAAATGA TCTTCAATAT ATAGCTATGG CCAAAAGATG GGCTAAAGCT 60

TATACAATTA CTGTAGCAGT GGGAGTTGTT ACAGGTACAA TTATAGGACT TCAATTATCA 120

TGATTTGGCC TACATTTATG GAAATGGGTG GACACGTATT GCACTTCCCT TATTATGGGA 180

ACATTGCGGT CTCTTGGAGC TATTTCTTAA GTATATATTA TATACTGGGA TCGTTTAAAA 240

TAATGGCACA TTCTTAATAG TATACCAGTA ATTATGGGGC CTTCTCAGCA TCTCATACTC 300

AGGAATCATT ATGAATACGC CTGCAGGTTT GAGTGAAGAT GGAAGTGGCC ATGTCACCnT 360

AGAGCGTGTT ACCCACGTTA AGTCGTCATT nCGAATACAC 400

(2) INFORMATION FOR SEQ ID NO: 1012:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1012:

CTTTATGGGA TACACTACAA ATCGAGACTA TAAGGTTTTT TATTTTATTT ATTATTACAT 60

TATCAATAGT TTTATAATCG AGCTTCAAAA CTTTAGAAAA TAGTAGAAAT AGCATTCAAT 120

ATAGTGCAAA AGTGCAAATT GATAACTTGA CACTTATCTC CTATAAACCG TACAATTAAT 180

TTGTATGATT TATATATAAT TTCATAAAGT CATATTGAAT TTCATATAAA GAGCAAACCC 240

TAGAAAAAnGA GGTGTTGTGG AATTATTAAG CTCCTACTCA TTTGCGGGGT CATCTAGGGT 300

GTGGAGGATG TGTGCCGAAT TGTGCTCAAA nATCCCAGCA GCAACGCGAG TTGAACAGCC 360

TAAGACGCAA CAAAGGATCT GnnAAGGACC ATCAGGCACG 400

(2) INFORMATION FOR SEQ ID NO: 1013:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1013:

GTCGTTGCTG ATACCACGCC AGTATTGGTT TTAAATGATA AAAAAATCTG TGAGATTGCA 60

TCATTGAGAC AAACATCGCT ATTTGAAATG GCCGAATATA TAGGGTTTAG CGAGCCACAG 120

AAATTAGTAC AATTATTTAT TAACCATGAT AGGAAGGTGA GACGCCAATG AATCAATATA 180

ATACTATAGG TTTTCACCCG GGAAATAGTC GTATTCATCA ATTAAATGCG ACTGTTAAAC 240

TTTTATnCTT ATTAGTTGTT CTATTCTGCA ATGGTnCTAT GCACAGGTAT TnATTTAATT 300

AGGCTCACAT TTATGGGCAA TTCTCAATGA TGAACAGTCG TTGTGTAATC TCG 353

(2) INFORMATION FOR SEQ ID NO: 1014:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 627 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1014:

CAAAGCCTTC AACAAATAAT CCTTTATTAG TACTGATTGG TTGCACAACA TAAGTTACAC 60

CAGGTTCATC TTTAAATGTA ACTTCCTTAT AGAAGAGACC TTTTTTAGCA CTATACTCTG 120

TTTTTTCTGA TTTAATTTTA TCTTTTAGAT TTTTCTCTTC CAAGTAACTG TCAATTAGTT 180

ATGAAATAAA TAATATAATG ATAACTTTAA TCGCGTTTTt TTTCTTCTTC ATTATGTAAC 300

TCCTTTTTGC TTATCTATTC AGTATGAACG AATCAATTTA TTTAATAAAG AGTTTTTACC 360

AGATTGTAAC AAATTTTTTT ATTCTCAATA TTATTATAGA AATCGAATTA CATACACGAT 420

GCTTTTAAAA AATTTAATAA CAAATTTTAT TTTACTATCT ATCAAAATAA TTGACTACTT 480

TTAACAATTA AGGATGATAC AATTACATTT TTTTCAATTT AAAAAATCAG TCATATCAGT 540

AATTACCGAT GAAAATACTA AGATATCGAT ATATTTTGCA TTATTTAACA TTTAAATTCn 600

ATTATAGACA ATTCAATAAT TGCGATG 627

(2) INFORMATION FOR SEQ ID NO: 1015:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1015:

TAGTGTGACA TTAACACTGG AACAAAAAGA AGCTGCAATT GCAGAAGTTA ATAAGCTTAA 60

ACAACAAGCA ATTGATCATG TTAACAATGC ACCTGATGTT CATTCAGTTG AAGAAATTCA 120

ACAACAAGAA CAAGCGCATA TTGAACAATT TAATCCAGAA CAATTTACGA TTGAACAAGC 180

AAAATCAAAT GCAATTAAAT CGATTGAAGA TGCAATTCAA CATATGATTG ATGAAATCAA 240

AGCTCGTACT GATCTAACAG ATAAAGAGAA GCAAGAAGCT ATTGCTAAGT TAAATCAATT 300

AAAAGAACAA GCAATTCAAG CGATTCAACG TGCGCAAAGC ATCGATGAAA TAAGTGAGCA 360

ATTGGAACAA TTTAAAGCTC AAATGAAAGC AGCTAATCCA ACAGCAAAAG AACTAGCTAA 420

ACGCAAGCAA GAAGCTATTA GTAGAATTAA AGACTTTTCA AA 462

(2) INFORMATION FOR SEQ ID NO: 1016:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1016:

TGATTGGTCC CATCGACTCG TTATAACAAA TTGAAGGTAC AAAAGTATCT TGTGATTTAA 60

TAAATTCAAG TAAATTCGTA CCTGGTTCTA CAAGGTAATT CTTTTCCATC AAGTGTAACC 120

ATAAATTGCG CATATCCACC nAAAATAACG ATGCCCCACA CATCTTTCAG ATAGG 235

(2) INFORMATION FOR SEQ ID NO: 1017:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1017:

GTTGAAAACT ATAAGATCAn ATAAAGGTAA AACAGTGGTT TGTGTCATTA GTGGTGGTAA 60

TAATGATATT AATCGAATGA AAGAAATTGA AGAACGTTCA TTACTATACG AGGAAATGAA 120

GCATTACTTT ATCTTAAATT TCCCTCAACG TCCAGGTGCA TTGAGAGAAT TTGTAAATGA 180

CGTATTAGGA CCTCAAGACG ATATTACTAA ATTTGAATAC TTAAAAT 227

(2) INFORMATION FOR SEQ ID NO: 1018:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1018:

GTCTTACTTG CACAAGGTAT TATTTCTATC TTACTCGTTG CTTTCGCAAT CATGCTATAT 60

ATCATTAATA TTTTAGATGC ATATCGTAAT GCTGAACGAT TTAATCGCAA TGAGGAAATA 120

AAGGATCCGA AGCGCGTATG GTGGCACATG GGACAAGACG TTCCCATACT TACTAATCTC 180

ACCAGGTACA TnCTTATTGA TATTGTAGTG TAATTCCATT ATATTATGTT GGAGTAGCAT 240

TACAATACAA TTATACACGC GCCTCGAGAC nACATAGATG GGTG 284

(2) INFORMATION FOR SEQ ID NO: 1019:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 779 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1019:

CAATCATCAC ACATAAATGT TCGAATAGGA TTGTTTTTAA GTCGTTTAGA CTCAGTTGTG 60

CACCTCAATA TGAGTTACAT GGTTGATTCG ATATGAATAA CCATCTTCTT GATTGTAAAT 180

AAAACTATCT ACACCATTAT CGCTGTAAAG TCGTTTACCG TCTTTTGCAA ATTGGAAAAA 240

TAAATAGGGT AATAGATCTA TCGGTATATC TAAATGATCA TGCTCATTTG ATAATCGAAT 300

AGTAGTTGCA GAGTCATGTG GTTCGGAATG TTTGAAAAAT GGTGTCATAT TAATGACAAA 360

TGAACCTTCT AACATGGCAC GTTTTTTATA TTTTATTTCT GAATTTAAAG TAGGCGGATT 420

AGTTTGTCCt TCtAGGATAG CaCGATTCCa TTCaTGaTTA TCTTCAAAGT CGATTGGTTT 480

TGAACCATCa AATACACCTT TTTCTAAATC TTCGATGCTA ACTTTTCTAT CATCGAAAAT 540

CCAAGTCGTA CTATCTAATG TTATAGGAAA CTTTACGGCT CCTTTAATTT GTATCATTTT 600

CCCACTCCCT ATCAATGTAT ATAGCATTAT TTTAACACAA ATTGCTAACG ACACATTTTA 660

AATCTACTTG CTTTTTAATA TTTAGTAAGA TAAACTTTTA GTAAGACTTG AGAATTTATA 720

TAGAGGGGGA GCGTGTCATG GCGAAACAAG CAACAATGAA AAATGCAGCT TTGAAACAA 779

(2) INFORMATION FOR SEQ ID NO: 1020:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 950 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1020:

TTAATGGTCC ATTAAGAATA ATGGCAGAAA ACCGTTTGCA TAAATCAAAC CTTGATTCAC 60

TAACTTAAGT AATACTCGCT TTTCnTAAAT CCTTTAGAAA GGAACTATnT ATCATGATTA 120

CTTCATTCAG ACATTCTGAA GATATAGATA AACATATTAT AAAAACACCA TTAGATCATA 180

CAGCGTCATG GATTAATGTA GTAGAnCCAG ACCGAGAAGA AATTGAAAAT CTTATGGAAC 240

AATATAATAT ACCTGAAGAC TTTATACGTG ACCCTTTGGA CTCAGAAGAA AGTTCCCGTA 300

TTGAATATGA CGAAGATACT GGTTACTCAT TAATCATTAT TGATTTACCT ATCGTCAATT 360

CAACTAATCG TAGCGTTCTA TCTTTTGTAA CGATTCCATT AGGCATTATT ATTGGCAACG 420

GTATTATCGT AACAGTTTGT GACGCTGAAA ATGAATTTTT AGAAAATTTA CCTAAGCGTG 480

ATATTAATTT AAAATTTCAC AGCAGATTTG CATTAGAAAT TTTAACTACT ATTGCCGACC 540

ATTATAATCG TAACTTACGA TTACTTAATA AAAGTAGAAT TCGTATTGAG AAAGAACTAA 600

AAAATAACAT TACTAACAAA CAACTTTTCA AATTAATGGA AGTTGAAAAA AGTTTAGTAT 660

ACTTTTTAGC TGCCTtAAAA GGTAACGATA CAATTATTAA AAAGTTATTC CGTTTACCTG 720

AAGCCATCGA AACAACAGAA TTACATCAAC GTATCTTAGA AAGTATCACA ACATCATACG 840

CTTCCTTATT ATCTAATGAT ATGAATACGA TTATGAAGAC ATTAACACTT TTCACGGTAC 900

TATTAACgTT ACCAAyACtC GTATTTAGTT TCTTCGGTAT GAATGTGTCG 950

(2) INFORMATION FOR SEQ ID NO: 1021:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1021:

AATATATAAA ATGAATACAT TGTGAGGCAA TTATCAAATG AAATTTAATA AAGTAAAACT 60

AGTTATACAT GCGTGTGTAC TATTATTTAT CATTATTTCT ATAGCGTTAA TTTTTCATCG 120

ATTACAGACG AAGACACATT CTATAGACCC AATACATAAG GAAACAAAAT TATCAGACAA 180

TGAAAAATAT TTAGTGGATC GTAATAAGGA AAAGGTTGCG CCGTCTAAAC TAAAAGAGGT 240

ATATAATAGC AAGGATCCTA AATATAAGAA AATTGACAAG TATTTACAAA GTTCATTATT 300

TAACGGTTCA GTAGCTATAT ATGAAAATGG CAAATTGAAA aTGAGTAAaG GTtATGGaTA 360

TCAAGaTTTT GAAAAAGGTa TTAAAAaCAC ACCGAaTACG aTGTTTTtAA TnGGTTCAGC 420

TCAAAAATTT TCAACAGGGT TACTGTTAAA ACAGTTAGAA GAAGAACATA AAATAAATAT 480

CAATGATCCA GTAAGTAAAT ACCTTCCATG GTTTAAAACA TCTAAGCC 528

(2) INFORMATION FOR SEQ ID NO: 1022:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1022:

GCATTnCGGT TAAAgTAkGt TTCAGCTTCT CTCaTTTTAG AAGTACCGaA AAtTGGTTGG 60

TTAtCTGGAT TTAATrtCAC GATAAATATT GCTTACTTTG TTACTTTGTr AAATGTACCC 120

ATTACGAGTC TCAATGTTAT TCCAATAAAT ATCACTTGTT GGTGCATGGT TTGGATATGC 180

ACAATGATTT CTTGAAATTG TTTGAACGAT TTCTAATGGA TCACAGCCAA ATGTACTGTT 240

TAATACTTCA GAGTCTCTGA ATAATGCACA AAnTGAAATA CAAGTTGTCC AGTTTGGTAA 300

AGTATCTTGC GTATAACCAG CCTCTATACG AACCATTTTA AATTTTGTTT GAATTAAATC 420

TGTAAAACTC TGTCTATCCA TTCTGTTATC TACCTTTCTG TTTGGGGAAT TTTATCCGGA 480

CACAAGAAAT TGCAATAATA CACATTTCTT GAAACACAGA TTACATCTTA ATATATTTTT 540

AATAAAATGA AAAGAGTCAA TTTCACATTT GTATTAAATT TTGATCAAGT CAACAAGAGT 600

TAAGTTTACT TTATAATGAA GCGAAAGTAA ATGAAGTAAA ATTTTATGCA TAATCACTAG 660

ATTTGATAAA ACTTACACTT TTATAATGaT ATCAAATTTA CAAaGGAAAA CTG 713

(2) INFORMATION FOR SEQ ID NO: 1023:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 570 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1023:

AATAAAATAG AAATGATTAT GGGTACAATT ATCGCTATCA TATCCTTGTT ATTAATTATA 60

TTACAAGCAT TTAATATTAC TTGGGGCGTT ATACCAATTA CAAATTTTGG ACATCAATTT 120

TTCTTTTTCA TTGGTATTAT TTTAGTAATT GCCGGCATAT TTTwyAAGCG ACTtGAGTTT 180

TCGGGaATcG GGTTATTATT TTGTcAAAAA ACCGTCGATG CAATGATTCA TAATCCACAA 240

TCAGCCCAGA TTTTTTCATT AATTATATGG ATATTATTAG TAGTTCTAGT TATATATTTC 300

ACAATTAGAT TATCTTCACG TACAAGATTA TAAATATGAT AAAACTATTC ACTTGaTTAA 360

TTGTATTAAT TGaGATGaAT AGTTTTTTTA TTGTTGGAAT AACTTTTGGT AATTTATAAA 420

TAATTTAAAA AAATTGTTTA TAAAAgGAAG CGTATATAGA ATGAAGGTTG GGTATATAGT 480

TTATTGAGGG AGGTGTCACA ATGAATAAAG TCACAaTTAA TCCTCAAATC CAATTAACTT 540

ATCAAATTGA AGGTAAAGGG GATCCTATAn 570

(2) INFORMATION FOR SEQ ID NO: 1024:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1024:

CTTTGTTGTG CTTGAGCATT ATTAAAAAGA GTATTTAAAT TTAGTTGTTG GTTTGTAATA 60

TCAGAATTAT TAACACTATA TTTCCCTTTA AATAATGGTG ATTCGrAATA ATGCTTATCT 180

TTATCTGCAG CTAACTGGAA TTkCCCTAAT GCAGAGTCTG CGATTGTTGG TTCAAGATTA 240

ATCATTGATT TCTCTTTTTT AGGATCATGT CCATATGACA tGTaATTTTC GATGCATTAA 300

CAACAGATTT AkGAATGCCA AGCCCTTTAA CAATTTCATC TGATGCATCT GCGCTTAATn 360

CTAATGAAGA TAAAAACGAt TAtCTTTCAT CkkTTCTTGG AACTTCACTT CATTTTCAAA 420

ACGGTCATTA AAATAATCTT TATACATTTT TGCTGTTTGT TGTTCACTTT TTAGGTATGT 480

ATTTTTC 487

(2) INFORMATION FOR SEQ ID NO: 1025:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1025:

ATATGTTATA AACAATTTTA CAGTTGTATC ATCTACTCGT TCTATTCTCA TATCATCTCA 60

CTCCTTACAG TCGATGAATA GTATCCACAT TGTATTAAAG CATCAAACAA AATACAATTT 120

ATTTGTTTGA TTTCTTTCTC TAAAmTATTT TGGTAACTTA TAATAACATA TTCGTTGTAG 180

CAAAACTATT TAAATGATTT ATACAGTTAA AGCATTAAAG CACTTTCTTA ATTTAATTTT 240

ACCTTATCAT AGCAAATGTT TCATCCAAAA CACTCTAATA TAGAGCTATA TTAACAATTG 300

CACATTTGaT TTAAAAGATA CTAAGCAATT ATTGtAAAAT TAAAACCAAA AAaGCAACAC 360

TATA 364

(2) INFORMATION FOR SEQ ID NO: 1026:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1026:

TGCCCCAGGG GAGTACnAAA AAAAAGnGGG GTGGGGAATT GGAAACCGGA ATTAGTGGTT 60

AAAGGGGTTT ATTGGATGTT GGGTCTAAAG TATTCCCAGA AATTTATCCA TCnATGATTG 120

CTTTAGCCAA GTTTTTTTCC AACCCATCTT TATGGAATTT AGTTATCTCA ATTACATTAA 180

CTTATATAAA AATGGCACAA TTATTTCATG TACCAACAAG AACAATATTA ATACGTCATT 300

TAACACCTAA AATTATACCG GCTATTATCG TTG 333

(2) INFORMATION FOR SEQ ID NO: 1027:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1027:

TGTTCCATTC GTTTTAATAA TGGTGATACT GTACCAGTAT CGAGTGCTAA TTCAGTTACG 60

ACTTTCTTGA CGTTTACAGG AGATTCATCC CATAAAATTG TTAAGACAAG AAATTGTGGG 120

TATGTTAGAT TGTACTTCTT AAAAACTTTG TTAGAGTAGT AGCGATTAAC TTGTCTTTGA 180

GCATTGTACA AACTAAAGCA TAGCTGTTCT TTTAAATTAT GTTGATCAGA CATTAAAGTT 240

CTCCTCCAGA CATACTATCC GTTTTTnTCT CTTTTCGGAT TGGTAATCAT TAAAAAGTTG 300

ATTGTTTATT AATTCACAAC TTTCTTTGAT TCAATGCCAT GCnAAAATTA AAGTATGTTT 360

AAAGTTTAGA AGATATTTTT GATTAAATCA AGCAAAAAGA TAATTTAATA TATATGTGAT 420

CATTTTTAAA AATAACTGTn ATAGAAAAGA 450

(2) INFORMATION FOR SEQ ID NO: 1028:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 535 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1028:

TGCATCTATA CCTAGAACTT TAATTTCGGA TTTTATTGCG TCTGTAATAT CTTTAATACC 60

ACTTTCGATA GGGAAACTTT CGTCACCTTC AACATATTTA ATACCAAAGC CACCACCAAG 120

GTTTAATAAT TCAACTTGAA TGCCTTGctC TTTaAGCCAA CGTAAAmCAA TTTTAGCaGT 180

TTCAATAAAt GCTTCTGTAC CTTCAAtCTG TGrACCaATA TGACAATGTA CACCTTTTAA 240

TTTTAAGTGT TTAGATTGTT GGACTTTGTC AATTGCTTTT TTAGCTAAGC CATATTGaAT 300

TGaTAATCCA AACTTACTAT CTTCTTGCCC AGTTTGaATA AATTCgTGTG TATGTGCTTC 360

aACACCTGGa TTAACTCGTA AtACAACTTG aACCGTATCA TTAGCATAGC GGTCTATTAA 420

AATTTCATGT TTCGTTTTAT TGTTACCATG GAAATGGATG CGACTCGGTT CAAAA 535

(2) INFORMATION FOR SEQ ID NO: 1029:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1029:

GAAGATGATT GAATTATGGA ATTTTTTTCG AGATATGTTA TTTCGGGGAT CAGATTTTGC 60

GATTTTGCCT TGGATAGAGT AGTTGCGATT TGTAAATACG TTTTTCAGGT TCGATTCAAT 120

TTCGTTGTTA AGATAATATG GATTAGTTTC ACTGACATGT TGATGCATGT CTTTTTTGTT 180

CTGATAAAGT ATAAAATGTT TACTTAACAT TACTTAGTAT GACACCTGCT AATTCAAACA 240

TTATTTGAGA CATTCTTTTC AAATTAATTA TAAATTTTTA CCtATAGACT AGTTTGATAT 300

TTATCTACAT CTCAAAATTC TCATCAACAA TCTGTCACAT CCAACATTTT TACTTnAGT 359

(2) INFORMATION FOR SEQ ID NO: 1030:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1030:

TACATTGGTA AATAATTCTC ATAGTTTATG TCTCGTTGAT TAATCCAATC ATTGTTTTTA 60

TCGGGTAAAA CATTCAAACT TTTCAAATTC ACAATTGATT GATGTTTCAT TAAAGTATCT 120

AATTTTTGCT CTCTAGTTAA ATATTCACCA ATGTCATTAT AATAGATATC GTGATTGTAA 180

CTTCCATCTT TAACTAAAAT AGATATAGCT ATCGGTGCTC TACTTCCTGA TCCAAATATT 240

TTTCCACCTT CTTTTCTTGa TTTTTCACCC TGTGTTCGTT GGTCGCCTCT CAAATTAATT 300

ATGtACAGaT AGTTAAATTC ATCGaTAAAA CTTTTCTAAA T 341

(2) INFORMATION FOR SEQ ID NO: 1031:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1031:

GTCTAACTTT AATGTTTAAA AAnCTTAGAA ATTTTCTACT CATAAATGGA TGCTTTATGG 60

AATATTATTA ACAGGCCCAG CTTCAATGCT AGCTATAGAA TTTGGATGGT TCTTAACAGA 120

GATGGGTAGA CAGCCTTGGA TTGTTCGTGG TTATATGCGC GTGGCAGAAG CAGCAACACA 180

GCAGCGGAAT AACCTTCGTT ACAATTTTAT TTGGCATATG TACATCATTT AAGTATACAG 240

TGCAACGTAT ATCGTAGTTA AAATAACCGC GTAGAGAGTA ACGTAGCAGA GCAGAGGAAT 300

GAAAnATTAG CTTATGnAAC GGTAGG 326

(2) INFORMATION FOR SEQ ID NO: 1032:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1032:

ACAATCAGGC TTGTGAAGAA TGAATTGCAT GACGTTTGTG TAATTGAACT GCGAGGTTTA 60

ATTTCTAAAA TGCTCCAGnC CTCCAATGTA ATCGCATCTT GATATAACAT AGCGATCGCT 120

TGATTTGTCG TTGTATCAAC ACCTCTAAAC AACGTTTCAC CTATTCGGCA ATTCATTTAT 180

TTTACCCAAA TCATTATATA AAAGTTGTGG TAACATGCTC GAAATACCAC CTGAAATAAT 240

nTCAATCGAT ATCCTATTTC TCT 263

(2) INFORMATION FOR SEQ ID NO: 1033:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 514 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1033:

TTTCTATAGA GGATCCTGTA GAGATGCAAA TTCCTGGTAT CGTCCAAATT AATGTGAATG 60

ATAAAGCTGG CATAAACTAT GTAAATTCGT TTAAAGCTAT TTTAAGATGT GATCCTGATG 120

TTATTTTAAT AGGTGAAATC AGAGATAAAG ATGTTGCCAA GTGTGTTATA CAGGCTAGTT 180

TAAGTGGTCA CCTTGTTCTG ACTACATTGC ATGCAACTGA TTGTAAAGGT GCTATTTTAA 240

GGCTATTAGA AATGGGCATT TCTGTACAAG AATTGATACA GGCAACTAAC TTAATTATAA 300

AGCAACAACT CCGATATTTC TTTTCCCaTA ATCATtCATT ACCATCATCA TTTAAGAACT 420

TAGAAGATAA ACTTGATGAT ATGACAAAAG CAGGTGTCAT TTGTGAAACT ACAATGCATA 480

AATACATTTA AACTACATTC TAAGAAGCGA CAAT 514

(2) INFORMATION FOR SEQ ID NO: 1034:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 598 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1034:

TTTTTCACGA ACATTTTTGT TTAAAATTTT CTTTCTTAAA CGTATACTTT CTGGTGTAAC 60

CTCAACAAGT TCATCATCAT TAATGAATTG TAACGCTTCT TCCAATGTTA GAATACGCGG 120

TCTATTCATT GTTTGTGTTT GGTCTTTCGT TGCAGAACGT ACGTTAGTTT GATGTTTTGT 180

TTTAGTGATG TTAACAGTTA AATCATTTTC ACGATTATGT TCACCAACAA TCATACCTTC 240

ATAAACTTCA GTACCAGGTT CCATGAAGTT TACACCTCTA TCTTCAAGTC CCAAAATGGc 300

ATAAGTACTT GCAGAACCTT GATCCATTGA AATTAATGCA CCATTACGAC GACCGCCAAT 360

TTGTGCTTTA ATACGTGGTC TAAATTCyTC aAATGTATGG TTAATAATAC CGTAACCTCT 420

TGTCATTGAC ATAAATTCAG TCGTATAACC AATCATACCA CGAGCCGGTA CATTAAAGAT 480

TAAACGTGTA AGTCCATTAT CAGTTGTAGT CaTATCAACC ATTTCACCTT TaCGTGcACC 540

TAAkGATTCa ATAACAGCAC CTGcATTTtC TTGTGGCACT TCACATTGCA CACGTTCA 598

(2) INFORMATION FOR SEQ ID NO: 1035:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1035:

AAACAGTGCT TCATTATCGG TATTGATATT GATCCACAAG CCGTTGACCT AGGGCGCACA 60

ATCGTTAACG TCTTAGCACC AAATGAAGAT ATAACAATTA CGGATCAAAA GGTATCTGAA 120

CTTAAAGATA TCAAAGATGT GACGCATATC ATATTCAGCT CGACAATTCC TTTAAGTACC 180

AGCATTTAGA AGGAATTATA TGAnTTAACC AATGAAAATG TCCGTAGTGC CATGCGCCTT 240

AAGTGGGCCA TGT 313

(2) INFORMATION FOR SEQ ID NO: 1036:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1036:

AATAATGAGT AGGTTTTGAT TACTTACGAG ATAACATGGT GAATTATTCT GAAGATAGAC 60

TAATGCGTCC ATTACATTTT GCAATCATTG ATGAGGTTGA CTCAATTTTA AATCnACGAG 120

GnCGACGCCA TTAATTATTT CTGGTGAACT GAAAAGTCAA CGTCACTTTA TACACAAGCA 180

AATGTTTTTG CGAAAATGTT AAAACAGGAC GAAGATTATA AATACGATGA AAAAC 235

(2) INFORMATION FOR SEQ ID NO: 1037:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1037:

nCAATATACC TCCTATCATC ACACAAAATG CGTTGTTTCG TATGATTTTC TCAACATCGT 60

AGACTAATGC AATCAGACAC AACACCATGC TCTATATCCA ATATTTGCTT TATTGCCTAT 120

CAATGAGCGT ACTGCGTGCT TTTAAATAAT CATCATCAAT TAATGACTGT ACAGGCACCT 180

CATGAAAATT ATCATCCGCC AAGTATTGCG CACGATCACT ATATGCTAAA TGCATCGCTT 240

GTATCAnATG ATGCAAGTAA TCA 263

(2) INFORMATION FOR SEQ ID NO: 1038:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1038:

ATTGTACCTG GCACAATCTC ATTATGTATT GGATTATCAT CATTACGAGC GCCAAATATT 60

ACCGTTATGA CATGTTGATC ATTTTTAGTn AATGTTAAAG CTATAACGTG TGATATTGCG 180

AGTCTGTCGG CATTCAATAT CTTCnAAATG CCCTACAT 218

(2) INFORMATION FOR SEQ ID NO: 1039:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1039:

GTTTAGACGC TAATGnTGGC ATATATTACT TGCCATGCAA ATGAGTCATA AGGCATAGTT 60

TTCAAGAAGG GTTCTGACAA TGAAGTGAGC AACATGTCAT GATGAGAAGC AGGACTATAC 120

AATGAGAATA ACCTTTTGAT TTTTCATGCA TAAGGCGATT CAATCAAAAG CAATCACCTT 180

CCAACTGAAT TGTCATTTTG TAAAATAAAA TAATCGATCC AATCGTTATC TAATTCATAA 240

ATGTGTAAAC ACATACGTTA TGAATGGATA ACGATTTTTT GTTATGTTAA AGTGGTACAT 300

TAATCATGTA TTTCGTATGA TAATTAACGA CAAGTGTAAT GGTTAAATGT ATTTTATGGA 360

TGGAAATGCn ATAATAGGCC TGGGTTACCA TGGnGC 396

(2) INFORMATION FOR SEQ ID NO: 1040:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1040:

AGCATTTTGT TTAAAAGCTG ATGAAGCAAT AATAAACTCT TCATATCCTC TGTCCATTAC 60

AATTTGACCT TGATATACAA TTTCTTTAAA GTTTTCGATT TCTTTAAATT CTCTGCTATC 120

ATTTAAAATA GGTGCATTCG TAATAACATT CGCTTCCTTC TTATATCCTT TAGATTGATA 180

ATATTCTTTT GCTGCATGAC TTACTGTTAC GAAGGCATTA ACACGATGTT TTACTATGTG 240

TTTTTCTATA CTTTCTACAA ACTTTGAAAT AAGTGGAACT TTATTAATAA AGGCATTTTT 300

CGCATATATT TCATGCGCAT CATAAACAAT ATTAGCTTTT TtATAATTGC TTAAATAGAC 360

CATTAATAAT ACGTCGAAAT CATTTGCATG AATCACGTCA 400

(2) INFORMATION FOR SEQ ID NO: 1041:

(A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1041:

ACTTGCGTTT CTATTTAGCT CAGACAGGAA AAATATTCGC TGGAAATATG TAGGAATTTT 60

ACTTGCAATT CAGCTTATCT TTGCATTTAT CTTGCTTAAA ACTACAATGG GAATCAAGGT 120

TATTGGTGGT ATTTCAAACG GTTTTAACTA CTTATTATTA AAAGCAGCAG ATGGTGTTAA 180

CTTTGTATTC GGTGGTATTC AATATATCGT CCCTAAGCAC CCACCCATTC CTCCTCCGGG 240

GAATAATAAC CAACnGAATT AATTCCGn 268

(2) INFORMATION FOR SEQ ID NO: 1042:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1042:

GTGAAGATAA GAAATTAAAG TTAAGACAAG GTTAAAAATA AGCAAAAAAT ATTGAAATTA 60

CAGATCATTG GAnTGGTATT CCAGAGGAAG ATCAAGATTC ATTTTTGATC GCTTTTATCG 120

ATGGATTAAA TCTCGTTCAA GAAGTCAAGC GGTAATGGAC TCGATTATCT ATTGCTCAAA 180

AAATCATCAA TTAAACGGnG ATCGATTAAA ATTAAAGTGA ATTAACAAGG AGCAACGTTA 240

AATCTATTTT AATCAGACTG AGACGTCATC AAGTCAT 277

(2) INFORMATION FOR SEQ ID NO: 1043:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1043:

TTATCATCAC AAGTGATTTT GAAAATAAAA AAATCGAAGA TGATGACAAT GATTCAGGTA 60

GTGTGCCGAT ATTGCCGTTT ATTAAACGAG ACAAAGCATA TCAAATTATC CAGAATTTAG 120

TACCAGATTT ATCTTATCAA CAAGTTAATG AAGGTATGCC TTTGTCAGGn TTCCACAGAC 180

AACCATTATT ATTGTTATTA CCGATATAAC CATAGTCATA TGGTTATTGT GATCCAAGGT 300

ACCTTATGTC AACAGCGGGT TAAAGCAGAG ACAATACATC AGATTCGGCA TGAACGAAAT 360

TATATTTAAn GCTnCTAAG 379

(2) INFORMATION FOR SEQ ID NO: 1044:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1044:

ATATTGAACT TGAAGACCAT GCAGATATAA ATGAAATAAC ATATCGATTA TCAAAAATTT 60

TCGGTATTAA ATCTATTAGT CCAGTATTAA AAGTAGAAAA AACAATAGAG GCAATAAGTG 120

CAGGGACAAT TAAATTTGCG CCATTnTGAA GAAAACAGCA CATTTAAAAT TGATGTGAAG 180

CGTGCCGATA AAAATTTCCC AATGGATACG TATGAATTAC AGCGTGAATT GGGTGGTGCA 240

GTATTGAAGC ACTTCGACAA TATTTCAGTG aATGTCaAAC GTCCAGATCA TGgAAATTCg 300

AGTGGGmAGT TtAGGmTTAG ATGCCAATTT TATATGGTAT GnAAGAAGTT GGTTCCGGGG 360

TTCCAGGTGG GATTTACCnG TTGGGTACTG GTGGGTnAA 399

(2) INFORMATION FOR SEQ ID NO: 1045:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1045:

AnGATAAACA GAGGAGCACA AAAATGAATn nAAATATAAT CATCAAAAGT ATTGCGGCAT 60

TGACGATTTT AACATCAATA ACTGGTGTCG GCACAACAGT GGTTGATGGT ATTCAACAAA 120

CAGCCAAAGC AGAAAATAGT GTGAAATTAA TTACCAACAC GAATGTTGCA CCATACAGTG 180

GTGTTACATG GATGGGCGCT GGAACAGGAT TTGTAGTTGG GAATCATACA ATCATTACCA 240

ATAAACATGT TACTTATCAC ATGAAAGTCG GTGATGAAAT CAAAGCACAT CCTAATGGTT 300

TTTATAATAA CGGTGGTGGA CTTTATAAAG TTACTAAGAT TGTAGATTAT CCTGGTAAAG 360

AAGATATTGC GGTCGTACAA GTTGAAGAAA AATCAACGCA 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 626 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1046:

ATAAACTTCT ACACCATCAT CTTTACCTAC AACATTTGTA GCTTTAACTT TTAGTCCAAA 60

GTTATCTTTA AAGAATTGTT CACCTACTTT TTCAAATTCT TTACGATGCT TCTTCACAAA 120

TTCAATCGCA TCTTTTTCTG CAGGTGGTTG AAAGCCTTGT CCTACATATT TTGAAGCTTC 180

CATTTCTTCT GGTACTGATT TTGTTTCTGT ATTTGTTTCT GTATTTGTTT CTGTATTTGT 240

GTCTTTTTTT GATTCATTAT TCATCGCTGA ACATCCTGAT AACAGTAGCG TTGCTATTAA 300

GATTAATTTC GCCTTTTTAA ACATAGCTCA TCACCCATTT ATGTGkTTAT ATAGAATATT 360

AAAAAGCATT TTAAAAAAAA TTTATTCATC TTTACGATAC ACTCCATATT CTATTGGATC 420

ATTATCATCA TAAAAGGCTT TTTTAGTATT AATAGTAGGC TTTCCTATTT GAATTGTAAT 480

TGTAGATTTT TCTGGCTTAT TTTTAAAATT ATATAGTTTA TCACTCAGTT CAATTACATC 540

ATCAACTGTA TTGTCTTTAG TAAAATTTTC CTTTGTACTA AACAATGTTG TTACTGTATC 600

TGTATTAGCA GCGnAATTCA CTTCTT 626

(2) INFORMATION FOR SEQ ID NO: 1047:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1047:

GACGGCGTTC AAAATGCAAC GGTCAATTTA ACAACAGAGC AAGCTAAAGT TGACTATTAT 60

CCTGAAGAAA CAGATGCTGA TAAACTTGTC ACTCGCATTC AAAAATTAGG TATGACGCGT 120

CTATTAAAGA TAACAATAAA GTCAACGTCA CGCAACTGAA GCGTACAACA TAAATTGATA 180

GnTATCATAT CAGCAGTATA TCTTACCACT ATAATGTAAT GTTGACACTT TCATATGCAT 240

ATACAGACTA TTACGATCAT GTCCATTATT TAGCnCACTG TCATTATATG GTGGCATTAT 300

GAGGGTATAA ACTTAGn 317

(2) INFORMATION FOR SEQ ID NO: 1048:

(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1048:

ATACGnATTA TGCAAAAAAT AAAGTGAGAT TGGCATATGT GTAAATCTAA AATACTGTTG 60

AAAAATATTT TTAGTGAAGT AATCAGAAGT TAAAGATTTA ACTGAAGTAA AAATATAATC 120

AAGATTACGA GTCATTAACA TTTAGCTTTA AAGAGGGAAA CATATCAAAG TAGGTTAGCT 180

AAGnAAAACA CCGACTAAAT CGGGGATATT TCGTGACATG TTG 223

(2) INFORMATION FOR SEQ ID NO: 1049:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 608 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1049:

AAATATGAAT AATGCAATTG ACCAACGTTC GATAACGTTG CCATACCCAT ATTAAATTTT 60

GTATAACCTT GTTCTTTACT CCAAAGTAAC ATATGCAAGT ATAGACCATC CATTAATGGT 120

AAATCTAACT CTGGCAACCA TCTAATTAAA TCGACTGAAA TGGCATCATT AAAGTATGTT 180

GGCATTAAAC TACAAAATGC AATTACTTCA TTTTCTTCAT TTCGCATTAC ACCAATTGGC 240

GCTTTAGATA AGTATTCTTC ATTAAATnCA CCAACAGAGA AATGCATTTC CyGACGATTA 300

TCTAGCCaTA AATcACTTAC ATGTTGAAGt TCATTTAtAA ATTCAGTTGr AAACGGtGGt 360

TCAATAATTT CGAACGAAAT ATTAAGTTCA TCGAATTnAT TTAAAGTCGC TCTAAATCCC 420

ACGGCGTTTT TTACCTGAAG TTGAAAATTG CGTTAAATCA ATAATTGCTT CTTCACCTAA 480

TTTGAAAAAT TGGTTACCGG nATTATGATA TAAAGGCATG TGTTGATCTG TAACTTGATA 540

GAATATAACA TCATAGCCTA AATACTCAGC GTAATTATAG AATGCTTCTA ACAATTCATC 600

AAAGGCAT 608

(2) INFORMATION FOR SEQ ID NO: 1050:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1050:

TGTTTTTCTA CGCTAAACTA TATGATAAAT TGCCTATGTA TTTACTGGTG TTTATGGCCT 60

TTACAGCTGT AATTTTGATT ATGATGTACA TACAAGAGAA AAATGAAAAT TACAAAGTTG 120

AAAAAAGATA TGTGGTTAGA TATCTCACAC TTAACGTTAT TGTGGGATAT ACTTTGCCAT 180

TGCTTTTTGT ATCTATTTAC GTTTTTGGTG TAGTCGGTTT TGGATTTGAT GTTTTCAATT 240

ATTGTCTAGG TAkTATCTTG ATGTyATwTA TTTCTTGGTT TAGGTnTATT nT 292

(2) INFORMATION FOR SEQ ID NO: 1051:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 734 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1051:

TAAATCnTCA AAGATTTCTT CTAAAACATT ATAATCTTCA ACGATACTCG AATAATAATA 60

CAGCTCATCA TTTCTGGGCT TGGTATAATA AAATATAACT TGCCCACCTC CATCGTCCAC 120

ATATGCAATT ACATATACCT TTTCCCACTC TACTGGTATC ATTTCATTGA TCTCATTTGC 180

AATTTTATTG TACATTTCAC TTAATTTTTC TTCGAAATTC ATGTTATCGC CTCTATTGTT 240

CAGCTTCTTC TTGCTCTTTA ACATATTGCT CGATTTCTTT AACTTTATTA ATTTCATATT 300

CCGTTTCTGG TAAAATTCCA AATTTTCTAT ACTTATAGTA ATTTTGTCGA CCTACTTGAC 360

CAAATTCTGA ATTTATCCAA TCAATATAAT CAAATGAAAC TTTTAATTCA CCTTCTCTTG 420

TAAAGTCAAA TTCGCATGAT GTCCATGGTT CATGTCCTTC TTCTTTAAAT AAATTCCTTA 480

AATTTTGAAA TTGTTTATAC AACTCATACA CTGAaTCCAT AAATTCCGAT TCCGATATAT 540

CATATTTATT TAATACACTA GTATAGTAGT ATAATTCATT ACTTCCAGGT TCTGTGTAAT 600

AGTAGAACAC TTCTCCTCCT CCGTCATCTA TATATGCCAT TGCATATACC TTTTCCCACT 660

CTACCGGTAT CATGCTGCTA ATCTTATTCG CAATCTCGCT ATACATTTCA CTTAATTTTT 720

CTTCGAAAGT CATG 734

(2) INFORMATION FOR SEQ ID NO: 1052:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 775 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1052:

ATTTTTAACC AAAATTGCTT TTTTATCTGA AAAGAAAGGC AATGTTAATG TTTCTTCAAC 60

AATTGGTGCA ATCTCTGTTT CGTATAAATT ATATTTCACA AAGTTAAAGT CATCTCTATC 120

ACTTTTCAAA AATTGTGATA TGATTTCTGC ACTTTGTTTT TCAACCAATT CAGGCACATc 180

TCCATAAATa GCTACAATAT TGTCGCTCAT TCATTACACC CTTTCATTCG TTTGACACAT 240

CAATAGATTA TATCATGTTT CTGTATCTAT AAACCACTTG CATTTCCATA AGAGCTTGAA 300

TCAACTTTTA AATTATCATC TAAGTCAATT GTAACTTGAC CGTTTtGTTG ACTATTGTAA 360

ATGCGtACTG CGAATCCTTT GCAATCGTTt aACAACTTCT ATATTAGGaA GwTGATACAT 420

ATTGTTCTTC CCAGAAGAAA TCAAACTTAT TTTAGGCTTA ATCATCTCTA TAAATTCTTT 480

AGAACTACTT GTCTTGCTCC CATGATGTCC TACTTTTAAA ATATCAATCT CCGGCAAGTT 540

ATATTTTTTT AGTAGTAAAG ATTCATTATT TTTACTAGCA TCGCCCATTA ATAAAACTTT 600

TTTATTTTGA TATGTAATCA TAGTAATAAT CGAATACTCA TTTTTATCTC GGCTATTTGG 660

AATAAAACTA TCAAAAAAAT AGAAAACTAC TATCTCCAAG TTTAAAACTA CTAACTTGTC 720

TTACATCCAT AAGTTTAATG GTTGTACTTA TGGGCTTAAT TTCCGATAAT AACCA 775

(2) INFORMATION FOR SEQ ID NO: 1053:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1053:

GAGACCAATC ATCATAATGA ACGACAATCA TGTATTTAAT ATTTAATAAA ATACTGAATA 60

ATGCTATAAC TGCCATTAAT TGAAGACCAA TCGCATCTAA TGCGACAACA CGATCGGCAA 120

GTGATGGGCC TAGCACAACG CGAATGAGCA TAGCTAACAT AGGAnGTGAC AACTATGATT 180

AATGCAATAA CGATGAATAA CCTTGATGAn TCATTATAAT TCGCCCACCT CTCT 234

(2) INFORMATION FOR SEQ ID NO: 1054:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CTACTGGTAT CATCCACTGA TTTCATTTGC AATTTCATTG TACATTTGAC TTAGCTTTTC 60

TTCGAAAGTC ATGTTATCGC CCCTATAGTT CAGCTTCATC TTGCTCTTTA ATATATTGCT 120

CGATTTCTTT AACTTCTTCC ATTTCGTATT CCATTTCTGG TAAAACACCA AACTTTTTAT 180

ACATATAATA GTTTTCACGG CCTAATTGAT CAAACTCTGT ATTTATCCAA TCAATATAAT 240

CAAATGAAAC TTTTAATTTA CCTTCGCTTG TAAAGTCAAA TTCACTTGAT GTCCATGGTT 300

CAAGCCCTTC TTCTTTAgAA AGTTTCTCTT AACTTCTTAA ACAATCTATA TAAATCCGTC 360

CACAAATCAT AAAATACTTT TTCAGAGACA TTATACTCTC 400

(2) INFORMATION FOR SEQ ID NO: 1055:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1055:

GnGGCATATA TAGCGTTGGC GGTATAACAA AGAAAAATGT GAGATCAGTG TTTGGATTTG 60

TAAGTAATCC AAGTCTACAA GTTAAAAAAG TTGATGCTAA AAATGGCTTT TCGATAAACG 120

AGTTGTTTTT TATTCAAAAG GAAGAAGTAT CATTGAAGGA ACTGnACTTT AAAATAAGAA 180

AACTCTTAAT CGAAAAATAT AGATTGTATA AAGGAACGTC TGATAAAGGT AGAATTGTTA 240

TCAATATGAA AGACGAAAAG AAGCATGAAA TTGATTTAAG TGAAAAATTA AGTTTTGAAC 300

GTATGTTTGa TGTAATGGaT AGTAAGCAAA TTA 333

(2) INFORMATION FOR SEQ ID NO: 1056:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1056:

TGGGCAGTTA CATTTATGAT TATCAGCACA TGTTTAGCTT ATAAATTTTT ACGAAAGTTT 60

AGCCGTTTAT AAAGCACATG CATAATGAAA CGAGTATTTG CCACTTGATT AGTACTTCAT 120

TATTATGTCG AAAATAAAAA TAAGTGGTAT TTTTAATATA TTAAGAAGCA CTCATAATCG 180

GCTGTTAATT AATAATATTT TTCATAAGTA TTGATTCATC ATTTTCTTTA TGTTAAATAT 240

TAATACAGAT ATCAATATGG CnAAAGTGTT nnATGAATCA GAGGTAA 347

(2) INFORMATION FOR SEQ ID NO: 1057:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1057:

TCCAAAACGG AGAGCCAAGA GTTAACTCTA CTTATATAGG ATACGCGCCA ATTGATGATC 60

CAAAATTAGC GTTTTCAATT GTATATACAA ATCAGCCTGT ACCACCACCA TGGTTAACAG 120

GTGGAGACTT AGGTAGAGAT GTAATTAACT ACTACTTTAA GCAGTTAGGT AAAGATGATA 180

AAAATAAAGA CAAAGACAAA TAAAATTTAA CCTGACGATT GTGTAGCGCA TGGTTGTAAA 240

ATTTTAACTT TGCmAATATT ATAGATGTTG GTATAATAAT AAAGTCGTAT TtAGaAATGA 300

TwAGGaGGGA AT 312

(2) INFORMATION FOR SEQ ID NO: 1058:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 404 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1058:

GCCATTTTGC GATGCTAAAT CCATTGAAAA TGCAATACCT GAAAGTCCAC CAAACAAAGA 60

ATTGTTATAT TGACCACTCT GTAAATATGG TGCTAATTTC ATGATGTACT TATGCACAAT 120

TTGCTCAGTA TTAATATCGA AAACTTTTtG AtAAGCATCT AAAAACAAAA TGATACCTGG 180

TATACCATGT GATAAAGTTG AAGGTTCAAA ATAATCGGTT TCAGTAGATG CTTTTGAAAT 240

GAAATCATCT ACTTCTGAAA TCTCTTGAAA CTTCTTCTTC AATATTAGAT TCATATCAAT 300

CATTTTtGTC ACCACACCAA TGCTTTTGAG TTTTAACAAT TTCTTTTACA ATAGATAAAA 360

CAAATGTTTC TTGATCCTTA TCAATGCCAA ATATTCGATT GnAG 404

(2) INFORMATION FOR SEQ ID NO: 1059:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1059:

ATGTACATAG GnATGACATA AGTGTGCCTT CTTTTTCAAG ACCCTCCATA GAAATAATAC 60

ATGGATGTGC ACCACGnTAC TACCTCTTTA ACGTTACCAG AATTGATAAA TTAACTTTCT 120

CTTGTGTTGC TAAACCTACA ACTGGTGTAC CTTCTTCGAT TAAGGCAATT GTACCATGTT 180

TAAGTTCTCC ACCAGCAAAA CCTCGCTGAA TGTAGAAATT CTTAAGTTTA AGT 233

(2) INFORMATION FOR SEQ ID NO: 1060:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1060:

GCACCACTAC TGTTAATAAC ACACCTAAAA AAGTCGAAAT ATAAGGGTTA ATCGCTGTTT 60

TAAATGTATA TCCTAGTGCG ATTGCCATTA ATTATCCGAT AGCTTTTTCT GCTGCTTCCA 120

TAGTCATCTC ACCTAATGTT GGATGTGCAT GGATTGTTAA TGCGATATCT TCAGCATTCA 180

TACCAGCTTC AATTGCTAAA CCTAATTCAG AGATAATATC TGATGCACCA GTACCAACTA 240

CTTGAGCACC GATTAAAGTA TCATCTTCTT TAGTGTAATA AGTTTAACAA ATCCG 295

(2) INFORMATION FOR SEQ ID NO: 1061:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1061:

CAATGCCTCT CGTGTTGCAG CTTCTTCCGG TGAAAAACCA ATATTTTCAA GTGCAATAAT 60

TTGATCTAAG TCCTGCATGA TTACTTTTCT TAATACCATA AAAACACTTC CTTAGCCCTA 120

TATATCAAAA GTAATACCTT CATCTTTATA TTCATTATTT TCAAACTACC TTCACTATAA 180

AAAACGAGTC TTTTTATTGA AAGCCATTCG CCTTAATCAA TTAGACAAGT TGTATkATAC 240

GAATTAGTAA ATAATCATGA TTATAATTCA TTTTAAGCAT ACTCAAAAAG ACTGGTACAT 300

GTATACCAGT CTAATTCGAA AAAATATATT TAGTTAAAAC CATTTCAAAA ACGACTTCAC 360

(2) INFORMATION FOR SEQ ID NO: 1062:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1062:

AAGCTGCATA CTCTCCAAAC TTAGAACCAC CGAAGCGATT CACAAAATAT TTATTAGCTA 60

AAAAGTCGGC ACATAAAATT AATATTGTTA GCAATGCCAT AGATACATAA AACACCCATG 120

ATAAATGCTG ATTATGAAAG CCAAATTGAT AGATTAAAAA GCCAACCCAT AATACTAAAA 180

CAGAAGGAAT AATCGGCTTA ATCAACCCAA CAAATGCTAA CATGAAGGCA GCGATGATAA 240

GTAGCCATAA AATAATTGTC ATGTTGATAT CACATCCTCT TTTGTATTTT TTGATTTTTA 300

GTAAAGAATA TAAGTATCAT ACCTAACATG GTTGATGCTG CTGGATACCA AAAnATACAT 360

TTTCCCAAAC CTTACCCAGT GGACTCCTAG GCACCACCTT 400

(2) INFORMATION FOR SEQ ID NO: 1063:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1063:

TGGATCAGAA GGAATCTGGA TGCCTATTGA TGACAAAGGA TACTTTAATT TTGACTTCAA 60

AACGAAACGT TTCGATGATT TAGAGTTAAA GAAAAATGAT GAGATCTCAT TAACATTTGC 120

ACCTGATGAC GAAGATGAGG CATTGAAGTC ATTAATTTTC AAAACTAAGG TAACGAGTTT 180

AGAAGATATT GATAAAGCAG AAACTAAATA TGACCATACT AAAGTGGAAA AAGTAAAAGT 240

ATTGAAAGAT GTTAAAGAAG ATTTACATGT AGATGAAATT TACGGAAGCT TATATCATAC 300

AGAAAAAGGT AAAGGTATTC TTGATAAAGA AGGTACTAAA GTaATTaAAG GTAAGACTAA 360

ATTCGCAAAT GCAGTTGTGA AGGTAGACTC TGAACTAGGT 400

(2) INFORMATION FOR SEQ ID NO: 1064:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 434 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1064:

GTGGTCGTGA AGCAACTGAT TTCAAAGAAG AAGATATCGA GCTTTTCAAA GACATTGCCG 60

ACAAAGTAAA ACAAACAAAT AGTTATGATC TAGCGTTTGA TGAATTAGAA AAAGAAAAAG 120

ACTTCCTGCA AGTCATTGTC AAAAACGATG ACAAAAACTT ACCTACTAAT CAAAATGTCG 180

CTCAACTAGT AGAAGATTTA CGCCTAGAAA TCCAGAAAAT GCGCGAAGAA CGTCACCTAC 240

TTGGTCAAAT GATGAATCAA GTACATCAGC AACAACAAGA ATTAAAAGAA CTTCAAAATC 300

AACTTACATC TAAAATCGAT TCAAATAGCG AATCCTTAAA AGCCATCCAA ACATCACAAG 360

AGGCTATCCA AGAAGCGCAA GCCTCTCAAG CAAAAGCATT AGCTGAATCC ACCAATAAAG 420

TTGGAAAGAA TGCT 434

(2) INFORMATION FOR SEQ ID NO: 1065:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1065:

TAAAACATAT GGCTTGATAT TGCAGAAGAA TTGAAGTTAT CGTACCAGAA ACGGTACATA 60

ATCATGATTA TATGGAAACG AAAAAAATAA AAATGGGTCA TTTAATATAG GAGGATTTAA 120

CATTGAATTT TGAAGGTAAn TAATTGGAAA AGATTTGAAG TTGCATCGTT ATTATCGTTT 180

AATGATTTTA TCACTGGAAG ATTACTTGAA GGTGCAAAAG ATACnTTGAT TCGACATGA 239

(2) INFORMATION FOR SEQ ID NO: 1066:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1066:

AAATATCTAT AGACCTTTAT TCGGAAATGG TTCGTCTCCA GAATGGAAGG ATGAAGTACC 60

GAGTATTGAA AGGTAGAAGG TCTCCAAACT TTACCTGnAC GTGCACGAnA TCTAACTGAA 120

GATGATTTAG CAATTGAATT GAAACAGCCA ATTGTCGGTT GTAATAACTT AGGAGAGTTA 180

(2) INFORMATION FOR SEQ ID NO: 1067:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 749 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1067:

CTACAATTCG ATCAACGCCG AAGTTAGATA CACCGATTGC TTTAATTTTA CCATTTTCTT 60

TTAACTCTTC TAATGCACGC CATGAGCCAT ATACGTCATT GTAAGGTTGG TGAATAAGCA 120

CTAGATCAAG ATAGTCCAAA TTTAATCGTT GTAATGATCG TTCGATTGAT TTGATAGTAT 180

CTTCATAGTT AACATTTTCA ATCCATACTT TAGTCGTAAT GAATAGTTCA CTTCTATCAA 240

TACCTGAAGC TTCAATACCT TGACCTACTT CAGTTTCATT TAAATAACTT TGTGCTGTAT 300

CAATATGTCT ATAACCCGCT TTAATTGCTT CTTTAACCGC TTCTGCnGTT TGTTCTTGAG 360

GAATTTGAAA TACTCCGAAA CCTAATACTG GTATCTTTAC ATCTTTACTT ATTTCAATAT 420

GATTCATAAA ATGAACCTCC TTTATCTtGT ATGTCCACTA TAAACCATGG AGCGAACTCT 480

ATAGCAAGCC ATAGGTTTAC TTTCTCTCCC AAAGACGTTC AACATTGTCA TCATAATTAT 540

CACTAGCATT GATTTTAGCA ATATGATTAT CATAATTATC AATTTTATAT TGTAGTAAAT 600

CTCTCGCATC ATGAATTGTC TTTAAGTTTT CATTTAATTC TTCGAGTTGC TTATTTAAAA 660

TTTGCTTTTG CTGTGCTTGA ATATTTTCAT TTTTAGGCAA nTGCGCTAAC CTGCAAAATT 720

CGATAAGCGA TTCAATACTG ACGCCTGCA 749

(2) INFORMATION FOR SEQ ID NO: 1068:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068:

TCCTCGAGAT AGACAAGAAT GGTGGTACAA TGTTTTTTAT GACGATGGCA AATATnATAA 60

GAAnATAATT AAGAATGACA TGTCAAAAAT TAGGCGTAAT TTTTAGATTT ATCTATATAT 120

TTATGCCACC GCTCAAACTT TTATnAAAAG TAAAAAGACA ATATTTATAT TGAACTTGTG 180

ACGTGAATTT CTAAAACACA ACCAACAATC CACAAGGAAA CTAGTAAATA AGTTTAAATA 240

TACTGACTAA AAAGATTTTG AAAGTGATTA AGTATTTAAA ACACGCCAAT CTTAAACCGC 360

TATTGACAAA TATGAAGCGG AACCACCGTT GTnTTTCTTT TnCAGGTCCA ATTGAATAAA 420

TGTTGATGAA TAGAAT 436

(2) INFORMATION FOR SEQ ID NO: 1069:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 551 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1069:

TTCTCAAGTA ACAGGTATTA TTGTTACTGG TACAATCAAT AGAGAAAAAT ATGGCATTAA 60

CTTTAACCAA GCACTTGAAA CTGGTGGCGT AATGCTAGGC AAAGATGTTA AATTCGAAGC 120

ATCAGCTGAA TTCTCAATCT CAGAATAATC TCATTACACA ATCCTCATTG TTTTAATATA 180

TATACGAAAT GCCAACTATA TCATCCCTAG GTATAGTTGG CATTTTTCGT TTAACTCATG 240

TGTAACAAGC ACTAACTGTT CACCCTAATT TTAGACGCCT TTCATTCAGG TAGGTCTTAT 300

TGAAACTGAA AACTTTGaTG ACCTTTTGcA AaGCCATTAA CTGTATAAAG CATAGATCCT 360

CCGCCCATTT CTATATCATT GGAACAAATG ATGAGTTGAT TTGTTCCAGG TATAAATTGC 420

GGATGAGTAG AACGTAACAT ATGCCCTTCA TCTCGGCCTG GTATCAATAT TTGTCCTATT 480

GGATAACCCC TTTTATTAAA AACTAACACT CGACCTTGGA CCATACATTG CTACGGATAA 540

ATTATCGGCA C 551

(2) INFORMATION FOR SEQ ID NO: 1070:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1070:

TATnATGGTA ACGCATGAnC CTGTTGCAGC ACGCTATGCA AATCGAGTAG TGATGCTAnA 60

AGATGGTCAA ATTTTCACTG AATTATACCA AGGGGATGAC GATAAACATA CCTTTTTCAA 120

AGAAATAATA CGTGTACAAA GTGTTTTAGG TGGCGTTAAT TATGACCTTT AACGAGATAA 180

TATTTAAAAA TTTCCGTCAA AATTTATCAC ATTATGCCAT CTATCTTTTT TCGTTAATTA 240

CAGAGTCATA TCCAATTATA CnGGC 325

(2) INFORMATION FOR SEQ ID NO: 1071:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 771 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1071:

TAAATGCCGC AATTGGATAG CTTTAATATA ATTAATAGTC AAGGTATTnC CAACAAnAAT 60

ATATTATCCA CCCGAAGGAA GCGGGGTATn TTTGTTACTG ACGTCCCACA AGAAGCACAn 120

ATATTAGATA GTGCTTACTC TGAAATTAAA AAATTAAGAG ATTATGATGA AAAACTAATT 180

ATCCCAGGAT TTTTTGGCGT ATCTCATGAA GGATATATAG TTACATTTCC ACGTGGCGGA 240

TCAGATATAA CTGGCGCCAT CATATCAAGT GGTGTTAGAG CCACAATTTA TGAAAATTTC 300

ACCGATGTGT CTGGTATTTA TAAAGCTAAT CCAAATATCA TCAAAGATCC TGAATTAATC 360

GAAGAAATCA CTTATCGAGA AATGCGTGAA TTATCTTATG CTGGTTTTAG TGTTTTCCAT 420

GATGAAGCCT TACAACCACT TTATAAAGAT CGCATCCCTG TGGTGATTAA AAATACGAAC 480

CGCCCTCAAG ATAAGGGTAC ATTTATAGTG CATGATAGAG AAATAAATGC GAAAAATGTG 540

ATTAGCGGTA TAAGTTGTGA TAAAGATTTT ACCGTTATTA ATATCAAAAA GTATTTAATG 600

AATAGACAAG TCGGCTTTAC TAGAAAGATA TTAGGTGTCT TAGAGGATAA TAATATTTCA 660

TTTGATCATA TGCCTTCAGG TATTGATACT ATCAGTATCG TTATGCGTTC AAAACAAATT 720

CAAAATAAAG AAACAAAAGT ATTAAATGAA ATTCGTCAAA AATGTGATGT T 771

(2) INFORMATION FOR SEQ ID NO: 1072:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1072:

CGGTGGATCC GTTTGATCTT GAGTGAGGTG CCAATGAAAG TTATGAGCCA CGTTGTCGCG 60

CGCACCATAT CGTAGCACCT AGTGATAATA ATAAGGAGGA ATTATAAGTG TTTGATCAAT 120

TAGATATTGT AGAAGAAAGA TACGAACAGT TAAATGAACT GTTAATGACC CAGATGTTGn 180

(2) INFORMATION FOR SEQ ID NO: 1073:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 733 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1073:

CTTCTTGTGA GGGCGTTACA TCACCGGATG GATGATTATG AACTGCGATG ATTGCATTGG 60

CATTTTCTCT CACCGCAATA CTAAAAATTT CACGTGGATG TACAATCGAA CTATTTAATG 120

TACCTTTAAA AACACAGGTT TCTTTAATCA CTACATTTTT TGAATTTAAC AATAAAATGA 180

CAAAATGTTC TTGTGTTAAA TCTTTCATTG TTGGAATCAT ATAATCAGCA ACATCACTTG 240

GTTGCGTTAT TTkTATACGA TTATTTTCAG CTCTTCTCCC CATCCTTTCC CCTAACTCAA 300

ATGCTGCTTT TAAAGTAATT GCTTTTTGTA ATCCAATCCC TTTAACTTTT ATCAAATCGT 360

TAATTGAAGA TTTTTTCAAT TCATTCAGAT TcGAAGCAGA TTTAAGCAGT TCATTACTAA 420

TGTCTATGCT CGAGAATCCT TTTCTTCCGG TGTTAATTAA TATAGCTAAT AATTCTGTAT 480

TCGAAAGACT TTTTGCACCA TGGCTTAACA AACGTTCTCT TGGCATTTCT GAAGTTACCA 540

TTTCTTTAAT TTTCAAAAAT ATACGCCTCC TAAAAATTGA TGGATATCAT TATAAAAAAG 600

TGAATTGATA AAAAAGGArA TAAATATAAA TGGAACAAGG GGTAATAGTT TAATCGGCTT 660

AAATATCATG GTAATTAAAG CAACTAAACC AGCAATGACA AATGTAAATA AnATGACATA 720

AATAGTGAAT TGG 733

(2) INFORMATION FOR SEQ ID NO: 1074:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1074:

ATGGTTATTT TTTATGCTCT AAATCGTATG TGTTTATAAG GTTCAATTTC TTGCCATTAT 60

TAATTTTGCC GAGCAGTAAT GGGTTGTTAA AGTATCCATC AATTATGCTT AGCAATATTG 120

AAAAATTTAA ATGAAAAAGC GGTTCAATTC TTGAAAAATA GTGTATATTT ACATTTTGGT 180

AATAACTAAC TATAATTTAC ATAAGGAGGT TGTCATTTGG TAGTATTGTT ATCTTATAGT 240

TATTTACATA GAAGATCGAA ATGTGATTAT TGTAATTCGT CACTCAAAwG GTATGAATTA 360

ATGCCGATTA TTAGTTTTTT ATTATTAAAA GGGCGATGTC GAAACTGTCG AAAGCGTATT 420

TCCCTAACAC ATTTCTTAGG GGAAACCTTT GCTTTAATAC CTATCGTCTT TATTAAGTAT 480

GATTTCACAT ACGTAAATGt ACGCTATTTA TAACTACATA TGTTtTTCTG CTTATTTTTA 540

CTATGACCGA TATCACTTCT TTAATGTTAG ATTGTCGCTT AATTATAATT TATTGTATCG 600

TTTCTCTCTC GTTAAGTATG ATTTATCCAG TAGCTTTTAT CATTATTAGT ATGACCACGC 660

ATATATTCTA CTTTTTATTT CGGGCATATA TTGGTTATGG TGACGTTTTA CTAATATCTG 720

CACTTTCTTT GTTTTTCCCC TCTCCAATTC ACTATTTATG TCATTTTA 768

(2) INFORMATION FOR SEQ ID NO: 1075:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1075:

TCATATTCAT TTAAAATACC ATTCATCTCA GCTTTTCTCA TTTTCTCTTT ATAAAGTTGT 60

ATTTCGTGTC TTAATTCTGG CTCAGACATC TCACTCAATT TCTTCTGTTC CATCGGCAAT 120

ACCACTTTCT TCTAATTTAG CTTTAATTTT ATCATATTTA TATCCTTTTC TCATAAGGCC 180

TTCGATAGTT TTTGAAATTA ATTTCTGTTG CGTGTACTTC TTTCGATTTT TATTATAAAT 240

TTTTTCTAAA TCTCGTTGTA ATAAATCGTC TAAAACCGCT TCATCTTGTG TAAAATCCAT 300

TTCATTCAAT ACAGCATGAA TGGTTTCCAT TTCAAACCCT TTTTGAATTA AAGATTGCAT 360

TACTTTTGCn TnAACTnTAT TTTGTGGCCC nTTTTTTGTT 400

(2) INFORMATION FOR SEQ ID NO: 1076:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1076:

TTAGGTCAAA ATATGTTTTA TCCAAAAGGC ATTTTATCTC AATCTGCTGA AGCAAAGAGT 60

ACAACATATA ATGCAACTAT AGGTATGGCG ACAAACAAAG ACGGAAAAAT GTTTGCATCA 120

CAAGGCATCG AAGAATTACG TGATTTATGG CAACAAAAAA TGTTGCGTGA CAATCCAGAG 240

CTATCAATCG ACAACATGTC ACTACCAATT GTTACGAATG CATTAACACA TGGTTTATCT 300

TTAGTTGGCG ATTTATTTGT AAATCAAGGT GACACTATCT TGTTACCAGA GCATAATTGG 360

GGTAATTACA AACTTGTTTT CAATACGAGA AATGGTGCAA ACCTTCAAAC ATATCCTATC 420

TTTGATAAAG ACGGGCATTA TACTACTGAT TCACTTGTAG AAGCTTTACA ATCATACAAT 480

AAAGATAAAG TCATTATGAT TTTAAATTAT CCTAATAaTC CGACAGGTTA CACACCTACG 540

CATAAAGAAG TGACTACCAT CGTCGATGCA ATTAAAGCAT TAGCTGATAA AGGTACAAAA 600

GTTATAGCTG TTGTGGATGA CGCATACTAT GGTTTATTCT ATGAAGATGT GTATACTCAA 660

TCATTATTTA CTGCATTATC TAATTTAAAT TCAAATGCAA TATTACCTGT TCGTTTAGAT 720

GGTGCAACAA AAGAATTTTT CGCATGGGGA TTC 753

(2) INFORMATION FOR SEQ ID NO: 1077:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1077:

AGAAGCGATT TGACaATAAA ACAATTGAAA AACTTTTGGA AAGCAAGTGG TGGGAGAAAA 60

CGCCTGACAA ACTAAAAGGA TTTTCGGTTG AATATTTAAA TAAAAAGGAT ACTTAATGAT 120

ATGAGAATTT TAAATATTGT ATCGAGTAAT ATTGTTCAAG ACCCAAGGGT ACTTAAACAA 180

ATAGAAACAA TTAAAGGCGT TACGGATGAT TATAAAATTG TTGGAATGAA TAATTCACAA 240

rCTACTAATA AGCGATTGGA AAATTTAGAT TGTAATTATC GTTTGTTAGG TAGCAAGGTA 300

GATCCAAAAA ATATTCTTTC TAAATTAATT AAGCGTATAA GATTTGCaAC AGGTGtTATC 360

CGAGAAATTA AAGCTTATAA AcCTGACGTG AtTCATGCaA ATGAT 405

(2) INFORMATION FOR SEQ ID NO: 1078:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 504 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1078:

CATATTCACA CCTCAATATT CCATAACTTT TACTTTAATA TCAATCCACT TAAATCCATT 120

CACATCATTG AGTATAAAAT AATATGGTGA TATACGTTGA AGTTGATTAT CTTATATATA 180

AGTATACTTC ACAGAATTTA TAAAATTGTT TAGTCATCAT CTTCAGTGTT TAATTCAAAA 240

ATATAGAATC TACTGTATTG CATmATAaAT TGAAATGCCA CAAATTGTGC TCCAGCGATA 300

ACCAACATGC TCACAATAAT TATAAACTTA GATTCTACGA CATTAGGmAC CAtATATATT 360

CGATAATTTT TTCAATATAT ATAAATGAGC TCAACGCAGT TAATAATAAA CCGAAATGTG 420

TTTTAGTTTT ACCACCCCAA CGTTTTGTTA CTTTAGGTAA TTTTAATAAC GTGAACATTC 480

CGCCAATTAC TAATAACAAA TAAC 504

(2) INFORMATION FOR SEQ ID NO: 1079:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 645 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1079:

CATTCTTAAT CAACTTCTTC ATAATGGGAA TTTGGCATGG TAnCGAAGTG TATTACATTG 60

TTTATGGTTT ATACCATGCA GCATTGTTTA TAGGTTATGG CTATTATGAA CGTTGGCGTA 120

AGAmACATCC GCCACGTTGG CAAAATGGTT TCACAACAGC ACTTAGCATT GTGATTACAT 180

TCCACTTTGT AACATTTGGC TTTTTAATCT TCTCAGGTAA ACTTATATAA TAAAGGAGAA 240

TTTAATTATG GAATTTAGAG AACAAGTATT AAATTTATTA GCAGAAGTAG CAGAAAATGA 300

TATTGTAAAA GAAAATCCAG ACGTAGAAAT TTTTGAAGAA GGTATTATTG ATTCTTTCCa 360

AACAGTTGGA TTATTATTAG AGATTCAAAA TAAACTTGaT ATCGAAGTAT CTATTATGGa 420

CTTTGaTAGA GATGAGTGGG caACACCAAA TAAAATCGTT GAAGCATTAG AAGAGTTACG 480

ATGAAATTAA AACCTTTTTT ACCCATTTTA ATTAGTGGAG CGGTATTCAT TGTCTTTCTA 540

TTATTACCTG CTAGTTGGTT TACAGGATTA GTAAATGAAA AGACTGTAGA AGATAATAGA 600

ACTTCATTGA CAGATCAAGT ACTAAAAGGC ACACTCATTC AAGAT 645

(2) INFORMATION FOR SEQ ID NO: 1080:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1080:

AGATGCCAAA ATCAAAACCA ATAATTTGGC AACAACATAT AAGTCCACTT TACCGGACCT 60

nTAAACTTAT CGTACTGTTA AGAACCAAAC GACTGCCATT ATTTGGTCCT AAAGCCACGA 120

TGGTGGTAGC CnTTGTAATA ATGCTGGCGT AGAAATTAAC CGCCACCCCT AACACCGAAC 180

TATAACGCGG ATAAACCAAT AAAATTATGA TATAATCATC CGTTAAGTCA ATCCATAGTT 240

TAACATCCCT TATGTTTAAT TTACTCT 267

(2) INFORMATION FOR SEQ ID NO: 1081:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1081:

ATATTTGTCC ACTATTAGAA GATTGTAGAG AAGGACAAAA ACGTTATAAA GCTAGTTTGA 60

AAGAAGCGTG ATAACATGAC AAATATTACA AAAGAGGTAT TTGATAATTT AGAACAAGAG 120

ATTGATTTAT TTGCCAAAAA TAAGACATTA GGTTCTAGTG AAGCAAAGCC CTACTTGGAT 180

GAATACCATA GTAAAATTAT TGATTATTTT AAGCAGGTTA ATGACATAAC TGGCAATATT 240

GATTTTGATA AATTAAATCA ATATCCTGTT GTGCCAATGA ATTTTAAAGA AAGATATGAT 300

TATATGATTG AACGTAAATA TCATTTTATG GGCTATCGAC AAATGAAGAC CTTTAAAACT 360

GAATTGATTA AAATGnATGC TAGTTATCAA ACAAGGTTAA AGAATAAGCA GGTATnGACA 420

AGATTGATCA TTTCCTAGTG T 441

(2) INFORMATION FOR SEQ ID NO: 1082:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 410 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1082:

AAAATTTCTT AGtTGATGGT TATTGTTGTT GATTTGAATA ATTTGTAGCG AATATTTTGT 60

AACAGGGCTA CTAAGAATTT TTATAACAAG AAGTGATTTC AATCGTACTA ATTTTCAGCG 120

TTTGATGACA AAAGTGTATG TCCAAACTTA AATAATGGCG ATAAAATTTA AGTCATGGGT 180

GTTGAATATC AATAAAAGAT TAGCAAGTTA GTTCAAAATG GCTATGTATT GTTTTTTGAA 300

ATACATAGGT TTGAAATCTA TATTAATTAT GCACCAAATA ATTTAATTAG ACTCTATCGA 360

AAATTTCCAA ATTTTGCTTA CTATCTTTCT AATTTTACTT TTATATTGTG 410

(2) INFORMATION FOR SEQ ID NO: 1083:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 586 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1083:

CAGATATTCC CTTCTATTTA CAAGTTGGTA ACCCATATTT ATCAGACAGC GTAGATAATC 60

ATACCGAAAA GTTGTTAGAA CGCTACGAGC AGTTGGTGGA TTTAGTTATG yAAAGTAATG 120

ATATGAATCA CGTTTATGTG TTACCACAAC TTCATACATT ACTTTGGAGC AATAAAAAAG 180

GTGTATAAAG GATAACTTAT TTTACTTTTT GCAAGTCATA TCTAATGAAT AACAATATAT 240

TAATTGATAT AATAGTTGAT TGAAGTATAA CGAACAGGAG TCCATCATGA TTGTATATAT 300

ATTAATTAAT ATTGCTATCG TCGTACTTAT AACTGGATTC AATTTATATA GGCATCAAAT 360

GCAACATTTA TCATTAAGTG CAATGTTGTt ATCTATTACG ATaAACGCCT TTATAAATAC 420

ATTCATAATT GATAAATATA ACTTTATTAC TCTGTGTACT ATAACGATGT TTATCATTTG 480

GACGATACTA CAGTTTTACA TTGATAAAAA ATTAAAACCT GTATACATTA CAGACCAAAA 540

ATTTATTGCT ATCATATTAA CGATTGTTGT CAGTTTAACG CAACGT 586

(2) INFORMATION FOR SEQ ID NO: 1084:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 638 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1084:

AACACAAGGT AGCGTCATTA GCATTTAGAT TTTATTGCCA AATTATATAA CGATTTATAC 60

ATCAATAAGA AAACAATAGA TGATGTATCT GCAGTTTCTG AAGTGAAATA TGATATTAAA 120

TCACAAATGA GTGATGATGA GATTAAGCGT TTAGAGGAAC AAGGACTTCA AGCTATTAAA 180

GAAGGACAAT TTGCAGTACT TTTGATGGCA GGTGGTCAAG GAACAAGACT TGGTTACAAG 240

TTAAAAACAT TGAATCATCA ATCTGGACAT ACGATTCAAT GGTATATTAT GACAAGTGAT 360

ATCAATCATG AAGAAACTTT AGCTTATTTC GAAGCACATA GTTATTTTGG ATATGATCAA 420

GAAGCAATCC ATTTCTTTAA ACAAGATAAT ATTGTGGCGC TTAGTGAAGA AGGGAAGTTA 480

ATTTTAAATC AACAGGGTCG TATTATGGAA ACGCCGAATG GTAATGGTGG CGTGTTTAAA 540

TCTTTAGACA AGGCAGGATA CTTAGAAGAA ATGTCTAATA ATGGCGTTAA GTCATATTTT 600

CTTGAATAAT CATCGACAAT GTTTTCAGTA ACATGTTG 638

(2) INFORMATION FOR SEQ ID NO: 1085:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 618 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1085:

ATTGCAATAT TATCCGCTTG GTTCAACACG TCATCTTTaT tAaTACcATT TATTGgAAaT 60

tCcACCcATT TCCcGGgCTt CTtACTTCCc TTTATAAAAC TGcCCATTTA ATGAATACTG 120

TTTAGCTTCA TCTATTCGTA CTTCCACTAG TTTACCAATC ATTTCTTTAG GCGCTTTGAA 180

ATTAACTAGC TTATTTTTAT CAGTGTAGCC AGCAAGAACC TGATCATCTT TTTTACTACT 240

TCCTTCACAA AGTACTGTTA CAGTTTGTCC TTCGTACTTA CTcATAGCTA TTTGTGAATA 300

ATGACCAACT TTTTTATTCA AACGTTGCAA TCGTTCCTTT TTGACATTTA AAGGTACATT 360

ATCTTTCATT TTAGCAGCAG GCGTACCATC ACGTTGTGAA TACAAGTACG TATATGCATG 420

TTCAAAACCA ACTTCATCAT ACAGAGTTAA AGTTTCTTCA AATTGTTCCT CTGATTCATT 480

TGGATACCCT ACAATAATAT CTGTAGTTAA TGCTACATTA GGAATTCTAT CTTTGATTCG 540

TTTTACTAAA TCCAAATAAC TTTCTCGTGT ATATTTTCTA CCCATTATnT TTAATACTGC 600

ATTATTTCCA GATTGAAC 618

(2) INFORMATION FOR SEQ ID NO: 1086:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1086:

CAGCAATATC ATGATCAGTT TAATTCATCA AGAAAGTCTA TCTATACTTT TACAGAAACA 120

GTTCAACCAA ATCGTGTTAT TTATGATTTT TATGATTATG ATCCGTATCA ATTAGCAGCA 180

AATAATGCGA AAGCATTAAA GGATCATATT GAACAAAACT TTAACTTTAA AGTCCAAAGT 240

ACCGGTGTTA kTTACTTTAG TGATGGTACA GTTAATATCA TTCAAGGTTC TGAAGAAAGA 300

GATAAATATG TTGATACAGT TTCAACAAAA TCTTCGTTAC GACGTATTAT TAGCGAACCA 360

nAGAGCTATC TAAACACCCT TTAAATAAAG AACAGGTTGA nCAAATCACA GCTATATTCA 420

AGTAAAATCA AAGGCATAAT AATCCATTAC GCTCGATACG CACTATGGTT ATTATGCCTT 480

TAAATTATTT CTATATATAA nT 502

(2) INFORMATION FOR SEQ ID NO: 1087:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 429 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1087:

TTGCCTGATG GACGATGGCC ATCACAGACT GAGTTTAGAT TGTCTTTAAT GCAACAACTT 60

GCTGTAAACC AAATTACGAG TGGTAATGAA AGAATAAGTT CAGTTAATGG GCCACCAGGT 120

ACAGGTAAGA CTACTTTATT AAAAGATATA TTTGCTCATC TAGTAGTTGA mAGAGGTAAA 180

GAGTTAGCTA AACTAAATAA TCCTAAAGAT GCATTTGTCA ArACAAAAAT TCATGAAACG 240

GATGATAAAT ACGTATACTT ACTAAAGGAn nTATTGCCAA ATATAAGATG GTAGTCGCAT 300

CTAGTAATAA TGGAGCTGTT GAAAATATAT CTAAAGATTT ACCGAAAATT GAAGAAATTA 360

TAAGAnATCC CGAAAAATGT AAATTCCCTA AATATGAACA GAATTATGCA AATTTAGCAC 420

ATGAATTAA 429

(2) INFORMATION FOR SEQ ID NO: 1088:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 611 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1088:

TAAGACCTAA TATTTTGGnC CAATACTATG GTGCAGGTnA TTTATATATG ACACCAACAG 60

ATCCATTATT ACATGAGTTT GGTACGAAAA AGTATCCAGA TGAATATCGA TATGGTTTCT 180

ATGCTAAGCC AACATTGAAT AGACTTAACG GGGGATTCTT TGGACAAGTC TTTACTGTTT 240

ACTATAATGA TAAGTATGTA GTTGTACTTG CATTAAATGT AAAAGGAAAC AATGAAGTTC 300

GAATCAAACA TATTTATAAT GATATTTTAA AACAAAATAA ACCTTACAAT ACGAAGGGTG 360

TTATTGTTCA ATAATTAATA TAGAAGATAT AACATGTATA TGGCATTAAG GCATCGACCT 420

TATCTGACCA GTATACGAGT TATATCTTCT TTTTTATAGT GGTAAAAAGT TTAAAGTATA 480

AGGTTGAAGA AGGATGAGTT TAAAAATATG TGTTAACTGA TAAAAGGGGA nATCATTTGG 540

TGAGTTGGCA TCAGnCTAAA nTGAATGAAG ACGAATACGT TGGTCCATGC GTGGTGTGAn 600

TGTTTTCTAA A 611

(2) INFORMATION FOR SEQ ID NO: 1089:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 644 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1089:

CTGGATAATC GCTTTAATAT GATCAATTTG CTTTTCACTC ATATTAAGCT TATCTAGCCC 60

TTTCATTTTA TTCATACCTG GAATCATTTT CATAATATCA TCCAGTGGTC CTAGATTTTT 120

CACCyGwTCA AGTTGTTCTA AAAAATCATC TAAAGTAAAC GATGACTCAC GCATCTTTTT 180

CTCTAAATCT TTTGCTTTTT CTTGATCCAC ATCTTGTTGC GCTTTTTCAA TTAAACTTAA 240

CACATCACCC ATACCTAAAA TACGTGATGC CATACGTTCA GGATGGAATA GCTCTAAACC 300

ATCTAACTTT TCACTCATAC CAACAAATTT AATTGGTTTT TGTGTCACCG AACGAATAGA 360

TAAAGCTGcA CCACCACGTG tATCACCATC TAATTTAGTT AAGGtAACAC CTGTGACATC 420

AAGTTGATCG TCAAAAGATT CTGCAACATT GACAGCATCT TGACCCGTCA TTGAATCGAC 480

AACTAACATA ATTTCGTTTG GTTTAGCAAT GTCTTTTACT TCTTTTAATT CGTTCATCAA 540

TGCTTCATCG ATGTGTAATC GACCTGCTGG TATCAATGGA TTACAAAGTC TAAATGTTCT 600

TCTTTAGCAn GTTTTAATGC ATTAGTTACA ATTTGGTGTG GGCC 644

(2) INFORMATION FOR SEQ ID NO: 1090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1090:

GATCCTATCG TTTTAGTGCA TGGTTTCAAT GGGTTTACAG ATGATATTAA TCCTTCAGTG 60

TTAACTCATT ATTAGGGCGG TAATAAAATG AACATTCGCC AAGATTTAGA AAAAATGGTT 120

ACAAAGCTAT GAAGCAAGTA TAAGTGCTTT TGGAAGTAAC TATGACCGCG CATTGAACTT 180

TATTATTATA TCAAAGGCnG TCGnGTA 207

(2) INFORMATION FOR SEQ ID NO: 1091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1091:

GACTCTAGAG GATCCCCGCT CAAATGCCAT TTGGTGATAT TCGTGAAGCT GCTGGCGAAA 60

AAACATTTAA TCCAGTGGAA GATCGTTTCG TAATAAAAAA ATAATCAATA TATTGTTAGG 120

AATGGGACAG AAATGATAAA GATTCATTAG TTATTCATTA TGTTGTAGTT CTTACACATT 180

AGCCGCTGCT AATnGCAACT TAAGAnTAGG TT 212

(2) INFORMATION FOR SEQ ID NO: 1092:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1092:

TGGACCTGCA ATTGGTTGCC AGCAGCAACT TTAGCTTCAT AGCTAGCTTT GTGAGCAAGT 60

GGTAAACCTG GAACGATATC ACCAATTGCA TAGATATTGC TGATAGACGT ACGGCTTTGT 120

TTATCAACnn CTAATAATCC ACGTCAGCGA ATTTAACACC TAATTCTTCT AGGCCTAATT 180

CGTCGTGTTT GGACGACGAC CTACATTA 208

(2) INFORMATION FOR SEQ ID NO: 1093:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 902 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1093:

CTTAAAAGTT GTnTCAATAA TGATTGTATT AGTTGCATGC TTATTATATA TGAATCATAG 60

TATTGATTTA CCTACCCTTA TTATGATTTC AATTTTTTCA TTTGTGATAT TTGATAGTGT 120

TGAAAATATT AATAGTGCTG CACACGTACT TGAAATGATA GATATGACGA TAGATGATAT 180

TGmAAAGATA AAAAATGCTC CAGAACTGGA TGAGAATGGA AAAAATTTGA CGATTAAAAA 240

TGAAAATATC GCTTTTCAAA ACGTGAACTT TTCATATGAT GATAAACAAG TGATAAAGAA 300

TGTGAATTTT GAGATACCTA CACAAACATC AACAGCAATA ATTGGACCTT CAGGAAGTGG 360

GAAATCTACA TTATGTCACT TACTCTTGCG CTTTTATGAT ATCGATGATG GAAATATTCG 420

CATCGATGGT GTTGATATTA AAGATATGAC ATTAAGTACG TTAATGTCGA AAATTAGTGC 480

AGTATTTCAA AAGGTGTATT TATTTAATGA TACGATTGAA AATAACATAT TGTTTGGCAA 540

TCCAGGTGCA ACGAAAGAAG AAATTATTCG TGCCGCGAAG CAAGCATGTT GCCACGACTT 600

CATCATGTCA TTACCTGAGG GATATCAAAC AATGCTAAAT GAAAAAGGTA GTAATTTATC 660

TGGCGGAGAA AAGCAAAGGA TTTCTATTGC TAGGGCGATA TTAAAAGATG CACCAATAAT 720

TATTTTAGAT GAAGCAACTG cAAGTATTGA CCCTGAAAAT GAACAGCTGA TTCAAACGGC 780

AATTAATGAA TTAAGTAAAG GCAAAACAGT AATTACAATT GCACATAAAC TTGAAACTAT 840

TAAAnATGCA GATCAGATTA TAGTGCTCAA TGnAGGTGAA ATAATTCAAA AAGGTAGTCC 900

TG 902

(2) INFORMATION FOR SEQ ID NO: 1094:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 632 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1094:

ACGCAAGGGA TATGATTAAA CACCATAATA TACAATCACC TTTTTTATAC ATGAAAGCAC 60

TAATAGAATC GATTCATTTA AACATAAAAC ATGATTTTAA CCAGCAAGAT TTGATTGAAA 120

TACCAATTGT GTATGGTTCG AAATATGGTC CGGATTTAGA ATCACTTTTA AAACATTACA 180

AAATCAAGCT AGAAACTTTT ATTGAATTAC ATTCTAAGGC GCAATATTTT GTTTCGATGA 240

TGGGATATTC ACCTGGGTTt CCTTATTTAA CTGGATTAAA TAAGAAATTG TATATTAATC 300

GCGGTATTGT AACTACGGAT ACAATTAATG ATTGGTTAGT TATTGGTTAT ACACCATTAT 420

CACTTTTTAA TCCGAAAGAA TCAGATTTCG CACGCTTAAA GTTAGGCGAT AATATTAAAT 480

TTAGACCTAT CAATGAAAAT GAATTAGAAG TAGGAGCGTT TAAAGATGTC AATCATAATT 540

GAAAAAAGTG GCTTATTCAG TAGCTTTCAG aCTTTGGCAG AAGGGGATAT GAACATGATG 600

GTGTAATTCC ATGTGGTGCA CTTGATACTT TA 632

(2) INFORMATION FOR SEQ ID NO: 1095:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1095:

GCAACACGAT TGCTAAAAAA TGATATACTT ATTAATTGTT GCAACACTTG TTTATGTGAT 60

ATACTGATCA TGGCATTGTG GCGGATTGAT GACCATACAC ATGACGTGAC AATGATAAAT 120

CATTGCCACT ACTTGTTAAA ACAGCAATTT CTCAAGTGGA AGCTGGTGCn ATATATTnCG 180

CCAATAATAT GATGGATGGT TTGTTGCTGA AA 212

(2) INFORMATION FOR SEQ ID NO: 1096:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 466 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1096:

AATGAACTGG GTATTnCTTT TGCCATGCTT GCCCACTGCC ATGCATTTGC TGAAGAATGT 60

TTTTGTAGAA CCGgCTTAAG AATTTGAAGT TTGTAGTAGT ATCTAAAAAG ATTACTTGGT 120

GATACTCAGG ATGAATTCCT TGTTcATTAT TTTCAGCTCC TTTGCCCTGA ACCATCTGGA 180

ACAGAGTTAT TTGTGAGTTT TTACCCAATA CTGTGTAATT ATAAAGGTAA TTAATTCAAA 240

ACGCAAGCCC CTATATAATG TTTATTAAAT TATAGGTCGA CCCGTTTTAG TACTTTCTTC 300

TGCAGACTTT TGTAGCTGCT TGAAGAAATC TtCATTATTC TTAGACCTTT TAAGTTTGCG 360

AATAAATCTT TCAGTAAAGT CAGTTGAGTC AGTGAATAGA TTTCTTAATT GCCATAATGT 420

GTCTAATTCA GATTTACTTA TCAACAATnC TnCTTTACGC GTTGAA 466

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1097:

TTTTGATTCA ATAGGCGGTT CCGTGTTATC ACTGACAACT TTAGTTGTAG CTTCATCTTT 60

ATGTATTTCT TCGTTAAATC CTTCAAGTTT TTAGTCGTGG GATTTTAACC TCAGGATGTT 120

CCATCATGTC TTGACTATCA AGTCCTTnTA CACGTGTCTT TATGTGATGC TTGATTGCGT 180

nCCCTTACTT TTTGAATAGG GGTAGTAA 208

(2) INFORMATION FOR SEQ ID NO: 1098:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1098:

CCTTCAACGA AAATAGCATA TTGACCATAA ATATTATGAA TTGTTTGTTC AACATCTTCA 60

GTTATTGGAT CTTGACTCAA AAATACATTA AATACTTCAA TACCAAATTT ACGTGACATT 120

TCTACAGCTT CATACGTATC AATAATACCA TCTTGACTAT AATTAAATGC AGACGGTTCG 180

CCGTCTGAAA ATAnGATTAA AAATCGTTGA TGTTGATTTC GACGCATTAA TCGTTCACTT 240

GCAACTCTAA TAGCAACACC ATCACGATTA TCATCTTGAG GTTCAAGTGC CATAATACGT 300

GGGCCATCTT TTTCAAAGGT TGAGTAATCA TAGTTAATAA TTTCATTAAT GATATTTGGT 360

TGTGCATGCT CGTCTGAATC AAAGGCATCC TCACTGAATG ATAAAATTTC ATGTTTAATG 420

TTCAATGCTT TTAACGTCTC GTGGAATAAC ACTACACCTT TCTTCGTTTC AGCCATTTTA 480

TCATGCATAC TTGCTGgACG CATCAATTAA CAATGTAAAT GTnCGCATCA AATGATTnAC 540

TTAAATCTTG TTTTTTGTAA AACAATTTAT A 571

(2) INFORMATION FOR SEQ ID NO: 1099:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1099:

TGCAAGTGAA CAAGTCATTA ACTTGTTTAA TACACGTGGG GCACAAGTCG AAGAAGTTTG 60

GGTGAAGGGC CATGAAATTA CAGAAACTGG ATTAACGGCT GGTCAACAAA TACTTGGGAA 120

ATAACAGTTC TATTAAGAAG CGGACAGATG GAAAAGATTT TACCTTTCAT CTGCCGCTTT 180

TTGATTTGAA GGCCGGACCn AATTTACCAn GGAA 214

(2) INFORMATION FOR SEQ ID NO: 1100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1100:

CACCGTATTG TACAAAGAAT TTAAAGTTTT CGATTTCTTn TCTTAATTTA TCATCAGCTA 60

TCGGTTTGGT TGGGATAATT TTATTATGTT CCATTTTTAC TGGATATTCT TTTTCTTTAC 120

TACGTGAGTA TCCTnTTTTA TCTTCCCATA ATTCCCTCAC AATAAATTCA CCTTTTGTCG 180

TTCTGGTATT GCGGTCTACA TACAGGACCA ATCCTCTGGA TTCCaTATTc TTTCCATTTG 240

TTTCTATTGT CATTTTAGAG TGAATTATCC aAGTGCCTTT GTCGCCCTTT TCAAACTCTT 300

GATCTCGAAA GCCTTCCTTA TCATAAAAGT CTTCAAGATT TTTAGTTGGA TACAGGCTCA 360

ACGTTTTGTT GAAGTTTTCT TTAATTTGTT TATCTTTACT GCTTTCTTCC TTTTTCATTC 420

CGCAAGCCCC TATAAAAACA GCTAATAATA CTAAATACAG CCAGAGCCTC AACCTTTTTG 480

AGTGAATCAT CATTTCACAT CCCCATTTTT ATTTTTGATG CAAAGTTAAG TtCAAATTCC 540

AATATTAATA ATATTAGAGG aAAtTTtATG ATTAAaTCCT CGTGGATTtT AATTGTTAGT 600

TGTATTTTTC ACATATCAAC ATCACAAATT ATTTAAAAAG CGCAAATATC TTTATAATTT 660

TTATTGGCCT AACCAACTAA TTAATTAAGA TAAATTGCGC TTATATTTAA AATAATAACA 720

CTGAAACTCA ATGTATTTAC TTATTAAAAT TGATGTTTAA ATACAACTTT ACTAACATTC 780

ATTTTTCGGT TTACATTAAT TkGTTAGATA ACGATATATA TCAtCTCTTA CAGCTTTATC 840

CAGTGCTAAA TCCATCGTTA CTACGTTTGA ACCATTCGGC ATTTTATCTT GCTTTTCTGA 900

ACCTTCTATA TATCCAGCAG TTCCTAAATA ATAAAAATAT ATACCATCAT CATCTTTTTT 960

CTGTACAAAA ATATACATTT TAATTCCTTT TGCTCTATGG GACAAAATTT TCTGAACTTC 1020

TTTTGATTCT AGCGTTCTAT TAGATTTAGT AAACCATTTT AATTCATCTT GACTTAAAAA 1080

TGGCATTTCT TGGCTTTT 1158

(2) INFORMATION FOR SEQ ID NO: 1101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1101:

CCAAATGCTA TAAATGCAAA AATnGCTAAT GCGATATTTT TATAGAAAAT ATCTGGTCCT 60

AAATTTTGTA AATACGTGGT AAACGTTGCG TATGACAATA AGCCAATCAC TACAGCGTAA 120

ATATGTGAAA TAATTAAACC GAACCGTCTC GCTCTTTCAA AAACAAGTGT TGCTAAAATA 180

ATAATCAGTA ATCCAAATGA CAAGGGTTGT CGCCAACTTA ATGGTAAAAA CTGACCTAGA 240

TAGCATCCTA TGCCAAATAT AATCCAATAA TACATAAAAT AAAGCCACAC TTTACTTAtT 300

GATTGAGCAT GCTGGTTTTG ATGATAATAT GAATGATTTG TATTTTGCGA CAA 353

(2) INFORMATION FOR SEQ ID NO: 1102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1102:

CCCACACGTC TTCCACCGGA TAGGTTTCGA GCTCGGGCGA ACCGGGCAGG GCGGTGACCA 60

CCCCGTGCGG TGTCTTCTTG GCCAGCTTGT TTGCGAGCTT GGCCAGCGTC TTCGTGGGGC 120

CAATGCCCAC GCAACACGGG ATGCCCACCC ATTGGAGGAT CTGGGCACGG ACCTGGCGGG 180

CCATCGCTTC GnTG 194

(2) INFORMATION FOR SEQ ID NO: 1103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1103:

TCGCTTTTGC TTTTGCATCA GGTATTGCTG CTATTTCAGC ATACTTTTTG ACTTTCAAAT 120

CTGGTGATCA TGTCATCTTA CCCGATGGAT GTATATGGGC GGTTACTTTT CGTCTCACTG 180

TGGCAAATTT TGGATCGATT TAATATTGAA TTTTACAACC 220

(2) INFORMATION FOR SEQ ID NO: 1104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1104:

GGACATTGTA TCGACATTTC AAAGATAAAA GCGATTTATG CTACTACGTC ATACAAAGAG 60

ACCTTGATAT TTTTATCACT CATTTTAAGC AAATTAAAGA TGACTATCAT TCTAATTATG 120

AGGTTATGCA AGTGTCGTCA TCGCTTTTAA ATAAGTCATA ATAAAAATCA AATAATTCTT 180

GATAAAATGC GCTTTGGTAA AAACGTAATT TATTGTTGCC TGCTTCAATA CATTG 235

(2) INFORMATION FOR SEQ ID NO: 1105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1105:

GCGGGGGCAG GTAAATCCAC TTTGACACAT CTTATTGCAG GTGTTTATCA GCCAACAATA 60

GGTACTATAA GTACAAACCA GCGTGATTTT AATATTGGGA TACTTAGTCC AnAGCCCTAT 120

ATTTCAGGCT CTATAAAAGA GGATATTACG ATGTTTAAAG nTATAGAAAA TAATACTAAT 180

GAAGAAGTGC TAGACGAAGT AGGGTTTATT AGACCAAGTG CCATCCTTC 229

(2) INFORMATION FOR SEQ ID NO: 1106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 596 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1106:

rAATTAAAAT CAAAATTTGA TGAAGTAAAT GTAATCGCGT CAACAAACGG TAGAAAGTTT 120

ATTAATGGTG AAATATTAAA GCAATTTTGC GATAACTATT ATGACGAATT TGaAGACCCT 180

TTTTTAAATC ATGTAGATAT AGCAAATAAA CATGACAAGA TTATTATTTT ACCTGCGACT 240

TCTAATACGA TTAATAAAAT TGCmAATGGT ATATGTGaCA ATTTATTATT AACTATTTGT 300

CATACAGCTT TTGrAAAACT TTCTATATTT CCAAATATGA ATTTACGAAT GTGGGAAAAT 360

CCAGTTACTC AAAATAATAT TCGATTATTA AAAGATTATG GTGTATCAAT ATATCCAGCA 420

AATATTTCAG AAAGTTATGA ATTAGCGTCA AAAACATTTA AAAAGAATGT TGTCGCACCT 480

GGAACCATAT AAAGTTCTGG gAATTCATTT GaGATTAGAA TATGGAAAAT CaTAAAGCGC 540

GCkATTGATT AGTTTAATGA ATGATTGGAG TCnTTTGAAG ATnCGATTTA CAATGG 596

(2) INFORMATION FOR SEQ ID NO: 1107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 673 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1107:

ACTAGCTAAA AATAATATTC TATTCTTTTT AACATGGGCA GTTCCAGCGG CAATTAGTGG 60

TATTTATATT AAATATATAA ACAAGGCTAC GGTAGAAAGA TTTTTTAAAT TAGTATTTTT 120

CATATTTTCT GTTTCATTTA TTTTTGTAAT TTTAATACCA AAACTTACAG GTGAGATACC 180

TAGCTATATC AATTTTGGAC TTATGAACTA TCAAAACGCT TCGTACCTTT CAGCATTTAC 240

TGCCGGATTA GGCATTTATT TCATTATGAA AGGTTCAGTT AAACATAAGT GGATATATGT 300

TCTATTTACA ATAATTGATA TCCCTATTGT GTTTATACCA GGAGGGCGTG GAGGTGCTAT 360

TTTATTAATT CTTTACGGCT TATTTGCATT TATACTTATT ACGTTTAAAA GAGGAATACC 420

TATCGCAGTA AAAAGCATTA TGTATATTTT TGCATTAAGC ATATCTAGTG TATTGATTTA 480

CTTTCTTTTT ACAAAAGGTT CGAATACTAG AACATTTTCA TATCTACAAG GTGGAACACT 540

TAATTTAGAA GGTACTTCTG GgAAGAGGAC CGATTTATGA AAAAGGTATT TACTTtATTC 600

AACAAAGTTC GTTATTAGGC TATGGGCCAT TTAACTATtA TAAACTAATC GGAAATATAC 660

CACATAACAG CAT 673

(2) INFORMATION FOR SEQ ID NO: 1108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1108:

TCACAGTGGC GGCACAAAAA GTAAGTGGAG ATTATTTTAA TTTAATTGAC CATAACGATG 60

GCACAATGAG CTTTGCTGTT GCAGATGTCA TTGGAAAAGG TATACCAGCT GCTTTAGCAA 120

TGAGTATGAT AAAGTTTGGC ATGGATTCTT ATGGACACTC ACAATTACCG AGTGATGGTT 180

TAAAACGTTT AAATCGTGTT GTTGAAAAGA ATATTAATCA AAATATGTTC GTCACAATGT 240

TTTATGGTTT ATATGAAGAA ATGAACCATT TATTGTATTG TAGTTCAGCT GGTCATGAGC 300

CTGGATATAT TTATCGCGCT GAAAAAGAAG AATTTGAAGA AATTTCAGTT AGAGGTAGAG 360

TGTTAGGAAT CAGTTCACAA ACACGATATC AACAACAAGA AATTCCAATA TACCTTGATG 420

ATTTAATTAT CATTTTAACG GATGGTGTGA CTGAAGCTAG AAAAGTGAAG GTACCTTTAT 480

AGATAAACAA AAACTTTTAG AATATA 506

(2) INFORMATION FOR SEQ ID NO: 1109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 552 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1109:

TGATATTGAA AAAGATGTCA TTGTTAAAGC ACAAGAAAGT AAAATTGCTC AAGTTATCAC 60

GAATTTGTTA ACGAATGCAA TTAACTATTC TTATGAAGAT GGAGATATTA ACGTTCGTGT 120

GTATCGAGAT GACTTTCGTG TCATTTTCGA AGTACAAGAT TTTGGTATAG GTATTAAATT 180

AGAAGACCAA CAACGTATTT TTGAAAGATT TTATAGAGTA GATAAAGCAC GAAGTAGnAG 240

ATTCTGGTGG GACAGGTCTT GGATTATCAA TTACAAAGCA TATAGTAGAs GCCCACCAAG 300

GCAATATTGA AGTGAATAGT CAAGTTGGCA AAGGCTCAAC GTTCAAAGTT ATTCTAAAAG 360

ATTATAAAGA ATAAnAATTA AAGTGGTAAC AGCGCGTGTA TTTTTCACGA AGTTGTTGCT 420

GCTTTTTTAT TTCGTTCAAA TCTCTATTGG TATTAAATTA GAGTTAATGA AGTGGAATAA 480

ATTCGGTTGT CAATTTTGTC ATTTGTATAT GTCGATTTGT AAGTTATAAG TAATAGATTG 540

TTGTGAATCA nG 552

(2) INFORMATION FOR SEQ ID NO: 1110:

(A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1110:

AACAGATCAA CAATTGCAGA TCAATTACTC GTCATATTGA TCAATTATCT CTGACAACGA 60

GTGATGATTT ATTACGTCAT TGATTGATCA TCACAAGATA AGTCGCTATT GATTTCTCAA 120

TTTTACAACG AnATTAGGAA AGCTGnAGCA GATAATTGGC TAAGTTGGAC GATAAAGGTT 180

ATCAATCGCC AATCGTTGCC ATTGAAGAAC TTTTGCTCAC TGGCGCACGC TTCAGATGAT 240

ATTT 244

(2) INFORMATION FOR SEQ ID NO: 1111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1111:

AGTATTGAGT GTTTTGATTT AAGAGACTTG GAAAGTGAGT CAATAATCAA AATCTTACTC 60

AATACTTTTA TTTTGGTACT CGCAATTTAG ATTTGTTAAC TAATTTTTTC GCTTATTATA 120

AAACGAAACA ATCAAGTAAA CGATAAAGCC TACAAAGATA CCCAATAAAA TAGATAGTAC 180

TGCCGTCACT ATTAATGGTA ATTTGAAAAA TATTTGTAGG AAAATmCCAA TGATAATTGC 240

GATAATTACT GCAAtTaATG TGACTGTATT TTCATTTGAA ATGTTCATtT ATttTCACTC 300

CTtAACAATA ACATTATATC ATGCTATAGC TTTCCAAAAT ATTGAAATAT GTAGATATGG 360

CTATTGACGA TATTTCTTAA CTTTTATATG ATTAATCGGA ATGAAAAAAG AGAAGTAGGT 420

GGCAATATGA AGTCAAATAA ATCGCTTGCT ATGATTGTGG TAGCCATCAT TATTGTAGGT 480

GTATTAGCAT TTCAATTTAT GAATCATACG GGTCCTTTCA AAAAGGGGAC GAATCATGAA 540

ACTGTACAAG ATTTAAATGG TAAAGATAAA GTACATGTTC AAAGAGTTGT GGATGGTGAT 600

ACATTTATTG CAAATCAAAA TGGTAAAGAA ATTAAAGTTA GGCTTATAGG GGTTGATACG 660

CCAGAAACGG TGAAACCGAA TACGCCTGTA CAACCATTTG GCAAAGAAGC ATCAAATTAT 720

AGTAAGAAGA CATTAACAAA TCAAGATGTT TATTTAGAAT ATGATAAAGA AAACCAAnTC 780

GCTATGGTAG ACCATTGGCG TATGTATGGA TAAGTAAAGA TCGTA 825

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1112:

TCCCTATAAA TCCCCACAAA AAAAGGGTAA ATCCGAACGT CAAATTTCAT CTCTTTATGC 60

CAATCAACGA TCGATTTACC TTTTAAAATT TAAAATGTAT CTGTAATACT CTTAGCAATA 120

TTTGTATATG CTGCATCTTC CATAGGTGGA TTGTGTAATC CTGCACGCAT GTCACGATAG 180

TAACGTTGTA ATGGTCGATT CATTTCTAAG CTTTTAGCAC CAACTATTCT CATCGCTAAA 240

TCAATCACTT CAAGCCCTTG ATTCATTACC ATCACTTTAC TCGCACTTGT TGGATTTCTT 300

ATCTGACTGT CATCTTTATA TTGTTGATAC CCTTTTGCTG TACTCCATAA AAATTGTCTC 360

GCACATAACA ATAGCGTTTC CATTTTCCCT AAATTTTGTT GCACAGTTGG CAATGTTGCA 420

ATCGTTCCTT CAATACTATT AGGGCTATGT TGGATTGCAA AGTCTACAGC ATAATTTCTA 480

GCAGCTTGTG CTATACCTAA ATAACAGCTT GGTATATGCA ATATCCAACC ATTTGGCGCT 540

TTACTTTTCT CTGTTTCCAC TAAATGTTTT AATGGTACTT TTACATCATT TAATATTAAA 600

TCATGACTTT CTGTCGCTCG C 621

(2) INFORMATION FOR SEQ ID NO: 1113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 619 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1113:

GTACCTTGTT TTTCAGTGTT AATTTCCCAA ATATAACCTG GTGTAATACC GTATTGTTTT 60

GAGAAGTACT TGAAGGCACC TTCACTTGTa ATCATGGCAC GTTGTTCTTC TGGAATGTCA 120

TTAAATTTGT CTTTACTGTC TTTACTGTCA TTATTTAATT TTTCCAATTG AGCAATGTAT 180

TTGTTACCTT GCTTTTCATA ATCTGCTTTA TGTTTTTTGT CGTTATCGAT AAATGTTTGT 240

TGAATTGTTT TTACGTATTT AATACCGTTA TCTAAACTTA ACCATGCGTG TGGATCTTGT 300

TTATCTTTGT TGCCTTCTTC ACCGTTTAAA TAGATAGGTT TAACATCTTT TGATACTGCG 360

ATAACTTTTT TATCTTTTAA TGATTTACCA GCCTGTTCTA AGGCTTTTTC AAACCAACCG 420

ATATCyTTAG GTTtAACyTC aTAwTCaTGA GGATCTkGAC CAACAGGTAC AATACnATGA 540

ATATCGACGT TGTCTCCACC AACATTTTTA GCCATATCAG ATAGAATTGA ATTCGTCGnT 600

ACTACTTTnA ATTTGCCAT 619

(2) INFORMATION FOR SEQ ID NO: 1114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1114:

GAAAACCGCA CGACAATGAA AAAAGATATC CGGTTAAAAT GGTCGATAAT AAAATCATTC 60

CAACAAAAGA AATTAAAGAT GAAAAAATAA AAAAAGAAAT CGAAAACTTT AAGTTCTTTG 120

TTCAATATGG TGACTTTAAA AATTTGAAAA ATTATAAAGA CGGAGATATT TCATATAATC 180

CAGAGGTGCC GAGTTATTCG GCTAAATATC AATTAACTAA TGATGATTAT AATGTAAAAC 240

AATTACGCAA AAGATATGAT ATACCGACGA GTAAAGCTCC AAAGTTATTG TTAAAAGGTT 300

CAGGGAATTT AAAAGGCTCA TCAGTTGGAT ATAAAGATAT TGAATTTACG TTTGTAGAGA 360

AAAAAGAgGA AAATATATAC TTTAGTGaTA GCTTAGATTA TAAAAAAAGC GGAGATGTAT 420

AATCATGGCT CAATCAGAAT ATGAAATCAA TCCCGGAAAA AGAGAGTGAT GAAATGATAA 480

AACGTGTAAA TAAATTAGTG CTTGGTATTA GTCTTCTGTT TTTAGTCATT AGTATGCACT 540

GCTGGTTGT 549

(2) INFORMATION FOR SEQ ID NO: 1115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1115:

TGTTATTGCA ACTATTAAAA ATATnAAAAA CAAAGACTTA ATTGATTATT CTTTATATAT 60

TAAAAAAGGT TTAGTGGAGC CATTTATTGT ATTCTATAAT CAAGAAAATA TATTCTACAT 120

TAGCAATGCT GTTATAGATA TCATCAGTGT ATCCAAAGAT ACTCTTGATT ATATAAAGTC 180

AGAATTCAAT GATCACTGTG tTCGCCATAC TGATTTTATA GCACAGAGAA AAGCCGTAGT 240

TTATCATCTT CGATGAA 317

(2) INFORMATION FOR SEQ ID NO: 1116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1116:

ACTATGACTG CAATGCCAAC AATGAATGTT ATTGCATAAA GCATATGCAT TTAATCAAGC 60

TTATGTTATT TAGCAAGGGC AAGCCACTTC TCGATTCATG GCTTGCCTTA TTTTATTGTA 120

TATTTTTAAT TATCGTTGCT GGGCCCTTGA TTGACAATCG TATTAAAATG GCCTTATTAA 180

GTCAACTTTG TCTATACGGT TTGGAATCTT CTACCCAATG TCTTATAAAA GACAATCCCG 240

CACCTGAAAC ATAACTCATG AAnATAAGAA nATGGTATAC CATTAATnTG AATCCATTTC 300

CAnTTTATAA CGTTGTAAAT GACACATAAT TAGAATCATA AAGTTTTTCG TGGGATATTG 360

AAACTTTACC CATACGAGAC ATCATGGATA AAAGCGAGGC 400

(2) INFORMATION FOR SEQ ID NO: 1117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1117:

TGCATATAAT GTTCAAACGG CAATGATTCC ACTGTATAAA CCTCTTGTCG TGGATGATCT 60

TTAATTTGTT GTTTTAATAA CTGAACTCTT TTTTCATGTT CATAATGAAC ATAAATAAAT 120

GCACTAAGAT ATATCACAGC TAAAACTAGT GATGCACCTT TAATAAAATT AACATTGATT 180

GACTTATATT TCCGAAATTC TTTTAATAAA ATAATTAAAA TGATTACATG TATCGTATAA 240

ACAATCAAAA AATTACCTGG TTCTATTGGA GTAACAATGA CTAGTGTCGA CGCCGAAACA 300

CATATTGCAA TAAGTAAGGA ATATAAAGTG ATTTGTGTTT TACGATCATT AATAGACAAA 360

TAAATACCTA CAAATATCGA AAACGCAAAG TAACCACATA CAATTACGTT CACAAAACCA 420

ACCAATCCAA TATCTGTATT TTTATTTAAT AAAAACTGAT TGTAAAATAG TAAATAATAA 480

AGCGGTAAAG TGATAAATCC TATCATAATG ATACGACGCT TTAATATTGT TAAATGTACA 540

ATCTGACTGA AAATGACACC ATATGGAAGT GACGTTGATA TCATTTCTGC AAATTTTGAA 660

AAGATACCTT GATTATTTGA AACTTGTTGA TATTCT 696

(2) INFORMATION FOR SEQ ID NO: 1118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1118:

GCAGTGACAA TCAATAATTT GTAACTAGAA GATAATAAAG AGAACGCTCT ATAGAGACGA 60

ATTGAAGGTT TGATTTTAAT GTCTGTTAGT AAGAATCATA TCAATGAGAT GCCTATAGTA 120

CTCAGAnTAT ATTAAATTAA AACCGTCATT AATTGTTTTT CCGAAAACCA TTTGTAACCA 180

TTTnAATGTA GTTGGACCTA CCTACGTTCT CCAATAATCC ATT 223

(2) INFORMATION FOR SEQ ID NO: 1119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1119:

CTGCTTTACC TTTTCCAACT TTAGAAATTG CTACATAGGG GCCTTCTGCT TTACCGCCCC 60

AATTCCAATT CCACATTTTC AAGAAATAAG GAGGCAAAAA TGTTCATATA TGAATTGGAA 120

TTATTTGTTT TCTTATTAGG CCGAGATGCG CCGCGTGCGG cTGCTGGAGA TGGCGGACGC 180

GATGGATATG TTCTGCCAAG GGTTGGTTTG CGCATTCACA GTTCTCCGCA AGAATTGATT 240

GGCTCCAATT CTTGGAGTGG TGAAT 265

(2) INFORMATION FOR SEQ ID NO: 1120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1120:

CATGACATTA CATGCTTATT TAGGTAGAGC GGGAACAGGT AAGTCTACGA AAATGTTGAC 120

CGAAATAAAA CAAAAaATGa AAGCAGATCC GCTTGGAGAT CCAATCATTT TAATTGCGCa 180

ACTCAAAGTA CATTTCAATT AGAAcAAGCC TTTGTCaATG ATCCGGAATT AAATGGTAGT 240

TTAAGAACAG AAGTGTTGCA TTTTGAACGA TTAAGTCATC GTATTTTcCA AGAAGTTGGT 300

AGTTATAGCG AACAAAAGTn ATCTAAAGC 329

(2) INFORMATION FOR SEQ ID NO: 1121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1121:

ACACCTCTTT TTTAATATAT GTGAACTATA TATAGTGTAT AGAGAGGTTA CTTGTTACTC 60

AATATAAACA AAAATCAACT TTGTCAAAAT AAATGTGACA AAATTAAATA AAGTGTCATC 120

AATGTGACAG TATAGATCAT TTTGCAAAAA GTCAAAACAA AAAAATTGTT TTAGGGATTT 180

TTCAAAATTT TCATTGTGGA AAATGATTTG nCAAAACAAA ACAACACnTT GTGAGCAATG 240

AAGCTTCAAT GG 252

(2) INFORMATION FOR SEQ ID NO: 1122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1122:

nAATAATAGG CGCCACCTAA TAAACCAGCT GGAATGCCTA TCATTGGTGT TGTGAATGAG 60

CTTAATACAA TAACAAGTAT TGTTAAAGCA ATGACGTTAT ACCAAGTTAC AGTCAAATTT 120

TTCAAATCCT CATATGATTG TTTTACTAAT TCTCTAAATT TCATGATTCA ATCTCTCCTT 180

TTCTTAAATC AATTAATAGT TATACTGCAT TGCTTAAAAT CAAnATATCT AATGAAGCAT 240

CTTTTAATCG TAAGTGTTAA ATGGTTTTCT TAATCAATTT GTTTGAATGT ATAAnAGCAA 300

TTAAAGCAAA AGTAATGTAA ATGAGGGTGT ATACAACAAT TACTACAATA ACCGGCATGA 360

AGGAAATATT ACCCATCAAT TTCATAAATG CGATTGCGGC 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1123:

AATACAACCT TTTATCATAG TGTAAATGTA TTCTACCAGT ATTGAGAAGT TTTCATATTA 60

TTCAATACCT GAAATCGCCA TAGTAATATT ACTAAATGCA CACTGCATAT GTTGTTTAAC 120

AACACAACTT TAAAAATATA TTCTAACTCT ATCTACGAAT GTACTTAAAT ATCATAACAA 180

TCTATTCCAA ATCnAATTAC ATTATTAGCT ACCTTAAAAA CCAAACCGAG GCCTTAGGCC 240

TCGGTTTAAA TATATATAAC GnGCGACATG 270

(2) INFORMATION FOR SEQ ID NO: 1124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1124:

GGTCTTCTGT ATCAAATTAT ATTATGAGAG TTAGACTCAG TATTAATGAA ATCGTTGATA 60

AAGATCAAGT GCTTGCATCA CAAATAGGTG GATTACTATG ATGTTTAATC AAATTAATAA 120

TAAAAATGAA TTAGAAGAAT CATATGAATC TGAGAAAAAA CGTATAGAGA ATGAACTGCA 180

AAATTTAAAT GAACTTAGGC ATAGAACTCG AAAAGAAAAT GAACGTAGTT ATGATGTTTT 240

TCAATATTTG AAGCACGAAA TGAATTATAG TGAAGATGCC CAAAGGAAAA TGACGAGAAA 300

TATAGAAGCG TATGAGCAAG AAATCAATGA GATAATTAGA AAGCAAGAAT GGAAATTAGG 360

AAGAATATAA AGAAGACTTA AAAAAGTCTT ATGAAAAGCA 400

(2) INFORMATION FOR SEQ ID NO: 1125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1125:

AAATATAyTC GATCATTGAT AATATGTGCT TTACTATTCC AAATAACTTT CAAATTTTGA 120

TAATATTCAT CAATACTCTC AATATAACTA ACCAGTTTAT ACAACCATTC GCCATCGACT 180

TTCACATATT TTTGAATACT ATTTCCAAyT TtAAGACGTG TTGGTTCATT TACAAAATGC 240

CCCAAATTAA TACCACTTAA TAATCCAAAT GGAGTTGGAC GTGTTGACAT TCTAATTAAA 300

TATTTTAATA AACTTTCTTT AGCATCTCTA ACCTTCTTGT TATCGCCATC AAAATTTATT 360

nCnTGTAAAG TACAATA 377

(2) INFORMATION FOR SEQ ID NO: 1126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1126:

GTTACATTAC TGTTCATGTC CACAACGTTT GTCAGCGATT ATCATCATTG TGTTATATCT 60

TATTTATAGC AAGTGCATGG TCTGGATAAG TAAAGGTATT CATACTTAAG TAACTTGAAC 120

ATTGGTTTAG GACTATTTTA ATGGTnCTGC TTnAATTGTT GGCCAACTGG TTCTTATTTT 180

AAATATGTAA CTAGCTCTAC GGGTAGTTAC TAAACACATC CTGGTTT 227

(2) INFORMATION FOR SEQ ID NO: 1127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1127:

CCAATGATAC CGTTATAGCA TGTTAATGTT TTTGTACGAA TATAATCTAA AACTTCGAGT 60

TCATCACTTA ATTTCCACGT TTCTGCTTTG TTTAACCACA TTAAAGGAGT ATGAATGnCA 120

AAATCTTTGT CCATAGCTAG GCTTAATGTT ACGTTCATTG ATTTTATAAA ACTATCGCGA 180

CAGTCTGGGT AGCCTGAAAA GTCTGTtTCA CATACGCCTG TAATAATATG CTTAGCCCCA 240

ATTTGATAAG CTAGAGCGCC TGCAAACGAC AAGAAAAGTA AATTTCTAGC TGGAACAAAT 300

GTATTAGGTA TACCATCTTC ATTATTAGTA ATTTCCATAT CATGTTGTGT TAATGCGTTT 360

GGAGTAAGTT GTGATAATAA TGACATATCT AAAACGTGAT GTTTCATTCC TTGATCTTGT 420

AGTTCAACTT CTTTGAAATG TTTTTTTGCA TAAAAGAGAC ATGTTGTACT GTCTTGACCA 540

CCACTAAAGA CAACGATGGC TTTTTCATTA TTTAATACAC TTTCCATTTT GTAATTGCTC 600

CTATCATTAA TAATATTAAT AAAGAGGTTA ATGGCATTGA TAAGCCCGTT TTTAATTTAT 660

AAAATAAAAA AAGCCnATCT CCATAAAAGA TAGACGAnAG AAATGGGTTG CTCCTAT 717

(2) INFORMATION FOR SEQ ID NO: 1128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 595 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1128:

GATTATTGCA TTGACAACTT ATATCTATCT AACGTTAGTA GCATTTAATT TCATTTCCGG 60

GGTTCTAACT TTACCAGGAT TAGCGGCGTT GGTATTAGGT GTAGGTATGG CTGTAGATGC 120

CAATATTATC ATGTATGAGC GTATTAAGGA TGAACTTCGA ATAGGTAGAA CGATAAAGCA 180

AGCCTTTTCT AAAGCAAACA AAAGTTCATT CCTAACAATT TTTGATTCTA ACTTAACAAC 240

AGTTATCGCC GCAGCAGTAT TATTCTTCTT CGGTGAAAGT TCAGTTAAAG GTTTCGCGAC 300

AATGTTATTA TTAGGTATTC TAATGATCTT TGTTACAGCC GTGTTCTTAT CAAGATTCTT 360

ATTATCATTA CTTGTTTCAT CAAATATATT CAAAAATCAA TTTTGGTTAT nTGGTGTTAA 420

AAAGAATAAA CGACATGATA TTAATGAAGG TGTAGATGTT CATGACCTTA AAACTTCATT 480

CGAGAAATGG AATTTTGTTA AATTAGCTAA GCCATTAATT GGAGTAAGTA TTTTAATTGT 540

AGTGTCGGTT AGTTATTCnT TATATCTCAA GTAAACTTAG GAnTGAnTCT CAAGT 595

(2) INFORMATION FOR SEQ ID NO: 1129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1129:

ATTTTAACTT TCTAAGAACA AGTTGTCAAG ATTTTTTCTT AACATATCAT GTTCTGTTAC 60

AATATTAATA ATGAATACCG AAAGGACGAA TTGCAAATGA AAAGCGTTGG CTTAATCACA 120

GAATATAATC CCTTTCATAA TGGGCATCAA TATCATATTA ATCAATCTAA AAAACTTACA 180

ATCTATAATA AGTTACTCGT GCAAAATGGC TTTCCACCGC TGTTTAGTTT CGGACTACCA 300

GCAACTGCAG TTATCACTGG CGnCATTTGC GACTGCCGTT AAGCGCGGTT TTGGTGCGTA 360

CATGCnTGGn G 371

(2) INFORMATION FOR SEQ ID NO: 1130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1130:

ATGATGATGA GATTATGACT TTGCGAAAGA TATCGGTGCG CCTTATGAAT TTAAAACAnA 60

nTAAAGACCA TGGTCGTTAC CGGTAGTTAA CTTTGCAGCT GGTGGCGTTG CGACTCCTCC 120

AAGATGCTGC TTTAATGATG GAATTAGGTG CTGACGGTGT ATCCGTTGGA TCCGGGAATT 180

TTAAAACCAG AAGATCCCGG 200

(2) INFORMATION FOR SEQ ID NO: 1131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1131:

ATGAGCTAGT CGATTAAAGT TAATATTTGA AAATGAAGCA GGGCATTAAA TGCAATAAAT 60

TAAATAAGTT GTCATTAAAG CATTAATAAT AGAAATGATT TTAACAGGAA AAAAGTGATG 120

AATATTTGGA AAAGATATAT ATCGTGCACT GTCCTGAGAG ATTAGATTTG GGAAACCAAT 180

TTATCCnTGA ATCGAGATGT nGC 203

(2) INFORMATION FOR SEQ ID NO: 1132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1132:

ATCTAACAGT ATTGAAATCT TTGTTAGCGT CAATCGACCA TGTATTTTTA AGTATTGTCT 120

CTAACAACTT AGCACGACGT CTTAACCCTT TAGTAAACAA TCCTTCTTTA GnTTTAGTAC 180

GT 182

(2) INFORMATION FOR SEQ ID NO: 1133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1133:

CAAATTTAGC CAGGnATACA AATACATATA ATAAAACTGT TTGTAAGCTT ACGTTGACAA 60

TCTGGCGTAA TTGGAAAACT AATGAATTTT CTCCAAGTAG GTTTTACCCT GTAAACmAAA 120

TAACAATTCm AATAATATGr AATCACAAAg CGACTAGAAA TCCGGTAATA TGACTAATCA 180

TATATTCAAT GTGTAaTAAT TTTAACAGCA ATAAATAGAC AACATAATAA TTTAACGTAT 240

TAATGCCGCC AACAATGATA AATTTTAAAA TTTCAGCATG CGTTTGTGTT AGTTTCATAT 300

GTGTACTCCT CAACATCAnA ATATATGCAT AACTACGTTC TCGAACATAC TCGAATATGC 360

GAGCCAATCC GCTTCACTTC AAATATGCTT ATTTCAATCT TTATACCCTT TCACAGCAAT 420

TTAGTCTCTT TnCCCTCATC CTTATAGGCC nTATATGTAA CCGATTATCG GGTGGACTCA 480

TTGGC 485

(2) INFORMATION FOR SEQ ID NO: 1134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1134:

CTTGTTTTAT CGACAGATGC TGAACACGCA GTCaAAATAA ATAAATTACA TAATAAAATT 60

CCAATTAATC TTTTCATAAT ATCATCCTTT TGTTTTTCAA TTGATATTCA TTTTCAATTA 120

TAAAATATTA rAAGAATTAG TCAACGCCTG TGAGTAATAC ACATCAGTAA CATTTCTATT 180

TTCATTTATG ATATTATCTA ATTATTAATT TAT 213

(2) INFORMATION FOR SEQ ID NO: 1135:

(A) LENGTH: 526 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1135:

TGTGACTCCA TGTATTCATG TATCATTGTA CATTTGTGAA TTGGTTGAAA ACTGATAGTG 60

CCCGTTTAAT TACAGGTACT GAGGATGCTT TCAGGACATG GATTTGTTCG AAAATATGAC 120

AATATTTCAC TATGGCTCTT CACTTCTCTA GGGAAATTGC TATCTTGATT AATCCAATCA 180

ACCAATTCAC CTAATGGTGT GTCATCACCA AGAAAACTTT GCATAAATTC GTAAAAGCTC 240

AATACCTCAC CTCGATTaAT ATACTTGAGC CATTaATATA ATACCATAAA AGAATGTGTA 300

TTTTaCATAA AACTTTTTaT AAAGCAATTT TATAAATCTA AATTTATTGA ATGTTTAAGA 360

AGTTGTGTAT AATGAAATAA ACGTGTTGAA ATAGTTAGGA TGATGTTAGT GGATATCAAA 420

CATATGAAAT ATTnTATTGA AGTCGTTAAG CAnGGAGGCA TGACTAATGC TTCCAAATCA 480

TTATATATTG CACAACCTAC AATTAGGAAA GCnATTAAAG ATATTG 526

(2) INFORMATION FOR SEQ ID NO: 1136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1136:

AGCAAAAGCA ATGATGACAA AAGAACAAGC TATGTTAGCA GATGGAAGTA TTAAACAAGA 60

TCAATATGAT AAACAACTGT TATCGAnAAT CGGAAAATCA CAATTAGATG AATTGTCTTC 120

TAAAGATTTA CAAGTTTTAG CTATTTTTCC GAGAGATGAA TGCAGGAACA GTTTTAGATC 180

CACAAATGAT AAAAnATGGA AGATGTTCAG TGCAAAAAGA GTATGGCAGC AGTTTTCTCC 240

AGCAACTTTT CCAnATTTAC CCAGGTGTTT AACACGTCCT ATTGGATTTG GGCTTAGGAC 300

AATTATTCCA TATGGGCGGA T 321

(2) INFORMATION FOR SEQ ID NO: 1137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1137:

ATAAATCCTT ATAAAATCAT GAGTTGGACG ACTTATCCAC ACAATTATAC TTTTTCAGTT 60

CTCTATATGT CAAATACCTG TGAATATGTT GCTAAAAATA GTATAACTTT GTGTGTAATT 120

TCTAATTATC CACAATTCTG AAAACTATAA ATGTGCATAA GTGGATAmCT TTcCTTCTAT 180

AGAGTATCTG TTAGTGAGTG TATCAAAaCA GTTTGGGAAa TAATTtATAA AGTnTGTATA 240

AGAnCTGTAT AAGGTGTTCG AACATTGTAA ACACTCATGC TTCGGACCAA ACTCATGGTG 300

ATGTTATGAA ATTTGATTGC TCGCATCGnG 330

(2) INFORMATION FOR SEQ ID NO: 1138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1138:

CTTGATAAGG GAAGATTTGC CAGCACCATT CGGGCCCATG ATACCAATTA TTTCGCCGCG 60

TACTGGTATC GATAAGGAAA TGTTTTTAAG TACATGCTTA TTACCTAAAA ACAGATTTAA 120

ATCTTTTGTT TCTAACAAAC GTTTATACCT CCTAATTAAA AGTTTAGGCT AACCTAATTA 180

ATTGTATAAT AAACTGAGAA TATTTATCAT GTCAAGTAAA TTCGTGATAT AATATAGACA 240

ATGTATGTGA GGTGAAAGTA TGTTAACTGA AGAAAAAGAG GACTATTTAA AGGCAATCCT 300

TACGAATAAT GGCGATAAAA ACTTTGTGAC AAATAAAATC TTATCTCAAT TTTTAAATAT 360

TAAGCCTCCA TCTGTAAGTG AAATGGTAGG ACGTCTTGAA AAAGCAGGCT aTGTTGAAAC 420

AAAACCATAC AAAGGTGTTA GATTAACAGA GGATGGTTT 459

(2) INFORMATION FOR SEQ ID NO: 1139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1139:

TAAATACTCT CGCCGGTTAT TTCGCTTCCT CTATACGGAT TGGCGAAAGA TACGGTGCAT 60

CGGTTTCAAC TAGCAAACGC TCCATTGACA CATGCTTAGC AACTTCTTTA GGCTGTTTAG 120

(2) INFORMATION FOR SEQ ID NO: 1140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1140:

ACCTGAATGC CCATCAATGA CAGACTGGAT AAAGAAAATA TGGTACATAT aCACTATGGA 60

ATACTATGCA GCCAGAAAAA AATGAGGTCA TATCTTTTGT GGGAcATAGA TGCAGCTGGA 120

GGCCATTATA TTTAGTAAAC TAATGCAGGA ACAGAAAAAC AAATACTGCA TGTTCTCACA 180

GCAGGAGCTG AATGATGACA ATTCATGAAC ATAA 214

(2) INFORMATION FOR SEQ ID NO: 1141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1141:

GTTTCTAGTT GTTTATAGTT ATCGCATCTC TTGATGTAAA ATCTAAGATG TTTATGCATT 60

TCTAGATGTT AATTCTTCGC TGCTTAAGAA TTATCTTGAT GGTAAATCTA GTTGTGCCAT 120

GCATTTTCTC ATGATGAATC TAAGGTGTTA ATTCATTGAT GTGTGCTGTT TCTTGnnGCT 180

TCATTATCTT GATGGTGAAT TTCGTTGTCT AATGCACTTT TTCAAATGA 229

(2) INFORMATION FOR SEQ ID NO: 1142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1142:

TTATGAATCG TAAACACTAT TATGAAATTG CGAGAGTAGT ATGGACAATT AGAATGATGG 60

TTTGAGATnA ATGAGTGTTA TTAACCAGTG CGTCATTTTC AAAATTAGAT GCCATTTGCT 120

GTTTATAATA AGAAGATTTG ATAATTAACT ATGATAAGAA AAAATAATAA TCCCCTAAAT 180

GGTAAATGTG TGAATAGGAA TATCGTTaAA CTAGTTGTGT TCATGCTAAT TTTAGTTGTA 300

GCAGTAGCGG G 311

(2) INFORMATION FOR SEQ ID NO: 1143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1143:

GATCATGCTG CTTATGAATT ATTAAAAGAG CAATTAGAAG ATGTGCTTGA TACATTAACT 60

GATAGAGrAG AAAATGTATT ACGATTAAGA TTTGGTCTTG ATGACGGCAG AACAAGAACA 120

CTTGAAGAAG TTGGTAAAGT TTTCGGTGTT ACACGTGAAC GTATTCGACA AATTGAAGCA 180

AAAGCACTTA GAAAATTAAG ACATCCAAGT CGTAGTAAAC GTTTGAAAGA CTTTATGGAT 240

TAATTTATAT CAATTTTAAT GATTGATACC AAGACATGAA TAAGCGCTTA TTTATTTTTA 300

GATTAAGATT TAACTTGAGT GAGGTTGGTA CATTGAATAA TGTTCAACCT CTTTTTTCAT 360

AAAGGAGAAT AAAATGATTT CGTTAAATAA CCGATTAACG ACn 403

(2) INFORMATION FOR SEQ ID NO: 1144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 612 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1144:

nTTTTTATTG ACGAATnGAT TTGGATGCCA GTGGTTTGGT CCTAAATCTT GAATGGTAAT 60

CGGTATTTTG AAGTTGTCAT GTGCTACACG GTAACCGATA CCnATAAGTA CGAGTGCGAT 120

GACAATGGTT GTTACGAGCA AGATGTATTG TAACCATTGC TTGAACACAA CAAGTTGTAT 180

ATAAGGCTTC ATTGACGATA CCTCCAAACC AATACAGCTA AATTAATTAT CAAAAGTGCG 240

ATGAAsCTAA GATAGAAACT AGGGTGCAGT TCTAAAATGT AGTTGTTTAA AATAATTTCT 300

AACAATTGAT TTGTTACAAC TGCGAACGGT TGAATATTGA AAACACCATT TGCTATATGT 360

TGTAAAAAAA TCGTAGGTAT TGTTAAACCA GATAACACCA GGATGACAAT AGCTAATATG 420

ACTTTACTAA TACTATTCAA CAAGCCTGTT GTTAAAAGTT CGATGAGTAA TAACCACAGT 480

AAGATATTCG GAATACTGAA CACAATCCAA ACTACACCAA CGATACTCCA TAACATAGTA 600

TAAAACCATG Tn 612

(2) INFORMATION FOR SEQ ID NO: 1145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1145:

GAATTAATTA CGCAATATCC GCATCTTAAA TCAGTAATCG AAAAATATGC TTTAAAATAA 60

AAGTGATCAA TGAAGTGGTT TGAAGGTTGT nAATAAACCT TTGAGTCACT TCCATTTTTA 120

AAnGTATCCT GGATGGAACC AGAATAGATT TGAAGCTTCA GCGGTTTTTA ATGAAAATAG 180

CCATTAAATG ATTTGGAAAC GGTAAGAGGG GGTATTTAAA ATG 223

(2) INFORMATION FOR SEQ ID NO: 1146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 598 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1146:

CGCTACGGTT GTCACGTAGA GATTAAAGAC ATTCGTTTTA GCAGTCTTTT TTATTGAAGT 60

AGACAATGCA AGATTAAATG GTAGTGTCAT TTCATTTTAT TCAACTGCTA GTAATACAAT 120

ACTCAGTGTT ATTTCTGAAG ACTGGTTGAT AATGAGACAT GCATATTTAC AAAACTGTGT 180

ATATTGTGTA TATTGTATAT ATACAGAAGT TGATAGGGGG ACGTTGATGA AAATAATTTT 240

AAAAAACAAT AGTGATTTTC CGATTTATGA ACAGATTAAG CAACAAGTAA AACAAAATAT 300

TTTAAAGGGA CATGTTGCTC CTGGAGAGCA TTTGCCGTCA ATGAGAGAAC TTGCCAAAGA 360

TCTTCAAGTA AGTTTGATTA CTACCAAACG TGCTTATGAA GATTTAGAGA AAGACGGTTT 420

TGTTACAACA ATTAGAGGAA AAGGGACCTT TGTTAAGGAG CAAGATAGTT CTATTTTAAA 480

AGAGAAACAA TTTTTTACCA TGAAAATTTG GGTTAAAGGA ATTGGGTTAA TTAAGCnCAA 540

GCCCATCCGA ATTGCCACTT GAGGGAnTTC CAGGATATTT nACCGTCATT TATTGAGG 598

(2) INFORMATION FOR SEQ ID NO: 1147:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1147:

CAAATCCAAG TGCAACAGCT TTATCAACCG CTAAAGCTAA ATCCGTATCA GCTTTTTCAG 60

CTTGAACTGG TTTGATTTGT AACTGTTCTG TTAGAAGTTG GCGTTCTTCT TTACTGACTG 120

AATCAAAGTC TCCCACTGAG AAAAAAGGGA TAATTTGATG CTTCAATAAA ATCAAAGCAC 180

CTCTATCAAC GCCGCCCCAT TTACCTTCAT TACTTTTGGC CCAAATATCT TGCGGCAAGT 240

GTCGATCAGA ACATAATAAA TTTATATGCA TATACACTCA ACCTTTCAAT GCTTGTGTGA 300

CTTTTTAAAA TCCCCTGGTT AAAGGAAAAT GAACnGGTTA CCAGCATTGT AGGCACCATT 360

TCAACACCAA CTTCGGCGGA TCnGGATTAC GCCTCCATCC 400

(2) INFORMATION FOR SEQ ID NO: 1148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1148:

TTTTATGGGT CGTATTTTTT AAAGAACAGT CATCTCAATC AAAAGAATAG AATTATGATT 60

AAAATTGATG TrGTGTAATT AAAGTAAGAA ATrrkAAATT TCCTAGATAC TAGATAAATC 120

GTTCAATATT TTATTAATAA GGAGGCCAAT GAyTGTGAAT TATCTTAAAC ATAAGTTTTA 180

TAACTTGTTA ACTACAATGA TTGTTCTCTT TATTTTTGTA CTTTCTGGTG CGATTTTTTT 240

AACATTTCTA GGGTTTGGTT TATATGGATT AAGTAGAATA CTTATTTATT TTAGGTTGGG 300

TGACTTTACA TATAATAGAA GTATGTACGA TAACCTATnA TATTATGGCA GT 352

(2) INFORMATION FOR SEQ ID NO: 1149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 916 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1149:

GGCAAGTGTC GATCAGAACA TAATAAATTT ATATGCATAT ACACTCAACC TTTCAATGCT 120

TGTGTGACTT TTTTATAATC CTCTTGTTTA AAGAAAAATG AACCTGTTAC TAGCATTGTA 180

GCACCATTTT CAACACAAAC TTTCGCTGTA TCGGTATTTA CGCCTCCATC AACTTCAATA 240

TCAAAGTTTA ATTGACGTTC CATTTTAATA GCATTAAGAC CCGCTATTTT TTCTACGCAT 300

TGATCAATAA ATGATTGACC ACCAAACCCT GGGkTAACTG TCATCACTAG TACATAATCA 360

ACAATGTCTA AAATAGGkTC AATTTGTGAT ATkGGkGTAC CAGGATTAAT TACTACACCA 420

GCTTTTTTAT CTAAATGTTT AATCATTTGA ATAGCACGAT GAATATGAGG CGTTGATTCG 480

ACATGAATTG AAATCATATC GGCACCATGT TCTGCAAATG ATGCAATATA CTTTTCTGGA 540

TTTTCAATCA TCAAATGTAC GTCTATAGGT AATGTTGTGC CTTTTCTTAC TGCATCTAAT 600

ATTGGTAAAC CAATAGATAT ATTAGGCACA AATTGACCAT CCATAACATC AAAATGAACT 660

CCGTCGACGC CTGCTTCTTC AAGTCGTTTT AATTCATGTT GTAAATCCAA AAAATCAACA 720

GATAATAATG ATGGATATAG TTTTGTCATT TAATATCTAA CCTTTCTATT TGAAATTTCA 780

TTAAATAGTT GTAAATAATG GTCGTATCTA AATTGCGCAA TATTCCCTAT CTCTAATTGA 840

TGCnTAACCA TTACCATTAG GGTCCTTGGn AAGGnTACCA ATCCCAAACC TTACCATGGT 900

TCCCCCATAA CGGTTT 916

(2) INFORMATION FOR SEQ ID NO: 1150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1150:

AATTGGTTGT GGCTTCATAA TGTGCAGTTG CTAGACTGAC AACAACATCG TTTTCTAAGC 60

CTACGATAAA GACATAATCG TTTTCGGTTT TGTTGTTTTC TAATGAGCGT TTGATGATAC 120

GTTTATCTTC AGTTAAAGAT AAATTTAACT TAGTATCGTA AAGTTTAAGT GCTTCGTTGT 180

AATGTGGATC TTTGACAGAT TGAATGGTTT TAAATTCCAT AAGAACACCT CCCCAATTTA 240

AATAATATTA TAGCATAATC GCCTGCTGTA AAAGACTGTT CATAAACTTT TAAATGGTAT 300

AAAAaACTGT ACTATCTTAA ATTAGACAGT ACAGTAATCT CATTTTGAAT TCAGTGTGAT 360

AACTAAGCtT TGGGACCTTT AGATGCnTTC ACAAAATGTG 400

(2) INFORMATION FOR SEQ ID NO: 1151:

(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1151:

CACCGTAGTT GCTACCGAAT ACCACCATGT CGCCAGGTTG TGCTAAGAAG TCCGGTGTAT 60

TTTGGTATAC AGTTAGCTAA TCCGTCGAAG TTGTTAGCGA CGGnATATCT TTTGACCTAA 120

ACCTTTTAGA GTAATCCAAA CAAAACTTTC CAACCA 156

(2) INFORMATION FOR SEQ ID NO: 1152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1152:

TCAATATATT TATTTTCTAA TGTTAGCATT AGACTGTCAA TTAACTTGCT AAGTTGTTCT 60

TTTTTAGTAA TTAAATAACG CATATAATCA TCTAAATTTT TCATTTTTTC ATCTAGCATT 120

AAAAGGTAGT GCTTGATATT ATTTCTACTG TTGCTCCAAA AACTGnTCAA ATATACGTCA 180

CATAGTCATA CTACACCTTT ATATAGTTTA AATACCAATn GCATGACCTC GTG 233

(2) INFORMATION FOR SEQ ID NO: 1153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1153:

TATATTAnCT ATCGTTTAGT GAATCGTTTT TTTAAAGTAA AGAGAATTTC ATATATTACT 60

GGTACAACTA CAAGTGTTAA TAAAGTTGAT GAAATTmAAC CACCAATAAC TGTAGCAGCT 120

AATCCTTTCG AAATAAGAAT CGnGCTATCT TGACCAAATA ACAnAGGAAC TAATGCACCA 180

ATTGTTGCAA TCGCCGTCAT TAATATCGGT CTAATTCTAG TACCGCCTGC TTCGATTAAT 240

GCTTCTTTCA TCTCCATGCC CTGTTGCTCA TTATTAATAA CACGGTCTAT TAACACAATG 300

GCATTTGTTA CTACGATnCC AATTCAACAT TAGCATACC 339

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 817 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1154:

GTCACCCGAG GAGATATnCA ACTATTACCA TCAAGATGnG AAAAATGGTg CCTTGGGCAA 60

TTGGTTTTTT CATTTTAATC TTAATTATTA TATTGTTCTT TTTACTAAGA AACTTCAATT 120

CACCTGAAGC GCAAACTAAA ATATTAGTGA ATGCGATTGA GAATAATGAT AAACAAAAAG 180

TAGCAACATT ATTAAGTACT AAAGATAATA AAGTAGATTC TGAAGAAGCA AAAGTATACA 240

TTAACTATAT CAAAGATGAA GTTGGGCTTA AGCAATTTGT CAGCGACCTT AAAAATACGG 300

TACATAAATT GAATAAGAGT AAGACCAGCG TAgCTTCTTA TATTCAAACC AGATCTGGTC 360

AAAATATATT ACGTGTAAGT AAAAATGGCA CACGTTATAT CTTTTTCGAT AATATGAGCT 420

TTACTGCACC TACCAAGCAA CCAATTGTTA AACCGAAAGA AAAAACAAAA TATGAGTTTA 480

AATCTGGTGG TAAGAAAAAG ATGGTTATAG CTGAAGCAAA TAAAGTGACG CCAATAGGTA 540

ATTTTATACC GGGGACATAT AGAATTCCAG CTATGAAATC AACTGAGAAC GGTGATTTTG 600

CAGGCCATTT AAAATTTGAT TTTAGACAAA GTAATTCTGA AACGGTAGAT GTTACTGAAG 660

ATTTTGAAGA aGCAAATATA TCTGTAACTT TAAAAGGCGA TACAAAATTA AATGaTAGTT 720

CTAAAAAAGT AACTATAAAT GaCCATGAAA TGGCATTTTC AAGTTCCAAA ACGTATGGTC 780

CATATCCACA AAATAAAGAT ATTACCATTT CCAGCTT 817

(2) INFORMATION FOR SEQ ID NO: 1155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1155:

AnAGAAAATC TACTCTTTTA TTTCACCGGT CCTTTCnTAT CTCTCATTTG GCATACTCCT 60

TTTTCCATAT TTTCCACTTT CAnTACAGTG AATTTACATG TAATTTTACA AATACAATAG 120

GAGTGCACAA TGGAATATAA CACTTATCTT TATAAAATTA TTTTATATAT TGaCGCACTT 180

AAAACAATCT ACAAATAAAA TTATTATTTT TAGTTTTCAA TGAATAATTC ATTCTTATCT 240

ATTTAAAAAT ACATTTAACT GC 322

(2) INFORMATION FOR SEQ ID NO: 1156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 777 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1156:

GTTTCCAAnG GAAnGnGAAA AGCGTCAACC AATGTAACTA TTTAAAGTCA AAGTGTTTGA 60

CCAAATTTGA CTTAATATGT AAAATAATGA GTAACAGTTA TTACAAGGAG GAAATATAGA 120

TGAATTTAAT TCCTACAGTT ATTGAAACAA CAAACCGCGG TGAACGTGCA TATGATATAT 180

ACTCACGTTT ATTAAAAGAC CGTATTATTA TGTTAGGTTC ACAAATTGAT GACAACGTAG 240

CAAATTCAAT CGTATCACAG TTATTATTCT TACAAGCGCA AGACTCAGAG AAAGATATTT 300

ATTTATACAT TAATTCACCA GGTGGAAGTG TAACAGCTGG TTTTGCGATT TATGATACAA 360

TTCAACACAT TAAACCTGAT GTTCAAACAA TTTGTATCGG TATGGCTGCA TCAATGGGAT 420

CATTCTTATT AGCAGCTGGT GCAAAAGGTA AACGTTTCGC GTTACCAAAT GCAGAAGTAA 480

TGATTCACCA ACCATTAGGT GGTGCTCAAG GACAAGCAAC TGAAATCGAA ATTGCTGCAA 540

ATCACATTTT AAAAACACGT GAAAAATTAA ACCGCATTTT ATCAGAGCGT ACTGGTCAAA 600

GTATTGAAAA AATACAAAAA gACACaGATC GTGaTAaCTT CTTAACTGCA GAAGAAGCTA 660

AAGAATATGG CTTAATTGAT GAAGTGATGG TACCTGAAAC AAAATAATTC AAAGTAAAGA 720

GTAGACTAAG CnGTCTGCnC TTTTTGTATG AGTAAACCAA GGTGTCAATA ATTTGTn 777

(2) INFORMATION FOR SEQ ID NO: 1157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1157:

TAATGTTGGT AAATGGGTTA AGGCTCAAGG TCGTATTGAA GAAGATACAT TTATTAGAGA 60

TTTAGTTATG ATGATGTCTG ATATTGAAGA GATTAAAAAA GCGACAAAAA AAGATnAGGC 120

TGAAGAAAGC GTGTAGAATT CCACTTGCAT ACTGC 155

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1158:

GACTGGTAAA ATTTACTTGC AAGTAAAGCT AAAAGGTCAA ATAGATAAAG AACAACTTGT 60

TTTTCAAAAT GACAAAAATG AAGAATTTCC TTTTGTTATA AAAGATGAAA AGGATGACAC 120

AATAGTAAGA ATTTTAATTG AACAGCATAT GGATAAAATC AATATGCATG TTAAAACGTT 180

GGCTGAAAAG AAAAATCTAG ATAACAAAGA AATGGTGTAT TCTATTCATT TTAAAGAGAA 240

AAAAGTACAA CATGATGATG CAAAAGAAGT GCCTTCAAAA CATCAAAATC AAGAAAATAA 300

TCAAGATCAG CTTAAAAAnAG ATATTGATGA CAAAnAAGAT AGTCAAAAAT CAGATACTAA 360

GGGAAAGACG TACTAGCCTT TTTACTGGAA AAAGGGTTTA 400

(2) INFORMATION FOR SEQ ID NO: 1159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1159:

GTTGGTACAG TGTTGAGTGG CTTTGAATAT CGAACACAAA AAGAAAAGTA TGACAATTTA 60

TATAAATTTT TCAAAGATAA TGAAGAGAAA TACCAATATA CAGGCTTTAC AAAAGAAGCA 120

ATAAACAAGA CGCAAAATGT CGsATATAAA AATGAATATT TTTATATCAC TTACTCGTCA 180

AGAAGCTTAA AAGAATATCG TAAGTATTAC GAACCATTsA TTCATAAAAA TGATAAAGAA 240

TTTAAAGAGG ATGGACCAGC CAGAAAGAGT GATTACGCGC TATCAGTCAG TACACATGTT 300

AGTCCAGGAA TTTCTAGCAT CnGTGTGTGA ATGAnGGGTA CTTTATn 347

(2) INFORMATION FOR SEQ ID NO: 1160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATAGTTATTA ATTAGTAGAA TGAGGATATT TAAATATAAA GGATAGTGTT GAACTTATGG 60

ACATGAATTT CGATTATACA TGAACGGTGT TGTAGAACAA GCAAGGAATG AAATTGAATC 120

TGCGGGATAT GAGCAATTAA CTACTGCAGA AGATGTTGnA AAGTCCAAGA TGGnCACCTA 180

GTTATGATCA TCTGTATGTG GTG 203

(2) INFORMATION FOR SEQ ID NO: 1161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1161:

AATTTTCCnT TTCCATTGAC ATAACAATAT TTAATGGGGC CCAGTTACAG GAAATATCAG 60

TTTAATTTCG TCTTCAATAC CATAGTCATA ATATTGAGTT TCTTGTGTTG GAAAATTTCC 120

TACATAGTTA CTCATTTTAA TTTGTnCAAT GTTTGAATTC GGAGGCACTC TGTTAGCATA 180

TCTTTAAACA TTAAATATGG ATA 203

(2) INFORMATION FOR SEQ ID NO: 1162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1162:

GCCATTTTGT TGATAAAGGT ATACTAAAGG TTATCGTTTT GAAATTTTTA GTAACTAGGA 60

TATGTTTCGT GTTATAGGAC CGGAATTTGT GGTATACGGT AAAATTTTAA TGCTATTGGA 120

ATTTTTAAAA ATGGAAAAAC ATGGACATTn AAATTGGAAT TTCATAATAT GTCCTAATTG 180

GACTTAACTT GTTGGGAGTT CATTTTACTA TTTnTATGGT 220

(2) INFORMATION FOR SEQ ID NO: 1163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 409 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTCACGTGCT TTGCCATCTT TTAAGAAAAA CACAGAAGGC TTTTGCATTT GATTGTAATT 60

GGATGCCATA GAGTAATGAT ATGCACCAGT TGATAATATA GCAAGATAGT CTCCACGTTT 120

GACTGGATGA AGGTAATTTA GCGTCTTTAA TAATGATATC ACCAGACTCA CATAATTTTC 180

CAGCTATAGT TACACTGtCA TCTGCTTCTT CATTTCTATT AACAAGCAAT GCTTGATACT 240

TTGCGTCATA AAGTGCAGTT CTGATATGAT CACTCATACC GCCATCGATT GAAACATATT 300

TATTArTCTC TGGAATTTCT TTAATGGtTC CAACTTCATA TAAAGTAACG CCAGCtTCAC 360

CTACAATTGA TCGTCCCGGT TCAATACCTA TTTCTGGTGC ATCTATACC 409

(2) INFORMATION FOR SEQ ID NO: 1164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1164:

CTAAATAATT GTTTAAATTT TTCTTTACTA TTTAGACTCT TTCGTTTGCC ATGACTTTGT 60

TGACTTGCAA TGATATGAAC TTAATTTTTG CGAAAAAAGG AATCTAGATT CATATATTCG 120

GTAAATCTAC CTTCTTCATC TTTTTGAACT TGTAATTCTA GCAATTCACG TTGTATCAAA 180

TTTTGAATAA CCATTGTAAT ATCACGTGGT TGCATAGTTG AGCCCTTCTG AAGCAATTCA 240

ATTGAAGGCG TTTATTTGAG TTTCGAAGCA TAAATCAATT TAAGCAAAAG ACTAAATCTG 300

CTCATCTAAA CCTAAGTCAC GTAAGGTCTA ATAATCnCTC GTATCACTAC GGTCTGCTTT 360

AATGATATTA nCCAGTnCGT GCCCCTTTAA ATTAACCAnA 400

(2) INFORMATION FOR SEQ ID NO: 1165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1165:

TCGTGATTAT TATTAACATT TTTTAGTAAT TGATAAAAAT CTTTTCTCGC TTCTGTAGGG 60

CTAGTGATAA TCATATAAAC CCTCCTTTGT TTTCTGTTAC GCTAATTATA GCGTACGCAC 120

TTGAGTACGT CATATTACCA ACGAGTTCAT CGTATnCTTA ATACCTATAT GCTATCGTTC 180

GGACACACTA CCGTnCCCTA CCGCTTAACC ATTTTCGGGC TTAAATATTT TnAAAATTTT 300

GTGAGGATCC GCTTAAAAAA CCCCATA 327

(2) INFORMATION FOR SEQ ID NO: 1166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1166:

TTAGGATTTC AAAAATATGT CAGGTTTTCT AACATAAAGC TTAAAACATT GATATAACTG 60

CGATTTCGAC TTCTAAAACG aCATrAAACA ATCTACAGCT AAAATATTTT TTCAATTTTT 120

AAAAATAATC nGATAAATCT CCGCAAAA 148

(2) INFORMATION FOR SEQ ID NO: 1167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1167:

nAAGGTTATC GCTCGTAAAG ATGTTGTTGA AGAAGTATTT GACGACAGAG ATGAAGTGGA 60

TTTAAGTACA GCGCTTGTTA AAACCCTGCA TATGAAATTG GTGTATTACG AGAAGAGTAC 120

ACTAAAGTTT TGGTCGTGTA GGTCTCAGCA GCGAACAGCA GTATGCACGT CTnCGTGTGC 180

TGACGTGAAT TTTATTTGAG GATTATAGAC AAGAGAGACA ACTTACTGGA TTTTGCCCTG 240

TTG 243

(2) INFORMATION FOR SEQ ID NO: 1168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1168:

TTATATACTA CTATAAAGTA ATCCAACTCT CAAGAAGGTA AATGGGCAAT CAAAAGCTAA 60

CTACGATATG ACGCACAAAT GTTTAGGGTA GGTGTTGACA TGTGTACAAA AACCAGCAGA 180

AAATGGTTGT ATTCTTAGGG AAGCATTCAT CCTGTTTGTT TATGGATTCA TGTTACGTTA 240

CGCAATATGT TTTTATGTAG CACAGCGAAG TTACAAGTTT ATACGCTATA TATCCnTTGA 300

TnATAAGCAG ATGAAAnCGG C 321

(2) INFORMATION FOR SEQ ID NO: 1169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1169:

TCTACATATA AAATTACTCT AAAAATATGT ATAGTCATAA ATTGTTGGTT GATTTAATTA 60

AAAGTATGGA AATTAAGGGG CTCTTATGTA TATAAAAAAA TGAATTATGA TAAAATGTAA 120

GAnAATATTT AGGGTCGATT GGAGAGATAC CAGTGGTACC AATTAGAAGA CGACAGTTTA 180

ATGTTACCAT A 191

(2) INFORMATION FOR SEQ ID NO: 1170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1170:

AATGTGGCAA GGATGTGTGA TATGACTACA CATTTAATAT CATCCTACAT AATAATTTTG 60

CGCGCCAAAT TATCACACAT ACCACACCTA CGATAACAAC CAGCAAATAA GGAGATAGCT 120

ACACGTATTT ATCGTCCAAC GCACTACTAT ATGTTGTTGn ATGGGCACAA GTTACAAGTG 180

CTGCGCGATA nCAAAAGGTA TACCCCTAAA ACGTCCCAAA AnAATCGGTT GCCCTCTAAA 240

TTGTTTGTGT GCCATGATTA GTAAGCTCCT ATGTTAGAAA CAAATTTTTA ATATGTATAT 300

TAG 303

(2) INFORMATION FOR SEQ ID NO: 1171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1171:

AAAAAGGTGA GAAGACAATA ACGnACGCCA ACACTAAAAA ATCCATTAAC TGGAGAAATT 60

ATTAGTAAAG GTGAATCGAA AGAAGAwATC ACAAAAGATC CAGTTAATGA ATTAACAGAA 120

TTCGGTGGCG AGAAAATACC GCAAGtCATA AAGATATCTT TGATCCAAAC TTACCAACAG 180

ATCAAACGGA AAAAGTACCA GGTAAACCAG GAATCAAGAA TCCAGACACA GGAAAAGTGA 240

TCGAaGAGCC AGTGGATGAT GTGATTAAAC ACGGACCAAA AACGGGTACA CCAGAAACA 299

(2) INFORMATION FOR SEQ ID NO: 1172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 821 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1172:

CCATAGCACC ATACCCATAA CCAACCCGGA TCCACTAACA AATAAGTAAT AATTnACACG 60

TAAAGAAGTA AATAGTTTGT TTAGTTTTTT ATCAACATTA TCAATGTTTT CCTCGACAGA 120

CACTGGAATT TTAACGATAG CTGTACCATT TGTAATTGAG TAGTTCGTTA TTTCACCCAT 180

ACTACTATTT GGTAAAATTG TTAATTCTCC TGAAATTGTA TTGATTCGTG TTGAACGAAG 240

TCCAATTGAT TTAACTGTTC CCTCTGCTAC AGTTGTACCA CCGTTATTTA TCTTAACATA 300

ATCACCTACA TCAAATTGGC TTTCAAATAT AATAAAGAAT CCTGTAAtTA CGTCTTTAAC 360

TATAGTTTGA GCACCAAAAC CTACTGCTAA GCCTACGACA CCAGCACTGG CAATTACCCC 420

TTCAACACTA ATGCCAAATT TACTTAAAAT CGTCGTAATA ACTATAAACC AAACGATATA 480

CTTCACTACA TTTTGAACAA GAGATATTAA AGTTTTAGAG CGCTTTTTGT TACTCTTTTT 540

ACTTTTATTT TGAATCTTAA ATCCCTGTTC AATCATTTTA TTCAGTATTT TAATAACTAT 600

GAGGGCTACG ATAATATAAA TAACAATCAT AGCGATTTTA GTTGCAATGT TTTCATATGT 660

TTCTATTTTT GTTAATGGCT CAAATAGAGA TGAAATAATA TTCATGACTT GATTCATGAT 720

AAGCGTTACT CCCTTCTATA TGATATATCA ATATTGtATT CATATTTtga TATACTTCCC 780

AACCTACGAA AGTCTCAATA TATCTAGAAT CAAATGGTCA C 821

(2) INFORMATION FOR SEQ ID NO: 1173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1173:

CCCGAAATTA AAATAATAAT GTATGAATTT TTAAATATGA TTTAAACGTT TTCAGTTTTT 60

ATGAAAACGC ATGCATTTTA CAAATAAAAA TGGTACGATG GCACTGGTTA AAACGTTTTA 120

CTAAAAACAA ATCATGAGGT GTATAACATG GCTGTCTCTT GATCAGATCT TGATCCCCTG 180

CGCCATCAGA TCCTTGGCGG CAAGAAAGCC ATCCAGTTTA CTTTGCAGGG CTTCCCAACC 240

TTCCCAGAGG nCGCCCCAGC TGGnCAATTC CGGTTCGCTT GCTGTCCATA AAACCGCCCA 300

GTCTAGCTAT CGCCATGT 318

(2) INFORMATION FOR SEQ ID NO: 1174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1174:

GTTTTAAAGC GGTTATAAAG GTAAATATGC AATATTATAA ATATCTTCTT CAGAACTAAC 60

CGAATCTCTT AAACTCATCT GTTTAGATAG CGTTTCAAAT TGATAAGTTT TAATTTTAAC 120

CGTTACAGTT TTAGCTGACT GCTGTAATTT ATTTGACGTG CAGCTGTTTT CCTGACAATn 180

CCATACTGTC TTAAAnCTCT GCATCA 206

(2) INFORMATION FOR SEQ ID NO: 1175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 653 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1175:

TCTGCATCAT GATATTTTAC ATCATCACTT ATAAGAACGT CACCTACATT TAAACTTTCA 60

TCTAAAGCTC CAGCAGAACC TGTATTAATA ATGACGTCCG GTTTAAACTT ATTAATTAAT 120

AATGTCGTAG AAATTGCAGC ATTAACTTTT CCAATGCCAC TTTGGGTAAT CACTACTTCT 180

CTATCTTTTA AAATGCCAGT ATAAAATTTA ACATGTGCAA CTGaAATTTC GCTTAATTGT 240

TTTTGATTCA CCTCTTTTAA AAAATCCTAG CATTTGTTAT TTTATCACAT TTTAATCACT 360

ACAACGACAA GTATCATGAT TTTCATTACT GTATAAAACT TTTGCTTTAT TTTTATAAAA 420

AGCTCTTTCA ATAACTTGGT ATCATAAATA ATTATTTTTG AACTCATAAC AGTGAATTCG 480

ATGCTTCTAA TTTGTCTATT TTTCAAAAAC TAATCATATC AATTACATCA ACCAATCGTG 540

TCAAGAAACT TTATTAAATA ACAGGAAAAT GATATGTTTA AAATAATAAT GATGAAATAA 600

GAGGATTTTA CAATGGCTGA AAATAATCAA AATAGTCTCG TAACAAAGAT AGC 653

(2) INFORMATION FOR SEQ ID NO: 1176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 410 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1176:

ACATGGCCGT TnGnATCAAG ATCGTCAACG ATTGATTGGT ACAATTGAAG TGCCTATGAC 60

ATTGGCAACC GTTGGCGGTG GTACAAAAGT ATTACCAATT TGCTAAAGCT TCATTAGAGC 120

TACTAAATGT AGAGTCAGCA CAAGAATTAG GTCATGTAGT TGCTGCCGTT GGTTTAGCGC 180

AAAACTTTGC AGCATGTCGC GCGCTTGTGT CAGAAGGTAT TCAACAAGGT CATATGAGTT 240

TACAATATAA ATCATTAGCT ATCGTTGTAG GGGCAAAAGG TGATGAAATT GCTAAAGtAG 300

tGAAGCTTgA AAAAAGAACC CCGTGCAAAT ACACAAGCAG CGGAACATAT TTTACAAGAA 360

ATTAGACAcA ATAGTAAAgG CGAtAGCGAT TaAAGAAAGT TAAGTCAGTC 410

(2) INFORMATION FOR SEQ ID NO: 1177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1177:

CATCAAGATA ACTACGGTTA TAATCCAAAC GACCCAACAT CATATAACTA TACTTACACT 60

ATTGATGGCA CAAGGTAACT ACCATTACAC ATGGGAAAGG TAACTnGCAT CCAAGTCAAT 120

TAAACCAAGA TAATGGCTAC TACAGC 146

(2) INFORMATION FOR SEQ ID NO: 1178:

(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1178:

TGTTCCTGGT GGAACTTTGG TTTCTTAATG TCATTCCAAA TTGCTGTATA TTCATTCATT 60

GGTATTGAAC TTATAGGTGT ACTGCTGGTG AACGAAAGAT CTGAAAAAAC CTTACCGAAG 120

CAATTAATAA TGTACTATCC GTATTTATAT CTATATCGTG GTnATATAAT ATGTCATCAA 180

CTGGATnTAC GTCAATAGAC CTTCGTAACC TTAATATCGC GACAT 225

(2) INFORMATION FOR SEQ ID NO: 1179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1179:

TGTACGCATA TGGTATCACT TGATGACCAA TTCACTTTGT CGAGAATAAC GTTATTTAAA 60

GACATTGATT TAAAGAATTG GTATTnCGTT AATTGTATTA GACTTTTCAC AGAAGTAGCG 120

ACAACAATGA TTTCATCGTA ACACGTGCGC ATATnAAGCA TGGGAAAAGA CATGGnCTAT 180

TGACCTGGCC TTTTGTGCAC TCGTACGATT GGTCAAACGT GGCTATATTG AAAGTTTGAA 240

ACAAGATGCG ACGGACACAC ATGCACGGGT GGGGATAGAT CTTGAGTCTT ATTGAGACGC 300

TGTGACTGTG GCTGACATC 319

(2) INFORMATION FOR SEQ ID NO: 1180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 654 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1180:

TTTTATCTTG GTTTTGAACT AGATATGTGT AGTCAGGTAT AACATAATCA ATCCCTAATA 60

AGTTATCATC AGGGAATTTG ATACCTGCAT CGATAATGAC AATTTCGTCT TTATACTCAA 120

CTGCATAAGT ATTTTTACCG ATTTCACCTA GACCTCCAAG TGCATATACA CCTACTTCAT 180

TTCGTAATCT AAATGTGCGC CCTCTAATTT AGTGATAAAT TCGATATTAA AATTACGATC 300

TTTCAAGTAA CGACGTACTT GTTCTTCTGT TTGAGCTTCA ACATAAAGTG ATTGTGTATT 360

TTCACGCACA ATTACCTCGT CTCTGTTATG TTGATAaAAA ACTTTAAATA CTGCCATGTT 420

AAAAATTCCT CCTAAGAATG TTTGTyTAAT TTATTGTTAA CCCTAGtAAA ATCGTATTGG 480

AGTATATATC GATAAATTCA TTCCAATCAT CTCTATAATG TAACTTAATA ACGATTTGGT 540

TAATAACTAG GTTCATCATG TCGTTCATTT TAAAAAATTA GTGAAATAAC ACTAAAATTT 600

CAGTTAAATC TTATTTTACA TGATGAATGA TAATAAATAA AGCAGTTTAT CTCA 654

(2) INFORMATION FOR SEQ ID NO: 1181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1181:

CGGGTATATT ATAGACAACG TTTAAGGACT TCTTTTTAAC TAACTTGTTA AATGTTGCTG 60

TATTTTTGTA TTCAACACTG TAATATAGTT CTTCTGACGC TGATGCATTA CTCATTGTAA 120

TAGATATTAA AAGACTCAAT ATTATTAaAC TAATAATAGC GCGCTTTATG ATTTTCATAT 180

TCTAATCTCA AATGAATTCC AGAACTTTAT ATGGTTCAGG TGCGACAACA T 231

(2) INFORMATION FOR SEQ ID NO: 1182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1182:

TAAGTTTATT AAGCTCTTGT CCGTTAGCAA TCACGCTACC GCTAGAAATT TGGTCAATTG 60

AACTTAGTAC ATTTAATAAG GTTGTCTTAC CTGATCCAGA AGGCCCCATA ATCGCACGAA 120

TTCGCCTTTT TGTATGTCAA GTAATATCTT AGGCTGAATG GTGCTTTACG AGTTTGAACA 180

GTGCCGAAAA CGCAAGCCCC TTGATATCTT AAATGTGGAG ACTACAACnC ATCAGTGnCA 240

CGGGA 245

(2) INFORMATION FOR SEQ ID NO: 1183:

(A) LENGTH: 490 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1183:

AGGTAAAGAT GATGGTGTAG AAGTTTATGT GCATTGCGAA GATCATGGCA TTGTATTTAA 60

TGCAAGTCTA CCTTTGTACA AAGATGCCAT CCATCAAAAA GGATCAATGC GTAGTAATGA 120

CAACGGTGAT GATATGAGTA TGATGGTGGG TACAGTGCTG AGTGGCTTTG AATATCGAGC 180

GCAAAAAGAA AAGTATGATA ATTTATATAA ATTTTTAAAA GAAAATGAAA AGCAATATCA 240

ATATACAGGT TTTACTAAAG AAGCAATTAA CAAGACGCAA AACGTCGGGT ATCAAAATGA 300

ATATTTTTAT ATTACATATT TATCAAGAAA TTTAAAAGAA TATAGAAAAT ATTACGAACC 360

ATTGATACAT AArcAATGAT AAAGAGTTtA AAGAAGGTAT GCAACGAGCT AGAAnAGAGC 420

TAAACTATnC TGCTAATACA AATACTGTAG CAACGTTGTT TAGTACGAAT GATGAAAGGA 480

ATAGAAAAGA 490

(2) INFORMATION FOR SEQ ID NO: 1184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1184:

CTCGCATTTT AATAAATCAT ACTCTTCTTT TCTTGCATAC GAATTAGAAT AACTCGCGAG 60

ACCTATAAGT CTCTTTCCTC ACTAGATAGT TTATACTTTT GGTCnGTTGA AGTCAATAAT 120

TTTATCTAAA GCTATAAAAA ATCTTTTGAT AGC 153

(2) INFORMATION FOR SEQ ID NO: 1185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1185:

TCATTTATAT ACTGTATCAC GCTATCTTTA GTATGTGTGC ATnATCATTC GTTAGTGCGT 60

AATGAACGTT ATATTTTAAT TCATGATTTA CTAAGACCAA CAAT 164

(2) INFORMATION FOR SEQ ID NO: 1186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1186:

CACAAGTGAC GTCATATTAT AAAAGTCACT CGGTTTGCGA TACGTTCTGT CTAAGAAATA 60

GCGACGTGCA ATTTCATATT TTnTATAAAC ATCCGTTGAA AAAGGACATA AAACCATGCG 120

TTGAACCAGG GTCTATACTT TCT 143

(2) INFORMATION FOR SEQ ID NO: 1187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1187:

CGTACAAGTT AAAACGTTTA TACGATTACG AAAAACCACC GAAGAGTGAG AAAGATCCAA 60

TGGTTGTATA TGCAGTAAGT GCAGGATACA AATGGTTCTT TGCTTATCCA GATGAACATA 120

TAGAGACTGT TAATACATTA nCAATCCCTA AAGATGTCTG TTTATTAGCT CAGCATGAnC 180

ATACAGTTCG GTCACATAGT GTCAATTCA 209

(2) INFORMATION FOR SEQ ID NO: 1188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1188:

TTGGAATCGC TGTCGACGGA TAGCAACCTG GATTGTAAAA ATAATGTTGG CTTTAAAAAT 60

ACCGTGGCAA TATTAAATGA ATAATCGCTG CTGAATATAC ACCCAATGCA CATTGAACTA 120

ACATAAnCCC ATTTGACTCA TCTACGCCCA CTATTGGCTT TATAGTCACT GAACTAAGCT 180

TAT 243

(2) INFORMATION FOR SEQ ID NO: 1189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1189:

CACCAGGCAT TACCATACCA GCACTCATAC CACCAATCAC kCTCGATAAC ATCAATACCG 60

AAAAATTGTG GCCAACTGCA AACATAAATT CTGACACTGA AAACAAAATT AATCCTATAC 120

ATATAATTAA TTTCTTCCCT AATTTGTCAG CTAGCGTACC ACCAAACGGC GATATAATCA 180

TTTGAGATAA CGCAAAAGCA GCAACTAGTA ATCCTAAATC ACTACCAGTT AATCCCAAAT 240

CTTTTAAATA AACAGGCAAG ACTGGTATTA CTAAACCGaT ACCTAAAAAA ATCAAGAAAA 300

TATTAAAATA TAAGACAAAA ATCTGTTTAT TCATATGCTC ACCTCTTTTT TCTCCATGTC 360

ATGCTTAAAG CTGTTATTCT TCTTTTCCAC GACAGATTGC AATTCATGCT AAATATTCGT 420

AAAAAGTTTC TATATTGTAT TACAACATTG CTACATTTGA CAATATTTTt TCTTTGTAAT 480

TATCACTATn TTCCATTTAA TTGTATAATT AATGACATAT TnnAATA 527

(2) INFORMATION FOR SEQ ID NO: 1190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 889 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1190:

AAAACGTGGC AGTAATTCAG TGTATGTTCA ATATGATGAT ATTATGTTTT TTGAATCATC 60

AACAAAATCT CACAGACTCA TTGCCCATTT AGATAACCGT CAAATTGAAT TTTATGGTAA 120

TTTAAAAGAA CTGAGTCAAT TAGATGATCG TTTCTTTAGA TGTCATAATA GCTTTGTCGT 180

CAATCGCCAT AATATTGAAT CTATAGATTC GAAAGAGCGA ATTGTCTATT TTAAAAATAA 240

AGAACACTGC TATGCATCGG TGaGAAACGT TAAAAAAATA TAATAAGATA ATAAAGTCAG 300

TTAACGGCGT ATTCAATTGT AAATCTTGTT GGATTTTAAC AAGATAACTA GCAAATGCAC 360

TGTATAGCTG GCTTTTTAAT TTTATTAACA AAATTAAATA TGACGCGTGA ATTAAAAAAT 420

CTCTACAATC CTATGGCGCA ATTTTTAACA AAATATACTA AATtTGAAAT TGACAGTTTC 540

CATAAATAAA ATGCTATAAT TTCCTACTCC GTGAATCTTA TTTTGTTTTA AAAAACAGTG 600

TAGCACAAGm TTCAACTTGT TTCCTACACT GTTTTATAAA TGAATTATTT AAAATGCTTG 660

TTCAACCTCT TGTAATGTTG GCAAACTATT AATAGCACCA TACTTCGTTG TCACTATTGC 720

AGCAACGCGA TTGCTAAACG CTAAAATTTC CTCACCTTCA TTTTCAAATA ACTGAGTTAA 780

ATTTAACACA TCGGTTGCTA AAATCCTGCT AATAACTGCA CCAATAAATG CATCCCCTGC 840

CCCAGTTGTA TCAACAGGTT TTACCTTATA GCCACTATGA TAATGATTA 889

(2) INFORMATION FOR SEQ ID NO: 1191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1191:

AGTTAAAGGC GTTGAATTAA TGGCCTTCCC ACACATGACA TATAAACAAG CGTGCGCCTA 60

TGGTCTGATA ACCAGATACA CGTTTGAATG GATTAATTGC GTTCTCAATT AGGCGTGATA 120

TGGCTTTAAA GATTTnAGTC TGTTGAAATG ATGGTGAATT AAAGCATTGC GCTAAAGGTG 180

CACTGACAAT ATCTCGTAAA GATATGGTGC TTTAACAGAT TTGTAACATC TATGGTCTAA 240

nGATACGGGG TTAA 254

(2) INFORMATION FOR SEQ ID NO: 1192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1192:

GGCTCATAAG TTACACCTAA TGCATCTTCA TCTGGAAGCT GTGGTTTATC ATCTTCTAAA 60

TCAGCAGTTG GCGTTTTTTC ATATAATTCC TTTGGCGCAC CAAGATACGC TAATAATTGA 120

GCTGTGTATn CTAGGCATCC ATACCGTATT CGTTAAACCA GTATATTTCA GCTGAATGAT 180

CTGTCCTAC 189

(2) INFORMATION FOR SEQ ID NO: 1193:

(A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1193:

TTGATATTGA TCGATGACCG GTGATGTGAA ACTGAAACTG ACCAATGAAT GAAAAAATGG 60

GCAATGTTTT TGACAACAAT GGTCATTTAC CAAATAAAAA TATTGnCACC ATTAATACCT 120

GnCAAACGTG TTTGTTCCTA AACCTAAAAT GATAAATCCT ATTGAGATTA TGGACTTGGT 180

AAGCTGCAAT CTTTTTAATA TCTTTATAAG CAATG 215

(2) INFORMATION FOR SEQ ID NO: 1194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1194:

AGAATTTGCn ACTGGTTTAC CAACGCATCT ATGTTCGGTC GCTATACCGC ATACAGATGT 60

CGAACATATT AACCATAGAA CGTAGGTGTG GTGTTCTAGA AAAAGAAGTG CCGTTATTGA 120

AATGGGACAC TTGATCAACA GCCGAGTGAA ATCGTTTT 158

(2) INFORMATION FOR SEQ ID NO: 1195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1195:

ACTGATTGCC GTGTCTGTGG TTGATCATTG ACTAATTGTT GGCCATCATT GGnTTCTTGG 60

TCTAATAGTC CTCTTGCTCC TGCGTCGTAA CATTGATGCC AATCATGCAC CACAGCCTTT 120

CGGTTCATCA TAACATTTCT GCCAATGTCT CTACATGACA CGGGCTCATA TTTCTTTCTG 180

(2) INFORMATION FOR SEQ ID NO: 1196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1196:

GTTAAAGCGA ATTATTCACA ATATAAAAAA TCATCTGATC AAGTCGTATT AGAATTAGGT 60

ACAAATGGCG ACTTTACTGT CAAACAGCTC GACGATTTAC TTAATCAATT TGGaAAAGCC 120

AAGATTTATT TAGTTAATAC ACGTGTTCCA AGAaTTTmTG AGGgCAAATG TAAATCGATT 180

ATTaGCTGAC GCGGgCGAAA CGGAAGTCCC AATGGTCACA TTAATTGGAT TGGGTATTAG 240

GCGCTTCACA AGGGACCTTG GTGGAATATT TTTG 274

(2) INFORMATION FOR SEQ ID NO: 1197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1197:

ACGTAACCTA TATTCATCTC TGTTCCCAAT AATAATAACA ATACATAACT GATATTAGCT 60

GTCTTTCATC TCTAATTAAT ATGCGTCATG AGCTAATATC GGTTATTTTT TTGTGTCAAA 120

nAATTTTTAT TTTATCTCTC CATCGCATTA ATTG 154

(2) INFORMATION FOR SEQ ID NO: 1198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1198:

AATCCTCACC CGTAATAAAC TCGTTTTGAA TGCGTTGTTC GAACTCACGG TATATTAAAG 60

CAATATCCTC TAACTTATTT TTAGTTCGAG TTTGCATATT TTTATCAGCA ATAAAGTGTT 120

CTAAATGTTC AGGCGTTACT GCATATTTTT TAAAATCTTG AATTTGTTCT GTTAATTTTT 180

CACTAAACCC ATAATATTTT GCTTGTGATT GATAAAGTTT TAAATACTTT TGTTGTTCnT 240

GAACAATGn 249

(2) INFORMATION FOR SEQ ID NO: 1199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1199:

TTGGTAAAAA TCGACATCAA ATACTAAATC TGATCCATCT GAATCCCATG TTTAAAACCG 60

AACTTGTGCA TTAATTGTAA AGTTCAAACT CTTCATCTTC ATAGATCGCG ATGCGTCTTT 120

TAATTCTTTA GGTGATACTT TGTAGATCTA TAACAAAATT AnCTA 165

(2) INFORMATION FOR SEQ ID NO: 1200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1200:

TTATTAGCGA TTAAAAATAT GTCCTTTTTT AATAAAGGAG ATATATGTTT AATTGGATGT 60

CAACATCGGA GTCATTGGCG AAAAATAGGG CTGCGGTCGA TGGAGTTCAA AACTATTTTA 120

ATGCATTACA TGTTGTGAGT nAAGAGCAGG CGTACTTTTC TTTTCAAGGA TGTGACATAT 180

CACAGAGCGT ACAATAGAAA CTCAGATACC ATTACATGGA nAGTCCGCGT CCAATG 236

(2) INFORMATION FOR SEQ ID NO: 1201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1201:

TAATGCTAAA CAGTATTATG GAGATAATGG CTTAGTTCAA ATTTCTGATG nAAGTCAACA 60

CTTCTAAAAT TTGTAAATGA AGCATTAGAC AATAACGAAC AATCAGTTGA AGATTACAAA 120

AATGGTAAAG GCAAAGCTAT GGGCTT 146

(2) INFORMATION FOR SEQ ID NO: 1202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1202:

ATTGATGATA GTATTGATGG TAATACCATA AACATACAGC ATTATCACAA GTAAAAGTAA 60

GCCTAAATGT CCATAAAATC TACTTGTCAC AATATATGTC GGTATTATCG TAACGGGAAG 120

TCATTTCGTA CTTGATTAAA CTTTTGTGTA ATTGCTTTAG TACCTTCTAA ATACCTGGTT 180

GATGAGACCA CATACTGATA CCACCATAAC CATAAACAAA AGGTACACCA GAATTGGGCA 240

TACTTCTTAT TCCATCCAAA CCTCCGTAAC CTAATTGCTA CGGGTAATAT TCCAGCACAC 300

TAATAGTATT GATGTAATTA ACTGAACGGC CGCTnGATAA TAAGTCTTAC AGTCTTAAAC 360

GTCCATGCGC ATCnTnACCC ATTCA 385

(2) INFORMATION FOR SEQ ID NO: 1203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 580 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1203:

ACATTGAACG AGTACAGAAA ACTTATTGnA AATAAAGGCT GTTAAAGATA AAGAAGAAGA 60

TACTTACAGA GGTAAGTATT TTGCGGAAGA AAGAAAAAAC GAAAAATTGG AAAAAGAAAA 120

TATAAAACTA AAAAACAAAA TTTATGAATT ACAAAACGAA GAAGATAACG AGGAGGACGA 180

AGAAGACAAG GAGGACGAGA ACGATGTATT ACAAAATTGG TGAGATAAAA AACAAAATTA 240

TAAGCTTTAA CGGGTTTGAA TTTAAAGTGT CTGTGATGAA GAGACATGAC GGTATCAGTA 300

TACAAATCAA GGATATGAAT AATGTTCCAC TTAAATCGTT TCATGTCATA GATTTAAGCG 360

AACTATATAT TGCGACGGAT GCAATGCGTG AyGTTATAAA CGAATGGATT GAAAATAACA 420

CAGATGAACA GGACAAACTA ATTAACTTAG TCATGAAATG GTAGGAGGTA TGAnAAGTGA 480

ATGATTTACA AGAGAGAGAA TTAGAAACAT TCGAACAAGA CGACCGATTC AAAGTAACTG 540

ATCTAGACAG TGCTAACTGG GTTTTTTnAG AAACTnGGAT 580

(2) INFORMATION FOR SEQ ID NO: 1204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATCGTATGGT TGAGGCGAAT TTAACTGAAA AATTAGACAA CGAATCTTGA TGAAAAGAnA 60

ATGATTGGCT AAAATAGCAG CTAATCAAAT CAACGATAAT GAATGCTTAT TTATCGTGCT 120

GGTTCATCTA CATTGGAGC 139

(2) INFORMATION FOR SEQ ID NO: 1205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1205:

AGGAGGATAT CAGaCTTACA rACTATTCTT TATCATACTG rAATTCAAAT AGACACCTTA 60

ATTGaAGaAG GCGTTGACGC GCTACTTTTC rAAACGTATT ACGACCTnGG AAGnGTTAAC 120

AAATGTCATT TCCACGGAAC GGGGAAAGGA AATACGGCGT TGCCAATCCA TTGCTCCAAT 180

TGAACCGGTT GCAAACACAA ATTGACTTGG TTGAAGGGGC AGGCATGCA 229

(2) INFORMATION FOR SEQ ID NO: 1206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1206:

TCGACAAGTT TTTAACAGTT CGTTATTATA TGAATGTAAG TAAAAATTTC TTAGCTACAA 60

CTTACATATT ATAAATGCAT AAATTAAACA AAAAGGGGCG AAAAAAGTTG ACTCATTTAT 120

CAGATTTAGA TATTGCGAAT CAATCAACAC TACAACCAAT TAAGGATATT GCTGCATCAG 180

TAGGTATTTC AGAGGATGCA TTAGAACCTT ATGGTCATTA CAAAGCTAAA ATCGACATTA 240

ATTAAAATTa CGCCAAGAGa AAACAAAGGG AAgTTGTTTT aGTTAACTGc GATGaGCCCA 300

ACACCAGCTG GTGaAGGtAA tCmACGGTTA CAGTTGGtTT AGCTGaTGcA TTCCmTGaGT 360

TaATgAAAAC GTTATGGTTG ccTTaGGGGG CCTGCCTTT 399

(2) INFORMATION FOR SEQ ID NO: 1207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1207:

ATAAACAATA CGATTTGTAT GCTACTTGTC TGAAGACAAC ATAAAACAAT ATGTTAACTG 60

ATATTGAGGA TATGGGCTTT CAAAATCCAn TTCAAAAAAG GTTATGTTGA AATATGACGC 120

GGTTGTTGAA AGAGACCC 138

(2) INFORMATION FOR SEQ ID NO: 1208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 655 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1208:

AGTCGCCTAA CTTTTATTAT CAGTCCAATC AGTTTCATCA AGTATAAATG TTATTGCTTA 60

TTTTTGTATT CTTGGCGTAT TTTTTGTTCT TCTGCATAGC GCTCTGGATT TTTCTTATAA 120

AAATCTTGGT GATAGTCTTC GGCTTTGTAA AATTGTGACG CTGGTArTAT TTTTGTTGCA 180

ATTGCCTTAT CAGCATTAAT CGTATTTTTA AGCTGCTCGA TATAAGTCTC AGCGAGTTCT 240

TTTTGATGAT CATTAGTGTA GAAAATAGCT GTTTnATATT GAGGACCACG GTCTTGATAT 300

TGACCACCTG TATCTAATGG GTCAATGACT GAGAAAAATA TTTCTAATAA CTTATTGTAT 360

GAGAATAATG CAACATCATA TTGAATTTCA ACAGTTTCTA AATGACCACT CGTACCTGAT 420

TTTACTTGTT CGTAAGTAGG ATTTTCAATA TGTCCGCCCA TATATCCAGA AGTTACTTTT 480

TCTATGCCGT CAAAGGTGTC AAATGGTTTC GTCATACACC AAAAGCAACC TCCGGCAAAA 540

TAAGCTGTAT TAATATTCAT TTTTGACATC CTTTCCATTA GACCTTAGTA CGATTTATTA 600

AGAAATCACT TGCTTTTTGA ATTGTTTTTA TATAACGTTA ATAnGnGATT ATnAT 655

(2) INFORMATION FOR SEQ ID NO: 1209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1209:

CCGnCCCCAA TGGAAATTAC CTTTGGTnCC CCATTTTAAT TGTTAAATTA TTGGAGTGTT 60

AATCTCACTA TCTTCAAATA AGCTTGTGTA TAGTTTAACA GCTTCTTCAG CTTGGTTATT 180

AAACATTAAA AATGTCGTGA TTTTTGGAAT ATC 213

(2) INFORMATION FOR SEQ ID NO: 1210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1210:

TTGATTGCAA CTTTGATAGT GAAAACATTT ACATGATGTT GTCACTGGTG CACGGGCGTC 60

GAGAACAATC ATTGCGTTAT TGACGGTGCT GCCCTGCTGT CTCAGTTTGT TGATGCAAGC 120

ACTACACGAA ACCCAATAGC nTCACCAGG 149

(2) INFORMATION FOR SEQ ID NO: 1211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1211:

AATGTTTCTC CTAATTTTAA ATGTTTAGGA ATATTAACTA GGATAATAAA TCCAGCGACA 60

TCCCAAATGG GATTCATATA AGAATGTTGG ATGATAATnT TGGCCGTTAA TATACATATT 120

TTCTATTATA AAATTGGGCA AA 142

(2) INFORMATION FOR SEQ ID NO: 1212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1212:

TTTAAATTTA GTCACTTCAC CTTTTAAAGC ATGTTCATAA AATGTTTGCA TCATCAATGC 60

ACGTTCTGAA CCAGAGCCTT CAACACAAAG ATAAATTTGT ACAGCAATAC CGCCTCTAAC 120

TCTTCGTTGC GATGATGGCA ATACCACTCA ATCCAACGCT CnG 163

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1213:

GTCACCTTTC ACGTCTTGAA GAAAAAGGCT ATATAAGAAG AGATCCAACG AAACCACGTG 60

CTATAGAAAT TGTAAGTGAT CAAACAAATG ATAATATTAA TATGGAAGAA ACGATTCATG 120

TGCCAGTTAT TGGTAAAGTC ACAGCAGGTG TTCCTATTAC CGCAGTAGAA AATATTGAAG 180

AATATTTTCC ATTACCTGAA CACTTAACAT CGACACACAA TAGCGACATA TTCATATTAA 240

ACGTCGTAGG CGACAGTATG ATTGAGGCTG GTATATTAGA CGGAGACAAA GTAATTGTnC 300

GCAGTCAAAC CATAGCAGAA AATGGAGACA TTATTGTTGC TATGACTGAG GAAGATGAAG 360

CAACTGTCAA ACGCTTCTAT AAAGAAAAAA ATCGTTATCG ATTACAACCT GAAAATAGTA 420

CAATGGAGCC AATTTACCTA GACAATGTTG CTGTAATTGG GaAAGTAATT GGTTTGTACC 480

GCGAAATGTA ATATTTTAAA CCGTTATATA TTATCGTAAT TGTTAAGCCC TCATTTTTAT 540

AAATTTTGGG nCTCTTGAAA AAGTTACGTT TTCAAGAGGT TTTATTTATT CTAATCTAAA 600

TTCAGTTCAA ACAGAAATTG CGAATTGTTA GATAATCTCA TTCTTTArTA TAAATnTTGA 660

ATTACAGATT TCTGCAAAAT GTTACACAAA TTAAAACTCG CCCCCGTAAT AATTTACAGG 720

AGCGAGCCAT TATTATTTTT TTCnTTCTTT TTTATTAAGT ATATC 765

(2) INFORMATION FOR SEQ ID NO: 1214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 495 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1214:

AGTTGCCATC AAAAATACAG AACCTAATnA TnACCTTTTA TGATTTTTTG TGAATTCAAA 60

GTCACTTTCT TTTTnAAGCT TTAAATTTCT CCCCATTTTT TTAGCCCCCT ATAAGGATTG 120

AATATCAATG CCTTCTTTCA TTAAAATTTC TCTAATTTTC GAAACAAATA ATAATGCATG 180

TTCTCCATCA CCATGCACAC AAATTGTATC TGCTTGTAAC GTTACTTCCT TATTGTTTTT 240

TGAAATAACT TTATyyyCCt TCACCATCTT TAAAACCTGC TTAAGTGCTT CGTCAGTATC 300

ATCAGCAAAC ACTTCAGAAG CTGTAATTAA TCCGACATTC TTTGCTTCTG AAATTAGATA 420

TGAATTTGCT AATCCTACTA ACACTAGTGA TGGATCAAAG TCATAAACAG CTTGTGCTAT 480

AACGTTTGCn ATTnC 495

(2) INFORMATION FOR SEQ ID NO: 1215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1215:

AnTGTCCAGG TACCCGTGGT CCAAAATTCG ATGTACGTAG ACCATTGnCT CGTATTTGTC 60

AGATTGTGTT AATGATTGTC TCTGTATTAG GAAGTTTATT CTCCATTTTA ACAATTAGAA 120

AAATAGATCC GTTAAAGGCG ATTGGGTAGG AGGTGTGCAA ATGTTGAAAT TGAAATGTAC 180

AAGTCATTAA GTGGATCTAC ATGAGCGTAA GGTCATTGGA ATAGGTTTGC TGTGACTCGC 240

CGA 243

(2) INFORMATION FOR SEQ ID NO: 1216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1216:

GGGCTTCTTT CTAAAATAAC TAAGTGAATT ATCTATATAT GAAGAGGTCT CCAATACTTT 60

TTATATAATT CGTGATTACA TTCTATACTT TTAATTGTAT TTTCTGCGTA GGAAAGTGGT 120

TTTATTAATT CGATTAGTTC GAACTACAnT CAAGAAAAGG TAAAATTTGT GCATGAGCAA 180

GAGAAACATA CCTGAACCAA AGGCACCCGA ACAGTACCTA GGCCTAAGCG GCTAATTATA 240

AATGCTCAAG CGCAnG 256

(2) INFORMATION FOR SEQ ID NO: 1217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1217:

TTTATTTTTT CTTCTAAACG AAACATTGCT TCTTTTTGTG ATTGTTTTGT ATTCTTGTTC 60

AACACAACAC TTACGCGCTT CCATTTATCT GTGTATGGAT CTTTATACTT CTCGTAGTAT 120

CTGTATTTAG TTTCGTTATT TTTGTTTTTA AATTTTTCAA TCCACATGTT TATACCTCCT 180

GAGAGAACGT ACGTTCTGTA AATTTGTAAA AAATAATAAG GGTAGGTGGG CTACCCAAAA 240

TTTAGTACTA GGTACTAAAT ATGTTATAAT AAAATAAAAA GTAGGTGATA AGATGACTCA 300

ATTTCTAGGG GCGCTTCTTC TTACAGGAGT TTTAGGTTAC ATACCATATA AATATCTAAC 360

AATGATAGGT TTAGTTAGTG AAAAAAACAA GATTATCAAT 400

(2) INFORMATION FOR SEQ ID NO: 1218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1218:

CCAAGTGTCA ATTTTAGATG ATTTTTTTGT TGACCTATCG CCTTAACTGA AGAAACTGAT 60

AAATCATCCA TTTCAAAAAT AGGTCTAGAA AAATCTGTTC CGAAGGtCTT AAACGATTCA 120

TATCACGAAT ATTTTTAATC GTTATATCAT TTTCTGTTAA TAATACATCT ACTTGCTTTA 180

CGGGATCTAA CGAAGTTGTT TTAGATAATT CTTTCATCCA TTTATTTAAA CCTTCAGCTA 240

ACGATTCTAT ATTTTCAATA TCCATCGTCA TACCTGCAGC CATATGATGG CCGCCAAATT 300

TAGCGATTAA CTCTTGATGT GCTGATAGTA TTTCAAACAT CGACACTTGA TCAATTGATC 360

TGGCGGAGCT TTTGCATGAT TTTGCTCCCT ATCAATATTT 400

(2) INFORMATION FOR SEQ ID NO: 1219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 458 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1219:

AAGATATTAG ACATAAAATC TAAAnACAGC AGTAAGATGA TTTATGATTA GAAACTATCT 60

TACTGCTGTT CACTTTTTAT AATACTTCTG AATGTCTTCA CTTATACTTC TAGTCACAGA 120

GCATTCATTT CTTGTcTAGC AACGTTCTAC TCTAGCGGAA nTAAtTAGCT ACCATCCTCG 240

CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGcTCTCGC 300

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 360

TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT 420

AAAAAAAGAG ACCTCACGGT CTCAACTTGG CCTGGGCA 458

(2) INFORMATION FOR SEQ ID NO: 1220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1220:

CAAAATTTAT TTCTTGTAAA GTACAATATA AGTTAAATGT TGTTGTTAGG ATTGATTCTT 60

TCATCTGAGC ATTTAATTGT AAGTCGCTAT ATTTAATTTG TTCAGTATTT AmAAATAAAT 120

TGAAAAATTC AACTGATAAT AAAGGTGTTC TAATCATACA AATACTTGAC GGTTCGTAAA 180

TAGTGTTCAT TTGTAAGCAC CTCACATATT TGAATAGACA AATAGAGCCC TTTCAGGCTC 240

TATTTGCTGT AATCTTAACA GCAGAAGCTA TTAAAACTAC CAGTCTTAGC ACAACCAGGA 300

GTACATAAAC TATGACTTGT AATACGTTCG TCACCTGCTG AATCATTTGA GTnATTGTTT 360

GCTTTAACTT GCACGTCTAA ATCAAGAACT TTTTCCATAG ATAAAACCTC CTATTATTAG 420

TTGAAGTTAA GGCCTACTTC AATTGTCATA TTATCCCTTT TCACACAACA AATCAATAAA 480

TTATATAATT ATAT 494

(2) INFORMATION FOR SEQ ID NO: 1221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1221:

ACTATTATTT TAATAGTGAC GACAGTTTTA ATTTTATTAA GTATTGCTTT AATTACCTTT 60

ATGCAATACT ATTTCACACA AGAnACCGAA AATGCCATAA GAGAAGATGC TAGACGTATA 120

AGTTCACTGG TCGAACAATC ACATAATA 148

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1222:

TCGCTTTTAC ATCAAATAAA TTATCTTTAT ACAATTTCGT ATGAATTACT TCTTTATAAT 60

TATAAAAATG AGGAATTTTT TGATTGTTTA ATTCACTTGC TAATTGATTA GCTTTTTGTT 120

GGTCTTTAAT TGTAACGTCG TGTGGTGCAG TATATTTTAT TTCACTTGAT AAGGACGCTC 180

TACTTATAGC AGCAAAGCAA AGAACTGAAA CAGTAATCGC TGAAATGATT GCCATGACCG 240

TAAGTGAAAA AGCATTTTTC TTAATACGAT ACATAATAGA TGATGAGAAC ATGACATCAT 300

TtACACTTAT AACACCTTkT CTAAACtTCT TCACCATTTT AAAAACTAGA GArACAGAGC 360

TTTTAAAAAA TAAGnGTGCC CCAATCACAG TTGACAAnAA A 401

(2) INFORMATION FOR SEQ ID NO: 1223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1223:

CTTGACCAAA TCCATTTTTT AACAAAAGTG GTCAAGTGAA ATCCCATCTT TCCAAATCAA 60

AAAAGAGCTA AAGCAAAATG CTCTAGCCCT TGaTATTACT GATTTCCCAT CATTGTnTAG 120

CGTATTAATA TTGCTTCATG TACTGATCTC TTTCCCATTC AGAGACTTGA GTTCTG 176

(2) INFORMATION FOR SEQ ID NO: 1224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1224:

AATACTTTTA CGATAATTAT AAAGGTTCAT TCAAATCTTA GGGCAAAATG TATAATATTT 60

TTATGCAAAT TTAAAACAnT AACACTTATT TCAAGGTTCA ATATTTTGAG AATAAGGAGT 120

AATGCCAATC AAACTCGCTC GAAATAGGGG GAAACGAGGC nATCATTTTT GACAATGAGT 240

GTCAATAGGG AAGAATAACA ATTAGGAATG ACTCATAGGA GGA 283

(2) INFORMATION FOR SEQ ID NO: 1225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1225:

AAAAGAAGAG AAGAAAGTTG AAGAACCTCA AGCACCTAAA GTTGATAACC AACAAGAGGT 60

TAAAACTACG GCTGGTAAAG CTGAAGAAAC AACACAACCA GTTGCACAAC CATTAGTAAA 120

ATTCCACAGG CCATTACAGG AATTTAAGTC GGATACCACG TGAATnACGT CAGGATGTCn 180

GCCGTTCACA TGACACGCTC TACATATTCA CCACTCG 217

(2) INFORMATION FOR SEQ ID NO: 1226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1226:

TGGGTACTAT TTATTACGTA AAACTTTTCG TTAGCGATGC CGGCATTGCA AGAGCAAGGT 60

TTACAAAAGC GGACTAGGTT TGCACTTTCT GCTGTTCCAT CGCATATGGA TTAGTAAGGT 120

CTTTATGGGn ACTGTAAGTG ATCCGAGCAA TGTCGGATAA TCTAGGTCTT GGATAG 176

(2) INFORMATION FOR SEQ ID NO: 1227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1227:

AATGAAAATA AAGAAGATGA TTTTGTTGCA TATGGGTCTC CAGAACATAA TTATCAATTT 60

GGTGGAAGTT TAATCAAAAG TAAAAATTTA AGCACGTTAT TAAAACCAGT ACATCAAACC 120

GCGGCCGTTT TAATTTTGTT TTCAAGTTAA TCATACTTAC ATATAAAAAT GAAAAGTTGA 240

ATTTTTAGTA CAATTTCCAC TGTATTTATC TGTTAACCAC TTTATACCCG CAATATTTCG 300

TTGATCTTAT ATAAACACTT TTGGCTGCTT TTCCTTGACC TAGATTAAAA TTATAGATTT 360

TCCTTGTAAG AGTGTGTTTG TAGTATCATA AATATGTAAA 400

(2) INFORMATION FOR SEQ ID NO: 1228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1228:

ATCTAGCATG CTTTTGGAAA ACGATAAGAA TTTGGTGTTT GAATTTCATA ACCAACACCA 60

GCAGTTTCAA CAACTACGTG TGTAGGATAT AAATGTGTTA CTTGACCTTT GACATACGCG 120

TACATTATAG GCACATCCTT ACATACTCAn 150

(2) INFORMATION FOR SEQ ID NO: 1229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1229:

TCGGTACAGT GCATTTGGTG CGTCATGGTT TACAAGGnAA AAATAAGTGA TCACTATTTA 60

TCAGTATGGG AAAAAGCAAC GACGTATCAA ATGTACCATG GCTTAGCATT ATTAATTATA 120

GGTGTAATTA GTGGTACA 138

(2) INFORMATION FOR SEQ ID NO: 1230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1230:

TTGGTATGTA CCTCCAATAG TAATTTCAAT AACTTTGTCT GTTGAACACT AAGAGCAATT 60

CCTTGATTAT nCTAAGAAAA GTAAAAGCAC ACGGAGTATC CTATCAGAAA ACCAGTATAC 180

CA 182

(2) INFORMATION FOR SEQ ID NO: 1231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1231:

TCTCTTTAAA TTGTACACAA TTCTGGATAA CTATCCCCAT TTCTGTGGAT AAACACCTTG 60

ATGTCTTATT ACTTATCCTC GTTTTTATAT CCCATATTTA TCAACGGkTA TCGCTTTTTT 120

TCATAAAAAA aCACTACCGT ACCyCTTATT TAAGAAATAC AGTAGTATTA TTTTCAATAT 180

ATTTTAGCTA GCnTTTCTAC GTCGTACAGT CGCGATTAAA CCTATACCTG CTA 233

(2) INFORMATION FOR SEQ ID NO: 1232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1232:

GTTTTTGGTA AAAGTACTAA TATTAaCCAA GTATTGAGTC ATATGTTAAA ACAAGATGCG 60

AATGATATTG GCTTTGCTAA ATTACTACAA AATGAGAATA ATCGTATGAG TTATAACGAG 120

TTAATGAGTG AATGGCAATC ACATCAACGT GCATTTTTAG AAGAGTTGAG GCATGTTGAA 180

ATGTTAAAAG AAGAATCTAT TAGAGCATAT GATGTTTATA AAAATTGTGA GTCTTTCTCT 240

AAGATTGAAC AGGTTATTAA TAGTGAAAAA ACAAGTATTG AAGAACAGGT ATATCATTTA 300

GATAATGAAA CGTTACGAGA CAATAAAGAA ATAGAAGTTT GGGATAATCG ATTTAATTAn 360

ATTGnTAGCC CAATGGnCCC TTTAA 385

(2) INFORMATION FOR SEQ ID NO: 1233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1233:

CTGAAAAGAT TCAACTAATC TGAGTCAGGT TACAATCTCA TGATAACCGC TCGCACCTCG 60

GAGAAAGACG CTCAAACAGT ACAGAGCTCG ACCGCAGGAT ATTTTTTGTG AAAATGAACG 120

TATGAGCTGT TCAGAnGGCA CTTTATTGCG CAATAAAACG GTAAAAATCC TGAAGTGAAG 180

(2) INFORMATION FOR SEQ ID NO: 1234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 453 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1234:

ACCATTTTAA TTTnCnTTAT GACCTTGTAT GCCATTATCA aCAGTTATGA TTAATGTTAT 60

GCyTTCATCA TGAGCATTTC TAAATGCTAG TTCGTTTGGT CCATATCTTC GGTAAAGCGG 120

TTAGGAATAT GCCATCCTAC TTGTGCACCT AAAAGTTGTA ATGTTATCAC TAAAATTGTA 180

GTTGCGGTAA CACCGTCGGC ATCGTAATCA CCATAAACTA GGATTTTCTC ATCATTCGCT 240

ATCGCTCTTT TAATTCTTTC AATAGTCTTA GTCATATCGC TCAATTGnAG TGCATCATGA 300

TTGATATCTG TATCTGAAAT GATGGATTCT ATTGCTTGTn CATCAATAAT CGATTTACTT 360

nCTAATATTT TTTTTACGAT TGGCGTTAAC TTTAATTTTG ATGTTAATTC ATCACTTATG 420

TATTCAGCTG GTTTAGTTAA TTTCCACTTA TAC 453

(2) INFORMATION FOR SEQ ID NO: 1235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1235:

CGTGATTAAG TTGGATACTA AAATTTGGGA TGTTAGAGAA TGTGATGAAG ATTTnCAGCA 60

ATGTCCTGAA ATTAATGAAA TAAGAGACAT TGTTTTAAAG CGGTGGTTTG ATAGGTTTAC 120

CAACTGAAGC AGTTTATGGA CTTGCAGCGA ATGCGGCAGA TGA 163

(2) INFORMATION FOR SEQ ID NO: 1236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1236:

GTTAACACAT CGCTTATAAC GTGTAAATAT AAACACTGTT TTATAAAAAC TTTTTATACC 60

ATTACCGGCA CCGATAAATG TGTACTATGG AGCACAACAA TAACTGGAAT ACTTnGATTT 120

AATCCCGCTA TAACATTTCC TAAT 144

(2) INFORMATION FOR SEQ ID NO: 1237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1237:

ATAGTTTAAG GTGATATTCA AACAATATTA GGTTTGATTT AACTATCAAG CATCTACTTT 60

GTCATGTTTA ATACCAGCAA ATAATAAAAT CCATGTCACG ATAATAAATG GCATGTTAAT 120

GCAGGGTAAG CCCAACCGGT CCAGCCATGG TGGTGGTACC CTAnTTGGCC nCCACCTACC 180

GGTTAATTAA CCACCCCCAA AAAA 204

(2) INFORMATION FOR SEQ ID NO: 1238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1238:

CGGTCATTTT GGTTATTnAA CAACTATACC TGAGGGGTGG TGGGTAATTC GTATTGCCGA 60

TTCAGTTTTG TTAATATGCT GACCACCTGC ACCAGAAGCT CTGAATGTAT CAACTGTGAA 120

TAGCATCCGG ATTGGTTTCA ATCTGCTATG GCATCAT 157

(2) INFORMATION FOR SEQ ID NO: 1239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1239:

TTAAAGCATG TTCATAAATG TTTGCATCAT CATGCACGTT CTGGACCGAG CCTTCAnCAC 60

AAGGTAATTT GTACAGCATA CCGGCTCTAA CTCTTCGTTG CGTATGCCTG CAATTTCTTA 120

CCTCGATACT TAAGTCAATT TTCCGGGCAT AAGGGTGTTC ATTT 164

(2) INFORMATION FOR SEQ ID NO: 1240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1240:

TTGAAAAACT GAAAACGGTG AAGTTTTACA AACAACTAAA ACAGATAAAG ATGGTAAATA 60

TCAATTTACT GGATTAGAAA ATGGAACTTA TAAAGTTGAA TTGAAACACC ATCAGTTACA 120

CACCACACAA GTAGTTCAGA ACTATAAGTT GATCAATGTC TCACACAGTG CATAATnGAA 180

CAACATGCCG GTCTCAACAC TCACTAGGCA GAGGATCATA ACGGTCGTnG TAAGCTCGG 239

(2) INFORMATION FOR SEQ ID NO: 1241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1241:

TGATAAATAA TAGCGCCATC ATAAGTTGCA GGGTGGTAAT CATAATTTCT ACCATGAGTC 60

TTTGCCTTGA AAGACCGTGC ACCACTTTCT TTTAAATCGG TAAACGATAA TGnCAAGTTT 120

AAAATAATTT GGCGTGTTGG CATTTGAGTA TC 152

(2) INFORMATION FOR SEQ ID NO: 1242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1242:

ATCTTTACCT TTCACTGTTC ACTTATGTAC CATAATACTT CTGACAGTTA CTAATTAACA 120

GCAACTCTAA CTCATTTATA TTTAACTA 148

(2) INFORMATION FOR SEQ ID NO: 1243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 588 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1243:

GGTACCAATC GATCGTTACA AACGTTTCGT TAAAGACGAT AAAAAAGTAC CAACAGGCAA 60

TGAATATCGT GAATTAGTAT TAAAAGCAAT TCACATGATT ATGCTTGGTT TCTTGTATAA 120

ATATATTGTT GCTTACTTTA TTAACACATA TGCAATCATG CCGTTACAAT TAGACTTACA 180

TGGCTTTGTC AATTTGTGGT TATATATGTA CGCATACAGC TTATATTTAT TCTTTGACTT 240

TGCAGGTTAT AGTTTATTTG CGATAGCATT TAGTTATTTA TTCGGTATTA AAACACCACC 300

AAACTTCGAT AAACCTTTCA AAGCGAAAAA TATTAAAGAT TTCTGGAATA GATGGCATAT 360

GACATTATCA TTCTGGTTCA GAGATTGTAT TTACATGAGA TCTTTATTCT ACATGTCTCG 420

TAAAAAATTA TTGAAGAGTC AATTTGCAAT GTCCAACGTG GCATTCTTAA TCAACTTCTT 480

CATAATGGGG ATTTGGGCAT GGGAACGAAG TGTAATACCA TTGGTTTAAG GGGTTAAACC 540

ATGGCCAGCC TTGGTTAAAG GGTAnGGnCC AATAAGGACG GTGGGCGG 588

(2) INFORMATION FOR SEQ ID NO: 1244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1244:

ATTGCTGGAG AAAGGCAAGG CTTTGCAGGC GGATTGAACT CGACATTCAC TAGTATGGGT 60

AATTTCATAG GTCCTTTAAT CGCAGGTGCG TTATTTGATG TACACATTGA AGCACCAATT 120

TATATGGCTA TAGGTGTTTC ATTAGCAGGT GTTGTTATTG TTTTAATTGA AAAGCAACAT 180

AGAGCAAAAT TGAAAGAACA AAATATGTAG CATAAGTATT TTGGTGTATA TTGATATAAA 240

GTAAAGCGTA ATATTATGAA TGATTAGCAT CGTTTTTCTT ATGAATTTTA TTAAGAAAAT 300

GTTATATGTn ACAAAA 376

(2) INFORMATION FOR SEQ ID NO: 1245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1245:

CAATTTGTTC TAAAGCAAAT TCTTTACATT TCTCACGGAA TTCAGCTGTT GACATTTTCT 60

TTCGGTCAAC ACCTTTTTTC GTTAATGGCT TGTTCAATTG GGTAAACCAT GTGGTTATCC 120

CCCAACCTGG GTACCGTATG GGGTGGCCAT TAGGAAACCC CTTGGCAATA GGTTTTTTAA 180

TAAACCGGTA nCAAATTAAA AGGTCCTTTT TTAAAAAATT TTTGGTTTCC AAAGGGGCCA 240

ATGGnTCCCC CAATTAATGG TTAAAGGTTT TAACCCCAAT TTTCCGGC 288

(2) INFORMATION FOR SEQ ID NO: 1246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1246:

CATCATCAAT AGAACGGTAT TCGCAACGTC GTAGAAATCC CTTAAACGAC GAGAACAAAG 60

CAAGTCGACA TCAGTAAAAC ATTAAAGATA TTATGGCTGA AGCAGAGAAC TTAATAACTT 120

TTTATAAATC TATACCnTCC AAAATGTAAA ACTACCAAAA T 161

(2) INFORMATION FOR SEQ ID NO: 1247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1247:

TCACTACGTT GTTTAATTGT GGTAATTGCA GTTTTACAGG CTTGTCTAGT GAAGATTTAA 60

AACTTAATTC AAGTGTTTTA GTCATGAATA TGTCCTCCTG ATTAAATTGA TAAAGATTTG 120

TTAATTTGGT CGTTTGATGC ATCAGGGTTA ATGTTAGCGA ATCGACGCTT AAATTCTGTT 240

TGTTTGCCGT TAGCGTCtAC TTTAGTAAAT GaTAATACAA TAGTGATGTG GTTTATTTtA 300

CTCATATTTT AAAACCTCCT TTCACACTAT ATATCGAAAC AAAATAATAA AATGGCTAAT 360

TTTATTTTCT ATGTTTAAAA TCTATAAAAn AGGCAATAGA TATGTGTAAC TAAAATATAn 420

G 421

(2) INFORMATION FOR SEQ ID NO: 1248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 409 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1248:

ATAAGCTGCT GTTGATAATC CAAGTGCTAA AGTTAAATAT AATATAGTGC CAAAAATTTT 60

ATTCTTCTAT AAAAACACCT CTTCATATTT AATCCATATC TCTTTTTCGT TATTTATACA 120

GAATTTTCTG AAAATAGTCA AGGTTAATTT ATTTGCTGCA AATTTCAACC ACTTTATGTT 180

AAATGGACAT CAAAGTATAA TTGTATTATT ATTAAATTGT GCAGTGTATA AATAGACGAT 240

ATGCAGGAAC ATGTCGCCTA TTGAGCCCGT TAAAAAGACG GTGACTAAAT GAGATTTTCT 300

TTAACCATCA TTCGTTGTCA AAGTTTGGAA ATgATGGTTG TTTTTTATTG TTTAAATTAA 360

TCATTGCGAC TTCTATATCA ATGAAAGTTA TCTTAATATA TGAACTTCA 409

(2) INFORMATION FOR SEQ ID NO: 1249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1249:

CTTTCAATTA CGAACAAATC ATTACTAGTT TATTTAATGA TAATGACTGn AATTTAGCAA 60

AAAACGTAAC ATGATCATTT AGCTTGAATT GGTAAAACTG TTTATCCAAC ATTTCCAGAC 120

CAAATCACAC CGGTAAAACG TCAAAATATA TTGTnTCTAT GCCCGTTTTT ACCAGTTATC 180

TCATTGCAGG TATATTGATG AATTCACAAG TTGGTAT 217

(2) INFORMATION FOR SEQ ID NO: 1250:

(A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1250:

CAGAACGTGC GGATCGTTTT TATGCAACCT AAACCAGGTA CGGATTTAGC GTGGTTAAGT 60

GGCAGTGCAC TAAGTATATT CATTGATCCT GCATTTACAC GATGAAAGCA TTTATTGCAT 120

GAGTGGGTAG ATGCATTTTG CTGGAATGAT TCACAAATGC ATTAGAGnAC ATTTAC 176

(2) INFORMATION FOR SEQ ID NO: 1251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1251:

TTTCAACTTT CTAAATTATA ATATATCTTT TTAAAATAAG CTAGAATTTC TATATAATAA 60

ATGTTAATAA CGAAAAGGGA TGATGCATAG TGATCGCAAG CACGCCAGAG GCCGATTTGA 120

TATTGCGAGT TAGTTTATAT GGTTTGGGAT GATATGGATA GAATTGGTAA ACATCTCCTA 180

AAGCATGGTA TAGTGCAATT nAAAAnCTGT GT 212

(2) INFORMATION FOR SEQ ID NO: 1252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1252:

CAGTAAGTCA ATTGAAATGG CTAATTTATT AAATCTATAA AAGCATAGAG CACTGTTGTG 60

AGTTCATAAT CAAAGATTTA TAAATGTnTC AGACTGCCAA TATAACATTT AGGACCTAGA 120

ACATTGATTA T 131

(2) INFORMATION FOR SEQ ID NO: 1253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1253:

TTAGTAGTCA TCGGTATTGG TGGTTCTTAC TTAGGTGCAC GTGCAGCAAT CGAmATGTTA 60

ACGTCATCAT TTAGAAACAG cAATGAATAC CCTGAmATTG TATTTGTTGG TAATCACTTA 120

TCATCAACAT ATACGAAAGA GTTAGTTGAT TATTTAGCAG ACAAAGATTT CTCTGTAAAC 180

GTTATTTCTA AATCTGGTAC AACTACAGAA CCAGCAGTTG CATTTAGATT GTTCAAACAA 240

TTAGTTGAAG AAAGATACGG TAAAGAAGAA GCACAAAAAC GTATATTTGC AACAACGGAT 300

AAAGAAAAAG GnGCTTTAAA ACAGTTGGCT ACAAACGAAG GTTATGAAAC GTTTATCGTA 360

CCTGATGATG TAGGTGGAAG ATATTCTGTT TTAACAGCAG TAGGATTATT ACCAATTGCA 420

ACAGCTGGAA TTAACATCGA AGCTATGATG ATTGGTGCTG CA 462

(2) INFORMATION FOR SEQ ID NO: 1254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1254:

ACTCATAAGT GAATGGTTGA TTACCACTAG TTAAAACTTC ATATACTATA GTTTCTTTTT 60

TTATTTTGCA ATTAGTTATT TTCATTATAA ACTTCCTTTC AAACACTGCT GAAATAGACG 120

TCTTTTTCAA ATAAGCATGA TTAATACTTC AATTCTTTAA TCCACATATA TTTAAAAGTG 180

AGGTAGTAGG TAATAAATAT AAGACTTAAA GTTAAGATTG CTTTTTTCAT GTTTCATAAT 240

TAAAACCTCT GTAAATTTAA GGTTAGTATT ATGAAATAAT GGATTGGTTT ATTCTTTAGT 300

ACTAACTTCG TAGTAAATTA TATAGTTCGC TAAATTGTAT TTATCTACTA TATTTTTGGA 360

ATAAACAATT TCCTTTTCTT TCTTCAGTAA ATTATAAAAA 400

(2) INFORMATION FOR SEQ ID NO: 1255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1255:

nAATCTATGT ATGGGGGCAT CCAAAGATTT CATAGACTAC TTATTTGTTG ATGAAGCCGG 120

ACAAGCAATC CTCAAGC 137

(2) INFORMATION FOR SEQ ID NO: 1256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1256:

TGAAATGTAG AAATTGAATT AGAAATGAAG ATTAAAAATC nACACGTATC GTTCAAGTGG 60

TGCAGGTGGT CAGCCGTAAA CACAACTGAC TCTGCGTACG TATTACCATT TCCACTGGTG 120

TCATTGCAAC ATCTTCTGA 139

(2) INFORMATION FOR SEQ ID NO: 1257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1257:

TTACCAnTTA TTTTAACACC ATGTTTAGAC CAATTTGATC TGACTAAATT AATCGCTGTT 60

TGTACCTCCA AATTGTTACA ACGTACACCT TTAGTTTTTC TAAATTAATG TATATTCATC 120

ACATCTTCTT CAGTTAAGGG TCAAAGTATA ATTTGTCGAA ATTGTGAAGT CGTTGTA 177

(2) INFORMATION FOR SEQ ID NO: 1258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1258:

AAGACCAACC GAAATGAATA TCGACATGGA TTAAGCCTAT ATTCAGATGT AAACGGCGAT 60

TATATTAAAA AGCCAATTAC AGAATGTAGT GGTTAATGAA ATATGCCCAA GAATGGGCTG 120

TATCACTTAG GTGTATCAAA CTGACCAAAA ATTGGAAGGA CTTTAGGCCA AAAACCATGC 180

TTAATTTTTC 250

(2) INFORMATION FOR SEQ ID NO: 1259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1259:

ACATTTACGG GACATTTCAT TACATCACCC TGCTTTATTT TGGATTATGG CCTAATTTAT 60

ACTGATAAAT CTAGGAGGTG GAAAAAAGAA TGCCCTGCAA TTTAATTnCA TTTAACCAAA 120

TAATGAAACA ATAAAAAACA TTATATCGTT ACTTATTAAG TAATTTGGCA 170

(2) INFORMATION FOR SEQ ID NO: 1260:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1260:

TTTGTACTCC GATACGTTGT ATTCAGGTTG ATGACACTAG GAATTTGTAA TGATCAATTT 60

CTCTAATTCT TTACAATTGA TAGAATTCTT CGATTTGTGG ATAGACATTC ATATCATTGT 120

CTAATGATTT TTGGTGATTC ATAAATTGTG ACTAAAGCTT GGATGCTTTA GGATTGTAGC 180

TGAGACACAT GTTGCGTGAC TGnGGATTTA TCAnATAATC TCAATCACGT GATCCnATCA 240

CATTCATCAG CTCACTAAAT CAAGATGATC GTCGTTTATG GGCGATTAAT GGCGTACCGC 300

CAGTGTCCGC ACG 313

(2) INFORMATION FOR SEQ ID NO: 1261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1261:

TAGCGATCAT TTAATCAAGG TTAGATTATT TAATGTCAGC ATTACGTTTG ACAATGAACT 60

GTTTGAGGTT ATCACAATGC CATTTAACAC TATGCGCACA TGGCTGAACT AATnAGCGAC 180

GAGATGACTT CAAACCTTGA TTAGGT 206

(2) INFORMATION FOR SEQ ID NO: 1262:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1262:

AAGTGTGTAC ACGATAGCTA AACTCAAATA TCACAGAACA ACAAATGTCT TAGTACTTTG 60

TGCCGGTGGT GGTACAAGTG GATTATTAGC CAATGCACTA ATAAAGCAGC TGAAGAATAT 120

CATnTGCCAG TGAAAGCGGC ACTG 144

(2) INFORMATION FOR SEQ ID NO: 1263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1263:

ATAACGACAC CTAATGCAAT TTGAATAAAG CAGTAGAATT TGTGGGAATC GATTATTGAT 60

AACCGAACTA ATAATCACAG CAAAAATAAA ATTAAAAATG CTCTAATAGT GCCTACATnC 120

TCCTCAAATT TT 132

(2) INFORMATION FOR SEQ ID NO: 1264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1264:

TATGTCAATT TCGTAGAATT GGTTTTAnGC GCTATTTAGA ATAGCCATCA GATAAAATCA 60

TTATTTAAAC GTATAATAGG TCAAAATATA GAGAGTTACT ATACAAATTT CTAACTTTCA 120

CTTAAAATAA AATATATATA ATTAAAGTGG AGGAGAAGG 159

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1265:

ATAGCTCAAG CAATCATTAT GTTTATAATG ATTGTATGGT TCTTTATAGA TGCTTTATTG 60

ATTAATTAAT AAAAAGCTTA TTGCAAAATA TGTTTTTCGG TAACTGTAAT TTAGTGATTT 120

TATCATTAAC AG 132

(2) INFORMATION FOR SEQ ID NO: 1266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1266:

CATGGATTTA TCTTAGCGAT TGGTCTAATT TTACCTTTAG GTGCACAAAA TGTATTTATT 60

TTTAACCAAG GAGCTAATCA ACCAAAATAT AGATATGTAT TGCCTGCAAT AATTACAGCC 120

GGGTTGTCAG ACAGCTTACT TATTATTATT GCAGTGGTAG GAGTwTCTAT CATTATTATG 180

TCTTTACCTG TACTTCAwGC AwTTATTTAT ATAGTTGGTT TAATTTTCTT GATGTATATG 240

GCTTGGACCA TTTGGCATGA TAAACCCTCA ACAGATGGAG AAACTCAAAT TATGTCTCCA 300

ATGAAACAAG TAAGTTTTGC TTTATCAGTT tCATTACTCA ATCCACATGC TATTTtAGAT 360

ACAATTGGAr TAATTGGtAG TAGTGCTGCA TTATATAGTG GCnGC 405

(2) INFORMATION FOR SEQ ID NO: 1267:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1267:

TCTTTATATT GCAGTACAAA ATTCGCGTGG AGGTTTAACA CAAGTAGACC GCACAAGATT 60

TAGCGTCTGA AGGTATTACT GTGTAATGCA TTCGCACCTG GnTATCGTTC AAACACCAAT 120

(2) INFORMATION FOR SEQ ID NO: 1268:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1268:

TTTGCCCAAG TGACGTAAAG TACCCAATGT CCATTTGTAC TTGTATCGCC ATCAACAGTA 60

ATCATATTAA ATGTATGGTC AGTCGAAGAT TTTAATAATT GATGAAGTGT ATTCGATTCA 120

ATCGATGCAT CGTGTTATAA AAGCAAGCAT GTAGCCAATT GGGAATCAAC CCGAnCTTGG 180

CACACATGTA CGTTACACAT TAGAACnCAA GTGACCGACG GTAATCCTAC CCGCTCAACA 240

CAAGCGC 247

(2) INFORMATION FOR SEQ ID NO: 1269:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1269:

TCATTGTATA TGAGCAGATT GGCTAGGCGG TGGCTGGACT GACGGAATCG ACACCCGGCT 60

GGGGTTGGGA AAAGTACAAG ACGCAACATG CTATGATTTT CCTATGTGGT TATCGTCCGA 120

TTTAAAGTGA GCAGCGCACG GTCAGTCATC TCTCACAGnA CCTAAAAAGA ACAGTAAGCn 180

CAACCTAAAG CAGTGGAACT TAAAATCATC AAGGT 215

(2) INFORMATION FOR SEQ ID NO: 1270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1270:

ACAATAAAGA CTATTAAAAG AGATATAGGT TAGATATTAC ACTTTTAGAG CAAGACGGTA 60

TAAATGCAAG TAAATTCGTG TATTTATCAA TACAGCAGGT nGAGTGAAAG GCCCAGCAG 119

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1271:

CGTGGCACGT TAAGCGTTTA ACCATAGCAT TAAGATGATT GTCTAGCAGA GGCGATTTGC 60

GGGCTCACTA CAGTGCATGA TGAACTTAAT GCTTCAAATG TAACATTAAA AATAAAAGCA 120

ACGATGTCAC TTCTTACTTC TACATCTGCC ATnTTCGTGA TTTCGTATCT ATCCCGCATC 180

TCATCTTGAA CGTACGAGCC TAATCGCCCn GCGCGATCCT GCC 223

(2) INFORMATION FOR SEQ ID NO: 1272:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1272:

TAGTTACAAT ATCTGTCAAT TTCTGGAGAA CCACTAAAGC TATGCATAAT CCCGCCTACC 60

TCTTCAGCAT GCTCCTCCAA TAAGATATCG GTACAGTCTT GAGnTGCTTC ACGGTTATGA 120

(2) INFORMATION FOR SEQ ID NO: 1273:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1273:

TTGCGCGGCA GTAAAATTCA AACTATTGGC GTCATTTTGC CTAGCTTAAC AAATCCGnTT 60

TTCTCAGCAC TGATGCAAAG TATTCATGAC CATAAACCAT CTGATGTTGA TTTATGCTGG 120

TTAACA 126

(2) INFORMATION FOR SEQ ID NO: 1274:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1274:

GATTCTGAAG GATCAATACn ACATGTACAA TTTTGGCGTA GGTGCAAAGG CATCAGGTTT 60

GCTTGCTAAT CTACATCGAA GCGGCTACCT AAATTAATGA GAAATCACAC TCAGTTAATG 120

CATGTACTAG C 131

(2) INFORMATION FOR SEQ ID NO: 1275:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1275:

TGGAGTATTA CCTCAAGTGA ATACAACATA CCTGTTGGAA GATTTTTCAA AACTTTAATT 60

GGACCAAGTG ATGCCATTGA TGAGTTAAAT CCTAATAGAT TCAGGTTACC TCGGATGATT 120

GATACTAATT TGGCCTGGCG CACGCTTTAG TAnTAGTGG 159

(2) INFORMATION FOR SEQ ID NO: 1276:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 577 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1276:

GAAGTAAATA ATATATAGAA TATAACAGGA AATAAAATAG ATAATATTAA TGTTGTTTTT 60

TTACGCATTA TAACTTTAAA TTCGATTTTC AAGTAACTTA GTATCATAAT TAGATCCCCT 120

TTGCTTTTTA TTGnTGAAGT ATGAATCAAC AATTGAGACT tTTTGTATTT CAATATCATC 180

CAAATTAATA TGAAGTTGTT GAAGATATAA AATCGTATCA TTTACATTTG AAGTAATAAT 240

TTTsATAGTG CCATTATGAT TTTyycTGAA TAACTAAATC ATCTTTATCT AGTTTTAACT 300

TTCTTATATA TTCATCGGAT AACGTAATCT GAGATTGCTG ATTGGTTCTA ATATGTGACG 360

TTGAATCATT AAGTATTATT TCTCCATTTT CAATGAGAAT AATTTTGTCT GACATACGTT 420

CGACTTCTTC AATATAGTGC GATGTATAGA GTATCGTTCG ATTATCTTCT TTTAAATTTT 480

CAATAATTGA CCAAAAATAT TCTCTAATTT CTATATCCAT AGTCGATGTT GGTTCATCTA 540

(2) INFORMATION FOR SEQ ID NO: 1277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1277:

CTAAAnTAAG GTAATAGTTA CCAAGTACCA TATCTTGTGG ATGGTGTACT ACAGGTTTAC 60

CATCTTTAGG TTCAAGATGT TTTGATGACT GCTAACATCA ACATTCTTGC TTCAGCTTGT 120

GCCTCTTTTG A 131

(2) INFORMATION FOR SEQ ID NO: 1278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1278:

GTTTGCGATA TTTTAGGCAG ACAACCTAAC TTTACAGAAA CAGGTATCTT TTCTGTTATG 60

TGGAGTGAAC ATTGCTCTTA TAAACATTCT AAACCGTTTT TAAAGAATTT CCTACGCAGG 120

TGCCATGGTT TGGGCTGGAG TCAGGTGCGT TGTGTATAGC TGATnA 166

(2) INFORMATION FOR SEQ ID NO: 1279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1279:

CATAATTATG AAAATGATAT GATTTTTATT AGACCATTTA AAAAAGCATA ATTTAAATCG 60

AAGGCAGGAC ATTGAAATAT GAAATTTTCA ACTTTAAGTG AAGAAGAATT TACCAACTAC 120

ACCAAAAAGC ACTTCAAACA TTATACGCAG TCTATAGAAT TATATAATTA TAGAAATAAA 180

ATAAATCATG AAGCACATAT TGTGGGAGTG AAGAATGATA AAAATGAAGT TATAGCTGCA 240

TGTTTATTAA CAGAGGCACG AATTTTTAAA TTCTACAAAT ATTTCTACTC TCATAGAGGT 300

ATTCATTTAT AAAAATAGAG GAGTATTTAT TCTTGTTGAT CCATATnTAA TAGAGAAT 418

(2) INFORMATION FOR SEQ ID NO: 1280:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1280:

GACATATCAT AAATTACATG GTGATAAAAT TnTCGGCTAC GATACTAACG GATTCCCGAT 60

TACCTGGTTT TATCCATTAG GTGAAAAGAA AGTTGAACGT AAGGCACCAA AATTAGAAAA 120

ATAATTAAAT AAAACAGCTT AATGATGTAA TGAAATTAGT GAGTTAATCA CTGACTTCTA 180

CGTCATTGAG CTGTTTTTTT GTGCTTTGTT ACAAAGCATT ATTGAATTTA TTTTACGTGT 240

TCATATTTTG AAACATCAAA GCCGTCTTGT TTAGCTTTGT TGATAATGTC TTTGATTGAA 300

TGTAGTCCTT TATCGGCGAA GTATGATCTT AAGTTGTCTT TTGTAGCTTG GTCAGCATTC 360

TTATCTAATA ACACATCAAT ATAACTTAAT TCATGTTCTA AGAAGTTTGC ATCATCATGT 420

AGTACGAGTC CATTTTGAGA ATAAACTTT 449

(2) INFORMATION FOR SEQ ID NO: 1281:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1281:

TATTTATATG TACTGATGAT GAAGTTTATT ATCTATCAAG TGGATCAAAT CCGAAATATA 60

ATCAGTATAT GGGTGCATAT CATCTACAAT GGCATATGAT AAAATATGCA AAATCACATA 120

ATATTAATAG GTATAATTTT TATGGAATAA CAGGCGTCTT TAGTAATGAG GCGGATGATT 180

TTGGTGTTCA ACAATTTAAA AAGGGTTTTA ATGCACATGT TGAAGAATTA ATTGGTGATT 240

TCATCCAACC AGTAAAACCC ATTCCAATAT TAATnTGCCA AACCTnAAT 289

(2) INFORMATION FOR SEQ ID NO: 1282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1282:

ATTCAGGTCG AGGTGGCCCG GCTCCATGCA CCGCGACGCA ACGGGGGAGG CAGACAAGGT 60

ATAGGGCGGC GCCTACAATC CATGCCAACC CGTTCCATGT GCTCGCCGAG GCGGCATAAA 120

TCGCCGTGAC GATCAGCGGT CCAATGATCG AAGTTAGGCT GGTAAGAGCC GCGAGCGATC 180

CTTGAAGCTG TCCCTGATGG TCGTCATCTA CCTGCCTGGA CAGCATGGCC TGCAACGCGG 240

GCATCCCGAT GCCGCCGGAA GCGAGAAGAA CTAATTGATA CAACACTTTC TCAACCTGAT 300

CTTCTTTACC TTCTACATAG CGCGTGAgCA GAACcATCTT GATGgCACAG CTAAATAATG 360

CaATgGGAAT GATGTATGAC ATTCGGGGTG CATAATTTCT CT 402

(2) INFORMATION FOR SEQ ID NO: 1283:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1283:

TATTGACAAC CAGAGTACAA ACAGCAGCTA TATTATAGAC TTAGGTCTGA AGTGGTAGTG 60

GCGGTGGACT ATTGTTGCGA CTGGACACCC GAGATATTGC TCAGCAnAGC ATCATATACA 120

GGAAGTATTA AAAGAGACTT GnCGAGTAAC AAATACTGAA GTAATAAGAT TAAAAGAGTG 180

AGGTGTATAA TTATCCTCGT TCTTTTATAT TAGTATGATA GAGA 224

(2) INFORMATION FOR SEQ ID NO: 1284:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1284:

CGTGGGAGAT TGTGCATATT GATTATGCAA GGAAGnACGC CATAAAAGTG GATGGCCAGA 60

CATCATTAAT ATTATTGATA CCACATCAGA AGGTATTCAA AGTGAATCGG TGATAAGTGA 120

ATCAATTAAG TCTGCCAAAG AAAAGA 146

(2) INFORMATION FOR SEQ ID NO: 1285:

(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1285:

ATTTCGCGTG ACTGGACTTG GATCCGCAAC TTGGTAATTT AAGGAATTCT TGTCATTATA 60

AGCCCTCCAT TTCATGATTT GATTTGCCAC TCGGTAACCA TTGGGGTTAC AGCTTCACTA 120

GGGGAnATAC GAACCTC 137

(2) INFORMATION FOR SEQ ID NO: 1286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 594 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1286:

GCTATTGATT ATGGTTAGCm TGTTGTTCwC TTTACTCATT GTTCCTTGGt TAAGCTCrAA 60

AAAAGCACGT ACTTTAAAGA AACATGCAGC TAATGAACAG GCCCGATTTT TAAATCATTT 120

TTATGATTAT AAAGCTGGTA TGGATGAACT ACGTCGATTT AATCAAATTA ATCATTATCG 180

AGATAATTTG ATGGCTAAAT TAAATCATTT TGATAAATTA CAACTTAAAG AGCAACGCTT 240

TTTAACGATT TATGATTTTA TATTAAATAT TATTGCTATG CTTTCGATTT TTGGTAGTTT 300

AGTTCTAGGA TTAATTCAAA TTAATGCAGG CCAACTAAAT ATTATTTATA TGACGAGTAT 360

AGTTTTAATG GTCTTAACTT TATTTGAACA AGCTGTACCA ATGACAAATG TCGCGTATTA 420

TAAAGCGGAT ACTGACCAAG CATTGCACGA TATTAATGAA GTGATATCTG TACCTTCTAC 480

TAATGGAAAA AAACGTCTTA ATGATAAGTA TGATGCAACG AACATTTATG AAGTTAAGGA 540

TGCTAGTTTT AAGTATTGGA ATCAGCAAAC GTATGTnTTG TCGGATATTn ATTT 594

(2) INFORMATION FOR SEQ ID NO: 1287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1287:

TGAAGTAGTA ATAAACCCGG AACCCTAAAA CTGGATGGAG GATGAAACCA AAAAGGAACC 120

AGCCAAGCCA AATTGGGGAA ACCAGGACGG CCCAATGGAG GTCCAACCAA TCCAAACCCC 180

ATTCCGCTAA TGnCTATGGG TCCCAATTAG GAATCCAATG GATGGATGGA TTn 233

(2) INFORMATION FOR SEQ ID NO: 1288:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1288:

AATCCCTGTA CGTTCGTAAA GCTAGCTGGn TAATAAAAAA GAGTCTGGAA AGTAGGCAAC 60

AATCAATGAC AATGAGCAGA TCCAATCGCA GTATGCTTAC TCGTGTAAGA AACGCAAACA 120

TGGTGCGTCA CG 132

(2) INFORMATION FOR SEQ ID NO: 1289:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1289:

TATCTGATAA TTCTGTACCC AGGCGTTTTA ATATGTTTAT CTGGTGTCAT GATACATAAA 60

CATTGTACCT TTAGGTCATA CGATGTCGCA AATAACTGCT CTTGCCGTTA CAACACCATT 120

ACGGTTATAC ACTTnTAGCC AATCATTATC TGGG 154

(2) INFORMATION FOR SEQ ID NO: 1290:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1290:

AAAAGTGGCA CATGCGGCTG TAAAGTCCTC TGTTTCTGAT AAATCATAAC CTATATACAT 60

GTCTACCTTC CAACTCATCT AAGAAATAAG TCATATTTTT TTGAATGTTG GATAATCAAT 120

(2) INFORMATION FOR SEQ ID NO: 1291:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1291:

CTTAATGCTA TATATTCTTT GTTTTTGATA CCATTTCATC GTCTTCTCTT GATTTCTAAA 60

CAATTTAGAA AATAAAAGAA TATACGCTTC AGACTTATTA AAACCCGCTA TATCATCTTG 120

ATATTGTATT AACAATTGAG TAAAGCTGTG TATTAAGTCA TCTTTCTTCG ATGCAATGGT 180

AGTTAATGAT TTTACACGAT AAGCATATTT ATCTGTAAAT AACTTAGCAA CTACCCCACC 240

TAAATCATGT CCTAGAATAT GTGCCTCATG AATATTTAAC TTCTCCATTA GAATTTTTAA 300

ATCCTCAACG TGATCGTTTA AATCGTATGA TTCACTTTTA GAAGACTTGC CATGAcCTCT 360

(2) INFORMATION FOR SEQ ID NO: 1292:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1292:

TGTGTTAGTT GTTTATGTTG TTGATATATA CTGCTCGTGC ACATGGTACC CAGACGATTC 60

AACGnTGAGT ACACAAAATA CAAAATCTAC GGCACATGGT ACCGTTTATA AAAGATGTGG 120

AACCTTACTA GCATTTGTTG AGAACGCTAC ACGTTTAAAT CAAG 164

(2) INFORMATION FOR SEQ ID NO: 1293:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1293:

TTAATTTTCT ATATATTTCT TAGGTTATAT TGGTATCTAT GCCAGTAAGT GACATGACGT 60

TAGATCATTG AATCCAAGAT CGAnACATTG GGACATATTT ATTAACGACA TGGCTTCAAC 120

(2) INFORMATION FOR SEQ ID NO: 1294:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1294:

GTCATGCnTA ACAGGTGAAT ACCTAGTAAT TCAGATATTA TCATTTATAT ACCCTCTTAT 60

ATTTTAGTGC ATTATCTCGA AATCGAGATA CTTAATGTAA ATTTTTAGTG CAGCCTACAC 120

TTCGTGATTG GGCAnTAGTT CTTAAACGCT GTGGTAAGAT GTTAATTCAT CCTTGGTTAA 180

CACACAAACG CTTGGTTAAT GCTCAGCAGC TAG 213

(2) INFORMATION FOR SEQ ID NO: 1295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1295:

AAGAAGTTTG AAGTCTATGA AAACAATCAA AAATTGCCAG TGAGACTTGT ATCATATAGT 60

CCTGTACCAG AAGACCATGC CTATATTCGA TTCCCAGTTT CAGATGGCAC ACAGATGAAA 120

TGTTTCTCGn CCAATGAGAG GGAGAACATA GTATCAATAG ATG 163

(2) INFORMATION FOR SEQ ID NO: 1296:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1296:

TAGCTTTAAT ACATTCTGAT TTTTAAACGC TTCGAAATGT TTTCAGTAAC TAATTTTGCC 60

ATAATCCCAA AAACTCCTTG ATTATTAACT GCnTTTTGAT TGGCTACATT AAGGCTTTAT 120

ACACATCAGC TCACCATGCC CATATCTACT AATGGTTATA TCCCTAGAGT CCCAGCGATA 180

TAACATCAAC GCTTACnGGA GTTTCAG 207

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1297:

ATGGCATCGG TTGGTTATGA AAAGnCAAGC CATGGGGAGG CCATATTTGG GGTGGAATCA 60

TACCTGGAAC CTTTGGTGCC TACCACCAAT TGGTAACGGT TTTACCATCG GATTTTTAGT 120

GATACAGCGA TATGTTTTGT ACAGG 145

(2) INFORMATION FOR SEQ ID NO: 1298:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1298:

TCCAAAAGTT AAAGGTCAAT TGAAACAGAn AAAGCTTATT ATGTCTGGAA AAGTATTAAA 60

AGTAATGGTA TCAAATGACA TTGAACGTAA TCATTTTGAT AAGGCATGTA ATGAAGTCTT 120

TCAAGCGTTG AATTGTGGT 139

(2) INFORMATION FOR SEQ ID NO: 1299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1299:

GATATTGGCA ACCTTCAGCC GATGACCTCA TGGCAAATGA TTGGGAAGTT ATAAACCCAA 60

CTAGAGACCA GGAATTATTG AAGCAATTAT AGAAATGCTA TCAATGATAC TTTTTAAATT 120

GTTTTTAAAC TCATTTTCAA AGTAAACAAC AGTCTTGTCT GAAATTGTTA CATGATAAAT 180

AGTGTTACTA GCATACACGC CGTTTAGGAA CCCAGAGTTT TTAAGTTTAT TTAAATCGTA 240

TTTTACATCT TCGAAATGTA GTTTTTGAAA ATACTTTGTA TGTATATCTT TAGCACTTCC 300

AAAATTTATT GGCAGGTTAA TTTAATCGAA CCTAACTTTA CACATTCTAA ATAATCTTTG 360

(2) INFORMATION FOR SEQ ID NO: 1300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 693 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1300:

CTACAGTGCA ATTTAACCAT GAAGTTGTTG ATTTTGAACA ATTATCAAAT GGTCAATGGG 60

AAGTTACTGT TAAAAATCGC CTAACTGGTG AGAAATTCAA ACAAGTAACT GACTACGTAT 120

TCATCGGTGC TGGCGGTGGA GCAATTCCAT TATTACAAAA AACAGGTATC CCTGAAAGTA 180

AACATTTGGG TGGATTCCCT ATCAGTGGTC AATTCTTAGC TTGTACAAAC CCaCAAGTTA 240

TTGAACAACA CGATGCCAAA GTTTATGGTA AAGAGCCACC TGGTACACCA CCAATGACTG 300

TACCTCATTT AGATACGCGT TACATTGATG GTCAAAGAAC ATTATTATTT GGACCATTTG 360

CTAATGTTGG ACCTAAATTC TTGAAAAATG GTTCTAACTT AGATTTATTC AAGTCTGTTA 420

AAACATACAA CATTACAACT TTATTAGCAG CAGCAGTnAA AAACTTACCT TTAATTAAAT 480

ACTCATTTGA CCAAGTAATT ATGACAAAAG AAGGTTGTAT GAACCACTTA CGTACTTTCT 540

ATCCAGAAGC ACGTAATGAA GATTGGCAAT TATACACTGC TGGTAAACGT GTACAAGTTA 600

TCAAAGATAC ACCTGAACAC GGTAAAGGAT TCATCCAATT CGGTACAGAA GTGGTTAACT 660

CACAAGACCA CACTGnAATT GCATTATTAG GTG 693

(2) INFORMATION FOR SEQ ID NO: 1301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1301:

CATACTTGGG TAATGCTGCC CATGGnACGC TGGnACAAGG TAAAGTTGCA CGTTTAATTT 60

GTGnATGTAT ATAAAACAGA TGGGAACACC ATTTGAAGGG GATCCTCGTG CAAACTTAAA 120

ACGTGTATTA AAAGAAATGG AAGATTTAGG cTTCACAGAC TTTAACCTAG GACCTGAACC 180

AGAATTCTTC TTGTTTAAGT TGGATGAAAA AGGGGAACCA ACTTTAGAAC TTAATGATGA 240

TGGTGGATAT TTCGATTTAG CACCTACAGA TTTAGGTGAA AACTGTCGTC GTGATATTGT 300

TCAACATGAA AtTGACTTaA ATATGCAGAT GCTGTTACAG CATGTGATAA TATCCAAACA 420

TTTAAATTGG TTGTTAAAAC AATCGCACGT AAACATAATT TACACGCAAC A 471

(2) INFORMATION FOR SEQ ID NO: 1302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302:

CATGTGATTA AGAACGTTCA CTGATGAATT TTTGATGATC GTTCGGTTTT TGTTTGGATT 60

TTAATGATTA TTTATACAAA AACAGCCGTA TTTCAAGCCG TACATTTTAA ATTTAACTAA 120

ATTTGCATCT AGTTAATAAT TGCATTTATC AAATTTGTCT TATTGATCCA ATCTAATTTG 180

TACTCACAAA CTAGTTTrAA ATTCTAACTT TATCTCTCAG TTCGTTATCA ATCATCAGAC 240

ATAAACCAAT GAAGCAATCA GAAAACACTC TAATTTTCTa TTAGAAATTT GnTTTAATAT 300

AAAAAAACAG GCTTACTTCA TATAATTTAT GAAATAAACC CGTCAATTTT TGTTTAATAT 360

GCTTGGTGAT CTnTTATTCT GCGTAATAAT GCTAAACCTG 400

(2) INFORMATION FOR SEQ ID NO: 1303:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303:

AAAAGCTTAG TTGAACTTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGC 60

AAAAGACTGG GGTAAACTnC GCCTAGCTTA TGAAATCAAT GGATTTCAAA GATGGGCTCT 120

ACAACATC 128

(2) INFORMATION FOR SEQ ID NO: 1304:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCCTTCGGAT TCTAAATGGC ATTGGACAGT GTTTACAAGC TCGCATTTCT CCACTTTTTG 60

CAATTTCTTT TACAATTTCT AAAGCTTCAT CAAAGTTTCC TTCAATAGnA AACGATTTCT 120

GCACCATACA TTACTGACTT G 141

(2) INFORMATION FOR SEQ ID NO: 1305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1305:

GACTGGTAAA CACTAAGTGA ATTAGCTGGA CAATGAAAAA TATCCACAAT CATTAATTAA 60

CGTACGCGTA ACAGATAATA TCGGTTGAAG AAATGTTGAC GTTAAGAGTT ATGACTAAnT 120

AGAGTAGAAT GATGGTGAGG TCGATTTTAG TAGACTCTGG AC 162

(2) INFORMATION FOR SEQ ID NO: 1306:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1306:

TTCTTAGTTG CTCGAACTAA TAATTTGCTT AATAATGATs TAGCTGTTAT TGTGTCATAT 60

TCTAAAGGTG CCATAAATTT AAAAACTATA GTAGTTGTTT TAAATTTAGT TGTTGGTGAA 120

ACTTTGATAT GTATATTTGG TTGAGATTGT CTACTCAAAT ATATAGCCTC CTCTATATCT 180

TCTTACATCT ATATTTTTCT AGTGATTTTA AATTGAACTA AGCTATTTTT CATATAATTT 240

AATGAATACA AAATAGGTTC ATCTGATTCA TTATAGTGCG TA 282

(2) INFORMATION FOR SEQ ID NO: 1307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1307:

AAGGAAAAAA CCCTTGGCCT TTGGAAAAAA CCCAAAAGGA AAGGGGTTTA AAAAAAAAAA 120

AAGTTTAACC CGGTTGGCCC CAATTCCCGC CCGGGGAACC CAAAAGGAnT TTTAAAAAAG 180

GAAACCCAAT TCCCGGCCGG AAAAGGGTTT TTAAGCCCAA CCGGATTTTA AGGAAAACCA 240

TTTTAAGATT ACCTGGGAAA AAAAACCGTT TAGGAA 276

(2) INFORMATION FOR SEQ ID NO: 1308:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 692 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1308:

TGTATTTAAT GCTCGTACAC ACAATTACAA AACTGCAAGA GAAAAAGCAT TGAGTAATAA 60

TCATATTCCA GAAAATGTAT ATGACAATCT AGTAAAAACT GTACATAAAT ATTTACCATT 120

GCTACATAGA TATACTGAAT TGCGCAAAGA ATTGCTAGGT TTAGATGACT TGAAAATGTA 180

TGATTTATAT ACACCATTAA TTAAAGATAT TAAGTTTGAA ATGCCTTATG AAGAAGCTAA 240

AGAGTGGATG TTAAAAGCAT TAGAACCAAT GGGTGAAGAA TATTTAAATG TAGTTAAAGA 300

AGGCTTArAC AATCGTTGGG TCGATGTCTA TGAGaATAAA GGTAAACGTT CAGGTGGCTA 360

TTCATCAGGT GCACATTTAA CTAATCCATT TATTCTACTT AACTGGTCTA ATACTATTTC 420

AGACTTATAC ACATTAGTTC ATGAATTTGG GCaTTCaGCA CATAGTTAcT TCaGTAGAaA 480

ATTCCaACCg TCaAATTCtA GTGACTACaC TATTTTTGTC GcTGAAgTTG CaTCAACTTG 540

TAACGAAGCA CTTTTAAGTG ATTATATGGA TAAACATCTT GATGATGAAA AACGCTTATT 600

ATTATTAAAC CAAGAATTAG AnCGTTTCAG AGCTACATTA TTCCGACAAA CAATGTTCGC 660

AGAATTTGAG CATAAnATTC ATGCAATTGA AG 692

(2) INFORMATION FOR SEQ ID NO: 1309:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1309:

GGACTATTCG ATGATAGCTT TTTTGACTGG ATTTACTAAA ATGAAAGCAA GTACTATATA 60

atCGAGTAAT ATCTATATAT GACATTTTAA A 151

(2) INFORMATION FOR SEQ ID NO: 1310:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1310:

TGTGCATTTG ATAATATTCA CTATGATTCG TGGTCATTCA CATCGTCTAC GCTCACCGGT 60

CTAAACGTAC CTAACCCAAC ATGTAATGAA CAAATGCGAT ATTAnCACCT TTATT 115

(2) INFORMATION FOR SEQ ID NO: 1311:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1311:

CACCCAACTG ACCTCAATGG TATAATGCAT TTGTGAATAC CGAATATCAT TGGAATATCT 60

CCTATCATAG GAATATAATA TGTATATATC TTCGTAATCn TGTTCATTTT TAAGAAAATC 120

AATAGAAGTG TATCGATTAA AACTACATTT GAACCATTAC TTTG 164

(2) INFORMATION FOR SEQ ID NO: 1312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1312:

GAGGAAAATC GAAGTGAAAT TATTAAAATA TGGCGATGGT GGAATACGAA TAGATGGTGG 60

TTTAATAGGC GGCTTTATTC GGGTGTTATT GTATGTAAAG TGAAAAATTT AAnCCCATTT 120

CAAATTGGTG ATATCGTTGC G 141

(2) INFORMATION FOR SEQ ID NO: 1313:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1313:

AATTGGTATT ATGCATAGTG CAATGGATGC TGGTATTAAA nTCCAGAGGA TTACAATTAT 60

TAGTTTCAAT AATCACGATT AGTTGAGATG GTTAGCCACA ACTTTCTAGT GTATCACCAT 120

TATATGTATC GGT 133

(2) INFORMATION FOR SEQ ID NO: 1314:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 629 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1314:

TTGCAATTAG AATGCTGTTT CACCCCTTTA AACCATACTA TATATTTAAA TTTAGAGTCC 60

CATTTACACC AGGTTTAATA CCGAAAAGAC GCGAAGAAAT TGCAACTAAA ATTGGCCAAG 120

TGATTGAAGA GCATTTGCTT ACAGAAACTT TAATTAATGA AAAATTGAAA AGCGAGCAAT 180

CACAGCAAGC AATAGAATCT ATGATTCAAC AGCAGTTACA AAAGTTGACG AAAGATCAAT 240

TGTCAATAAA ACAAATTACT TCTCAAATCG tATTGATTTA GAACAAGTAT TACaAACTAA 300

TGGAAATCAA TATATTGAAT CACAATTgAA TAATTATTAT aCAAAGCaTC AAAACCAAAC 360

AATAGCATCT TTATTGCCAA ATCAACTTGT AACATTTTTA AATCAGCATG TAGATAACGC 420

AACAGACTTA TTATGTGATC GTGCAAGGAA TTATTTATCA TCTGCAAAAG GCACACAAGA 480

TATTAATGAT ATGTTGGATA CTTTTTTCAA TGAGAAAGGT AAGTTAATTG GTATGTTGCA 540

AATGTTTATG ACAAAAGAGA GTATTGCAGA TCGCATTCAA CAAGAACTTA TACGTTTAAC 600

ATCTCATCCT AAAGCAAGAA CAATTGTGA 629

(2) INFORMATION FOR SEQ ID NO: 1315:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1315:

ATACAGGTAC GTTCGTTATC AATGGTGCAG AACGTGTAAT CGTATCTCAA TTAGTTCGTT 120

CACCATCCGT TTATTTCAAT GAAAAAATCG ACAAAAATGG TCGTGAAAAC TATGATGCAA 180

CAATTATTCC AAACCGTGGT GCATGGTTAG AATATGAAAC AGATGCTAAA GATGTTGTAT 240

ACGTACGTAT TGATAGAACA CGTAAACTAC CATTAACAGT ATTGTTACGT GCATTAGGGT 300

TCTCAAGCGA CCCAAGAAAT TGnTGACCTT TAAGGGGACC AATGGAATAT nTACCGTAAT 360

ACCTTTAGGA GGAAAGACCG GCACCTGAAA CCACTGGAA 399

(2) INFORMATION FOR SEQ ID NO: 1316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 778 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1316:

ATAAACATTT TAAnATGTAA TTnAGAAATT TTTTTAGTAC AAAATCTTTC TTAATAATGA 60

TTAAGGAGGT CAGTAATGAT TGAAATTAAA ACATTAACGA ATAATGATTT TAATGAGTAT 120

AAGAGACTTG TTTCGACAGT CAATGAAGAA TTCACTCAAG ATTCACATTA TAGTCAAACA 180

ATGACtGACA CCTTAATACA TGACATTTTA AATCAAGGTT CACCGAAATG TATTGTATTT 240

GGCTGTTATG AAAACGAAAC ACTTATCGCA ACAGCTGCCT TAGAACAAAT TCGATACGTT 300

GGAAAAGAAC ATAAATCATT AATTAAATAC AACTTTGTTA CTAATAACGA TAAATCGATT 360

AATAGCGAGC TCATTAATTT CATTATTAAT TATGCACGGC AGAACAATTA CGAATCTTTA 420

CTTACATCAA TTGTGTCAAA CAACATAGnn GCTAAAGTTT TCTATAGTGC ACTAGGATTC 480

GACATTCTTG GTTTTGAGAA AAATGCAATT AAAATCGGAA ATACCTATTT CGATGAACAT 540

TGGCTTTTTT ATGATTTGAT TAATAAGTAA TACAGTTTTA TATATTCTAC rTTTCTCATA 600

AATTCAAATC ATATAGGTTC TATTTTTCAT ACAACTACTC TACTATTGAG TAGTTGTTTT 660

TTATTTGATA TGATAACAAT AAGTTTTTTT CAGAATATTC TATGTTTTAG GGGTGTCAAA 720

ACTTAATGGG TAACCGCAAT TATTCATGGA nTTATCnTAA GCGATTGGGT CCTAAnTT 778

(2) INFORMATION FOR SEQ ID NO: 1317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1317:

TGCACAAGGT GGTGCAGCAA TTGCAGCGTT CTTTATTATT AAACAAAATA AGAAGTTAAA 60

AGGTGTGGCA TCTGCCGCAG TATTTTCAGC ATTACTTGGT ATTACAGAAC CGGCTATGTT 120

TGGTGTTACT TAAAACTAAG ATATCCATTT ATTGGCGCTA TCGTTGGATC AGGTATTGGT 180

TCAGCATATA TTGCTTTCTT CAAGGTTAAA GCAATCGCAT TAGGAACTGC TGGATTGCCA 240

GgATTtATTT CAATCAATCC AGTACATGCA GGaTGGTTAC ACTaCTTTGT TGGTATGACA 300

ATATCATTcA TCATTGcTAT AACAGTTACT TTAAtTTTAT CtAAaAGAAa AGCAAATAAA 360

GAAGTTGTAG AATAAAAAAA GAGGTATGAC AGTAATCAAA GTATCAGTCA TTGCAAATGC 420

AATAGGATGA AACTTTAAGC TGTCATACCT TTnAATTTAG TTATA 465

(2) INFORMATION FOR SEQ ID NO: 1318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1318:

GACTTAATAT AACTGATCTT TTGCTATTAT TGAAACATAT TTATAAAGAA AATAGCATTG 60

CATAATACCC AAGCAATAAA TACTATAATA TTTTGGAAGT AACTAATCAA ACATCTAAGA 120

CATGATTGAT AnCACCACAG AAAAATAAGA 150

(2) INFORMATION FOR SEQ ID NO: 1319:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1319:

CCACCTTTTA ACGTACGTAT CCATGAATCA TATGATTAAT TTAATATCAT TATTACTTAT 60

TTCTTATCTT TATTnTCTTT TTTTCTTCTG AAAAGTAGTA ATGAACCTAT TGATGCTAAT 120

AATCCCCAAA T 131

(2) INFORMATION FOR SEQ ID NO: 1320:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1320:

TAGTGTCCAA ATGAAAGTGT GGCTACCTAT AGCTGGTCCA TGAAGCTTTA TTTTTAACTG 60

GTTTGTACAA TATTTAAATA TCAAAATCTT CTCGCGnTTT GGACAGTTTT TTTGGTATTA 120

ACCATTAATA AACGGAAAGA 140

(2) INFORMATION FOR SEQ ID NO: 1321:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1321:

CTTATTATAT AATTCTAATC CTAGTACATT ATACATTTTA TCAAATAGTC AACTGGATAA 60

CTTTGAAAGT GAATGATnCT TTTAAAATAA AGAAGATAAT ATAAAGTGCT TGATAATGGA 120

TTTGTAGTTG ATGATTTAAA 140

(2) INFORMATION FOR SEQ ID NO: 1322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1322:

TCGTTGCAAC ACAGGCACTA TTTTACCTTT ATATGTTGTA ATAGTTTGAT TGCTGCCATT 60

TAAACAACCA CCTTTCTTAC TCCACAAATT TACCATGAAT AGCGCGCGCG CCATAGCGGG 120

ATACTAAAGT GTTCTGCACC TTGCCTGTCT CCTTCAAnTT TCGATTACTG TAGAGCACAA 180

GTACG 185

(2) INFORMATION FOR SEQ ID NO: 1323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1323:

ACCTGCAATT TTCGTTATTC AAAACAATAA CTATGCAATT TCAACACCAC GGAGCAAGCA 60

AACTGCTGCT GAAACATTAG CTCAAAAAGC AATTGCTGTA GGTATTCCTG GGTATCCCAA 120

GTTGGTGGTA TGGTGCGGTA nTTGGTTT 148

(2) INFORMATION FOR SEQ ID NO: 1324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1324:

GAAAGCATTG ATGGACAAAG ATGAACCACC AAATGAATGG CGATTAGATT CCAATTGATA 60

TGGCTCACGG AAAATTTATG CTACAATTGC GTCCAGTAAA CAGTGGCACT AATAGTCCAC 120

TTAnGCTCCC TAGTGGATGA A 141

(2) INFORMATION FOR SEQ ID NO: 1325:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1325:

TTATACTATC GTGAAGGGTT TATTACTCAA TTAATGCCTA AAAAGGATAA AAGTTATTTA 60

GTTATTGATA ATTTTAATCG TATAGATACA GACATTTTCC AAACGTATAT TAATGTGTTA 120

GAAGGCTATG AAGTAACATT ACCACGTTAT AATAAAGACG GTAATATGAT TAAATGGTCA 180

CGACAAAAAG ATTCTTTCTA TTAT 204

(2) INFORMATION FOR SEQ ID NO: 1326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1326:

TTTGTTAAAA GTCTTCATTT CGGATGAAGC TTTATCTATT GAACGCTCCA AATTATTTAA 120

AGCAGCTTTT TCTTTATTAA CAGCTGT 147

(2) INFORMATION FOR SEQ ID NO: 1327:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 530 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1327:

CATTnAATGA AGAAACTGAA CCCnGAACTA TACGACGCAG AAGGCAATTT AATTAATAAT 60

AGTAAAACAT CCAGCTTAAT CCATTGATGT GTTATAAAAG TGAAAAGCTC CAATCAAAGT 120

TGACGCTCAA ATAGTTTAAC TTTGATCGGA GCTTTTTTAT AATGTATACC GAAAGGTTCA 180

AATATTATAT AATGGTAGAA TTGAAAGAGA ATATAAAAAA GTGAGGATAT AAAATGAAAG 240

TTAATCCTAA TAATATAGAA TTAATCATTA GTGCAGTAAA AGAAGAACAA TATCCAGAAA 300

CAGAATTGTC TGAAgTGCAC TGAGCGGTCG ATCTAATGTA GGTAAGTCTA CATTTATCcA 360

ATAGTATGAT TGGCAGAAAA AATATGGCAC GTACATCACA GCAACCCGGC AAAACGCAAA 420

CGTTAAATTT TTATAATATA GATGAACAAC TTATTTTTGT GGATGTTCCA GGGTATGGAT 480

ATGCTAAAGT AAGTAAAACA CAACGTGAAA AATTTGGGAA AATGATTGAG 530

(2) INFORMATION FOR SEQ ID NO: 1328:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1328:

AAGAAAGTTT GATCTAGGCC AACCTTTCTA ACAACGATAC GACAGTTTAA TAATGTCTCA 60

TATCTTGACT TCCCATGATG ATATGGTCGT TAATCACATC AATGACTTAA ATCTGGATnA 120

ATAGATGCGA ATGGATCTTG AAAAATCATT GTA 153

(2) INFORMATION FOR SEQ ID NO: 1329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1329:

TGTAGTTCGT TTGTGCTCTA ATTAAACGGT CGAAACCATG GATTAGACCT GCGATTACAA 60

CTGCAATGAT ACCTGAAGCA TGAACTTCTT CTGnTAAAAA GTATACGACA AAAGG 115

(2) INFORMATION FOR SEQ ID NO: 1330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1330:

AACAAGTTAT CTACATCTGC TGATAGGCAT ACTATTACTA ATAAATAATG CATCTTTTTG 60

CCAGATGTTT TCTTAATCAA TTGCACCAAC GAATGGCACT CTCATCTGTA Gn 112

(2) INFORMATION FOR SEQ ID NO: 1331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1331:

TTCATTGCAG ACAnTTGGTG AACCATGTGG ACGAACTAGT CCTAGATTAA GATAAGAGAT 60

TAGTGAnCAT TGCCACCACT GCAATTAAAC ATTCTTGGAA AAATTAACTT AAGTTAGAAT 120

CTTAATGCAT ACAGATACGG CGAAGATGAT GCCAAAGAAC GTCACGACTT TATGATGATG 180

ACTGAACCCA GTTTTTACGG AAG 203

(2) INFORMATION FOR SEQ ID NO: 1332:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1332:

ATGATGTACT AATATCTAAT AAGCTTGCTA AGTCTTGAGA CCTCATTTTA ATCACCTTTT 60

GACTATCTAT TTCTGTTAGT ACGTTTGACA TATTAATCAC TCCaCyTTAA CGCAaTAwAw 180

TTTAwTAGCG TTGGCTATTG TTGTTTAACG CGATGGnATT TACAACTTGT AACGTAAGAG 240

AATGAAAAAT AAGCTGnATA TGTTGTTTG 269

(2) INFORMATION FOR SEQ ID NO: 1333:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1333:

TAGCTTTTGC CCAATATGGT GAATCATGCG CCGTTCTGTA ATAATCTTCA CTTGGCATTC 60

TTGGAATTTG AACAACATCC TGTTCATTTT TATAGAnTGC TTAAATGGTA CAGCTGAAAA 120

ATCAAAGTAA TGTCCTTTTC TG 142

(2) INFORMATION FOR SEQ ID NO: 1334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1334:

ACTGATGCCC AATATGCATC TTGnCAATTG CAGGTGTGCA TGACTAAACA CATGACAAAT 60

CTGCCTGACT TTTTGCTGAC CCATAAATAA TTGGnCTAAC TTTTTGCATC TTGATCTTGC 120

ATCCTTGCCT TCCTATTTAA AATGCTACAA ATAAATTTGC CGGCGAGTGA ATTTTAATGT 180

TTTACAACGC TGTTCAATAC CTGGGAATAA G 211

(2) INFORMATION FOR SEQ ID NO: 1335:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1335:

CTTGAATCTC TTGTGCCTCT GTGATGTATC ATCAAATTAT TTGCACTGCT TCTTCTTTTA 60

TCCGCTCGC 129

(2) INFORMATION FOR SEQ ID NO: 1336:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 633 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1336:

CATGATGGCn TCTTACCAAA GGCGATTTTA AGAGCAATGA TACCAAGATA TTTTTAATAC 60

TGATCAAAGT TCAGGTGGTA GCACAATTAC ACAACAACTT GTTAAAAATC AAGTTCTTAC 120

CAACGAAAAA ACATATAGTA GAAAAGCAAA TGAATnCGCC TAGCAATTAG ATTAGAACAC 180

CTACTCTCAA AAGATGAAAT TATATATACA TATTTAAATA TAGTTCCtTC GGTAGAGATT 240

ATAATGGCGC TAATATTTCC GGAATTGCAT CCGCTTCATA TAGTCTATTT GGTATTCCAC 300

CAAAAGATTT ATCAATTGCA CAATCTGCAT ACCTTATCGG TTTGTTGCAA AGCCCATATG 360

GCTATACACC CTACGAAAAA GATGGAACGT TAAAATCGGA TAAAGATTTG AAATATAGTA 420

TTCAAAGACA ACATTATGTA TTAAAGCGTA TGTTAATCGA AGATCAAATC ACTGaAAAAG 480

AATACAACGA CGCATTAAAA TATGATATTA AATCACATTT GTTAAATCGA AAAAAGCGTT 540

AATTGATGCT CACTTTTTAA AGTAACCACA ACAATGAATC CAAATATTAA AAACAGCAGT 600

AAGATTATTT TCAATTAGAA AATTTCTCAC TGC 633

(2) INFORMATION FOR SEQ ID NO: 1337:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1337:

ATCAATATTT AGCAGTTATC ATTATGCTTG AACGGGTGGT AAAGGCGGAG AAGTCATCCA 60

CTTTTTCCTA TACTACAAGG ACCTTTACTT TAAAACAACG AATTTACAAA ATAAAAGGCA 120

TAATTTCTTT TCTGTCACAT CGCTCATTCT AACTACTAGA CTTTTAAAAT CGTTCCTGTA 180

ATTTAAACTC AATCAACTnT CAATTAATGA TGCATAATAT GATTATAAGT ATAGTAGTTA 240

ACTTCAAATA TCTTAGAAAT GTCCTGTACT ATATCTCTTT TATTCTCAAA AGTCATAGGT 300

(2) INFORMATION FOR SEQ ID NO: 1338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1338:

TACGGCATAT ACCTCGTTCA TCAATGTTCG TAAACATTAT TTAAAACATC TCTTACATCT 60

TGCGTTGGAA GTTCTTCATA GTCGAATTTC ATTGTnTTAT CAAAGTTTTC CATTTGCGAC 120

ACTCC 125

(2) INFORMATION FOR SEQ ID NO: 1339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1339:

GAGCTTCGTT CCATTGTTAT CAAACGATTG CCATTCTGAA ATGCTGTAAA TAGCATGCTT 60

CAAATCATCT TGTGCCTGCA GCAGTTTCTT TGnAATATGC TTCATATCAT T 111

(2) INFORMATION FOR SEQ ID NO: 1340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1340:

TCACACGTTT AGTTTTCTAT GAATACCAAT ATTTTAACAC CATGTTTAGC CAATTTGTCT 60

GCTAAATTAA TCGTGTTTGT CCTCCAAATT GACACGCACC TTTAGTTTTT CTAAATAATG 120

ATATCATCAC ATCTCTCAGT TAAAGGTCAA AnATATTG 158

(2) INFORMATION FOR SEQ ID NO: 1341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1341:

GCTTCAGGTC AATTAAAACG TTCAAGAGCT TTCACATCTC ACTTATTCGC AAACAAGAGC 60

ACTAAACAAA AACGTCAATT ACGTAAAGCT AGATTAGTGT CTAAGAGCGA TATGAAACGT 120

GTAAAACAAT TATTAGCATA CAAAAAATAA GAACAAATAC AGAAATCGGT AGGAATTACC 180

TAAGGAGGAA TTTTTTATGC CACGAGTTAA AGGTGGAACA GTAACAAGAG CGCGTCGTAA 240

AAAAACGATT AAATTAGCTA AAGGTTACTT CGGTTCAAAA CATACATTAT ACAAAGTAGC 300

TAAGCAACAA GTAATGAAAT CAGGTCAATA TGCTTTCCGT GACCGTCGTC AACGTAAACG 360

TGACTTCCGT AAATTATGGA TTACACGTAT CAACGCAGCA 400

(2) INFORMATION FOR SEQ ID NO: 1342:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1342:

GTTGAACAAG GGCAACAAAA ATTTCGAGCG AAACAGATTT TTGAATGGTT ATATCAAAAA 60

AGAGTAGATT CGATTGATGA AATGACGAAC TTATCGAAAG ACTTACGACA GCTTTTAAAA 120

GATAACTTTA CTGTTACAAC TTTAACAACT GTAGTAAAAC AAGAAAGTAA AGACGGTACA 180

ATTAAATTCT TATTTGAATT ACAAGATGGC TATACAATTG AAACTGTTTT AATGAGACAT 240

GATTATGGAA ATTCAGTATG TGTAACGACA CAAGTAGGTT GTCGCATCGG ATGTACGTTT 300

TGTGCTTCTA CACTTGGCGG CTTAAAAAGA AACCTTGAAG CTGGCGAAAT TGTTTCACAA 360

GTTTTAACAG TTCAAAAAGC CCTTGATGCT ACAGAAGAGC 400

(2) INFORMATION FOR SEQ ID NO: 1343:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1343:

GAAAATTTCA TCAGGTGTTG GCgTGGAACG TACATTCCCA TTACACACAC CAAAAATTGA 60

TTTACGTGGT AAAGCTGCTA GAATCCAAGA AATTCGTTAA TCAGCATTTA AACAAAGCTA 180

TGTATGAGTC AAATTCGACT CAAACAATAA AGCCATCTAG GTCACTTTTA TGGAGTGATA 240

TAGATGGCTT TTTTTGCTGT TTAGTTAATG TAAAGTTGAT AATGTAATTG TTTATTCCTT 300

CTCTATTCAT AACGTGTTTG CTCAAAATGG TTATATAAAC AAAAATCTAC TAAGTGCCAT 360

TGAAAAGGAC TTAGTAGATT TATTAAATAT ATGCGTAnA 399

(2) INFORMATION FOR SEQ ID NO: 1344:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1344:

AACTTACAAC ACCAGGTAAT AACAGCAATA AAGGCACCAG TTAGTGCGGT AATGCCAnTA 60

TCTAGGCCTT TAGGTTGCCA TAGTACGAGA TGTAGAGGTA CTAGAGGAAT GAGTGTCGCT 120

AAAGTTGTCG TCGT 134

(2) INFORMATION FOR SEQ ID NO: 1345:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1345:

TCATAATAAA CAAGTTCACA TGAATCACAA CATCTGAAGA CAATGTTCAA AATGAGGCTG 60

GCACAATAGA TGATCGCAAG TCGnATCATC ACACAGTACT GAAGCAAGA 109

(2) INFORMATION FOR SEQ ID NO: 1346:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1346:

CCATATCTGG nACGACCGAC ACCTTTACCA CCAACGATTG GTGCCATTTG TTTGCATAAG 60

(2) INFORMATION FOR SEQ ID NO: 1347:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1347:

CAATTGAAAG GTGAATTTTA TAGGTCCATG ACAAACTAAG GCTTGTTAAA GCTTATTAAC 60

ACAGTTTCAT CAAATAGTTA AATTAGTTTT TGTTTTGCAA TAAATTGGGT ATAGATTACA 120

AnTG 124

(2) INFORMATION FOR SEQ ID NO: 1348:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1348:

CATCAGTGGC CTGATCACCC CAACATTTGA CATCAATGCA TACCAGTTGA TTTGAACAAT 60

GATTGCATTG AGCTATCATC AAGTTTGTCT TTAAGCTACT AAACCCACGA ACCATGTTAA 120

CCCCGTGGTC ACCATCACCA ATTGCTCGAT CTAATTCAGT TAATTCAGAT TCATGTTTTT 180

TAAACGTTTC TTCTAAATTT AATAAACGTG CTTTCATATC ATcAtTTCAT TGTGCaCtaT 240

AAaTGtATAT TaTTCATATT CACTTCTnAT TTAAAGTATG ACTTGTTGTT GGTGCTAAAA 300

ATGCnTCCAA ATATTCTGGT TTATnAGGCA CGATAGT 337

(2) INFORMATION FOR SEQ ID NO: 1349:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1349:

CAGCACGTAA ATACAACAAA GCGATCCCCA GCTTGTGGCA CATCATTAAT ACCTGTAATT 60

TCAACAGGCG TTGATGGACC AGCCGTTTTG ATTCTTTGAC CTAAGTCATT ACATGCCGAA 120

(2) INFORMATION FOR SEQ ID NO: 1350:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1350:

CAATTTTACT TTGAATTTCT TTTTTATCTT TTCTAGTTTT ATCGTCCCAC TCTTCAATCC 60

ATTTTTTAGC TTTATCTTCA TTATTAGTCA ACTTGCCTAT TTCTTTTAAT ATTcTTTATG 120

ATTGTATTTA TTGTATGTAT ATGGGATTGT TGGCGCTATT TTTTGGTATT TTTTTATATT 180

TTTATCCATA GcATCTACAA CAATTAAATC TGGTTTTtGcT TTAGCAACTC TTTCAACATC 240

ATTTTCTCCA ATATAATCAA CCCCTTTTAA ATAAGGTTTT AAAATTGAAG AATCTTTAGT 300

TATATCTGAA ACAGCAATTG GTTTGATTCC TAACTTTATA AAATCACCAA CATAAAATCC 360

AGTTAATACA GCAACTCTTT TAAGGTTCTC nGGGACTTT 399

(2) INFORMATION FOR SEQ ID NO: 1351:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1351:

TAAAACTTAG GCGGTTTTGC ATGATTATAG CGCTCAACAC GTTTGAAATT ATAGGTCATC 60

TCTGGTATTC TTGTACGATT CTTTTTCCAA TCTAAATCAA AGTTTTCAAT TTCTTCTTTT 120

GAGTTTAGAC TTAATCGATC ACGTTCATGT TCTTTAAAAG ATGGAATAAC TTGTTTAAGT 180

GACCCTTCCA TTCTTAATTG ACCATGTGAA AACCAAGCTA TGTAGTTACT CACTTGTGaA 240

ATTTTATCAA TATCATCACC AATTGACACA ATCGTTAAAT TATTTTCAAT ATAATCATTT 300

GTTAATTCAA TCGCACGTTC CATAAATTGT GGTGTTAAAT AGTCAATAAC ATGATTTAAA 360

ATAATAATAT TTGATTTTGA TGAGCGTGCA ATACTTAATA 400

(2) INFORMATION FOR SEQ ID NO: 1352:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1352:

AAGGGAACAA AAGCTGGAGC TCCACCGCGG TGcGgCcGCT CTAGAACTAG TGGATCCCCC 60

GGGCTGCAGG AATTCGGCAC GAGCATATCT AGTATTTTAG GACGGAGGnA GTACATT 117

(2) INFORMATION FOR SEQ ID NO: 1353:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1353:

AGTTCAGGAG AGTTATAAAT ATTAGGGTGG TACATGCCCG AAATCATTGG AATTGTTAAA 60

GTAGATTTTA CAGTTTAGAG ATAACAGACA TGTCTATATG AAGGGCTGTC TACCCTCGTA 120

AGGTTATATC CTACAGnTGA ACGTATCAAG CTT 153

(2) INFORMATION FOR SEQ ID NO: 1354:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1354:

TGTTGTAACA GCTCTCTATG TTTACGTTGG AAGTATGGTT TATTTTTCAT CTTCACATTT 60

AGTTCCTTAT TTAAAAGTGA TAGAGCAATT GCACTCGTAG GTCAAGAAGC GGGATGCCAA 120

CACAAAGTTC ACAAGAnAAT ACACTTTTGA AAATATTGG 159

(2) INFORMATION FOR SEQ ID NO: 1355:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1355:

CGnCTTCCTT CAACCATTGT AGAAGTTGTC TCATATACTT ACTACGGCTT GCTAATACTC 60

(2) INFORMATION FOR SEQ ID NO: 1356:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356:

GGATTCATTG GTGCTTATTT ATTTACATTC AATAATGAGA nCTTTACACA ACCAATTGGT 60

CAAATTATAG ATGTCAACAT GTTTCTTCGA CACCTACAAA AGATGCACAA 110

(2) INFORMATION FOR SEQ ID NO: 1357:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357:

TAATGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGn GCCTCACTAT CATTTATCAA 60

ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCATTAGTC 120

GTTGAAGATA TCG 133

(2) INFORMATION FOR SEQ ID NO: 1358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358:

GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACAAATG 60

ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTCGAAC 120

GTCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCATATAG 180

ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTAAGTT 240

TAGGAATTGT AATCATATCA AAGAACCTAA TTGTAATGTT AAGCATCAAT TAGAGATAGG 300

GAATATTGCG CAATTTAGAT ACGACCATTA TTTACAACTA TTTAATGAAA TTTCCAAATA 360

(2) INFORMATION FOR SEQ ID NO: 1359:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1359:

CTGTTTTAGT CTTATTGATT GCCTGACCAT TAACTAAGTA ATTTGTGTTT GAAGCGGTTA 60

ATTGAGCAAT GATTGGAATG TCGTATTTCT TTCTCGTTCG TGAAATGACA TTTGTTAACT 120

CTTCTAGGTC GTAATACGTT TCGAAAAGTA GCGCGTCAAC GCCTTCTTCA ATTAAGGTGT 180

CTATTTGAAT TCAGTATGAT AAAGAATAGT TTGTAAGCTG ATATCCCCCT GTTTGGATAC 240

CTCTAAACCC CACCAACTGG GGCCCAATAT ATACGTAAnC TnTAATTGGC nGGCTTTTTT 300

GCGATGCGAC GGGGGGCTGG AGGATGCTTA ACCTTAACCT CCAGACCGAA CCGTTTAACC 360

TTTCCAAAAT TGCACCATAG GAATGGGTGG AT 392

(2) INFORMATION FOR SEQ ID NO: 1360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1360:

CCATGGTTAT TTTCTTCACA TTTCATGTAT ATATATTTGT TTATTATCTG TCTCTACTAG 60

ACTGTAACCT CCAACATATC TGTTTTATAA ACCAGAGAGC AGTCATTCAA TAAATAAACA 120

GATCTGAGGG CCAACTGGCA TGTTGTCAAC TTATGATATT 160

(2) INFORMATION FOR SEQ ID NO: 1361:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1361:

GTATCCTAAA GATTCAGTTA ATCGGAGCGT TGTATTGCAT GAAGGTACAT TGCGGAATGC 60

ATATTTATTC ACGATnTTAT TTAGCGAC 148

(2) INFORMATION FOR SEQ ID NO: 1362:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1362:

AAAATTACTA TGAAGATTGC ATTAGGATGC GACCATATTG TTACAGATAC AAAAATGCGT 60

GTATCTGAAT TTTTAAAATC AAAAGGACAT GAAGTCATTG ACTGACACTT CACTCATnAG 120

TGGCGACAGT GTACGTATCA GACTTAG 147

(2) INFORMATION FOR SEQ ID NO: 1363:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1363:

CTGGCAAAGA AGACAACAAC AAGCTGGTAA AGAAGCAACA ACAAGCCTGG TAAAGAGACA 60

ACAACAAnCT GGCAAAGAAG ACGGCAACAA GCTGGTAAAG AAGCAACA 108

(2) INFORMATION FOR SEQ ID NO: 1364:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1364:

GACAATGTTG CTGTAATGGG GAAGGnAATG GGTTGGTACC GCGAATTGAA TAATTTAAAA 60

CCGTAATATA TAATCGTAAT TGTTAAGCGC TCATTTTTAT AAATTTTGGA CCTCTTGAAA 120

AAGTTACGTT TTCAAGAGGT TTTATTTATC CTA 153

(2) INFORMATION FOR SEQ ID NO: 1365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1365:

TAAGAGAATT ATATGCATTC CAAACGAAAC nAACAGAAAA ACGGACCAAA CTAACTGTCA 60

CAAGTACAAT CGCTGTACTA CTGCAAAACA CGCAAAACGA ACACTTACGT ACACACAAAA 120

AGACCACCAT TCACGTCGGG ATTATTAAAA AGGTAGTCTC GTACATTTAT TAAACTACTT 180

ACGT 184

(2) INFORMATION FOR SEQ ID NO: 1366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 452 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1366:

ACATTAGATG GGTCAATCAT GTTATACACG GTGATTTAGG GGAGTCAATC AAATATAAAA 60

GGCCGGTAAT TGATGTTATT GAGGAAAGAA TTCCAAATAC AATATTACTC GGTGCTATGT 120

CATTAATTAT TACTTATATT ATCTCATTTG CTTTAGGAAT AACGTCAGGT AGATATTCTT 180

ACAGTTTGAC GGATTATACT GTGCAAATAT TTAATTATTT GATGTTAGCC ATTCCATCTT 240

TTATTGCGGG AGTATTTGCA ATTTnTATTT TTTCTTTTGA ATTACAATGG TTCCCGTTTC 300

AAGGTTCTGT TGATATTAAC CTTAAAGAAG GTACTTTTGA ATATtATATG AGTAAAATAT 360

ATCACACATT TTTACCTGCA TTCACTTTAG GTTTATTATC TACTGCTGGT TATAwTCAAT 420

ATTTACGTAA TGaTATTATT GAAAATTCTA AA 452

(2) INFORMATION FOR SEQ ID NO: 1367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1367:

TTGTGAGTAA TTGGACAATA TAAGTGTTGG TCTTGGATGG CATATCCTTG GTACGACCTG 60

GGCAACTTGC TTCATAGCGC AGTTAGGAAC TGATCAATCA TTGGCGTTTT GATACCTAGC 120

(2) INFORMATION FOR SEQ ID NO: 1368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1368:

TGGTGCAAAT TAAAACGGTT GCATATGCAC GTACGACGTA TTGCTAAATA CAATCAATTA 60

TTACGTATCG AAGATGAATT ATTTGAAACG CTAAATATGA CGGTATCAAA TCATTCTATn 120

ACTTAG 126

(2) INFORMATION FOR SEQ ID NO: 1369:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1369:

TGnAAAGTTC ATCAGGGAGC CATTTTTACA ACACAGGGCA CATACGGGTT GTGTTTAGGT 60

GCAATTGCCC CAAGCGGACA AAGCATTATT TAAAGTTTCA AGTTCTTCAA CGATTTATTA 120

GTGCACAGGA TCCTGTTAAG AGGTATTTTG AAGACTTCCG 160

(2) INFORMATION FOR SEQ ID NO: 1370:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1370:

AGTAATTCTG CAAATGCCGC AGATAGCnGT ACTTTGAATT ATGAGGTTTA CAAATACAAT 60

ACCAATGACA CGTCAATTGC TAATGACTAT TTTAATAAAC CGGCAAAGTA CATTAAGAAA 120

AATGGTAAAT TGTATGTTCA AATAACTGTC AACCACAGTC ATTGGATTAC TGGAATGAGT 180

ATCGAAGGAC ATAAAGAAAA TATTATTAGT AAAAACACTG CCAAAGATGA ACGCACTTCT 240

GAATTTGAAG TAAGTAAGTT GAACGGTAAA ATAGATGGAA AAATTGACGT TTATATCGAT 300

AATGGACCAn CTGATGTAGC AGGTGCTAAT GCACCAGGTA 400

(2) INFORMATION FOR SEQ ID NO: 1371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1371:

CATCAAGAAC ATGTGAGACC ACAATTTGAA TCACTTGAAA AAATAAATAA AGACATTGTT 60

GGATGGATAA AATTATCAGG AACATCATTA AATTATCCAG TACTACAAGG TAAGACAAAT 120

CACGATTATT TAAATTTAGA TTTTGAGCGA GAACATCGAC GTAAAGGTAG TATTTTyATG 180

GATTTTAGAA ATGAATTGAA GAATTTnAAT CATAATACTA TTTTATACGG GCACCATGTC 240

GGTGATAATA CGATGTTTGA TGTGTTAGAA GATTATTTAA AGCAATCGTT TTATGAAAAA 300

CACAAGATAA TTGAnTTTGG CAATAAATAT GGTAATCTCC ATTGC 345

(2) INFORMATION FOR SEQ ID NO: 1372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1372:

TTGAAAAGCA GTTTGGATTT ATGCTCAAAC CATGGACGAC GGTTAGGTTT ATGAATGTTA 60

TTCCAAATAG GTTCATCTAT AAAAACTAGT GGAAAGTGGA AAAAATnAGT GGACCTTCGA 120

TAATACGATG TATTTATCGT TAGAAGCAGT AATA 154

(2) INFORMATION FOR SEQ ID NO: 1373:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1373:

GAGCCTAATT ATTCAAGCCA AATCGCATAT GAAATTGATA AAGAAGTTCA ACGAATCGTT 60

CTATACnAGA ACTATC 136

(2) INFORMATION FOR SEQ ID NO: 1374:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1374:

ATCTTTAACA ATTAAAACCA TACTATCTTG AATCATCATC AAATTTAACG CATGTGCGTC 60

AAGTTGTTTC ACTTTAAAGA CTTCATTATT AAGACCGACC TTAGACTGCT TTTTAAAAAT 120

AGGTACATTC GTAATCATAC CTATACTTTG ATTGTCTAAG TGTAATTTGT TTTGGTGATA 180

TCGATTATAA TCTTGTGCAG TAAAAGCTGT AATCATTACT GATTGTCTTG AAAATATCGC 240

GCCTTCATTA CCAATGAAGT CTATTGGaAT aTCATCACTA GCCTGTTTTA ACTTGTAATA 300

AGCACGATTC TnTTCTAAAG AAGCTCTAAA TAATGTCGTT TCATATACTT TGAAGTCT 358

(2) INFORMATION FOR SEQ ID NO: 1375:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1375:

ATATTGTGTG CTAAATTTGC TTAAGTATGT TTTTTGTTTG nAAGTAAGCA TATGTTATTG 60

TCTTTTTAAT TGTTGTAAAA GTGCTGTTTT CATAGAATTA ATATCAGACA TCTTTATTAG 120

TA 122

(2) INFORMATION FOR SEQ ID NO: 1376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1376:

CATTTTCTTC GGTTTCTGTC TTTTTATGCG TAGATTTATT TTCTTGTTCT TGGTTATTAC 60

CGATAATTAC GATGGTAATA AGAAGTTTTT TCAAATATAA CGCCTCCATG TTAATGAAAA 180

GTAGTTGATA CGTGAAGCTA AATAATTnAT TTCAATATTG CCATAATCAT TTTAAAAAAT 240

AAATATTAGA AAAGTAGGCG ATATTAATAT TTTCATTGTt TTTTGTGTAC TTCAATTAGT 300

ATAACAAAAC TGTTATGTAT TTATAAATAT AATCATTAGT ATTTTTATGG CTGAAAAAGT 360

TATAATAAAA GTGTAAGGAA TAAAATATTT GTATGGAAAA GAGAGATAAT TATGAATAAA 420

ACCAGTAAAG TTTGTGTAGC AGCAACATTA GCATTGGGCA CACTGAT 467

(2) INFORMATION FOR SEQ ID NO: 1377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1377:

AGGTGTTAGA ATTTATTTTA AGTGTTATAC GTGTCTTCCA GAAATTGTAA TGGCATTATA 60

TTTATnAAAG TGTTGGCAGG TTATTTTCAG GTGTATTAGT TTAGGTATCA TTCGTAGTAT 120

GCTTGGGA 128

(2) INFORMATION FOR SEQ ID NO: 1378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1378:

GGACGCTAGA GGATCCCGGT CTGGAAAATA TCGTCCAGAA CTTAGAAATA TGAAAATATT 60

CCCAAGACCA ATCGATAATA TATTGCCAAT ATGGCGTGCT GTTGGTGGTC CACCTGCAAG 120

TGCTATTAAA GCGGGAAAAC AAGGTGTGCC AATGATGATT ACAACCCTTG GTGGCCCAGC 180

AATGAACTTT AAAGGTTCTA TAkATGCTTA TCGTCAAkCG GCAACTGAaG CAGGTTTCGA 240

TGCTTCGCCT AAGTCTTTAC CAGTAAGTAC AGCGAGTCTG TTTTATACAG CTGAAACAAC 300

TCAGGATGCT ATGAGAGAAT TTTATCCACA TTTGAATACA GGGATGTCAT TTATTCGTGG 360

TnGTTGGTTA TCCGAAACAG CAATnGCTAA TTCGTCAGTT 400

(2) INFORMATION FOR SEQ ID NO: 1379:

(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1379:

AACTACAACA ATTTAACGAC CAACCTTAAA AnAATACGCT CTTATGCATT GGATTAGTCC 60

TGATTATACA ATTTAACTGA ACAAATACCC ATCATTTAAA AGACTTAG 108

(2) INFORMATION FOR SEQ ID NO: 1380:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1380:

AAGTGGGGGG AATCAGTATG TTACATTTAC ATATATTAAG TATTAGCGAT TATTTTATTT 60

ATCGCTACAT ACTTAACCAT TTCAAAAATT CAAGGCGGnT CACCATTTTC CAACCCGT 118

(2) INFORMATION FOR SEQ ID NO: 1381:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1381:

TCATGAAAAC ATTTATTTTA AAATTTGATA TTTGTTCAAT AATATTCGAA ATTAACTTnT 60

GTGTATAGAT TTTCTTTATA TCCTGAGAGA CATGTACTAT AATGTTTGTG AATA 114

(2) INFORMATION FOR SEQ ID NO: 1382:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1382:

CGGTATTGAT CATATAAATA GTGTTTAGAT GCTATAGTCG GnTGACTTAA GTAATTTAAA 60

GTTTTCTTCT GCCTTGCTTA AAGATATATG ACAGGGTGCT GGCAT 165

(2) INFORMATION FOR SEQ ID NO: 1383:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1383:

TTTGGTGTGA TGGAGTATAT TTAGGTGTGG AAATCAAGAG GGAATTCCAT TTTCAAACAT 60

CCAATTAGAG TCGnAATAAG AACTCGCTAT CGGTCCAATT AACTGATTCA G 111

(2) INFORMATION FOR SEQ ID NO: 1384:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1384:

CATTTAAATA ACGTTGTGAC CATGTGCTTT ATGCTATGTG CTAGAAAATC CATGTTTTTA 60

TCTAATTTCT TAATAAATTG ACATTAAGTT GGATTCTTGT CCnCTTCACG TTTCGACATT 120

GGATGACTGA ACGCATGAAA TCAG 144

(2) INFORMATION FOR SEQ ID NO: 1385:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1385:

TCGTTGTGCA GCAACTGCAT TACGCTGTCT CATTAATGTA AGCGCAATGG CCATTTGGTT 60

TTTCnATAGT GGAATACTTG TCAAAATTGA ACATTGTATC TTC 103

(2) INFORMATION FOR SEQ ID NO: 1386:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1386:

CCAGnACAAA TACAACGTTA TATTCAACAA TTAGAAGACT TAGnATAGAT ATAAATTGAG 60

GGAGGACATC GATATGGCAT TTGAAGGGTT ATCAGAAACC TTGCAAGCGA CGATGCAAAA 120

AATGCGTGGT AAGGGTAAAC TTACTGAAGC TGATATAAAG ATAATGATGC GTGAAGTAAG 180

ATTAGCGTTA CTTGAGGCTG nACGTAAACT TTAAAGTGGT AAAAGAATTT ATTAAAACAG 240

TATCAGAACG CGCATTAGGT TCCGATGTAA TGCAATCATT AACACCAGGG CAACAAGTTA 300

TTAAAATAGT TCAAGATGAA TTAACGCAGT TGATGGGTGG AGAAAATACG TCGATTAAnA 360

TGTCAAATAA ACCACCTACT GTTGTTATGA TGGTTGGTTT ACAAGGTGCT GGTAAAACAA 420

CAACTGCAGG TAAATTAGCA TTATTGATGC GTAAAAAATA CAACAAnAAA CCTATGTnAG 480

TTGCAGCAGA TATTTATCGT CCAGCAGCGA TAAATCAATT ACAAACAGTA GGG 533

(2) INFORMATION FOR SEQ ID NO: 1387:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1387:

TTATTTACAA GCCATTAATA TATTTTAGGT TTGTTCTGCA TCGATTCATT GGTGCTATTT 60

TATTTACATT CAATAATGAG ACTTTTACAn CAAACCAATT GGTCAAATAT AG 112

(2) INFORMATION FOR SEQ ID NO: 1388:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1388:

ACACCTACAG TTAATAGTAT CAGTGCACAC TAAAGTCCTA ATACTTTCAA CCATGACTAA 60

TGATGTATCn TCTTGCCCAA CGAACGCGTT GTGCCAAATT GAATTAGACT GGACGGAC 118

(2) INFORMATION FOR SEQ ID NO: 1389:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1389:

CGACGACACA ACTTTATAAT AAAATCTTAG ACAATAACGA AGGGTATTAA CAGAACTTGG 60

TGCTGTTAAT GCAAGTACTG GAAAATATAC TGGTCGTCGC TAAAGCAAAT TTTTGCTCTG 120

ACCTnCAATG GTACTTGTTG GGGAATA 147

(2) INFORMATION FOR SEQ ID NO: 1390:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1390:

TTTTTGATCA TGATTTTTGG GCATGGATCA ATCACTTGCT TGGCCAATGG TCTTTCAACA 60

ATTTGGATAT CTGACCTTAT TCGCTTTATC TAGCACTTTT GnCAATTTGT TGGCATTGGA 120

AAACATGTGT TTAGATTTTT GTATGCCTCT CGCAGGCTTT T 161

(2) INFORMATION FOR SEQ ID NO: 1391:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1391:

GCCGCACGCG CGCGATTCTC GGCCTAATAA GAAAACAAAT AATTCCAATT CATATATGnA 60

CATTTTTGCC TCCTTATTTC TTGAAAATGT GGAATTGGAA TT 102

(2) INFORMATION FOR SEQ ID NO: 1392:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1392:

AAAATGCTAT TAACAACGTA TTAAATAATC AAGATTACCA TGGTATTAAA GATAAACCAT 120

TCGCATTATT CGTAACTGGA TTTTTCGACA ATGTAACAGA TAATACTGTT GGTATTAACT 180

TTAAGACAAA AGACGGTTCA ATAGCAGTAT TTATGCGTCC AGATATTGGA GAAACATTTA 240

GCGAGTTTAG AACATTCTTA GCCGTCTTGT TAATGTTGTT ATTATTTATC TCGATTTCAT 300

TAGTTATCGC ATCAnCCTAT TCAATCATTC GTCCAGTAAA AAAGTTAAAG CTAGCGACCG 360

AACGCTTAAT TGATGGTGAT TTTGAAACAC CTATCAAACA AACnCGCAAA GA 412

(2) INFORMATION FOR SEQ ID NO: 1393:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1393:

AGCAAnTGGA TTGCAATGAG TTTCTTATAT TTACAAGGTG GTAGATTGAT TGATGTTTTA 60

ACTGCGATAT TAGCAGTAGT CTAGATACCT AGTCACTGAG ATTTTAGATC GAGTTACACG 120

CACATTATCC GATCTGTCTA TATGGATATC CGTATGACTA CCTATCCCAC GGACTGCACA 180

TACTGG 186

(2) INFORMATION FOR SEQ ID NO: 1394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1394:

TCTTTAAAAG AATCAGGAGC TTGGAAGAAG TATATCAGGA TCATTAAGTC AACAAATTAC 60

GCGATATGAA AATTTGAATA ACAATTTGnA AAAGCATGCT TCCGATAATC AGCAAGCC 118

(2) INFORMATION FOR SEQ ID NO: 1395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGTTACCTCG GATGGATGAT TACTATTTTG GGCTGGGCGC CGGCTTTnGT TATTAGTGGT 60

GGCAATAGTG GCAAAGTGTC ACAAAAAAAT CCAATAGCTG GAAACCCGGG TATATTTGGG 120

TATTAACGCC GGTGGCCGGG ATTTGGCCAA TCGCATTAAT TTAATGGCCA TTGGG 175

(2) INFORMATION FOR SEQ ID NO: 1396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1396:

AGAAACTTAG ACGATTAGTA TCATATATTA GAACACnGCA CCGAACTTGA AATCATGGCT 60

GATATCGCAC CTTGAAGAAG CAAAAATGCC GCACGACTTG GCTTTGATAT ATTGGCACGA 120

CTTACATGGC AT 132

(2) INFORMATION FOR SEQ ID NO: 1397:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1397:

AGAGGTCCGG CTATCTATCA AATAAAGTGG TCATTTAAAG CGTACACTTC GGGTGCGTTG 60

ATTTCTTACT TTAGGTGTAG GACAATTGTA TCGCATCTAT CTTTACnCTA CCTGCATTGT 120

T 121

(2) INFORMATION FOR SEQ ID NO: 1398:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1398:

CGTTCGTATA ATCTCACTTG CATCnTGAAT TGAACAACAT CCTGTCATTT TAAGACTGCT 60

AAAnGTACAG CTGAAAACCA AGTAAGTCCG TTTCGTCTGG CTGTGAAATG GATCAAGGAG 120

AAACACCTCA TCCAAAGTTC AG 202

(2) INFORMATION FOR SEQ ID NO: 1399:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1399:

CGTTGGATCA CTGATGCATT CATAAATGGG TGAACnTAAT GTAATGTTAA ATCTATCACA 60

GCGCGATAAC AGCAAGAATA TAGTGAACAC CATAAATTGA GCATATCAAT GCCATATTCA 120

TGGATACACA TAGTTCACCT GGTGGTCGGT GAAAGCCTGT AGATG 165

(2) INFORMATION FOR SEQ ID NO: 1400:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1400:

ACACCTTTGT TTTTGCAAAG CTGTACCACA AAGTACTGGG TAGAATTCTA CGTTATATGA 60

GnCTTGGCGT ATAGCTTCTT TTAATTCATA AACTGTAAAT TTCTTCG 107

(2) INFORMATION FOR SEQ ID NO: 1401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1401:

TTTTGTCTAG nAACATCTGC TTCTAATAAT GATCGATCAG CAGCCATTGT GCTTAATCTT 60

TCATCCCACA TCACAATCTC AATAGAAGGA TAAGCTTCTA ATAATT 106

(2) INFORMATION FOR SEQ ID NO: 1402:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1402:

CAATGTTAAA CCTACACCGT TAACAGCACA CATGATACTA AATTGTTGGG GTGTCATATT 60

ATACAATGTT GAGTAnTAAA TGGCGATGCA GATGAATAAC TA 102

(2) INFORMATION FOR SEQ ID NO: 1403:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1403:

TTTATTATTT GTGCTACAAC TACTTAAAAA AATCAGTAGA TATAGCATTA AACATATTTT 60

CATCCCCyTG AATTTTAAAA ACTTTTTCAA AAGCAACACC TCTAAAAATA AATaCAATAT 120

ATTATAGCAA ATAGAAATTA TTATTTTGTT AAATTATGTT GTnCATGTT 169

(2) INFORMATION FOR SEQ ID NO: 1404:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1404:

TTAGTTGATA AGTAAATCCG AGTGACATTG GGATTCACCC CAACCGACTC TATTCCAGTC 60

TGAAATACGT GAACCCATAA nATCCTATGT CCAGATTTAT ATTTCT 106

(2) INFORMATION FOR SEQ ID NO: 1405:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1405:

TATTTTTGCA GCAGAGATGT TCGCGACAAG GTTTACGCCA AATTGTCACT GCTACTGCGA 60

TGTGTATTGC ATGCAAGTGC AGGnAATATA TTGAACATTT AAACGATCAG TTTAATTCGA 120

CTTTAATAAG CAATTTGTAC TGACTGTCGA CATTGCGTCA TGGTCTGTTT TTGTTTAACT 240

ATACTATnGG TGCGAAGTAG GCCTATGTTT AGAGGTCTAA CATGCCGTAG GTCTAATGGA 300

TCAGGAACC 309

(2) INFORMATION FOR SEQ ID NO: 1406:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1406:

GTGGACCTGC AGTTAATTCA ACGATTTCAA GATGGGCGCC AAGAACGAAA CGTGGCCGAT 60

ACTTAGGATT CTGGAATCAT CACATAATCG TGTGCATGAG GTGTTTCACT TTGGGGTCTA 120

ATGATTCTTC ATGGAAnGTA TAGG 144

(2) INFORMATION FOR SEQ ID NO: 1407:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1407:

ACCTTTGCGT CCAGAATTAG CTACATGGTA AAGCTTCGTG TTACTATTTT AGGGATATCT 60

TCAACnCGTT TCACTTGTAT AATTTGTTTT TGTAATTGGT GAAGTCATAG TATAG 115

(2) INFORMATION FOR SEQ ID NO: 1408:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1408:

ATTGGTATTG GCGCTGTAGT ATAGCTTCAT TATCTGATGC CATTAGTATA CGCACACTnT 60

TTATTTATGG GCGTGGTATT CATCCTTATC GGGATCAATT ATTGGGTTAC ATTTT 115

(2) INFORMATION FOR SEQ ID NO: 1409:

(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1409:

AACCAGATGa AAAGCAAATA TACATATATA ACTCTACATG GGGTCGTGGT TTGGATATTG 60

TTCATGATGC ATTCGGTATG CCAATGACAA AGCAATATAA AGATAAATTn CAAGAAGATA 120

AAA 123

(2) INFORMATION FOR SEQ ID NO: 1410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1410:

CTnTTTATAT TGAGGATTTT GTATCATATA TGGATAATCA TTAAAGGTGT ATGCTCTTGT 60

TATCAGATCG CTACGGGTAA AATCGCTTCT ATAGGGCATT TACATGCGGG CTTCTGCCGG 120

(2) INFORMATION FOR SEQ ID NO: 1411:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1411:

TCTCGTATTG CGTTTAGAGA ACATGCGCAC AAAGGACAAA TTCCAGGTGT TAAAAAATCA 60

AGTTGGTAAA ATCAAATTTC GTACTTTAGC CCATTTACAA TATCAATAAA ACAATGTACA 120

GTATATACGA ATGCTATAAA CTGAATGTTT TCTCATATTA ATAAGGAAAC ATTCGGTTTT 180

TAATTTGCAT TTAAAAATAA TTAGTTTTTA AAGGGGCTAT TTAAAGTGAA AATATTTGAT 240

TACGAAGATA TTCAATTAAT ACCTAATAAA TGCATAGTTG AAAGTAGGTC TGAATGTGAT 300

ACAACTATCC AATTTGGTCC GAAAAAATTC AAGCTACCTG TAGTTCCTGC GnATATGCAA 360

ACAGTTATGA ATGAGAAATT AGCGAAATGG TTTGCTGAAA ATGATTACTT TTATAATCAT 420

GCATCGTTTT GATGAAGAAG CAAGAATACC TnTTA 455

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1412:

ACAATGTCAA ATCACAATAG CTGTTGTAGG CATTTGATTA CAATGAACTA AAGGCAAAAT 60

TGGAGCAGTT ATCCATGAAT GATTAATAAC AACAnAAAGT ATGGGGTCAA GTTTAGGG 118

(2) INFORMATION FOR SEQ ID NO: 1413:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1413:

TGTTGACGAT ATAGGAATTA GCAAGAAATA GGCTAAGATA GTTTCGCACA ACTTGGGGCC 60

CAnCCACTTG CTTGTTTGTA GAATTAGGGG TCCATTTCTC GTGTTGGGGC CCGAACTAAT 120

AGTATGAATA TATATATCTA ATATTAAAAC GGCAATATTT ATATGGTATA CATTTTTATA 180

TTTAGTnTTT GTATAGACAT GCTAATTAGC ACTTTCTAAA AAGGGTTGAA ATGATATACT 240

GATGA 245

(2) INFORMATION FOR SEQ ID NO: 1414:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1414:

TTTTTGTTAT TCAAAATTTA GAGTGTGTTA TATGATAACG GTTTTTTCAT AGCGACTTGA 60

TCATTTTTCG AAATGATGAA AGATATGCAA GTTCAATCAA TCGGAACAAA AATACTATAT 120

TATGGTAAGA AnTTCCCGAA GACTAGCGCA CTCACACACA AGTGCATCCT CGCGAACAAT 180

GCGCACTTTT CACAAGCACA CAAACACAAG GCACAAGTGC ACGCAnTATT AGACAATGGT 240

CTACCTACCA GA 252

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1415:

ATCTGCTGGA AGAGAAAAAA GACGCTCTTA AAACTGGCTT TAGAAGGTCA AGATATAGAA 60

GnTATTAAAT CTAAAAAAGA AGGAACTTGA AAAAGTGATT CCAGGAATTT TC 112

(2) INFORMATION FOR SEQ ID NO: 1416:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1416:

CTCAATTACA TTCAAGAAAA TGGGTGGAAT TACACAACGT TGGACTGAGA AGTATAGTTA 60

ATAGCGCAAA TGCnATAAGC CTTATATAAA AATGGGCACA ATTATTTCAT GTACCAACAA 120

GAAC 124

(2) INFORMATION FOR SEQ ID NO: 1417:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1417:

TTCAAGAGCA CATACTGTAA CTCGTACGAG AATTTTTTCA AAATGACGCG TCAATCTCAA 60

TATCATCATA TGGTATTCCG AGTAATACCC CTCGnCACCT TTTTTAGGTA GCGTCAATAT 120

T 121

(2) INFORMATION FOR SEQ ID NO: 1418:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1418:

CTACGCCATC AAGAGGGTGT TAGTGCTATT AACTATTGCG GCGAGAGCAA TTAGTCGAAT 60

GCAAATTAGG ACAAGTTGAT GAGTAACTAC nGCCAATATC GGTAAGTTTC ATGGCGGTTC 120

AGC 123

(2) INFORMATION FOR SEQ ID NO: 1419:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1419:

CTTATAATCC TTACnGCAAT TTCACCTTGT ACGGAATTAA ACAACGGAGG CATTTACTTA 60

CCCCCTTTAC TTAATACGTA CCAAAACTTG GTCGTATTCA ACCATTGGG 109

(2) INFORMATION FOR SEQ ID NO: 1420:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1420:

GCTGTnGTGC TGCCAAGATG CTGATTGAAA AGTATATATG ATTGCATCAG TAGAAGAGCG 60

AGCAGAAAGA AGATATAAAG ATAATCAGTT AAGAGGTGTC GAATCAAATT TTGAAGATTT 120

A 121

(2) INFORMATION FOR SEQ ID NO: 1421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1421:

TGTTTTTACA GTCACATACA CTAGGCATCC TAGCATTATC TAAATTTAAT ACCATCGCAA 60

CTTGCGCTTT AATCTTCAAG GCCAATTAAA CCTCCTTCAT CTTTCTAACT GCTTAnATAT 120

(2) INFORMATION FOR SEQ ID NO: 1422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1422:

GCCAATCATT GTCAATGTTC AGGCATCAnA TTTATCGAAT GATTTTCATT TGCCATGATC 60

AGTCAAGGCG GGGATTTATT CAAAAATTAT GACGCCTAGT AAAAAATTTT 110

(2) INFORMATION FOR SEQ ID NO: 1423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1423:

ATTACCTTGC ATGAATTTCC ATCTGTCAAA TGTGCGCCTT CACGAATTTG TTCGATAAAG 60

ATACGTTGGT CACCGTGAAT AATTTCACCA GCTGCATTTn TCCATGGACC A 111

(2) INFORMATION FOR SEQ ID NO: 1424:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1424:

TGTTGTGTGA TTGCGTATTC TCAGGTGAAT TCTTACATAT ATAGTACTTT TTGTTTCCGC 60

TTGATTTGAC CTTGCATATC TTTCACATTC TTCGAAAATT GATCAAAGCn CTATTGAAAA 120

ACCGTATCAT ATACAnACCT CTAATTTTTT TGACTAACAA AAAGAATTCT TTGACGTATC 180

AACTATATCA TCATGACTTC 200

(2) INFORMATION FOR SEQ ID NO: 1425:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1425:

TTTCTATAAT TTTAGACTAT TTCTACCATG TTGCTGAACA ATTTACTTAG ATAAAAATTA 60

TnAAATTTTG GTCAATTAAC AAAGTTAGTT TGTTAAAACG TATACTTTAA TTATTCCGG 119

(2) INFORMATION FOR SEQ ID NO: 1426:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1426:

AAAATGGCGT TGCATTTTAC TCTAATAACG CTCAAGGCGA CGGCAAAGAT AAACTAAAGG 60

CACCTATTAT CGAACATAGT ACTCCTAnCG GACCTGGAAT TTAAATCAGA GCGGCC 116

(2) INFORMATION FOR SEQ ID NO: 1427:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1427:

TTTTATTTAC GTATAAGTGG GCGTTAGGTG TCACAGCGGT TGTCGATCAA AATATCATCA 60

TCAATCTTGT ATATGGGTTT GCGGATTCTT ATTTTATGAT TTTACAGAAC TATCCTAGGC 120

TTATTCTTTA TTAAAAGATG CAACnAGTTA TATAAAAAGA CGAATCTATC AACGCGAGCT 180

GCTCACAAGG CATCTCnTAT AGCGTCCACA TC 212

(2) INFORMATION FOR SEQ ID NO: 1428:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1428:

GAAAAATTGG TTCTGAATAT AATGGTGCCG TATACTTTAC GCCTCAAATC AAAGATTTTA 60

ATTTTAATGA AAAACATCGG TCGAATATAA CATAAAAAAA CGTCTATATC AAAAGCATCA 180

TGAATAAACA GAGGAGCACA AAAATGAnTA AAAATATAAT CATCAAAAGT ATTGCGGCAT 240

TGACGnTTTT AACATCAATA ACTGG 265

(2) INFORMATION FOR SEQ ID NO: 1429:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1429:

CGTACGAAGG ATTTGCAAAC TTCTTCATTC AACAAGCTAA AGAAGAACGT TTCCATGGAC 60

AAAAGATTTA TAACTATATT AACGACAGAG GTGCACATGC AGAATTCAGA GCAGTTTCAG 120

CACCAAAAAT TGACTTTTCA AGCAT 145

(2) INFORMATION FOR SEQ ID NO: 1430:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1430:

ACACCGCTAA GCGTATTAAG ACAGGATCTG AAAATGGACA CATCGCAATC GAATTATTGC 60

AATGCCAAGT CATATCGGGG GTGAACCGCA ATTTCAGGnA TTAAGTGGAT AGGTA 115

(2) INFORMATION FOR SEQ ID NO: 1431:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1431:

nATGTATTnG TGAAAAGGTC CTGAGTGGAC AAAAGACCTA AATATTTAAT GGTCGATTAT 60

CGCACGTCCA TAGTTGGTGA ACAGGAACTT ACACGTACAT CTAATCGCAG ACTATGCGTA 120

AACTTTGGAA ACTGCTAGTC ATTGAAGCGT GGTATGTGTA TGCACGTAAA TATGCATTAG 180

(2) INFORMATION FOR SEQ ID NO: 1432:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1432:

GGAATGATTG ATAAATTGGA CTACTTAAAG ATTTCGGTAT CGTGTCATTT GGCTCAGTCC 60

ATGTTTAATC ACCTATGnTG ACATGGTATG ATATTAGTGA CTACCAGAGA TATGGATGAT 120

TTGGAACGTG GAGGACTTGA TCGTT 145

(2) INFORMATION FOR SEQ ID NO: 1433:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1433:

TTTATTGCAT TTACATAATA ATATCCTTTT GTTGTTTTGG TATTTCTATT CATATACAAG 60

ACCATACCTT TAACTTTCAG AGCTTCCCCC TTATTTTGAG TTGCCATTTC AGAACCAATA 120

ATCCATGTAC CTTTATCATT TTTATCAAAT TCGTCATCAC GATAACCTn 169

(2) INFORMATION FOR SEQ ID NO: 1434:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1434:

GATCTATAGT TCTGTAATCT GACGTGCTTT GCCATGTGCA CCACTCGTCn TAAAAATCAC 60

TTACACTTAA CCCTTTTCCA CCTTTATCGT ATCCACCTTC AA 102

(2) INFORMATION FOR SEQ ID NO: 1435:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1435:

TTCTTATTAT ACAAATAGAA GCCATGTGTG CTTATATCGC AGCATCATGA CTCCTTTTTC 60

ATTTGAATAT ATAAATAATA CAGnCGCTTT CGAATAAATT TAGGCTAATT CTACCA 116

(2) INFORMATION FOR SEQ ID NO: 1436:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1436:

GGGGGTTTAT GTACTGGTGG ATCTGCAAAC TACTTGGCGT AAAGAATATA CAGATATGGT 60

AAnGAAAAGT TTAGATTCAC ACGCCATCAC AATGGATTAG AAAAACCGAA TTTCTTCAGC 120

AATTCTACAA TTTCTAGTAT ACGC 144

(2) INFORMATION FOR SEQ ID NO: 1437:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1437:

GTTGCTGGGn AACCTATGGT CGAACATGTA TTGGTAAAGT GTGAAAGGCT CTGGTGGCGA 60

TCAAGTTGGT AACCATCGTA GTACATGGTG CTGTAAATGT A 101

(2) INFORMATION FOR SEQ ID NO: 1438:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1438:

AAAGATGGTG ACATTTCATA TAATCCGAAT GTGCCAAGTT ATTCAGCAAA GTATCAATTA 60

AGTAATGATG ACTACAATGT GAAGCAACTT AGAAAGAGGT ATGATATACC AACTAnGAAA 120

AATTTAGAGT TTACATTTAT AGAAAATAAA GAAGAAAACA TCTATTTTAC GGATAGTATT 240

AATTTCAAAC CTACTGAATA GGGTTAATAG AAGTTTGAAA TGAAAATTTC nTAAAGTGTG 300

CAAAATAATT TGTCGCTTTA G 321

(2) INFORMATION FOR SEQ ID NO: 1439:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1439:

CAGTTGTAAT GGGACCTGGG CCAATCGGAT TACTTGTAGC ACAAGTGTTA AAAAGTAAAG 60

GCGCAACTGT TGTGGGTACT GGGTTGGGAC AATTGACCAA GTCAGATTAG ATTAAAGCCA 120

GAAnGCCATT GCCAC 135

(2) INFORMATION FOR SEQ ID NO: 1440:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1440:

AAATTATTTT GAACACTTTA TGAAATTTTT ATTTCAAACT TCTATTAACC CTATTCAGTA 60

GGTTTGAAAT TAATACTATC AGAAAAATAC ACATTTnCTT CTTTATTTCT 110

(2) INFORMATION FOR SEQ ID NO: 1441:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1441:

TCTCTTTTGG ATTCATTAAG ATTGCnGCAT CGATACCAAC GTTmAACGGT GATTGTGTAA 60

TGAATTTTTG CCACCAAGCT TTTTTAACAT TATTCTTTAA TTCAACACCT AAAGGACCAT 120

AATCCCATGT GTTTGATAAA CCACCGTAAA TATCACTACC AGGGAACACA AAACCTCTGT 180

GAAAACGCCC CATGGAAAAT AACAGCATAG TAAATATGCT TTACTTCCAT GGGACGAGTT 300

AATATTTTAA ATTGTATATA ATACAAAAnA AGTnACGTAT TTAACCCGCG GTTCCACCCA 360

AATTAGTGTA GTCACTCGCT TTTATTTTAA AATGATTCGT TGCGCCAATC TTATTGTTAA 420

GCTTACACTA TCCTTA 436

(2) INFORMATION FOR SEQ ID NO: 1442:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1442:

ATTTTTAGAA GCATACTGCG AACGTCATCA CATCGATTTA CATATCAAAA AGTTAGATTT 60

GTCGCATAGT CTCGACCGAA ATAACAGCAT TCAGAATGAA GCTCGAATTA AACGTTACGA 120

ATGGTTTGAT GAAATGATGA ATGTATTAGA AGCGGATGTA TTGCTAACGG CGCATCATTT 180

GGACGATCAA TTAGAAACTA TTATGTATCG TATTTTTAnT GGGAAATCAA CACGTAATAA 240

ACTAGGATTT GATGAGTTAT CGAAGCGAAA AGGTTATCAG ATTTATCGAC CACTTTTAGC 300

TGTCTCTAAA AAAGAAATAr AACAATTCCA AGAGAGATAT CATATTCCAT ATTTTGAAGA 360

TGAATCnAAT AAAGATAACA AATATGTTAG AAATGATATT CGTAAnAGAA TTATTCCAGC 420

TATTGATGAA AATAATCAAC TTAAAGTATC GCATTTATTA A 461

(2) INFORMATION FOR SEQ ID NO: 1443:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1443:

AAAGGTGATA AAAAACAAAG GCATTGTAAA TTACTTGAAA ACCAAGTGAG TTATTACACG 60

ATTCTAATTG GGATAATGCG CGATATTTTA TTCCACACTT GTTACATTAT TGCTTTACGT 120

GGGGGTTAGC GTGGAnTCAT CAC 143

(2) INFORMATION FOR SEQ ID NO: 1444:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1444:

TGGTGTTGGT TCATCAGTTG TAAACGCGAT TGTCACAAGA CTTAGAAGTA TATGTACACA 60

GAAATGAGAC TATATATCAT CAAGCATATA 90

(2) INFORMATION FOR SEQ ID NO: 1445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1445:

ATTGAACAGT GACAACAAAT GACAACAATG AATGACCAAC TGAGTTGCAG AATTGACCGA 60

CCTGACTTGC TGTnAGATGT GCATTGCCTG TGACCAGTTA ACTGCTGTTT GTACATTATG 120

ATTGTGCACG TGAAGTCTTT GCAAATGACT TTTAACATTA TGCTGCTAGA GCCATCTTTT 180

AAAGATGTTT GGACTAACGT nCATGATGTG AATATCTG 218

(2) INFORMATION FOR SEQ ID NO: 1446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1446:

TTTGACTTGA CATTATAGAA CACAAATTCA TTTGAAACTA TGTTTTCAAA TTTATTTATT 60

GTTACTGGGA ATTTCACATT ATTAGATTTA TTTATTTTCT TTTGA 105

(2) INFORMATION FOR SEQ ID NO: 1447:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1447:

AGACTGAAAA CTGCATATGC AGAGGCGATG AAACAAAATG CCAT 104

(2) INFORMATION FOR SEQ ID NO: 1448:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1448:

TTGAATTAAC TGAAGAAnTA GCAGTGCAAG CAGGATTGTT GATATGACAA CATTCGAGTC 60

AGAATGGCAA CAACAACGTG ATTCGTGCAC TCCAAGCACG TGCA 104

(2) INFORMATION FOR SEQ ID NO: 1449:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1449:

TATTAATTTT TTTTAATATG GAATATTCAT TGCATCGCTT TCCTATTCTT CAAGCCCACT 60

TTTTATCTTC ATATACATTA ATTAACCACC kTCAAACATT GTCGTTAGAT TCGCCAAATT 120

GAATCTATTT TTAGCACAGC AAAAAACCGA ACTGCTGAAA TAATGCATCT CCAACAGTCC 180

GGTCTATTAA ACTATTTACT TATCTTTATT AAACAATTGA CATGATTTAT TAGAATAACC 240

CAATTGGCAT GACCATGCAT CAGTAACATC CATGTTTAAT GGCTGCTGGT TTTTTAGGTA 300

AACCAGGCCA GAGTCATGGn TGGCACCTGn GCAACGCnAC GATAAAGCC 349

(2) INFORMATION FOR SEQ ID NO: 1450:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1450:

GATTTTATAT AAATATAGCT TTTCAACAAA ACAAATGATT GAATTTCTAG GAATTGAGTC 60

ATTAAAAAAA CACTTGAAAA ATTCAGGTGG GATTGCGCTA TTGCCGGAAT TTATTGTTGC 120

AGAAACAACA TTGaTAATTA ATCCTGAATC GAATAAGCAm GTACTTGAAT CTTTTGTAAA 240

AGATGTTTTT TTATAATTAT TGGTGAAAAC GTGTAGTTAT GGTGAAACTC AAAGATAATA 300

ATTTAAATGA GATGTTAATG AAAAAGTAAT TCAATATAnA ACAGGTGATT TAnATCTTAA 360

TAAGGnTAAT TCCAGGTTGA ATTCCAATTG CGGGCATCAT 400

(2) INFORMATION FOR SEQ ID NO: 1451:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1451:

TGCGTTATAG TTGCTATTCT CAATTATGTT CGCGATAATT TTAAGTAAAA GTAAGCACAG 60

ATATTGAATT TGATAGGAGT TAATTGATAT ATACATACGA ACTTTCATGG ATCACTTAAA 120

TTnG 124

(2) INFORMATION FOR SEQ ID NO: 1452:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1452:

TGTATTAAAA ACCTTCCACC TTTAAAAGCA ACAATGCGGT GTCCTTTAAA TTCAAACATA 60

ACCATATACG AATTACTCGA TAATTCTGTG TGTTTAATTG ACAGATGTCG TGTGAATTGA 120

TnATTT 126

(2) INFORMATION FOR SEQ ID NO: 1453:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1453:

ACTTTGGCAA CATCTGGAAT ATCATATAAA TCAAGTAACT TACCTAACCG ATGATTAATA 60

CTAACAGTTG TTTCCATGCC TACACCTCAC GATATTATCA CTATTCATAT TAACATTATA 180

TGTAAGAAAT TAAAATCTTT TGAAGCATTA AGATTACTTA TCATTTnTAA ATTTCAATTT 240

AAACTAACAG TAATTTATGT AGCTTTTGnA ATTCTCATAA 280

(2) INFORMATION FOR SEQ ID NO: 1454:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454:

ATATTCTTTA AATTAAACTG ATCACTTGAA TAATTAACAT TACTTAATTC TATGGCATTC 60

ATGATGATTC CTCCTCATAA ATGAACGTTA AAATATCCTG CAGTTCCTCA AGTGACATTT 120

CGATGGCTTG CGCTTCATTA ACCAATTCTT TAACCAAATT TTCAATGGTA AAAAATTGTT 180

TCTCTTTTAA AATAGGAACT ATTCTTnGCT CCTTAACAAA GGnCCCTTTT CCTCTAATTG 240

TT 242

(2) INFORMATION FOR SEQ ID NO: 1455:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455:

ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA 60

TTGATGTGAC AGATCAAGTG AGACTTGCAT AnTGGTATTT TATTCAGATG 110

(2) INFORMATION FOR SEQ ID NO: 1456:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 551 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456:

ACCAGTGGTT GCCTTTTTAA GTCCCGCGTG GGACAAAAAT TAACCTCTTT ACACTTGCAA 60

AAAGCGCTTG CAATATATTT TCGATTTGTt ATTCAACmAA ACGTTTTATT tTATTCGCTG 180

TAGTCAAATG TATACCCTTA TACTGACTCG aTAATCATTT GCTTATnATT TGAGAcTAGG 240

ACATAAATcA ATGCTCTAGA ATCCAAAAAG TCACATTAGT AGTAGTTAAC CGAACGAAAA 300

TGCACTTGTA ACAAGCTTTT TTCAATTAAA GTCAGGGGCC CCAACATAGA GAATTTCGAA 360

ATGAAATTCT ACAGGCAATG CGAGTTGGGG TGGGACGACG AAATAAATTT TGCAAAAATA 420

TCATTTCTGT CCCACCTCAC TCAAAATAAA TTTCACTATC CGTAAAATAA ACAACTAACT 480

ATTTAAGTAT CATCTCTCCC CTAATTAACA ATTATAAAAA TAAGAACCAA TATTCGAGAC 540

AACCTAATTA A 551

(2) INFORMATION FOR SEQ ID NO: 1457:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1457:

ATCnGGGGCT GCATAAGCGA TATCAAGTGT GAGCATTGAA CGATTCAGGA CTGACCAGCA 60

CGCCGTTTGC CTGCTTTGAA AGATCCACCG ACAAATCCGC CAACATCGT 109

(2) INFORMATION FOR SEQ ID NO: 1458:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1458:

ACCAGAGCCT CTTTGACTTC CTAAGTCGAA TAGCATCGTT GATATAGTTA AAGATGACGC 60

TAGATTTAGn AATCCAAACT CATAACACCT CCACCATTCC ATCACATCTG GA 112

(2) INFORMATION FOR SEQ ID NO: 1459:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CCCCAACCAA TTTTTTAAAA AAGGGGGCCT TTGGGGGGGC CAACCAAGGG GGAACCCCTT 60

AACCCCAATT TTGGCCAATT TTAAAGGGAA GGCCTTGGAA CCTTTTTGGG AATGGGCCGG 120

TTTTAAACCC TTGGTTTCCG GAAGGGGAAA ATTTTTAAAA AAACCGGAAT TGGTTGGCCC 180

CCTTTAAATT AAAAAGTTCC CTnAAAAAnA AATTCCCCCA AGGG 224

(2) INFORMATION FOR SEQ ID NO: 1460:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1460:

TTTCGACAAT CAATTCGACG TCAGTGCCAC TCCATCTATA GTAAAGCGTT GATACTTTCA 60

ATAATAACTG GATCACTGTC TAATTATAAA TGGATTCTTA CATCCCACCA TAATAAATTn 120

CATATGTTCA TCACC 135

(2) INFORMATION FOR SEQ ID NO: 1461:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1461:

TTATAGAACC TCGTACTCCT nTCGACACTT GAATTTAAAT CAGAGCCGCC AGTGGAGAAG 60

CATGAATTGA CTGGTACCAC TCGCAGAAAG TAATGATTCT AAGCCACTTG ATTA 114

(2) INFORMATION FOR SEQ ID NO: 1462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1462:

GTTGAATTGT TGGTGATGTG GTTACACGAA TTTCGAATAA TTGTTCTTTA CGTCAAAACG 60

TATCGTTCCA AGTAATCCCC CnGGTAATAG TTACCAACAA GTTCA 105

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1463:

TTGTATGACT CTTCGGACTT TGGTAAAATT GTGAACGCTG GnTGAATGAT TTTTGTTTGA 60

CAATTGGCCT TATCATCATT AATCGTATTT TTAAGCTGCT CGGATATAAG TTCTCAGCGA 120

GTTCTTTTTG ATGTATCATT AGTGTAGAAA ATAGCTGTTT GT 162

(2) INFORMATION FOR SEQ ID NO: 1464:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1464:

TAAATTGGAA AGTCACATTC AAnATGCGAA AATGTTTTAA AATGTCCTGT AGGTGCTTAA 60

TAGTTTTGCA TTTGCAAATT TTACTGAACC GGTTTAAACG AAT 103

(2) INFORMATION FOR SEQ ID NO: 1465:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1465:

AAATTGTATA ACTACCAAGC TTATATGAAA TGGTAAACAA AATATTATCA CTTGTTTGAT 60

AAGTAGCGTG GAAAATATTG TATCTTTCTA AATGTACACG TTAGAAnTCA TGCTTATGTA 120

TTACACGCGG GGCACTGGTA CCTAAGGGCC TAT 153

(2) INFORMATION FOR SEQ ID NO: 1466:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1466:

TTTCAGTAAC ATATGAAAAC TTAATTAACG ATGTTCAGTA GGTTCATACA TTTTACTTTA 60

TGATGCTTAA TTGAATTACA nTTAAGATAT GACCAGCTAA AAAGAGTTAA TGTGATATTT 120

AACC 124

(2) INFORMATION FOR SEQ ID NO: 1467:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1467:

AAGGAATTAA GTTTGCGACA CCAGCAAATA GTACTAATAA AGGAATATAT GGTAAGTCAA 60

TAATTGAATA ACCGATATAT AAGAATATAC CTAAAATAAC ACTGACAGTT ACTTGACCTT 120

GAATGTAAGA TTTTAATGTA AAGTTTAAAT CAGTTAATAA ATCTACGAAA AATACTTTAC 180

GTTCACCTTT GAnAAATTTA GCAACAGCTG GGATAAATTT TTCATGGTCT TTTAACATAT 240

AAATTAAGAA GAATGGAACC ATAATCAATA AGAAGATGGT TGAAATTAAT GATGTAATGT 300

ACTGTAATGA ATTAGATAAn ATATTAGnAA CGCCATCACC CATTGATTTA ACCA 354

(2) INFORMATION FOR SEQ ID NO: 1468:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1468:

TGCAAACTAG GAACAATAAT GTTAATATAA CTATGATGnA AGTTAAAAAA TAAAAAGGAA 60

CACTCTATAA TATGAATTAG GGTTTACAGT TTTTTGAGTA TTTTACAGTA TCAAAGTTTA 120

(2) INFORMATION FOR SEQ ID NO: 1469:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 476 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCTAAATGCT GACTAAAACT AGCAACACGA GACTCATTAT TATTAGACAC GATTGTAATA 60

GTGATTCCTT TTTCATTAGC TTCCTTAAAC CATGCTTTAA CACGTTCTGT AGGTTCTTTA 120

ACATCCCAAC CTACTAGCGT ATTATCTAAA TCTGTAATAA TACCTTTAAC GCCTTTGTCC 180

ACTAACTTGT CTAAATCAAT TTGAAATATT GATTGAACAT ATGAATTCGG CATAAAAAAC 240

TTGCGAACTA AACCCATTTA ACTCACCTTT ACCTTTTTAT AATTGAGACA CTAATGCTTC 300

AACAGTTTGA CTTGATGATA CAGCTGCTTT TTCTAAAAAT GCTTCGAAGC TCATTTCCGC 360

TTCTCCATTT GCTAAGTCTG AAACTGCACG AACTACAACA AATGGTACAT TAAATTGATA 420

ACATGTTTGT GCAATTGCAG TTGCTTCCAT TTCAACCGCC ATCGCATTTG GAAATG 476

(2) INFORMATION FOR SEQ ID NO: 1470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1470:

CACCATACAT GGGTAAGGAT ACTACTCAAA TCAACTTGAA ACCAATAATn CATGACCATA 60

TGTGTGCCAA TGAATTCAAT TGGAAAGACA ATGATGAGAT ACTATTAAAA CGATTATATT 120

TATTGTCACT TGTTCAAACG CACTCCTTTT CCAAAT 156

(2) INFORMATION FOR SEQ ID NO: 1471:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1471:

AACAAAAGTT TTGAAAAGCC GGGTGCCAGC GAAAACTTAA AAAGCACTTT ATCAGAAAAA 60

GCTAAGAAAA AAGATTAATA TTCATTCATT AAATATAAAT CCAATTTAAT TTGTTGTTTA 120

AGGTCTACAA GTGTATGTTT AATATACAAT TCATCGTTTG ACGGTAAATC AGATACTTTG 180

AAATCTTGTC GCTCAACCTC TAGTAAATCG AAATCGCTAC CAGCTGAATT ATAGGTTTTA 240

AGTTCACCCT CTTCAATGAT TCTGTTTTCA AAGTCTTTAA TAACTATAAA TACTGGTTTA 300

CCGTTGTTAT TAAACAACTT GTCTCTTTTG TCTAATAAGC TTATACAATC CAAATTCATA 360

(2) INFORMATION FOR SEQ ID NO: 1472:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1472:

CTAGGATTnC ATCTATTTGG GATGAAAATA AGCGTTTCCT GAATCCACAA GAATATCCAG 60

TCGATTTAAG CCAGGCATGT TGGGGTAATA ACATAACGTT TTTTGA 106

(2) INFORMATION FOR SEQ ID NO: 1473:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1473:

TATCTTACCT ACATTGTTAT CTGATGGCTG TAATCATTAA ATCTATAACA CCGAGTTCTT 60

CCATTAATTT TCAGCTTCAT TCGACTGCCT TTTTATnTTT CGTACTATTA CGAATTT 117

(2) INFORMATION FOR SEQ ID NO: 1474:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1474:

ATGCATGGCA CTGGAAnCAG CTGGGAGATA TAGGTAGTAT CCTAAAGAAG TTCAGTTAAT 60

CGGAGCGATT GTATTGCATG AAGGTAACAT TGCGGAGTGC CAACAGGCGA AGTAAAACTT 120

AACGGCAACC ATGCCTTATA TTAAATGCCC TTCCGGGAAA GGAC 164

(2) INFORMATION FOR SEQ ID NO: 1475:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1475:

ACAGCAAGAC GTGACAAATC AGATACTATT AGTCATCAGC GTTAACATGT GGATAnGTGT 60

GAGGTACGAA TAnCCGAAAG GAAATACGAC CTTTAACATT CGCGCACAAA ATGAGCTCAG 120

GCGCCTGCCT TGCCCATTTT TTAAATTATT TCCCTGGAAA TGATTCGCTG TGTGCTGTTC 180

TGTCCACAAC AACACGATTA ATGCCATGAC 210

(2) INFORMATION FOR SEQ ID NO: 1476:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1476:

AGGGTGATTT CACGGTTCGT CTGCCCATTT AATTGCGCAT TTTGCACACC ATCTACCGTT 60

TGCAATTTTG GTATTAATTG TTGCATGCAG TACTGTCCGT TGACTTTGnT GCAAGTGCAT 120

GCTCTTTC 128

(2) INFORMATION FOR SEQ ID NO: 1477:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 641 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1477:

AAAATCTGGT AAAGTAACTA GAGTTTAATA AATATATTGC ACATAAAAAA TGTGACCTTA 60

TGTGGAGGAC ACATTTACTT AAGAACTAAG AGCTCAACCT CTTAGTTCTT TTTTTGTTAC 120

CAAACAATAC ATAATGGTTC ATAGTGAAAT TCGAACTATC AATATAATTT GGTTAATACG 180

TTTAATAATG GTTCTCTGTC AAATTGGACT TATGGGTTCA ATATCGATTT TGGCACATAA 240

ATCAATGTAC TAGGACCTAC AATTTTCCTT TCAATAATAA ATCACGCCAT AATCTTCATT 300

AATTACAGCG TGATTCATCT ATTATTATGT TATAAATkCT ATCTATAAAC GTCACTTTAT 360

TAAATAACTC ATGCACTTTA TTAAAAATCC TCACAAATTT GAATATACTT AATTTAAATC 420

TGTACTTCTA ATTTGCAAAA TCAACCCATC ATGTACAGTT ACTTTCGCTT GCAAAGACTC 480

AATTTCATTT GAAATAGTTA AAGTAGAACC TATATnAAGC ATTTGTCTAG CTAAATTATA 540

GATAACTCTT ATCTTTTTCA ACTGTAGGTG ACCTTTAGGG C 641

(2) INFORMATION FOR SEQ ID NO: 1478:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1478:

TTAACCGTGA TGCAGAGTAG TAAGTGGATn CATGCTCTGT TATGGATGAC AAGACAAAGC 60

AGCGAATATT GCGTACTGCG ATTGATGAGC AGATGCATAT GATTGGATTG GTGCAGCTGT 120

C 121

(2) INFORMATION FOR SEQ ID NO: 1479:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1479:

ACCATTGCTT AGATAAATAC CTCGCAGTGA ACCGCATTAG TATAGCACTT CTAGCTGATC 60

GCATCAGTAA AGTATGCTAT TAATGTCTCA GTTTTATCTG TAATGCATGT TTAAGTTAGT 120

CATAGCATTA TTn 133

(2) INFORMATION FOR SEQ ID NO: 1480:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1480:

TTTTGGGGnT TTTAAATTTT AAATTCCCGn TGGGGGAAAT TCCCTTAAAA ATTCCCAACC 60

CTTTTAAGGG GTGGGGGTTT TTTTAGGGAA AAAGGGGCCC GGGGTTAATG GTTCCCAAAA 120

AATTGGGGAA AATGGCCCCC CAAATTTTAA ATTCCCGGTT TTAAAATTGG GGTGGGTTAA 180

ATTGGAAAAA CCCCCAAATT T 201

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1481:

CAGTATCAAG CATAGTAAAA AATGAGGGTA GGACTGAAAA TACGGCGTTA TTGGTGGTGC 60

ATTCACGGTA AATATGTTGC ATGACCAGCA AGTTTTGGnC TTCTGATGCA CC 112

(2) INFORMATION FOR SEQ ID NO: 1482:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1482:

CAAAAAACAA GTTCTGATAT GCAGTAGCTG AATAATTTTG CTAGTTACAC CAnAGTGATC 60

TTCTGGTGTT TTACTTTTTA TAAATGTTTT CATATATTTC ATATGTATAA AAATGGGATT 120

TAGCGTA 127

(2) INFORMATION FOR SEQ ID NO: 1483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1483:

AGTGGTGTAT TGGGTGAGTA ATGCTTAACT TCATACCTGG TGCATTGGCT GTTCAGTATC 60

ATTATATCTG CATGGGCGAT ACT 83

(2) INFORMATION FOR SEQ ID NO: 1484:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TATTATTGAT GTTCTTTGGT TCATTCTTTG GTAATAATTT TGCACTTGAA AATTTACAAC 60

CGTTAGCTGG AACCTAGnCA AAGGGATGGG TTTAGTGGTC TATTGTGGGT TTATTGGTAT 120

TCCGTGGGCC ACCCCATGGG GCCATTATGG TTTGGGAATT TTGGGAATAA ATTAATTTnC 180

CCAACCAAAA ACCAGGCCAA G 201

(2) INFORMATION FOR SEQ ID NO: 1485:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1485:

CTCACAGCAA CATCAAAGAG GCAGATATTA GTCAAGTTCA ACGTAATAAC ATCTACCTTC 60

ACAAGTCGAT AAAGGAGCAC CATCATTAAT AAGTAGATCA ACAAGTCAAC GAGAATTTTA 120

ATGTGCAGAA TAGAGAAGTA CACCACACAn ATAATCAAGC GATGTAATTA CTACTACATT 180

TTnCATGACA GAGTGAACCT CAACAGCGGT 210

(2) INFORMATION FOR SEQ ID NO: 1486:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1486:

CAGGTTATGT TTGCATTAGA AGTTCTTGGA AAATCTTTAT GGAACGTGGT TTACACCCTG 60

ACTTTGAATT GCATCGATCT GATGAAGATA AATGAAATTG AATGGGATGG CCnACATGGA 120

ATGCAACCTA TGACTTGGAT GGAATTAGAT GAAGCGGG 158

(2) INFORMATION FOR SEQ ID NO: 1487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1487:

TTGCAGCATA TAGAGGTAGA GGCATCGCGA CAAAGTTATT AACGTCATTA CTTG 114

(2) INFORMATION FOR SEQ ID NO: 1488:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1488:

TGCTAAGTGA TAAAAAGAAT GATAAGCCAG GTGTACCAAT GGGTCCTGGA TTAGACCATT 60

TGGGAGATAT CGTTGTACCA CATGTTGATC AACTAACGTT nCCACATG 108

(2) INFORMATION FOR SEQ ID NO: 1489:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1489:

CAAnACGTAA TTTCATGATG AAAGTGGTCG ATAATTTCTT GAAACATCGC TTTCAGTAAT 60

AACGCCTGCT TTAAGGTCAC GTTCCGCATA GGTGTACTGA GGATGTTGAT GT 112

(2) INFORMATION FOR SEQ ID NO: 1490:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1490:

CAGAACGTTT AAAACAAAGT TGGAAAAGTT TTCTAATCGT ATTAGCTGCA TGTTTAATAC 60

TTATTATTGC AAGTGAAACG CTTATTTTCC TTTAGTCATT TGACCGATGT TAAAGAGGTG 120

AGATGGTTAT TTAGAATCAT TGTATTGATT GTTTTTGCGG TAGTGATGTT CACAATTTAT 180

ATCTCTTATC ATCATTATAT GAATGACTTT TTAGTTACTA AGTTATTTAA TATTTCCGCA 240

GCGACGCCAt AGTTATTATG TCTAT 265

(2) INFORMATION FOR SEQ ID NO: 1491:

(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1491:

CnAAATTGGC CAGGGGCTCA TCCAATATTA AAATAGGCGT ACGAGGGATT AATAGACCAC 60

CTAATGAAAC GCGTTGGTTG TTGGACCTCC AGATAAATCC TGGGGGTCGG TGG 113

(2) INFORMATION FOR SEQ ID NO: 1492:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1492:

ACTAAGAAAA TCCGAAATCT TTTCCGCTTC TTTTAAATAC GTAATACTTC CTTTTTTTCG 60

CTCTAAATGT TTGGCATTCA ACTCATAACT ATTCATTAGT TTCGTTAAGC CTTCTGCATG 120

ACTCTCATTT TGAGAAAAAA TTTCCAAATG GTACGAAGAT GTTTCAGGGT TATTCACTGA 180

GCCACCTGCC AGAAAAGCTC CTCTCAAGTA ACTGCGTCTC ATTTCGTCAT CTTGAATCAT 240

TGAAATGATC AATTTCATGG CGnnAAAATG CCGTCT 276

(2) INFORMATION FOR SEQ ID NO: 1493:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1493:

GATGACGAGC GCCAATTATG TCACTTTTAT GGCAAAAGCT GGAACTAAAC AACCnAGCCT 60

GCCAGTAAAA TTGGCAATTG GGACGTTCTT AGCAGGTGCG TCATACATAC 110

(2) INFORMATION FOR SEQ ID NO: 1494:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1494:

AAAAAAAAGG TTTTTTACCC GGAATTCCAA AnTTTTAATC CCTTAAAAAA AATTCCGGCC 60

AACCCCCAAA CCCAAGGTTT TTTCCTTAAC CTTGGAAnTA ACCAAGGTTT TTTTTCCAAA 120

AAATTTTCCA AAAAAGGAAT TACCCAAACC CTTAAAGGTT TTAAAATTGG GGGGGGAAAA 180

AGGCCCTTTT AGGGGGGGAA 200

(2) INFORMATION FOR SEQ ID NO: 1495:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1495:

AAAAAATTTG GTGCATTTAT CATATGGAGT ATTAATCTGT AGAAGTAAAG GCGATATAAA 60

TGTTACTTTG GTAATAAAGA TTACAGCGAA CGTTATTATT GCTCAGGTCA GATCAAGAAA 120

TTGGTGTCCG GGTGACAAGA CTTGGTGGCG CGGTGTAGTT TGTCAGTTGT GTGGTCATCT 180

TAAATAACGC TATCGTACGG TGTGTATCAC ATGAAGGGAC TCTTACTAAT TCTGCAAGTA 240

CACGTCACGC nnT 253

(2) INFORMATION FOR SEQ ID NO: 1496:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1496:

ACGCTAGCTT CTGAAAAAAT AAGTGAACTA TGGATGCAAT GAnCCTATTC CTGAATGATA 60

TTAGACGTAG CGCACCTGGT GCAGAACGCC AATAAAAAGA CAAG 104

(2) INFORMATION FOR SEQ ID NO: 1497:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AGGGAGGCGC CCAAATGGCT CTATATTAAA AAAGGACTCT CAGAGCATTA ATGAAAAGTT 60

GAAGCTCAAA AGGAAnCGAA AGAAACAAGT ATCAAAACAT 100

(2) INFORMATION FOR SEQ ID NO: 1498:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1498:

TGGAACTTTG GGGAAGTCAA ACGGTTGTAA TCGTTGAACA TAAAGTTAAA CACATTCTGG 60

ATCATGTCGA nCGCGTCCAT TTGATGGATA TAACGGGAAT A 101

(2) INFORMATION FOR SEQ ID NO: 1499:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1499:

AGTTCTGGTG CATCGTTTTT CATTGTATTT GTGACGATTA TCATTCCAGC ATTAGAATAT 60

TATGCATTAT ATTTAGGTGT GATAGGTGCA TTTATAGGTG GTTTAACTGT TTATACACTT 120

TCAGGTG 127

(2) INFORMATION FOR SEQ ID NO: 1500:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 560 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1500:

TCCCCGCTTT AATACCTTCC ACGATTTCTT TAATTGCTTG CGGTTGGTCA CCTTGAGGCT 60

CAAAATCAGA ATGTATTTTA AAAGGATAAT GTTCAACCAT TGTCACATAT GCCTCCTCTT 120

TCAACGTATT ATTTATATTT CCGCTCAACT CTTTGCTTTC TCATnACATA TnTTAGCAAA 180

GTAGTCACAC AAAAaGCAAA CGTTkGTTCG TAAAAATGTC GAACAAaGAA AnACAAACAT 240

AAATACACAT TATATTAATC ATCATTTTGT TTCAACAAAT TTGTTTGAAA CATTATTTTA 360

AAGTTAATCT TAGCGATCTT CATCTTGATG TTTATGAAAT TCGAGTTGAT CTATAATTAA 420

ATAACCAGCT AATAATGACA CTACATCAAT AAAAATAATC CACTCGTTAT GGAAATACTC 480

TTTATAGATT GAGGCACCAA TTAAAATTAA TGTCAGAATA GTACCGACCC ATTTACTTCT 540

TGTTATTACA CTAAATAATA 560

(2) INFORMATION FOR SEQ ID NO: 1501:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1501:

ATTAAATCAT ACTnACAATT ACCGATGACA TTATTCCAAT TCAATCTAAT TCCGTGATGA 60

AAGAGCCACG TTTTGGTTAC TTCGTGGGCG TGAATTATTA TG 102

(2) INFORMATION FOR SEQ ID NO: 1502:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1502:

TATGGTAGCT CCAAATGGTT GTATCGTCAC ACCATCATCT TCAAGTGCAA TGCGATGTAA 60

TCGATTGGCT GTTGTTTCTG TTACCCATAG TACTTTTTCA TCTGTACTTA AAGCAATACC 120

ATTTGCTACG CTAATATTTT GAATGATAGG CGTCACTGTT CTAAAGTCCG GCGAAACATA 180

ATAAACGCCT CCTAGTGGAT TGGTAGAGTA TCCTCTAAAA TCTGTAAAAT AAAATCCACC 240

TTTAGAATCA AATACCATGT CATCAATACA ATATGCTGTT GAAAGATCTT CAATAATATC 300

TTGTAAGTTG TCACCATTTT CTGTAGCTGC AAAAATGCCT CCnGGAGATT TAAAATCTCC 360

nAAAATAACC AACGnATAAA TCGGGCAnCT TATGGAATTG 400

(2) INFORMATION FOR SEQ ID NO: 1503:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1503:

TACAGGTAGT TAACAGTTGA TGTTAAATGG CGTACTGGAT TCTTTACGCA CGATTTTTTG 60

TTAATAAGTA TGGGATAGCA CATTACTATA TCCTACTTAC GACTTATTGG ATATGTCnTA 120

GCTATTCTTA AGCTCGAAAA GTTTCACAGG ATACATAAGG GACCAACT 168

(2) INFORMATION FOR SEQ ID NO: 1504:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1504:

CTACTGATTG TGTAATGTCG TTGGTAGGCT TGGGCTGTAC GCAGTATTAG GTGTAGGCAA 60

CTTGGCTTTT GGCATCTACC TTGTATGTGT CGTGTATCTA nGGCTGGGGC TTGCTCCTTC 120

AGTTGTTAGA CAGTAGGGGG TAATCTCAGG GGTGCAATGT ACTCCCTCCG TCCTAAAATA 180

CTnTATATGC TCGTGCCGAA TTCCTGCAGC CCGGGGGATC CACTAGTTCT AGAGCGG 237

(2) INFORMATION FOR SEQ ID NO: 1505:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1505:

CGCATTTACC ACCATATGAT GGATCCAnCG ACGTTTTAAT AAAGATAAAA GTGACAGTAG 60

CGGGAAAACA GGnCCATAAT TCACATCTCT TTTGAAAAAT ATGTTCAAGC TAGGATCATT 120

AGGAGAGTCA TATTAATAAT AAAAATGTTG CAATCAATCG ACGTGCGTTG AATCTTAAAT 180

ACATAATAAA TGTTGTAGAA GATATGGGT 209

(2) INFORMATION FOR SEQ ID NO: 1506:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1506:

AAAATGTGGC TATTGATTTT GACTTGGAAC TTTTTGAACA TTTCTCTCAA GGATTTAAAT 60

GTAGGTAACA GGGCAGGTAC TACGGTACTT nCCTATTTTT TTATGCAAAT TTTAAAAAAC 120

A 121

(2) INFORMATION FOR SEQ ID NO: 1507:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1507:

AATGACAAGG TCAGCATTAA AACCATTTAA AAATAAACGC GTTATGGTTA CTGGACGTAT 60

ACAACGTGTT TTGTTTAAAA ATTATTTAGA TAGACATAGC ACATTTAAGC CGAATGTAAG 120

GATATTATTA AAAGAnGTAT TTGT 144

(2) INFORMATION FOR SEQ ID NO: 1508:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1508:

CCGATTGAAT CTGTGTACAC TTCACCAAAG ATATCTTTCT TCGTTTCTTC AGATAAACTT 60

TCCATTGCTT TCTTATCAAC ACTTGTTTCT ACTAATAAGT GTGTTAATTT GTGCTTnTTA 120

ACAAACTCAA TAGCTTGTC 139

(2) INFORMATION FOR SEQ ID NO: 1509:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1509:

TCTGCCTGCC TCGGCCTCCC AAAGTGCTGG CATTACAGGC ATGAGCCACC ATGCCTGGCT 60

CAAGTTAAAA TACAGATGTA AGACTTGACT TGATC 155

(2) INFORMATION FOR SEQ ID NO: 1510:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1510:

ATCCCAATGC TAATGAATTT GCATATACGA TAAATAATGC TTTTTATCAT CAATAAAGCT 60

ATGAATCTTT CAAGATCTTC ATTGAAC 87

(2) INFORMATION FOR SEQ ID NO: 1511:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1511:

ATAGGCGTTT ACCAGTTATT TTCGAATCCA TATAATTATG TTTGTCCGTT TGGTTTAATC 60

CAATTAATTG ATTAAGTTTT TCCAATTCCT TTTTTTTTAA TTAAAATTCC AATCCTTAAA 120

AAAAATTGGA AAAAAGCCTT AAAAAAAATT GGTTAATTTT CCCAAGGGAA TTAAAAATTT 180

TGGGGTTTTT TnAGGnCCCT TTTGGGAAAA ACCCAAC 217

(2) INFORMATION FOR SEQ ID NO: 1512:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1512:

TGACATTGCA TCGGATTATG TTACATCAnG GACAACGGGC CTCAAAAAGC GGTGCACAAA 60

CGTTCCGTAA TCATATGCCA GTGCAATCGG ATGTAAAGAG A 101

(2) INFORMATION FOR SEQ ID NO: 1513:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1513:

GATTTTATTG AAATGATTTT ACCTGTGATC AATTATTGTA ACAAATCTAC AATAAAATTG 60

TCTTACTGCA TGACCTAATA AnATAGCAAC AGATATCATA CACACTTGTA ATTT 114

(2) INFORMATION FOR SEQ ID NO: 1514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1514:

ACATATACAG GTACGTGTTT AGTCCGTCGT ATACTGCAAA ATTATGTCCG ATGAAATTAG 60

GGGAAAATTG TAGAACG 77

(2) INFORMATION FOR SEQ ID NO: 1515:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1515:

CCTTATAAAG TTAATGCAAG CAACATGGAC AAATTATTAn TTGAATAAAC TGCAAGAAAG 60

ACAACAATCA TTCTTCGGAA TGCTAGGAGA ATATATTTTA GA 102

(2) INFORMATION FOR SEQ ID NO: 1516:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1516:

CAATTTTAAA TAGGATTTTT AAGACCTTGG TTGGGTTTTG GTACAATTAA TGGGGACATG 60

ACTAGGTCTT GCCACGTTTA TATGCATCT 89

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1517:

GTAAGAGTGC ATAGTTTTTA AATGTTGCTT GTCTGGTnTC ATTTTGGCAC CATACAGTTC 60

GTACCTGGAT TAGGGAAATG CCAAATGTCC GCGTAGTGAT AT 102

(2) INFORMATION FOR SEQ ID NO: 1518:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1518:

GAGAACTCCT TACCACAATC AAAAGTAATT GATTTAAATA TATGAGAAGA TAAAATGAAA 60

AGGTGCAAGC AGTATTAAGA ATTTAGGTAG CAAGAAAACA AGAAGTGGTA CATACGATGC 120

TAACCTAAAA AGAATTGGAG ATTAAAATGA TTATTAACCT TGAAACACAA CAAATACATT 180

TTGATTTAGA ACATGAAATT CCCTATTTTC AAGCACCTGA GAAAAATAGG ATACGCTTAG 240

ATATTGATGT TCTCAATAAA AAGCnAATTT CTAATATTAT TAATGTTATA TTTAATAACC 300

AATCAAAGAC GAAATGTACA TTTTTGTCTG AATACTTATA TCCTGTTAAA TTTAGAGAAA 360

AAACAAGAAT TGGTCGTTTT TTTAATATTA CTAACTGGTA CGAAGAAATC CATTCTACCG 420

ATGAGAAGTA TGTnATTGCA ACTATTAA 448

(2) INFORMATION FOR SEQ ID NO: 1519:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1519:

ATGGACGAAA GAAGATGTCA TTGCTTTTGA AAACCTAACA AATATTAAAG TAAATTTAAA 60

AGGTAGCGGT TTTGTGTCCC ACCAATCAAT TAGTAAGGGA CAAAAACTTA CTGAAAAAGA 120

ATTCAAATTC AGATGGTnAA GAAGAAATCT GACAGTTAAA ACTGACAGGG ATAAGTCGGG 240

ACTnAACAGG AATGGGCTAC nTTTAAATTT AGGGATGGTA TTGGGCCACT ATTTGGTTTT 300

TGAC 304

(2) INFORMATION FOR SEQ ID NO: 1520:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1520:

ATGACGTCGC ATGCACGCGT AcGTAAGCTT GGaTCCTCTA GAGCGGCCGC CCTTTTTTTT 60

TTTTTTTTTT TTTCTGTTGG CCTTTGATAA TTTTATTGGA TCAGTAACAA CTTTTTGTGT 120

TTCAACTAAG ATAGCTAAAA TTCTAACACT TATATGTAAA AATTACACTC CATTTTAGCA 180

CAAATGTTAA CAGAAATTAA CAGCACAGTG CCATGAAGAA ATGAnAAATA CACAGCTTTG 240

GTAGGGnAAT GGTCCTGGAA ATAATGTAAT GCCAAGTnTC TGATCATTTA ACATATCACT 300

CACCTCCTTC TTCATCTGAT GT 322

(2) INFORMATION FOR SEQ ID NO: 1521:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1521:

TAAATACAAA CCCTTTAAAC ATATTTACTA AGTCGTTCAA TTGTTGATTT GATAAnTGAT 60

GTGATGTGGT ATTTTGCATC GGTCCTGCTT GATTCCAGAC ATGTC 105

(2) INFORMATION FOR SEQ ID NO: 1522:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1522:

GATCGTATTT CCCAGATGTA AATTCnGTGG ACAATTGGCG TCAAATAGCT TCTAGTGG 118

(2) INFORMATION FOR SEQ ID NO: 1523:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1523:

CnGCATATAA TCCCGCGACA TGTCTTTTAC GGGTGCACTT GTAATATTAT TACCCCCCGT 60

ATAACCCATG TATATCTATA CTTTACCACA TAAAATAATT CCGGGACTAT TTGGCACATG 120

TTTTGGGTGA ATTTCTTTAG TGGCACACCA CCCCTGG 157

(2) INFORMATION FOR SEQ ID NO: 1524:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1524:

ACTGAGGTAG GTTATGTAGG ACGAGATGTT GAAAGTATGG TTAGACATCT TGTTGATCCT 60

TGAGTAAGAT TAGTCAAGGC CG 82

(2) INFORMATION FOR SEQ ID NO: 1525:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1525:

GATACAAAAA AGAAGTTCAA TTTGAACTAT GAAGAAATTT ATATTTTAAA TCATATTTTA 60

AGAAGTGAGT CTAACGnAAT CTCATCTAAA GAGATTGCTA AGTGCTCAGA GTTCAAACCT 120

TACTATTTAA CTAAAGCTTT ACAAAAGCTA AAAGATTTAA AATTGTTATC AAAGAAAAGA 180

AGTTTACAAG ACGAAAGAAC AGTTATTGTT TATGTTACAG ATACACAAAA AGCAAATATT 240

CAAAAACTGA TTTCAGAATT AGAAGAATAC ATTAAAAATT AAATCAAGGT TAATTGCGTT 300

AAAATTAACT TAAAATTTAA ATATTGAAGA GCTTAATTAA 400

(2) INFORMATION FOR SEQ ID NO: 1526:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1526:

ACTGTCTAAT ATTCACTCCC TTAAAGTGTT TTTCATATTT TTCTATTAAT GTTCATATTG 60

TAGGGTGTTG AATGCATCTA AGCATTnCAA GTTATTCTCC AAGTTCATCA ATTTCAAAAT 120

GGAAC 125

(2) INFORMATION FOR SEQ ID NO: 1527:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1527:

CATGTTTATT TATGTTTCGG CTTTAATGTT GAAGAGTTTT ACAAAGTTTA CCGATTGCAT 60

TTTATAATTT TAATGCATTA TTGGAGCATT GGCTATCATC TATTACTGCG nA 112

(2) INFORMATION FOR SEQ ID NO: 1528:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1528:

GCGAAGATGA GGATGAGATG ACTAAAGGAA AATATTGAAA AACAACCAAA AAACTGATGA 60

ACATTATTAA AAATTTACAA AATCAAATCG ACAACTTGAG CGCAAGAACn AACAG 115

(2) INFORMATION FOR SEQ ID NO: 1529:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1529:

ATGGATCTTC CGCTTCTCTT AATTGATCAA TTAAATCAGA CATTTCATGT TTTTGTAAAT 60

AATGATTCGC TTTAATGGAT TTTTTACATG ACATCATGAT TGCTACATCT TCACGTAATT 120

TTTTGATATC TACTTTTTTC TCTTCCAAAA TTAGCTCAAT CATATCTTTA ATAATTTCTT 180

CTACTTCATC TTTAGGGAAC CAAACTGGAT AGCTACTTAC AATATAATCA TGACCACCAA 240

AATGTTCTAA CATGATACCT ACTTGTTGAA GCTCATTTTT ATATTGATCA ATGACTAATT 300

GTTCATCTTT TGAAAAATGA AATGTTAACG GGATTAATAA ATCTTGTACT TCATTGGTAA 360

CCTCACCTAT TTnATCTCGA AAATATTCAT ATnTTATnCT 400

(2) INFORMATION FOR SEQ ID NO: 1530:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1530:

TAACAGTCAA CCCACCCATT AATATATATT CAACGGCTGA CTGATACGAC GAACGTCAAA 60

GAATATGAGA GGAATAGGGA CAAGATCATC ACACATA 97

(2) INFORMATION FOR SEQ ID NO: 1531:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1531:

TCATAACGGT GCAACTTAGA GCTGACGTAT AGTTCATTCC AACTATATAC GATGTATCAA 60

CACCATGTTC CAGTTTTAGG TTAACGATAC TGTATACCGT ATTATGTCAG nGGCACCTTA 120

TCTTCACGTA CTTTACGGCG AGATGATGAC 150

(2) INFORMATION FOR SEQ ID NO: 1532:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1532:

ATTCATTCTG CTAACCAGTA AGGCAACCCC GCCAGCCTAG CCGGGTCCTC AACGACAGGA 60

GCACGATCAT GCGCACCCGT GGCCAGGACC CAACGCTGCC CGrCCTATCC TGAAGCCAAA 120

GGAAATGAGA TCGGAATT 138

(2) INFORMATION FOR SEQ ID NO: 1533:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 460 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1533:

GGGGnCCnGG CAATGGAGGC GTGCTTGGAT GGTGCTTGGA ATCATCCCTT TGGCCTCGAT 60

CATAAGCTTA AACTTTTGGT GCTGGnGCCA CTGGAGGGAA ATCTTCAATT CTGGCAAATG 120

GTAATTnCCT ATACCAACAT TTAAGGCATG TGGTAATGCT GGCTACTCCC GCTTCGTTAT 180

CAGCTACATG ACAAATACAG ATGCCATCAC CTTTGCGTCC ATTTTAATCG TTGATGCTTG 240

GAAATGTTTT TTGTAAATAT CAATGTTATC CTTCGCTGTA TGTATCGCAT TTATATCTGG 300

TAGCAAAAAT GTTCCAACAG AAAGCCCTAT ACCTAGTTCG GCAGCTATTT TGGCAGATGT 360

TGCGCTACTA CTTAATAACC ACATTTCTGG AAAATGATCA TGTGTGGTGC ACTACGATCG 420

ACTTGGTTAT CTTTATTGTT AGATAATACG GAATACGnAA 460

(2) INFORMATION FOR SEQ ID NO: 1534:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1534:

TACGCTAATA AATAGTTCAC TTTTCCATTT TGTGTAGTCA GCTCATTGTA TTCTTCAATT 60

TGCTCTTCAT TTAATGCCGC ATAAGCTTGA TCAATAATAT TTGGATTAAG TTGTCCAATA 120

TACTCTAACT GGTCATGATA AACAn 145

(2) INFORMATION FOR SEQ ID NO: 1535:

(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1535:

ACGCGATTTA ATCGTTCGTT CCAACGATGT CCACTCCCCT ACTAATAATT AAAATCATTA 60

CAAATTATTT CAAACTTTAC AATTnAAACT AACAGTTTTC TCAATAAAAT GCAAGCTTTT 120

CTCATTTGTT ATTTAGAATG ATTATGATTT A 151

(2) INFORMATION FOR SEQ ID NO: 1536:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1536:

ATAATAGAAT CATTACAAAT TATTTCAGAC TTTACAATTA AGACTAACAG TTTTCTCAAT 60

AAAATGCAAG CTTTTCTCAT TGTTAA 86

(2) INFORMATION FOR SEQ ID NO: 1537:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1537:

ACCAAACTGT AAAGCCATAT ACTGAACATA TTGATAGCAT ACTCAATGAG ATCAAATTAC 60

ATCGTGAATT TATTATAGAA GTACCTTATA TGAATTCAAG GAAATTTGAG CTACTGATTG 120

CTAACATTGA ACAACTTTCT GTCGAATGTC ATTTTAAGCG AACAAGTCGA AAGTTATTTA 180

TAGAAAAGCT TAAAAGTGTT CAATATGATT TACAAAATAT ATTAGATGGC GTAACACnAG 240

AGGGTACTGA TGGTTAAAAC AGTTTATGTA ACAGGTTACA AATCATTCGA ATTAAACATT 300

TTTaAAGATG ACGCACCTGA AGTACATTAT TTAAAACAAT TTATAAAACA TAAAATTGAA 360

CAACTGTnGG ATGAAGGATT AGAATGGGnG TTAATACAAG 400

(2) INFORMATION FOR SEQ ID NO: 1538:

(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1538:

ATATCGTTAC TGCTGTATGT TTCAATATCT ATATTCATAA ATTTCAAATn CTGACACCTC 60

AATTTCTTTA AAATAAGGGG CAGAACCCAC TATGACTATA GGATCTCTCA CAGGTCAATT 120

CGCAAATCAC TCGTGC 136

(2) INFORMATION FOR SEQ ID NO: 1539:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1539:

TAAATATCTC GGCACAATGA TGCGGGATAT TTTTTTACAA TAGGCATAAA GGCTGGAAAA 60

AACATATCTA GTGCTATGAT ACTTA 85

(2) INFORMATION FOR SEQ ID NO: 1540:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1540:

ACAATTTGTT TATTTCAACA AATTATCTTT ATTCCACGAT GTGCACAAGT GGTTGAAATC 60

AGCTGAAGAC ACG 73

(2) INFORMATION FOR SEQ ID NO: 1541:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1541:

TGCAGGAATT CGATATCAAG CTTATCGATA CCGTCGACCT CGAGGn 106

(2) INFORMATION FOR SEQ ID NO: 1542:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1542:

ACATCAACTC ACCCATAATA TATATTCACG GCTGACTGAT ACGACGAACG TCAAAGAATA 60

TGAGAGGAAT AGGGACAAGA TCATCAC 87

(2) INFORMATION FOR SEQ ID NO: 1543:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1543:

GCTTATTCTG AAAAATATTT AAATTGAAGA AAAGAATATT CTAACTACGG AAGTGGTATT 60

AACTAATAAC TAGTATCCTT TATAAATAAA CATAAAAATA TTCAAACGAA GGTCTACTAA 120

ATAACTATCC ATAAAGTGAG TATAAGTTTG TTTGTAAAAC TGAAGTAAAA AGCATAAGGA 180

ATTACACTTT AAATACATAT AGTACTTACG AATAGAAAAT AATCCCTTCA ACAGTAATTT 240

TTAAACAAAA ATAAGTGTTG TTTTATGTTG ACTCTACTAG AATAACTTGA TATTATATAA 300

AAGTCGTCAA ACGGCACTAA TATTTAnnAA ACAAATGTTT TAAGTTGTTG GATTTnAAAA 360

TATTGAATTA AAGTGTAAAT TTGGACTATT GGAAATTGCG 400

(2) INFORMATION FOR SEQ ID NO: 1544:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1544:

ATAACGCTAA TCAGCCACAT TCAGTATTGT TAAATGGACA CACAAGCAGT TGATGAAAAT 60

(2) INFORMATION FOR SEQ ID NO: 1545:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1545:

GGCTGTTATT GTTGTGGAGT TAAAAATGAA GGAAAATTAT AAACATGGTA AGCGTGTTTC 60

TCGTATTACT TTACTTAAAC nAACGGTATA ACCATACCTA ACTTAGTA 108

(2) INFORMATION FOR SEQ ID NO: 1546:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 554 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1546:

AAnTATGTTT CATATATTAT GAATCTAGCC TTAATCATAT TGCATTCAAA ATAATTTTAA 60

AAAATGAAAA GAAAGGATTT AGCATGCAAA AATTCAAAGA CTTTTTTTAC GATGATTTAT 120

CGGTTACACG AGGAAATTAT TTTTTAACTT TAATGGCAGC ATTTTTTATT ACTATCATTT 180

TATTTATCGG CATAGTTGTC AGTGAAGTAC ATTTACTTTA TAGCATGCTA ATTGTATTAG 240

TAGGTTTAAT TCTATTGAGG CTATTCAAAA TCAATTTATT CTCTTTTAAA AAATTAACAT 300

TGTCTCAAGT TATTTATATT ATAGGCGGTG CACTATTAAT TTATGGGTTA GATAATCTTT 360

ATTTATATTT TCATGACGTA CCGGCAATGA ACAACAATTA GAGCAAGCAA TACGGAAATA 420

CACCATTCTA TATTTCTATT TtCACTGTaC CATCATCCCC GCTATTGTGG aAGAAaTTGT 480

TTTtCGCGGT ATGATAATAA GGGkTATCTT CAGAAAACAC TTGTTTTTAG GGTTAATTGT 540

GTCTAGTTTA GTTT 554

(2) INFORMATION FOR SEQ ID NO: 1547:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TAAAGCAACA CTTTTAATCC CTTTTGAACT TAGTTTATCC GCTAAATCAT AAGCTTCTTT 60

TTTGCTACTT ACAAAAATCA ATCCTTGTAA AATTTCACCT GAATATCCAT AGTAATCTGT 120

CTTTTGAATA ATATAATTAA CTCTTTCATC AGAAGTTAAA TATCTCAGTT TAGTTACATC 180

ATCTTCTTTA ATACCTTGAT GTACATAATC AGTCACACCA AAATAATGAA ATGGGACATA 240

AAATATCACT TTCTAATGCT GCTTGTAACC TTATTTCATA TGCAATATTA TAATCAAACA 300

GTTCAAATAT ACTTAATTCA TCTGGATCTT TCTGGTGGTA GGCAGGTCAT TCCCAGCAnG 360

AACTTAGGGT TTGGAGGTAG GTTAAAATAC TCGGTTGGAT 400

(2) INFORMATION FOR SEQ ID NO: 1548:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1548:

CGCTCTAGAA CTAGTGGATC CCCCGGGCTG CAGGAATTCG GCACAGCATA TCTAGTATTT 60

TAGGACGGAG GGA 73

(2) INFORMATION FOR SEQ ID NO: 1549:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1549:

GTATCCAAGC AGCTTTTAAA CAATATGGCA TAAACATTAT TAACGGCTAT GGTTTAACTG 60

ATGGCACCTC TTG 73

(2) INFORMATION FOR SEQ ID NO: 1550:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1550:

GTAACATGTA TAGTGAAGTG ACTACTAAGA AGnCGTATTG TGATATTGAT AGCAGCTGAT 120

(2) INFORMATION FOR SEQ ID NO: 1551:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1551:

GGTATGTATT AATTAAAATG TGGTCATGAT TGAAACAGCA ATGTAAAAAT AGCACAACAT 60

AATTnATAAA GGAGAGAAAC GGCATGCATG AACAAGATTT TAGAATTTTA GAGGGTCAAG 120

ATATTACTTT GCCAGAATTA GGTAGAGAAT TAGAnAATAT TACAGGACAT ACGATTGCTG 180

ATTCTACTGG CG 192

(2) INFORMATION FOR SEQ ID NO: 1552:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1552:

CTAAGTTAGA TGCTAGTATA CAAGATTTAC AACAAAAGGT ACTGGAATCG AATTGTGAAC 60

TAGACAAACT AAACTC 76

(2) INFORMATION FOR SEQ ID NO: 1553:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1553:

TGTGTTGGGG CCCCGTATAT TGAAAATTTG TTATAGGTGT ATTTCTTTGG TTAACTATTG 60

TTATATAACT TGTAGTTTTA GGATGTTGAT TTTGCTTACC TTGTCTGCTA TGTAATGTCA 120

CATCAACATG ATTnA 135

(2) INFORMATION FOR SEQ ID NO: 1554:

(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1554:

TTTGAnATCA AATTCACTTC GCAAACGTGT CCAAGCGTGA GCAAAGGGCT AGATGATTAA 60

TAGTTGCCCC ACTAACGGGA TCGCCCCAGT TATCCAACTT ATCT 104

(2) INFORMATION FOR SEQ ID NO: 1555:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1555:

AATAAGAAAC AnGACACTAG CTCACCACGA CGCGCACGGC CTGCGTGTAA AAATGTTGGT 60

GGCGCGGGTT GGAGATCGTG TTCAACCAGA GCAGAAAATA 100

(2) INFORMATION FOR SEQ ID NO: 1556:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1556:

CAATGAAATT ATTTATTATT TTAAGTGCAT TAAACCCCGA TGATGGCTGT CCGGTACCAG 60

GTGCATTTTG GTGCCCATGG TTTACC 86

(2) INFORMATION FOR SEQ ID NO: 1557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1557:

GTCATGTTCC CATCAAAACT AATTTGTACT TACTAAAGGC TCAGCAGCGC AACAATTAGG 60

(2) INFORMATION FOR SEQ ID NO: 1558:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1558:

AACTGGTTAC AGAAATACCA CGTTCTTGTT TCAACTTTCA TCCAGTCACT TGATCGCAAA 60

TTTACCAGTC TTCTTCCCTT TA 82

(2) INFORMATION FOR SEQ ID NO: 1559:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1559:

CCACAGCGGC ACTATAGCCA GCCCCTAATA TATACAGTAT TTGCATCTGA CTCATTGGTT 60

CATAAGTATA TGCAGTGA 78

(2) INFORMATION FOR SEQ ID NO: 1560:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1560:

ACCATTTGCT AACTTTTTAG CAGCGCAATG TTCTTATTAA CTGCTTACGC CATCTATAAA 60

AATAAACGTT CAACAA 76

(2) INFORMATION FOR SEQ ID NO: 1561:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTGGAACCCA AATTTTTTTA ATTTTCCCAA AAATTGGGGG GGGACCCCCA ATTCCCTTAA 60

GGGTTTTCCT TGGGGGCCGG GGGTTAATTC CACCCGGGGT TAAAATTTTC CCAAAAATTA 120

ATTTTnGAAA AGTTTTAATT TAAGGAAACC CATTnGTCCG GAATTTTTAC CCCATCCTTA 180

TGGGGGGTCC CAAAGATTCC 200

(2) INFORMATION FOR SEQ ID NO: 1562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1562:

AACACAGAGA ATAACCAAGA GAAGACGTTT TCATCTGAAG AAAGTAACAG TAmGCCATTT 60

ATGGAAGAAA ATCAAAACGA TGAGATAGTT ATAAAAGAAG ATTCATATAA TCCATTCGTA 120

ACGAAAACAT CTGAAAGTTT AATAGCTGAT GATGAATCTT CTGGTTATAA TAATACACGT 180

GAAAAAGATG AAGACTACTT CAAAAAACAA CAAGAAATTT TACAAGAAAT GGATCAAACA 240

TTTGATTCAA ATGATGGTAC AACTGTGCAA AATTATGAGA ATAAAGCGTC TGATGATTAT 300

TATGATGTAA ACGATATTAA AGGAACAAAA AGTAAAGACC CTAAACGAGG AATTCCATAT 360

ATGGAATTGT TGGnCAGTCA TGGAACGTTA TTATTGCTCA 400

(2) INFORMATION FOR SEQ ID NO: 1563:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1563:

TCTTCATCAT CTTCTAATTT ACCAGCTGGA ATTTCTAGCA ATGGTTTTTC TACTGGTTTA 60

CGATACTGTT TCACTAATAC GACTTCTTTT TTAGGTGTCA CTGCACAAAC ArCAACTGCA 120

CCATTATGAT AAACTAATTC TCTTGTTGAC GTTTCACCGT TTGGTAATGT CACTGTATGA 180

ATTTCTACAT CTACAATTTT GCCATTATAA ATAACTGTTC GATCAATTGT TTTTTCATTT 240

AAATCCATTA TAATCACGTT CCTTTAAATT CATATTATAT ATTGATACAC TATGCTTGTT 300

AGCTAAAGTG TATCGAAAGG AGAACAGACA TGCAAAAAAA TATATTAAAA AGTGGTATTT 360

AAATTATAGG ATTGTGCTGT TGAAAATGGG TATC 454

(2) INFORMATION FOR SEQ ID NO: 1564:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1564:

ACATCTCGCA TCGTCACGAC TTGCTTGAAC CACTAGCAGG TCAAACAAAG CTGTACAGGC 60

AACATCTGC 69

(2) INFORMATION FOR SEQ ID NO: 1565:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1565:

TCCAGAACCA TTTTAAATCC CGGGAAATAT AATTACCTCC ACTAAnGTAA TATATCCAAG 60

CCAAGACTAA TCCTCCTTAA GCCGGTTTAA GTAACCAGGT TGAGAAGGAT TTTTTGG 117

(2) INFORMATION FOR SEQ ID NO: 1566:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1566:

TATTGAGATT AACAGTCTGG GAAAAATGAA CAGCAATTGT nTAATGTGAC GATGCTGATT 60

ACTTTTTAAC AGTATCATTT AATAACTCAG AGATGCGCTT TAT 103

(2) INFORMATION FOR SEQ ID NO: 1567:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1567:

AATGGATGGG ACAGCAATTA GTGCATAACG ACAATATATG CTCAATTTGT CGGCAACTGG 60

TTAAGAATCG TATTGTCACA A 81

(2) INFORMATION FOR SEQ ID NO: 1568:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1568:

AATGGATTCA GTAGGTATTG GTGAAGCGCC AGACGCAGCT GATTTGAAAG ATGAAGGTTC 60

ACATACTTTT AGCATACCTT 80

(2) INFORMATION FOR SEQ ID NO: 1569:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1569:

TTTTTAAATA CGATTTTAAG GAGGCCATTA TAATGGCGAG TAAAAGTAGC GAATTAATGG 60

TTTTGGTTAG GAATTGGTCG TTTAGGCATT CAGGA 95

(2) INFORMATION FOR SEQ ID NO: 1570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1570:

CCCAATAAAA AAAGCCTGTT GTCACAATGG TCATAGACAC GTACATACTT TAAAGGTTTC 60

TGTAATATAA ATATTTCATA TGCCACTTTA AAGTTGGnAC GTTCGTATGT TGTACTAA 118

(2) INFORMATION FOR SEQ ID NO: 1571:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1571:

GACTTGATCA ATGAAGCATT GTGTGACAAT TGGTCTGTTT GCACACCGCA CGGATTGnGC 60

GTCATTTATT TGTACTAATT CAAAAAACAT TGTTGTTTTC CTAG 104

(2) INFORMATION FOR SEQ ID NO: 1572:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1572:

CCGAACTGTA ATGGTCCTAA TGTTTTACTC ATACCATATT GCGTAACCAT TGAGCGGCGA 60

TTGTGTTGCA CGTCGAGCAT TGAGACCGTT GTACTCGTAA nGTATATCTC TGTACACG 118

(2) INFORMATION FOR SEQ ID NO: 1573:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1573:

AGGGATCAAA GGTCCATCCC CCATGCATTG GATAGTGGGG GATGACTTTT GATCCTATGT 60

TCCAGTTGCT TATT 74

(2) INFORMATION FOR SEQ ID NO: 1574:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1574:

AACCTTTTGA GTAAATTCAC CAATACTCAT CCCCTTATCA TTTAACAAAC TTTTATTAAT 60

GTTTTTGGTT ATATTATGAG TCTTTACTGC TTTTAGATTG TAAAAATTAT CGTCATAAAT 120

GTAATTAATG TAATAATAGA AAAGTGTATA TATCTCATAT CGCCACCTGC TATACAACTT 240

ATTAAATAAT TAATTCCAAG ACATATTAAT TATCTAATTA TAACCTTAGT TnACGTTATT 300

ACATAATATA AAAATATATA ATAACTTATC CnCCGGCnCC T 341

(2) INFORMATION FOR SEQ ID NO: 1575:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1575:

ACGTGTACCA ACTTTTGGGC ACCATTGATA ATAnGTGTCA TAGGGTGACT CAGCATAACG 60

GGCAAGCCTA TTAATGATAG CCAGATTAAG ACATACAGTA CATATGTTC 109

(2) INFORMATION FOR SEQ ID NO: 1576:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1576:

GCTAGATTGC GGGAATTAAC AATCATCAGC GATTTAATAT TTGCACTGGA GACGTCATGG 60

TAATAAAAAA TTGATGAGA 79

(2) INFORMATION FOR SEQ ID NO: 1577:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1577:

ATGATGGCTA TCATGAGATT GAGATGATAA TGACAACAGT TGATTTGAAA TGATCGTGTA 60

ACTTTTCAT 69

(2) INFORMATION FOR SEQ ID NO: 1578:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1578:

AAATTGTCAC TnCAGGTCAT AACCAACCAG GTGGGACTGC ACGAGCGTTA CTAATGATCC 60

AACGGTCTTG CTTTGTGATG AGGCAACAAG TGCACTTGAT CCGC 104

(2) INFORMATION FOR SEQ ID NO: 1579:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1579:

GCTCAATAGA TACAACTATT AGGACAACGG ACTATCGTTT ACAATTTATT CCAGATAAGG 60

ATCGCGCAGG TCGTATGCGT AACTATGCA 89

(2) INFORMATION FOR SEQ ID NO: 1580:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1580:

TTGTCTCTAA TAATGGnTTT GGCTTTTTCT AAAATTTCAG ATGTGGGTGC TGGTGAAGCA 60

CCGACTGGTT AATTTTCTTG TCGTCACGGC CACTTTTTGT TT 102

(2) INFORMATION FOR SEQ ID NO: 1581:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1581:

AAGGTGCTGT TATTAGGATA ATGnATTTAA ACCCCATGGT ATGAAGGATA TCTGGAAGTT 60

AGATTGGATA TCCCTTAACC ATGGGGGGTT TTATTTTTGG GG 102

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucl ic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1582:

TTCAGGGGAG CTGAACATAT TGACGACTTT TGGGTCAATT CATTTTGCAT TTTACTTTTA 60

AATGCGTTGT TGCATGTAAT TGTATTAACG ACATACATGG TGGGGCTCTA AATnAATGCT 120

TGACTAATTT CTTGGATGGA GACCACGATT TACCAACTCA 160

(2) INFORMATION FOR SEQ ID NO: 1583:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1583:

TAAAAGCAAG TACATTAGAG GTTAGATCAC AAGCTACTCA AGACTTGAGT GAATATTATA 60

ATAGACCGTT CTTTGAGTAT ACAAATCAGT CAGGATATAA AGAGGAAGGA AAAGTGACGT 120

TTACTCCTAA TTATCAACTT ATAGATGTAA CTTTAACTGG GAATGAAAAG CAAAATTTTG 180

GTGAAGATAT TTCTAATGTA GATATATTTG TTGTAAGAGA AAATTCTGAT AGATCTGGTA 240

ATACAGCTTC AATTGGTGGT ATTACTAAAA CAAAcGGTTC AAATTATATT GATAAAGTAA 300

AAGATGTAAA TTTAATAATT ACTAAAAACA TCGATAGTGT TACATCAA 348

(2) INFORMATION FOR SEQ ID NO: 1584:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1584:

AGCCAGCAGT AGATAGATAT ATTAATGAAT TCTTGGAGAA AGGTAGCTCA AATTGTCCAA 60

TTGAGATATT GAA 73

(2) INFORMATION FOR SEQ ID NO: 1585:

(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1585:

GTAAGGAATG GTCACGTATT CCACACTTCT ATATGAATTA TTATGTATAT CAATACGCAA 60

mTGGTTACAG TGCAGCTCAA AGCTTAAGTC ATCAAATTTT AnCAGAAGGT AAGCCAGCAG 120

TAGATnGATA TATTAATGAA TTCTTGAAAA AAGGTAGCTC AAATTATCCA ATTGAGATAT 180

TAAAAAATGC TGGTGTAGAT ATGACAACAC CTGAACCAAT TGAACAAGCT TGTGAAGTTT 240

TTGAACAAAA ATTGA 255

(2) INFORMATION FOR SEQ ID NO: 1586:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1586:

TTATTAGGTG AnTCCATTGG CAACATTGAT TGGTTTGTCA TTAGGACAAA TTTTATTATA 60

CATTGGCGTT ATTTTTACTA TCTTATCTGG TATTGAATAC TTTTATAAAG GTAGAGATGT 120

TTTTAAACAA AAATAAATAT TTGTTTATAC TAGATTTCAT TTTCATATGG AATCTAGTTT 180

TTTTAATCCC AATTTTAGAA ATTAGCCACG CAATTGTTTA TAATGATATA TTGTAAAACA 240

ATATTTGTTC ATTTTTTTAG GGAAAATCTG TAGTAGCATC TGATACATTG AATCTAAAAT 300

TGATGTGAAT TTTTAAATGA AATACATGAA AAAATGAATT AAACGATACA AGGGGGATAT 360

AAATGTCAAT TGCCATTATT GCTGTAGGCT CAGAACTATT 400

(2) INFORMATION FOR SEQ ID NO: 1587:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 561 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1587:

CAAAGCGTCT ATTATTGTTT GATTTTGATG AAACATATTT TAAACATAAT ACAAATGAAG 60

AAGTGATCAC TGCTGTATTG ACAGGAAGTA CATTTCAAAG TGTCATGGAT AAaATGGATC 180

AAGTTAATAT GACGTTTAAA CCATTACATA TCTTTTCTGA TTTGAGTTCT AAAATGTTCA 240

CTTGGAATAA TGGCGAATAT GTTGAATCAG AAACATATAA AAAGAAAGTC TTGAGCGAAC 300

CATTTTTATT TGAAGATATT GAAGATATAT TACGTCATAT TTCTGCGCAA TATAATGTCG 360

AATTTATTCC ACAAAGAGCA TTTGAAGGTA ATGAAACACA TTATAATTTT TATTTTCATT 420

CAACAGGTAA TCACAACAAT GATAGTCGTA TCCTAGAAGC ACTnnTCAGA TACGCAAATG 480

ACCAAAACTA TACAGCGAGA TTTAGTCGAA GCAATCCATT AGCTGGTGAT CCTGAAAATG 540

CGTATGATAT TGACTTCACA C 561

(2) INFORMATION FOR SEQ ID NO: 1588:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1588:

CCAACAGTTT TATCATTATG GCAAGTTCTG TTAAACCTGC TGAGAGTTAT TTTGCACTGA 60

TTGCAAAACC AGAAATTGG 79

(2) INFORMATION FOR SEQ ID NO: 1589:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1589:

GCAGATATGC AGCAATTTAT AGAGGACTAG TAAACGCATA TATGACTTAC AGCTTTCAGA 60

CAAATAGCTT TGC 73

(2) INFORMATION FOR SEQ ID NO: 1590:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCATTTTATG GTTGATCATA GGCGTCGTCT TTTTCCTTGG GGATTTTATC TTTAAATACA 60

CAGATTGGCG C 71

(2) INFORMATION FOR SEQ ID NO: 1591:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1591:

ATACAATACA ATTCACACCA TATATGGATA AAATGCAAGA TGCAATTACT GCAGTTGCAC 60

AGTGCAAGTA GCAATACC 78

(2) INFORMATION FOR SEQ ID NO: 1592:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1592:

CCAATTAATT AAAAACCGGA AAACCAATTT TTTAAACCAA TTAAGTTAAA AATTTTTTAA 60

AATTGGGCCC CAAACCTTGG AAAAAGGTTT AATTTTCCTT TCCCAATTTT CCCAAAATTT 120

TTAAACCCAA AAATTCCCGG TTTTGGGTTA AATTTCCCTn GGTTAAAT 168

(2) INFORMATION FOR SEQ ID NO: 1593:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1593:

TGCTAGAAAG TATAGAACCT GGTTCAAACG CATGGTTTTA TGTCCCTTTT TAAACnGATG 60

TTTATTAAAA AAATATGGAA ATTGGCCACG TCCGCCAATT TCCTTAGAAA AGAACGT 117

(2) INFORMATION FOR SEQ ID NO: 1594:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1594:

AGACGAAGCC AAAAAGTTAT TCGCCAAATC TGAAATATTT TCAAAGACCT TAAAGGCGTA 60
AAATAC 66

(2) INFORMATION FOR SEQ ID NO: 1595:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1595:

ATTTTATTTA GGCCAATAAC TGnCTACTTC TGAAATAAGT TGCTTTGCAT AGTCTGACGC 60
GGGATGTTTG GATAATATCT TCTGTGTTAT TGCATTGCAA 100

(2) INFORMATION FOR SEQ ID NO: 1596:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1596:

GACCAGACGG CCGTAAACCT GGATGAAACC GTCCATTAGA TTCTGAAGTT GGTATTTTAC 60
CTAGAACGCA TGG 73

(2) INFORMATION FOR SEQ ID NO: 1597:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1597:

CTTTATAAAA TTGTCTTTGA CTAACAGGAT TTTCAACGCT ATTCACAAAC CATGGTTTAA 60
CATATT 66

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1598:

TATGGCACCC TCTTTGATnT TGTGACCGTT TTTGGTAATT CACCATTATT GTACGAACCA 60

TGGAATTCGC TGCCTTCCTT TAGGCAATAA CATAATTATA TTTATCCCCT TCTTGTCACT 120

AGAGGTGCTG ACAACACCA 139

(2) INFORMATION FOR SEQ ID NO: 1599:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1599:

CTCCTCTGCA TGCACATCTT GTTGTAGCAA GGTTCACATG TAATTTATTA AATCGAAACT 60

CTATCCAACT ATGTTATAAA GTTCATTCTA AACAAATnAG T 101

(2) INFORMATION FOR SEQ ID NO: 1600:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1600:

TTGTACCAAG GTTCACATGT AATTTATTAA AGCGAAACGC GTATCCAACT ATGTTATAAA 60

GTTCATTCGT AAACAAATAA GTATAAAAAT TCAATATTTT TATTACTAGA ATATGGTTAA 120

ATACATTTAT TTCTTATAAn AATTTGATGT TTAAGATATT TTGCCAAATT GA 172

(2) INFORMATION FOR SEQ ID NO: 1601:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1601:

TTGGCACTGG CCGTCGTTTT ACAACGTCGT GCACTGGGAA AACCAAAnCA CGACGTTGTA 60

AAACGACGGC CAGTGCCAAG CTTGCATGCC TGCAGGTCGA CTCTAAGAAG GA 112

(2) INFORMATION FOR SEQ ID NO: 1602:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 679 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1602:

TGCAATGGTT AATCATCTCA TATAACAACA CATAATTTGT ATCCTTAGGA GGAAAACAAC 60

ATGACAAAAC ATTATTTAAA CAGTAAGTAT CAATCAGAAC AACGTTCATC AGCTATGAAA 120

AAGATTACAA TGGGTACAGC ATCTATCATT TTAGGTTCCC TTGnATACAT AGGCGCAGAC 180

AGCCAACAAG TCAATGCGGC AACAGAAGCT ACGAACGCAA CTAATAATCA AAGCACACAA 240

GTTTCTCAAG CAACATCACA ACCAATTAAT TTCCAAGTGC AAAAAGATGG gCTCTTCAGA 300

GAAGTCACAC ATGGATGACT ATATGCAACA CCCTGGTAAA GTAaTTAAAC mAAATAATAA 360

ATATTATTTC CAAACCGTGT TAAACAATGC ATCATTCTGG AAAGAATACA AATTTTACAA 420

TGCAAACAAT CAAGAATTAG CAACAACTGT TGTTAACGAT AATAAAAAAG CGGATACTAG 480

AACAATCAAT GTTGCAGTTG AACCTGGATA TAAGAGCTTA ACTACTAAAG TACATATTGT 540

CGTGCCACAA ATTAATTACA ATCATAGATA TACTACGCAT TTGGAATTTG AAAAAGCAAT 600

TCCTACATTA GCTGACGCAG CAAAACCAAA CAATGTTAAA CCGGTTCAAC CAAAACCAGC 660

TCAACCTAAA ACACCTACT 679

(2) INFORMATION FOR SEQ ID NO: 1603:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1603:

CATTTTAATT GATATAATTT AGACTTTAAC ATTTCATGCT GTTCACGGTT TTAATTTGAG 60

ACGTCATTTG GTATAACAAC TATAC 85

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1604:

ACTGGTGTGA ATAGCTCCAG CAATTTCTTT AACCGCGATC ATAATCAACG TCACCTTTTA 60

ATTTGCCA 68

(2) INFORMATION FOR SEQ ID NO: 1605:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1605:

TGGGGGGTnT TTTTGGGTTG GGTTAAAAAA AGGGAATTGG CCCAAGGGGG GAATTCCCTT 60

AAAAAAACCC CCAACCCCCT TGGGAAATTA AAAATTGGGT TAACCGGGA 109

(2) INFORMATION FOR SEQ ID NO: 1606:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1606:

GCTTATATAC ATGTTCCATT ATAAAAGGAG TACGAACGAA AGTAACGCAT GACGTTAATT 60

TAAAAATATT GTAATAATTA TGGATTAAAT TTAAAACCAn GGGGTATTCC AT 112

(2) INFORMATION FOR SEQ ID NO: 1607:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1607:

GTTCAAGTTG GTAACCTAAC AACACGnAAT TAGTTTAAAC GTTTGG 106

(2) INFORMATION FOR SEQ ID NO: 1608:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1608:

CACACTGATA CCATAGGATT TATGATAGAT CAACAGCATG ACCAAATGTA TGACCTAAAT 60

TTAAAAATTT ACGTACACCT TGT 83

(2) INFORMATION FOR SEQ ID NO: 1609:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1609:

AAAAGAATAA AGTCACTGAA CAATGGTCTT TCACAATGAT GTTGCGTCAA TGCACAAGCG 60

CATTATGTnT GTGACTTGGG CATTTTGGCT TATCAGCTGA ATATTATACG CATTTACATC 120

CCAATTAACG TA 132

(2) INFORMATION FOR SEQ ID NO: 1610:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1610:

TTTAATGCAT ACGCTTCTCG CTTAGCAATT TCTTTGCACG TCTAACAAGC ATTAACGCTC 60

TTAnTACTAT AATCACAACA AAACCAGCGA AATATAACAT GCGTATA 107

(2) INFORMATION FOR SEQ ID NO: 1611:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1611:

TTCGCACCTG GTATCGTTCA AACCACCAAT GATGGCCCGT CTCGCCGTGG CAACAGCCGA 60

AGACCGCAGG TAAACCCTGA ACGC 84

(2) INFORMATION FOR SEQ ID NO: 1612:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1612:

ACTCACATGT ACGATAACAC CCTTCGTAAA TCCATCTTTG GTTTGCCAAG TTCGTCGTTG 60

TAAACTGTCT ATACTCGTTA AACCGCTACA TGTTTTCCTA AAnCCTGTGC CTAAATGCTT 120

TACTGAA 127

(2) INFORMATION FOR SEQ ID NO: 1613:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: ~~129~~ base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1613:

CGTTCAACTT TTTCAATTTC TAACGGCGTT TTACTATCTT TATCTGTAAC TAATTCAACT 60

CCAAACATTA AGCCTCGTCC TCTTACATCA CCAACATTTC GATGACGCTT CAGCGCATGT 120

AACTGTTTC 129

(2) INFORMATION FOR SEQ ID NO: 1614:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1614:

nCAACTAGTG GATTTAAnAT AnACATAATT ATAAATGCAA ATGCTAATAG CTGAATACCC 60

GCACTAGGTG CATAATTTGT GTATTGAGCA AATAAAGCTA ATACAATGAT TGTAATTCCT 180

TTAATGACAA ATAAAGGTAA ATTTAATCGT TTTAAAGGTT GGTAAATTAA AAATACAATT 240

GCAGCTATAT GCGAGCCACT AACTGCCAGC AAATGATATA TACCTATCTC TTTAACACGT 300

TCCTTAAATT GCTCATTAAC TTCTTTTACG TCACCAGTAA TCAATGCC 348

(2) INFORMATION FOR SEQ ID NO: 1615:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1615:

GAGCTCCACC GCGGTGTCGC CCGCTCTAGA ACTACTGGAT CCCCCGGGCT GCAGGAATTC 60

GGCACAGCAT AT 72

(2) INFORMATION FOR SEQ ID NO: 1616:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1616:

CATCACGTTA AATCATAACG CGTGACGTGC TTTTGCTATT TGTCTCTCGG TATCTCTATA 60

TCT 63

(2) INFORMATION FOR SEQ ID NO: 1617:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1617:

ATTGAATTCA AGGGTGGAAC TCATGAATTG GCTGGAAAAA GGTAGATTTA ACTGGATGGT 60

TGnAGCCATA TATCGGTGCG TTTATTTATT TGGTATTTTA AAAATCAACC TCG 113

(2) INFORMATION FOR SEQ ID NO: 1618:

(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1618:

GTACAATAAA GTGGTAAACA ACATGCCAAT GGAAAAAGGG ATTAAAGGTG TTTATGTCAT 60

TCTTAAAGAT AGTAACGGTA 80

(2) INFORMATION FOR SEQ ID NO: 1619:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1619:

ATCTTATGTT TTTTTCCTAA AACTTCTGCT ACTTCATTTA TTTGATGTAT GGTAGATAAT 60

TCTGTTTGGA TACTCATATC AACTTTTTCT ATCATATCTG AAATCTCTTT TnTGGCA 117

(2) INFORMATION FOR SEQ ID NO: 1620:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1620:

CGATAAACCC TTCGTAATCA ATCTTTGGTT TGCCAAGTTC GTCGTTGTAA CAGTCTATAT 60

CGTTAAAAGC TACATGnTTT CCTAAGCCTG TGCCTAATGC TTTACTG 107

(2) INFORMATION FOR SEQ ID NO: 1621:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1621:

AATATCGTGT CTCTGTCCAG TGCTGTCCAA TCAATTTTGA TCCACCGATT GTCATACGTA 60

(2) INFORMATION FOR SEQ ID NO: 1622:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1622:

ACCATCTGAC ATCATCAATT ATGAATTAAT GATGATATTA AAAATAAATT TGAAACATTG 60

CCAATTGATA GTGCC 75

(2) INFORMATION FOR SEQ ID NO: 1623:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1623:

TACCTGTGTA TCAGCTCTAT TAACAACCTA ACATATGTGA ATAATTTGCG ATCCTTGTTG 60

ATAATGCTGT AATTTGAC 78

(2) INFORMATION FOR SEQ ID NO: 1624:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1624:

GCAAGCTTTT GCGGCTTCTG ATGCACCATT AACTTCTGTA ATTAAACACA CAAAGTGAAA 60

CAGGTAGGTA ATGCAAAACT GCAACGGACA ATCGA 95

(2) INFORMATION FOR SEQ ID NO: 1625:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATTGCGATTA CACAGTAGTG AATGAGATAT TTGACATGAA AGCTCCTGCA GCTTCTAAAG 60

AAGAGTTAGC AGGTTT 76

(2) INFORMATION FOR SEQ ID NO: 1626:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1626:

AAAAGCTAAA AAAGATTATC AGGTGTATCA CAAACTCAAA TTCTCATTAC CATTTATCTC 60

AGTGTGAACG TCTTAATTGA GAACTAATCT nAATTGAGAT ATTAGTCATA TAAGGATGGA 120

CAAGCA 126

(2) INFORMATION FOR SEQ ID NO: 1627:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1627:

TGATACGATA GAACATAGTT CAGCACATTG TTTGTTGAAA TTGGATATTA CCGCCATTTT 60

TTCACAATAT CAATAATACC TGAACGTGTT GGTTnTTCCA CATTATGATT GTACAT 116

(2) INFORMATION FOR SEQ ID NO: 1628:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1628:

ATTTTGTCCT ATCTTGAACA AATCCGATTT TTCTCAGACA CTGAATCCAA AGTATTCATG 60

TACCATAAAC CATCTGCATG TTGATTTATG C 91

(2) INFORMATION FOR SEQ ID NO: 1629:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1629:

ACAGAAAGTC AAACAGTAAA AGCGGCAGAA TCAACTCAAG GTCAACACAA TTATAAATCG 60

TTAAAATACT ACTATAGCAA GCCAAGTATA GAGTTAAAAA ATCTTGATGG TTTGTATAGA 120

CAGAAAGTGA CAGATAAAGG AGTATATGTT TGGAAGGATC GAAAAGATTA TTTTGTTGGC 180

TTGCTTGGTA AAGATATTGA AAAATACCCT CAAGGTGAGC ATGATAAGCA AGATGCATTT 240

TTAGTCATCG AGGAGGAAAC TGTTAATGGA AGACAATATT CAATTGGTGG TTTAAGTAAG 300

ACAAATAGTA AAGAATTTAG TAAAGAAGTC GATGTTAAAG TAACAAGAAA AATTGATGAA 360

TCATCGGAAA AGTCTAAAGA TAGTAAATTT AAAATTACTA 400

(2) INFORMATION FOR SEQ ID NO: 1630:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1630:

GCTTTCCTTT TCGAAATCTA TAAATCTAAT CCATTGAAGT AAACTAATTA TGATAATTAT 60

TAATTCTATA ATTGTnGTTA TCTTTAAATA ATTTGGAAAC CTTTCATAAT CTAAACCAAA 120

AAAGAAAGTT AGACATGAAA AAAGTATCAT AAATAATGAT GCTAAACTTA AGGCTTGTGC 180

ACCTGGCTTT CGAAGAATGT CTATATTTTC CTTAGTAGTC ATATTTACCT ATCTCCTATA 240

CATTGATTTT GTAATAGCAT ATTAAGTATT TAAAGTTATA AGTACTTAGA TTCTTTTCGA 300

TTAAAAGTAT AAAAGCCTAA AATTATCTTT ATATTATTAT TTGATGACAA CTTTATGGTC 360

TCTATTGTTT TTTACTTAAA CGCTAAAAAG CTAnACAAAG 400

(2) INFORMATION FOR SEQ ID NO: 1631:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1631:

TCTAGAGCGA 70

(2) INFORMATION FOR SEQ ID NO: 1632:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1632:

CAACGAAGAT ATTCAAGTGT TCAGTCATTA TTTTTGACTG CTAATGAAAC TGATTCTTGT 60

GG 62

(2) INFORMATION FOR SEQ ID NO: 1633:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1633:

CTAATGATTA GATTCAAACT AATAAAGACT ACAAAAACAA GTTGATAATG GTAAAGATAT 60

TATCCAACTT GACATCTAAA G 81

(2) INFORMATION FOR SEQ ID NO: 1634:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1634:

AATTTCACCT TTGTCTAGTA ATTTATTTGT GTAGTGTAAT CATTAATTGT TTTAATATCT 60

AGT 63

(2) INFORMATION FOR SEQ ID NO: 1635:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1635:

ACCAACTAGC TAAATGCCAG CGCGGnATCC ATCTCAnAAG TGCACAGCAA GACCGTCTTT 60

CCAACTTTTG AACCATGCGG TTCAAAATAT TATCCGGTAT TnAGCTACGG TTTCCCGAAG 120

TTATCCCAGT CTTATAGGTA GGTTATCCCC AGTGTTACTC ACCCGTCCGC CGCTAACATC 180

cAGAGAAGCA AGCTTCTCGT CCGTTCGCTC GACTTGCATG TATTaGGCAc GCCGCCAGCG 240

TTCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 300

TACTAAATAA TGTTTGTAAC TAATAGTTAC GTTTTTGGAA TTAACGTTGA CATATTGTCA 360

TTCAGTTTTC AATGTTCATT AATGTTCAAT CTCTTTTATT CTACTTCATT TATTTCTTGA 420

AGTCAATAAC TTTTTGAACG ATTACTTTAT TTATTCTATA TTGTTTTTAT AGTTATTTCA 480

ATGGtAAGTn TTACACTTTT GaaATTCTTC TTTAAAAACA ACTGCGTCGt TTTTGaCGcT 540

TTATCaTATT ATCmACTTTG GGaATTTAAA GTCAATAAC 579

(2) INFORMATION FOR SEQ ID NO: 1636:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1636:

TCGACATTAA GCAACGTTCT TCGCAAAAGG TAGCGAGCGA CACGAGTTAA CTTTGCACGT 60

TTCATTATT 69

(2) INFORMATION FOR SEQ ID NO: 1637:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1637:

CTGTGACTTC GTCGCGATGA CCTTCGCCGT TGTTCTCATG GTAAGCTTTA AGTATCGTCG 60

ATGCAGTCnG TTCGCCATGT GCGCCAGCAG ACTGGTTGTA ATGTCGCCTC GTCCGT 116

(2) INFORMATION FOR SEQ ID NO: 1638:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1638:

ACAACATTTA GGTACTTTCA CGCATATCAC TACAGCTCAA CGTGATGATT TACCAAATCA 60

AATTTCACAA G 71

(2) INFORMATION FOR SEQ ID NO: 1639:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1639:

GCGTGGCTTT GTGATTAACA TTGACAAGCA CGTGCAACAA CATATTCGAC GCGATAAAGC 60

GACATCTAAT ATT 73

(2) INFORMATION FOR SEQ ID NO: 1640:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1640:

CGCGATCATT TTCATTTCTA ATTAATCTTC CAAGTCCTTG TCTAAAACGT GTAACTGCAT 60

CAGGTAATAC ATATTCCTTG AAAGTTGAAG TGAATTCAGA ATCCATAAGC CAATATTTTG 120

CATTATGCTT GTTCATAAAC GGTAACTTCG CTATCATCAC ACATTTAATA CCATTTGCTT 180

GAAAATCAAA ACCTTCAAAA AATGTTGACG TACCAAGCAG TATGGCCTTA TCAAAATTAT 240

TAAACTGTTG TACTATTTTA TAATTTTGGT TCTGCTGTTG TGTTAATACA ACATAATCTT 300

CAAATTCTGG CAATTCATTT AAGCATATCT TGTACCATAT GCATCATTTT ATAACTCGTA 360

AATAAGACTA AACATTTTGA TGACGTTATA GTCGTATATn 400

(2) INFORMATION FOR SEQ ID NO: 1641:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1641:

ATTGTTGTAC CATGTATACT AACAATTGTA ATGTCTCATT TCAGTAAACA AAAAGCGAAA 60

GACATT 66

(2) INFORMATION FOR SEQ ID NO: 1642:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1642:

ATTTCGTCGG GAATAAATTT TGCCATTACA TAGAAATATC TAATAGATAA CGAAAAAGTA 60

TCGTATGTAT TTTTAATATA GTGTAAAATA TTATATGTAA AATAAAATGT AGGTTTTTAG 120

TTAGAGGCAT TATAAGAnAA TTTTGAGTAT AGGTTAGCTT TTAATTATGA ATCTTATTGA 180

AATTTGATTA ATAAAAATAT GATAGGGGAT TAAAATGAAA CTATTTTATA TCGTATTTCT 240

TATTATTATA TGGCTGAATA TATTTTTAGG AAATGAAATC ATCCATACAC TGACTGTTTT 300

AATAACAACA TTGTATATTG TTAATTCACG AnAGGGGATT AAAAATGACA GAGTTGAATA 360

ATATTATAAA CGCGCnTGCA ATCnTTGTTT GAGTCCGGAA 400

(2) INFORMATION FOR SEQ ID NO: 1643:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1643:

AACTAGAGGA GGACATCCTA ATGGAAGCAA AACCCGTTGC TAGAACAATA AGAATCGCAC 60

CTCGTA 66

(2) INFORMATION FOR SEQ ID NO: 1644:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1644:

TATCAATTTC ATATGCGATT TGGCCTTGCA ATAATTAGGT CTCACCTTGC CATATCTTTA 60

CCTAAGCAAT ACTTG 75

(2) INFORMATION FOR SEQ ID NO: 1645:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1645:

CATTCTCCTG CATCATAAAA ATCAACAATT GTATCATCAA AGTGTATCAA AATATTTTAA 60

TATCCCAATT 70

(2) INFORMATION FOR SEQ ID NO: 1646:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1646:

AGTGACACTT TCGTTCCACC ACATCGTAAA GAAGTACTTC AAGCACGTGA AGATGACATC 60

AAAGAAAAAG TTG 73

(2) INFORMATION FOR SEQ ID NO: 1647:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1647:

CTGTGATTGG TGTTGTGATT GTCTTGCTTC CTGGTTGTCC TTCTTGTTTC GCTCGCTCTT 60

CGCCGGGTTG T 71

(2) INFORMATION FOR SEQ ID NO: 1648:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1648:

AACTATAGAA AAATTCGGAA TTATACCAGA AATGGAATAT GAAATGGAAG AGGTTAAACA 60

AAnCGAGCAA TATATTAGAG AGCAAGAAGA AGCTGGAACA ATAGAGGCGA TAACA 115

(2) INFORMATION FOR SEQ ID NO: 1649:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1649:

TGTTGTCATG ATCTGAAAAG TCAAAGTCAA TAGAACATTG GCTTTGGCTT TTTATTTGG 59

(2) INFORMATION FOR SEQ ID NO: 1650:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1650:

ACCGATAATA GTACACGGCA TAATGnAACA ACTTGGCATG CACCCTTTTT ACGTTCCTTT 60

ATCTCTGCAT GATTGTCATG TTCATCATGG TTTGGCTTGC ATTAATAGAG AGGGTTGACG 120

CAGAA 125

(2) INFORMATION FOR SEQ ID NO: 1651:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1651:

TGATTAACGC GAATGCCACT TTTACTACCA ATGTTCCCAA AGCTGCTTCT GACAAACGCC 60

ATTGTACTCT G 71

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1652:

TCACTACATG CACCATAAAT ACAGTATGAA CGTATTGAAA TGGGCATTAC ATGATACAGA 60

(2) INFORMATION FOR SEQ ID NO: 1653:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1653:

TTAATTGAAA CAATTGACAA ATGCAATTTG ACGCCAAACT TTGAACTTTG AATGGATTAT 60

CACATTATGA TTGTTCATCC ATGGnCAATT AGCATGGACG TATTACATTC TGGATTATCA 120

AGC 123

(2) INFORMATION FOR SEQ ID NO: 1654:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1654:

CTATGACGTC GCATGCACGC GTAACTTGGG CCCCTCGAGG GATCCTCTAG AGCGGCCGCC 60

CTTTTTTTTT TTTTTT 76

(2) INFORMATION FOR SEQ ID NO: 1655:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1655:

TTTTAAATTT TCGTGAAATC GGAAATGTAC GATTAGTTAT TAAGCGTTAG AATGTGTGAT 120

ATGTGAACCT GGTATTGACG GCGCT 145

(2) INFORMATION FOR SEQ ID NO: 1656:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1656:

TTTAGAATTC CAATACGCTA TTGCCAGCGA TTTAGCCACT TGTGGGTAAT GATATTGAAG 60

GTGTTAGTCA AGT 73

(2) INFORMATION FOR SEQ ID NO: 1657:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1657:

CTTCTGAAAA GTAGTAATGT AACCTATTGG ATGCGAATGA ATCCCCAAAT TTAGTGGACG 60

TATGTGGCTT CATCTTCAGA ACCTGTATCT GGT 93

(2) INFORMATION FOR SEQ ID NO: 1658:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1658:

AAGTTAACAT GCAAGTTGAC GATGTAATGA CTCAAAAAGA GTGGAAACAA AAACACGA 58

(2) INFORMATION FOR SEQ ID NO: 1659:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1659:

TTAATCCCAC AAACAAATGT ATGAAATTGA GTCAGTGATA TTAAATATGG GCTTGAAAGT 60

GTCTA 65

(2) INFORMATION FOR SEQ ID NO: 1660:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1660:

TGCATTTTTG TAAGAACGCA AAGCATTGTA AATTAGTTTT TATAAATTAG GATATTATCA 60

TGTGTATTGA AAACAATGAA GTGTGCTATG A 91

(2) INFORMATION FOR SEQ ID NO: 1661:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1661:

ACATATCTGT CCACACAACA AGGACCATTT GTCTGAAGGG ACAGTGAGTG GGGAATATGT 60

(2) INFORMATION FOR SEQ ID NO: 1662:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1662:

TGGGGTTTTA ACCAGGGGAC CTAAAACCAG CCCCCATTTT CCAAGTTTGG ACCCCAAATT 60

CCCnAAATTT AAAAAAAATT TGTTTGGGGT CTAACTTGGG CCGGTGCCTT CCTGCCTAAA 120

TTTAGCCCAT GTCTAACATA GTACTTTGGG AACGTAAAAG TTTAATTTA 169

(2) INFORMATION FOR SEQ ID NO: 1663:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 677 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1663:

TGGCACAATT GCACCAATTA AATGAATAAC TTTATCATTT TTATATACAG GTACAACAAT 60

CGCTTCTTTT ACGAACTCAG ACTGGCGTAA TTGTGTTTCA ATTTCTTCTA ATTCCATTCT 120

GTAGCCATTC AATTTGATTT GGAAATCAAT ACGACCTTGA ATGAACCATT GACCATTTTC 180

AAACTTCGCT TTATCACCAG TGTGATATGT ACGAATACCG TCATCGAAAT TAAATACTTC 240

AGCTGTTTTT TGGTCATTTT TTAAGTATCC TAAACTTACA CTTTGACCTT CGATAACAAG 300

TTCACCTTCA TCTGTAGTAG ATAATCTTGC GCCTGGTCTT TCAACGCCAA CAGGTAATGT 360

CGGATATTGA TCTAAGATTT CTTGTGTAAT TTGAATACTT GTAACTGCTA CCGTAGCTTC 420

AGTTGGACCA TATGTGTTGT AAATCGTCGC ACTTGGGAAA CGGTTTACTA ACGCTTTTGC 480

TGCTCTGTGA GGTAGAATTT CACCACAGAA GAAGAATTCG TTAAGACTAC CATATTGTTC 540

TTCATTAAGC GTTGGTAATA ATAAACACAT TTCCATAAAT GATGGTGTTG ATACCCAAAT 600

GTTAATCGGT GTTGCTGTTA GCATTTCATT TAATAATTTA GGTTTATTAA TCATGTTTTT 660

ATCTACAAGA nTnAAnG 677

(2) INFORMATION FOR SEQ ID NO: 1664:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1664:

GTTACAACAA TAGTGGTATA AAACGGGAGC AATTAGAGAT CAATATATGA TTATTAAGAG 60

CA 62

(2) INFORMATION FOR SEQ ID NO: 1665:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1665:

GTTTACGCAA ATGATAGCTC GGTAAAACAT GAGCAACATG TTGAAGCCAA TTTGGAAATG 120

TGTTTATCGG AAACCACAAT CCACCTAATA CTGCTAAACC AATTGTTACG ATATTAGCTA 180

AAGCACTTGT TTTTTGAATA TCATTTAACA AAGAACCATA ATATGCCAAA AGTTATTAAT 240

AGAGACGCAC CTAACCATAA AAATATTCCT GACTCTAACC ATTGAACTGC ACTCATTGCA 300

ACACCTTTAT AAAAATGTCC AACCATAAAA ATAACTAATA TC 342

(2) INFORMATION FOR SEQ ID NO: 1666:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1666:

GTCCAAGAAT TCAAAAACGT TTTCAACTTC GGCCAAAGCC CAATTTnTCT TTGTGGTTTA 60

ACTTTTTAAT TTTGAACGTT TTAGGGCATA AAAAAAAAAA GG 102

(2) INFORMATION FOR SEQ ID NO: 1667:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1667:

TTGATAGTAG CCATAATCAT ACCACTTAAA TAATATGTTT GATCATCGGC ATAATTTTTA 60

TTTATTGTCt GTTCGCAATA TTTTGAGCAT TATCATAATT ACCACTAGTC ATATCATCTT 120

TG 122

(2) INFORMATION FOR SEQ ID NO: 1668:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1668:

AGAGATGAAA TTAAAATCGC AATTGAAAAT TTCAAATCAC GATGAGAGTG GGACAGA 57

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1669:

AACTACTGCC AATATTAATA GCATTGGTAC ATCTTAGAGG CATTGAATTC CTTACTCAGA 60

CTCATAATGC 70

(2) INFORMATION FOR SEQ ID NO: 1670:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1670:

TTGTCTGATA TAATCCATTT CGATTGGACT CCACACGTTA CACCGATACC TTCTTTACCA 60

GCCCGACCCG TAC 73

(2) INFORMATION FOR SEQ ID NO: 1671:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1671:

GAAGAATTGT ACTGTTAAAG TGACTCTAAA CTATCGCGGA AATAACAGTG AAATCACCAA 60

TTAGACTAGC GACACTGAAG TCATTAAAAA CAGACATTTG TAGTGGTGCn CTTATCACCG 120

CAAATACAAG AGAGTTTCTC 140

(2) INFORMATION FOR SEQ ID NO: 1672:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AACAACGTTT ACTATTGGCA CAGAACGGTT GGTACTTAGT CTAATACCAT TGTCATCAA 59

(2) INFORMATION FOR SEQ ID NO: 1673:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1673:

ATCTCTTTGA CTTGAAGGAT TGGATTTAAA TCTTGGTGAT TTGGGCCGTG AAATATTTCC 60

AGAAAATTCC TCAGACGTAT TAGTATAATT GTAACGnTAC ATTCTAATAT ACCTTTCTTC 120

GATG 124

(2) INFORMATION FOR SEQ ID NO: 1674:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1674:

CACCACCACC ACACACACAC ACACAAACAC ACAACCCCCC CACACACAAA CCACACCACC 60

AACACACCAA CACAnCACAA AAACCCACCA CACACACCAC ACACCAACC 109

(2) INFORMATION FOR SEQ ID NO: 1675:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1675:

TnGTCAACTG ATTTATGAAA TGGCAGAGCA TATGGCGTCA AAGGTTCTTA ATCGTTAAGC 60

CAGACCACTG GAGGACCATT AGATGCAGCG TTGCTTTCAA G 101

(2) INFORMATION FOR SEQ ID NO: 1676:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1676:

TTTTTAAAAT TTGnAAATTT TAGACCTTAT TTCACGTGCG ATTTAATCGA TGTGTTAATA 60

AAACAATACT GGCATTCAAC ATGTAATCCG ATAATAAAAT AAGGTTGCAA TTATGTTATT 120

GCATATTTTG TTTATTACTT AGAATAATAC GATGGTTAAG ATGAAATATA TGACAAAGAT 180

AAATAATGAC ATTAAATTCA AGATGTTTAC GCCTTTTAGA TCTTTTTTAA GCATTTTAAA 240

TCCTGTCACT TCkACATTAC CGACTAAGAG TAATAAGACG ATAAATACCC ACCAATTsTC 300

TTTTGGAAAA CTCATCGTCG TTAATGCTAA GACGAATAAT AACAACACAC CCATAATAAT 360

TCTCAAAATG CGAGTAAATA CAACTTCCAT TTTAAAAATA 400

(2) INFORMATION FOR SEQ ID NO: 1677:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1677:

TCTTACTCAT GCATATGAGT GCAAGGGCCT GAGCATTCAT CAGCAAGATT AGAGCGATTT 60

TTAC 64

(2) INFORMATION FOR SEQ ID NO: 1678:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678:

ACAGCTGATT TATTAAATGA TACTAAGTCC AAAGGCATGC GCATTATATC AGTTGGTACA 60

TTTCA 65

(2) INFORMATION FOR SEQ ID NO: 1679:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1679:

AGCGCCACCA ACTGACGAAT TAGGTGGTAG TTGGACACTA TGGAAAAATT TAGCGCGACA 60

AAGTCCTGAA TTTGGTAATC CTGATAAGTT TTGCCAAAAT ATTCCTAnAA AAAGTTGGTT 120

TGTTTCAGCA ACTTCTACAA CAAACAATAA AGAGATTATC GATACAATAG AAAGTATTTG 180

TAAACGTGAC CCACTTGGCA GGCAAAACAG TTACAGGCGG TATTATTACA ATCAATGATT 240

CTGcATGGCA AATGAGTTTT ACAATCAATC GTGCAGCAAC AGTTTGAAAG ACCAACCTGG 300

AAAATGGAAA TATCTACATG GGGTTTGATG CCTTATGATT CnGGnGTAAA CGGCGGTTGA 360

TG 362

(2) INFORMATION FOR SEQ ID NO: 1680:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1680:

AGATACTTCA GATTTAGCAT CATGAAGCAA CTTTAAAAGC AATCGCTGAC GCTGGTATTC 60

AGCCCGAGG 69

(2) INFORMATION FOR SEQ ID NO: 1681:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1681:

TAACCATTTC TTTTGACGTT TTATGTTGTT TTAAGAAATA AATACCAGTT AATGTA 56

(2) INFORMATION FOR SEQ ID NO: 1682:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1682:

(2) INFORMATION FOR SEQ ID NO: 1683:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1683:

CCCCAACACA ACAAACAACA CACCCACCAC CCAACCCCAC CACACCCACC CACCACCCCA 60

ACCCACCACA ACACCACnCA CCAACACACA CCACACAACA ACCCCACAC 109

(2) INFORMATION FOR SEQ ID NO: 1684:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1684:

ATTATGTTCG CGATAATTTA AGTAAAAGAA GCACAGATAT TGAATTTGAT AGGAGTAATT 60

GT 62

(2) INFORMATION FOR SEQ ID NO: 1685:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1685:

CATAAGGTAC TTAAATTAAG GCATATCTGC TGTCTAGCAG TCGCATAAAT CATTAGA 57

(2) INFORMATION FOR SEQ ID NO: 1686:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1686:

(2) INFORMATION FOR SEQ ID NO: 1687:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1687:

CTTTATAGTA TATTGCTTTT TGTTTTTCTT TTTCGTCATA TTTCACTTTT AAATAGATAC 60

CTGCAACACT AATTAATATG ATTAACATAA TACTAGTTAA TATTAAnATT 110

(2) INFORMATION FOR SEQ ID NO: 1688:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1688:

AATTACTAGT CTGCTTGTCC AAAGATTATT TATATTCTAG CTCAACATTA ATTTCTTTGA 60

TTTTGGTACC ATCTATCGTG TCACCCATGC GATGCGGTTG TAGTTTTTTT GTAAGTTCGA 120

AAGTATAAAA CTTATCATCT TCCATTTTAA CTACAATTTT ACCTTTTCTA TTATTAACAG 180

CACCATATAA TTTTTCTTCT TCCATCAATT TTTT 214

(2) INFORMATION FOR SEQ ID NO: 1689:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1689:

GCTAGTTGTA ACGTGCTTTT TCACCACCAG ATAAATCATA ATATCTTTTA ACATCTCTG 59

(2) INFORMATION FOR SEQ ID NO: 1690:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1690:

CCAAACTTTA TAATATGAAA TGCTTGGTAA TTACAAAGAT AAAATCATAC TCACG 55

(2) INFORMATION FOR SEQ ID NO: 1691:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1691:

TAGACAGCAA TCCATTGCTA TAGGGGTGGA TATCTCATTT GCGTTTGGAG CTGTGCTTGT 60

TATG 64

(2) INFORMATION FOR SEQ ID NO: 1692:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1692:

TGCATGGGAT TGCAGCTAAG AGAATCATAA AAATATATTA CTTTAATAAG TGTAGTA 57

(2) INFORMATION FOR SEQ ID NO: 1693:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1693:

CGATGTGTAC GTCTCACCTG ATTTCGCACG GTAAGCTAGT GCATATTCAG CACCGCTACT 60

CGCCCAGCCT AGAC 74

(2) INFORMATION FOR SEQ ID NO: 1694:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1694:

AACTTTTCAG ATGTTGATAG CTATAGATTT AGGCGCTATT CACCAnGTCT ACATGCAATA 60

CGTACGTTAT AATGCACTGC AACGAATCGC GCGTTATGAG TTGGTAATTG TTGTTCAATA 120

TTGGGTGTAT AGTTTTCAAC GTGGTTACAA GCAACTACCT AA 162

(2) INFORMATION FOR SEQ ID NO: 1695:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1695:

AATTATCTCT ACACCTTTTC TTTCACATAA TTGACGCAAT ATAATCCCTA TATCT 55

(2) INFORMATION FOR SEQ ID NO: 1696:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1696:

ATGCAACGTT GGCATTGGGA AATGGTCCTG CCTAAATTAA CACGCAATAA AATGTG 56

(2) INFORMATION FOR SEQ ID NO: 1697:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1697:

ACTGTGTAGA AGATGCTATT ATTGTAAAAC ATAGTTTTAA TTTTATTTTC TGATATA 57

(2) INFORMATION FOR SEQ ID NO: 1698:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1698:

AAAATTTTCC CCCGGGAACC CGGTTTTTTA AACCCCCCGT TTTAAAAAAA TTTTGGGGGG 60

CCCAAAATTT CCCAAAAAAA nAAAAAATTT TTTTTTTCCC GGGGAAAAA 109

(2) INFORMATION FOR SEQ ID NO: 1699:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1699:

GTGTTAACGT GGATTATATC AAnGAGGCGG TCAGGTACAG TCCACACGCA CAGCGCACAG 60

AAGTATCACA TCCAGTAAAC AAGGCTAGTA CAGCATTGCA 100

(2) INFORMATION FOR SEQ ID NO: 1700:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1700:

AAGGTTAAAT GAATTAGGTT GATCAATGCT CTATACTCAT TGCTAAGTCA ACGCACCTTT 60

ACCACCTTTT CCCAACTCAG TAAGGCATTC GACGTATTTC TTAGCCAAGn TTACATATCT 120

ACTCTGCAC 129

(2) INFORMATION FOR SEQ ID NO: 1701:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1701:

CAAGAGGAAC AACTCGGTAC TGCGCATCAG CAGAGATGGC GAAATCACAC TTAGAAGACA 60

AGG 63

(2) INFORMATION FOR SEQ ID NO: 1702:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1702:

TATTTAATAA ATCTTCAATA CCTTGTTCAT CAGTTTGTTG ATAAATAAGA CCTCTCCATT 60

TTAAATCTTC AATTAATACA TTCGTCATTA TTATTTCCTC CTATTTATAA TTATTTATTG 120

AATACTTGTT AAAATACTTT AAAGkTTTTT GAACGTAAAA AAAACCCTTA CAACAAATAT 180

GTAAGGGCGC GATTGCACGT TACCACCAAA CTTAAACATA ATCATAAGAT AATGTTCACT 240

CTATTAATGA TACGTTCATT AATAAACGTA GGACATGTTA GTTATAAAGG TGTATTCATA 300

TTATTAAAAA CACTAGTTCA CAGCGACCAC TAGCTCTCTG ATGATTTCAA ATAATATTAC 360

TTGTCCTTTT ATCCTATTCT GTATGCATTT TCCCTAATTA 400

(2) INFORMATION FOR SEQ ID NO: 1703:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1703:

TCAATATTGA TATCGAAACG CTTTGCAGAT TGATATAAAT TATCAGAATC AAGTAATTCA 60

TTTATTTTCT TTGGTGAAAG TACTTGGAAA ATACTATACT GATGAAAACT TAAAAATGAA 120

ATGAAGTATG GAAGTTGTTG CTTTGGGTAA GCnAAATTTC TAATACATAC TGATTAAACT 180

GTTTGTTTAT TGnGAATTGC AACGCATC 208

(2) INFORMATION FOR SEQ ID NO: 1704:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1704:

AAGCCGATGT AATTATTTAT GCAACACCTG TTCTAATGCA CAAAGAAATA TCTTAGCGAG 60

CTTATAG 67

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1705:

CCAACTTGCA TGTTATTTTA AGCTGACTTT CCACCAACTT CTGAGTTTGT GGCC 54

(2) INFORMATION FOR SEQ ID NO: 1706:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1706:

CAACTACACG AAAGGGTAGT GCTTCAAGAT AATAACGTCC AATTATTAGG AACTGTGGCG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 1707:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1707:

ACCATTCCAA ATGAACCTAA ACCACTTGAT ACGTTGACGA CAACAGGTTG TTCA 54

(2) INFORMATION FOR SEQ ID NO: 1708:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1708:

AAATTTGAAT AACTGTACAC ATTTTTTTGA TCATAGTCTA TATACTTTGT GAATTAATT 59

(2) INFORMATION FOR SEQ ID NO: 1709:

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1709:

GCACAATAGC CAATTAGATG GGGCCGGTGC GGTAACATTT TGCTTCATTC CTGCATTAT 59

(2) INFORMATION FOR SEQ ID NO: 1710:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1710:

TTACAATTCA ATCAAGTTCT TCATTATCAG ACGAAGAAAT CCACCGTATG GTAAA 55

(2) INFORMATION FOR SEQ ID NO: 1711:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1711:

TTTCTGCTTA TTGTCATTCG ATATCGAATT ATTAGAAAGT GCAGATTTCG CATCAG 56

(2) INFORMATION FOR SEQ ID NO: 1712:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1712:

TAAACCTTTA GGATTGCTGG CAATAGTAGT GCAGTTGGCT GGACTTGTCA TGCCC 55

(2) INFORMATION FOR SEQ ID NO: 1713:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1713:

CAAGAGGATT CGTGCAnTGA ATTCATGGAG ATATTTAGAT CTTTCACTGG AGAGAAAATA 60

AAAAGAAGAA AAGAGTAACC TTTAGATTGC TGGATnTGTG CAGTGGCTGC TTGCGTGCCT 120

TTAGGTGGCA TAAGGAGGCT ATACGCAGAC AACCACCGTC CCGGGGTTTT ATTGTACACT 180

GTGTAGGACG CAGACTTTAT GTGGTTG 207

(2) INFORMATION FOR SEQ ID NO: 1714:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1714:

TGGTTATCGA CTGCTCGTAT ATTTTGACTG TTTTGACTGT TGTTTCCGTA GCAATACTAT 60

CTCCTAAGCC TTTCATTGGC ATTG 84

(2) INFORMATION FOR SEQ ID NO: 1715:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1715:

GTTTGAATTG ACTGACTTCG TTTTACCGCG TGTTTAATAT TGTTATACAT ATAT 54

(2) INFORMATION FOR SEQ ID NO: 1716:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1716:

GAAGCCTGTC AGTGGATCAA ATTATTGAAG ATAACTTGGG TGGCATTTTT GGAAAGTCCA 60

AATGCTGGGA ATGGTCA 77

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1717:

GGGCCCTTTT TTTCCCAAAA AAAAAAACCC CCCCAACCCC AATTTTGGnC CCCCTTCCCC 60

TTTAAAAATT TAAAAATTGG GCCAAAAGGC CCCCCCAAAA AAAACCCCCA ATTGGAATTG 120

GAAAACCATT GGAACCAATT CCATTGAACC AGGA 154

(2) INFORMATION FOR SEQ ID NO: 1718:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1718:

ATTGTCTACA CTGCCACTTT ATTTTCATTA ACCATTTCAC AAATGTGTTC ATCATTCAAC 60

ATGAACATCA ATTGTTCAAT TACATCGACA CCTGATGCCT AAnCACGCAC CTTTTGCACA 120

(2) INFORMATION FOR SEQ ID NO: 1719:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1719:

TTCATTTGTT TGTAAAAGTG GCATTTCTAT GTCTTAAAAG TGACGAAACT TCAC 54

(2) INFORMATION FOR SEQ ID NO: 1720:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1720:

(2) INFORMATION FOR SEQ ID NO: 1721:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1721:

TTTGGATTAT AAATTGACAT GTAAGTACGA GGCAGCTGTA CCCGATATAT AATTGCTAAG 60

AGTTAGGGCT G 71

(2) INFORMATION FOR SEQ ID NO: 1722:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1722:

TTTTATCTTT ATTACTAAAA CCAACTGCAC CAAAGTTTGC AGTCATTACC ACACGTTTAA 60

CACCCGCATG TTCTGCAGCT CTTAAAATAC GTTGTATACC TTCAATTGCA GGCTTCGCCA 120

TCACTTCTGC ATCGTCTGTT TTACCGAAAA ACACCGGAGA TGCTACACTC AAGACATACT 180

TGCAATCTTT CATTGCTTCA TCCCAATGTn CATCTTGTGA TAAATCCGCT TCGACAAACA 240

TTAAATCGCT CTGTGGAAAT GCCCATGTCT TGCATTGTTT nAATTACTTT ATCAGCTTTA 300

CTTAAATCAA GnATCGTCGT TTGTA 325

(2) INFORMATION FOR SEQ ID NO: 1723:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1723:

CAGTATTGCA GTCACGACAA TGTGATGACT AAATTATCCA AAGTATGAAT TCCATGCGGC 60

ATTAATCCTA G 71

(2) INFORMATION FOR SEQ ID NO: 1724:

(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1724:

TTGCAACGAT ATTAGGCTAT CTAGTCGGCA TATTTGTAAA ACAAGATCCA ATT 53

(2) INFORMATION FOR SEQ ID NO: 1725:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1725:

ATCTATTCAT CTTCGTACAC GGACAGGAAA TGAGTCCAGT AGATGCACAT TGGGAATTAA 60

TCGAAGCTAG C 71

(2) INFORMATION FOR SEQ ID NO: 1726:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1726:

CATCTTGCAG GTCTACATTA TAAAATGTGA AGTTTTCTAC GATAACAATT GGGAAACTCA 60

GGGGCATCTC C 71

(2) INFORMATION FOR SEQ ID NO: 1727:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1727:

TTCnTTTTTA AAAATTCCCC ATTCCTTTTT AAATTTCTTT CCCGCTGGAT TAAATGGATT 60

TTAAAAATTC CACCCCAACT TAnAATTAAA TGGCTTGTGG AAAATTAACG GGATTGGCAT 120

TCCAGCTTAA ATGGTTTTTT TGGAGGCTTC CACGTTAAAA ATGGCGGGTG GCTTT 235

(2) INFORMATION FOR SEQ ID NO: 1728:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1728:

TAGAGTGGCT ATAAAGCTAA GTTCAATTGA CCAATTTACA ACAGGTTATT GAGGACAATA 60

A 61

(2) INFORMATION FOR SEQ ID NO: 1729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1729:

ATCACCAAGA AGTTCTAATG CTTGGTATAA ACGTTGAATA CGACGTTCGG TATT 54

(2) INFORMATION FOR SEQ ID NO: 1730:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1730:

CGTCCCGAAG CGTTGGAGGC GGGAACATCC AGAGTAATTG GCACAGATTA TGACCATAT 59

(2) INFORMATION FOR SEQ ID NO: 1731:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1731:

(2) INFORMATION FOR SEQ ID NO: 1732:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1732:

TATGTGGTGT TCAATGCAGT GGTCATTATG GTGCATCTTA CCAGATTCGG CATTCTTATT 60

ATAACTATAC TTGTAATAAA TGGCGACATG CAGACACGnC AATAC 105

(2) INFORMATION FOR SEQ ID NO: 1733:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1733:

TTTACGTTCC ATAGCAAAGT GATACAAACG TCAGCATCAA TGTAAGGCAT AGATCATAGT 60

(2) INFORMATION FOR SEQ ID NO: 1734:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1734:

TTCCATCATA CATTCGCGTT TTACTTTTCT TCTGGTATGA TCAAATATTC ACATAA 56

(2) INFORMATION FOR SEQ ID NO: 1735:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1735:

AAATGGGGAT GAAACAGTTA GTGTACAGGT GAAAGCTTAA CAGCAGCTAC AATTGCA 57

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1736:

GATTTGCAAT TAAACTTAAA TGTAATTTTT CGGAATGTGT ATTTGGTTTA CTTAAAGTAA 60

A 61

(2) INFORMATION FOR SEQ ID NO: 1737:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1737:

AAAGAAGCTA AAGAAAAAGT TGATAAAACA GCAAAAGTGA TTATTAGCTA CAGCATT 57

(2) INFORMATION FOR SEQ ID NO: 1738:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1738:

CAATAATATC GCTAAAACCG CCATTTGTAC CAAATGAATT TGATAATGCT GCAG 54

(2) INFORMATION FOR SEQ ID NO: 1739:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1739:

TAGAGCCCAA CCGGCAACCC ATCCATGGAA ATTCACCAAA ATAATACATT GACCCCAAG 59

(2) INFORMATION FOR SEQ ID NO: 1740:

(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1740:

CCTTTTTGGn AATTTAAGGG GGTTCCCAAC CAAATTCCCC CAAATTTTTT TGGGTTAAAA 60

AAACCCGGCC CAAAAATTTA AGGGAATTTG GAAAAAGGTT TGGTTCCCTT TTTTTCCCAA 120

GGCCCAAAAT TTGGAA 136

(2) INFORMATION FOR SEQ ID NO: 1741:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1741:

CATTCAACCA ACGACTGACA ACAGAACATT TAAGAGTCTA GGACATTGAT TGA 53

(2) INFORMATION FOR SEQ ID NO: 1742:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1742:

GCTCGTCTGA TTCAGTCACA AAATTGTCTT GTTATACTTG TCACCTATCA TC 52

(2) INFORMATION FOR SEQ ID NO: 1743:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1743:

TGTTATTTAA AGAGGCTCAA GCTTTCATAG AAAACATGTA TAGAGAGTGT CAT 53

(2) INFORMATION FOR SEQ ID NO: 1744:

(A) LENGTH: 94 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1744:

TCTGAGTTAA AGACGTCTCA CTTAAAGCTT TAGCAATTCC AACAATCAGA TATCTTCACA 60

CGTGTTATAT GTGTCCATTA ATATATCCTG TGGC 94

(2) INFORMATION FOR SEQ ID NO: 1745:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1745:

GGAAAAAAnn TTTTTAAAAA AAGGGAAAAG GGAATTGGGG TTCCCGGCCC CTTTTTAAAG 60

CCCCCAAATT AAGGAAATTT TAAATTTTGG GGAAGGGGAT TTTCCACCGG TTAATAAACC 120

GCCGATTTTG AGGGGGTTGA ATTAATTGGC CCAAATTTAA AAACCTGGAT GCTGGGTCCA 180

ATTTTTTACC GGGACCAATT GGTCCTGCAT GA 212

(2) INFORMATION FOR SEQ ID NO: 1746:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1746:

TATCTTCCGA TGAAGAACAA GATGCACAAG AAGTACGCCA ATGATTTAAG AAAGTGGT 58

(2) INFORMATION FOR SEQ ID NO: 1747:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1747:

AAAATTAAGn CCTTTTTTAA CCTTTCCCTT CCCCAATTGG GGCCT 105

(2) INFORMATION FOR SEQ ID NO: 1748:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1748:

AGTGCCTATT ACTTTGATTG ATGTCCAAGT TTCCTATCAC ACAACTTAAT TT 52

(2) INFORMATION FOR SEQ ID NO: 1749:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1749:

AAAGCATCAT CCGAACTCCA ATGATTATAC TCCCTAGATA TTATTATGTG ATGCTTTGAG 60

CATTAATTAG AGATGGGACG ATTCCATGAA AGATA 95

(2) INFORMATION FOR SEQ ID NO: 1750:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1750:

TTGACACATC TACTCACATT AAAAGTAGAT GAAGCGTTGA GATTAACATT TCCACATTTA 60

CAA 63

(2) INFORMATION FOR SEQ ID NO: 1751:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCGATATTTG AGACACGCTG CTGTAATAAA ACATCCTATA AAGTATATAC CAAGATCTAC 60

CAATATAAAC AGCGGCTATA TGATATAAAT GCTCAGACAC ACCCnCTGCG ATCCAT 116

(2) INFORMATION FOR SEQ ID NO: 1752:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1752:

TATGATTAAG CTTAGTGCAG ATTTGATTTA TTnAACAACG CTTCACTACA TTAAAAATAG 60

GGCACTCGCA CATATAGTTG TATCAATAGC CTTTATCAAT TTTTTGGGAA GGTT 114

(2) INFORMATION FOR SEQ ID NO: 1753:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1753:

AACTTCAAAT GTGCCAAGTG TTGAATCACA TCAAAATCAT TTTTATTTAA CG 52

(2) INFORMATION FOR SEQ ID NO: 1754:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1754:

ACTAATCCCT TGCGTGTTTC CAATCAATTG CATTATTAGT GGCCATTTGT TTGATATAAC 60

TGACAAGCTT TAACC 75

(2) INFORMATION FOR SEQ ID NO: 1755:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1755:

GTGAACAAGG GTAGATGTAA ATAGTTGATG CATGTGTACA CATCATAACA AAA 53

(2) INFORMATION FOR SEQ ID NO: 1756:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1756:

TTATTTGGGC AGGCAAATAC CCTTAATATA TTCAAATCAT GTTAATATCA TTGCTATTGC 60

TAAACC 66

(2) INFORMATION FOR SEQ ID NO: 1757:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1757:

ATTAATCGGA GCACTTGGGT TCGCAATTTA TGCTGAAATG GATCATTCTA CATCATC 57

(2) INFORMATION FOR SEQ ID NO: 1758:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1758:

CGAACAATAA CTCTAAGTAT CCAACAAATG CTGCAAGTGT ACCTACTGTG ATTGATCCAG 60

AAATAGCAAG ATATGCACCA ACACCGATGA CAATAATTGG TCCAATATCT GTAACTGTAT 120

TAATTGCGGC AAAGGAATAg GCATTCCATC TTGTATGTTT CAACGCACGT GTTAGGAAAT 180

TAGTATTCTT TTTATCAAAG TTTTTCGCTT CATTGTCTTC AATCGCAAAA CTTTTAACGA 240

CTGAAATACC TTGAACACGT TCATGCAAGA ATCCTTGAAC CTCAGCTAAT GCTTGAGATC 300

TTTCAnGTGT CAATTTTCTT AATCTTCCAA AGAAAACGTA CACCGTTAAA ATGTAAAATG 360

(2) INFORMATION FOR SEQ ID NO: 1759:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1759:

nATTATGTCA TGCTAGGTCA CTTGCATCAT CCATTTAGTA TAGAAGACGA CAAAATTAAA 60

TTATAGTGGG CTCCTTGATT GGCAGTATTC ATTTTCGGGA AGCGGGGTCC AGGCTTAAAG 120

GGTATTAGAC GTGGTTACC 139

(2) INFORMATION FOR SEQ ID NO: 1760:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1760:

TCGCCCCTCC AGGCTATTAT TTCATCTATA TCATTGTCAT CAGTTAAATT CAGCCTCGAC 60

ATTTCCATTT CAATAGACTG TTCATTCAAT TCTAAGTCAT TATTGTAAGT TTCTAGTTGA 120

TTTTCATAAT GATTTAGATT ATTTTGCTCA ATTAACTTTC TTTGAGACAA TTGCATTAAC 180

TTATCTTCAA TCTCCTTTGA GAGTTCTTGA TGCTGATTCA CATCTTGAAC ATACTTCTTA 240

TAATCCACCT CAAAATTAGT GATATTAnTA TATnTCGAGA GTGTTTCAAA TTCAGTGATG 300

AGATCTCGAC ATAAT 315

(2) INFORMATION FOR SEQ ID NO: 1761:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1761:

TAAATCCTCG AGATTCTTAA TAGGGTAGAT ATCTAACGTT TTCGCAAAGC TCTTTTTGAT 60

TTGTTCTTCT TTTGAATCTC CAATGATCTT ATTATCACCA TCACAAGATG TAACAAAGAT 120

CCATCCTCAT CATTCATCAT CTTCATCTAC CTTCGCgGCT GGAAATTCAA aGAaTCTATT 240

ACTGACAAAT CGCTTTTTCC ACCTTTTGAA AAGTCAATTT CCAACTTTTT ATAACCCACA 300

GAACTTCCTT TCAAATTACC ATCAATATGC ATTTTTAATA CCGGTGCTTT ATCAGTAGGA 360

ATATTATAAC GACTTCTTAA TTGCTTAACA TTTTCATCT 399

(2) INFORMATION FOR SEQ ID NO: 1762:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1762:

GTATAGAAGA CGACAAAATT AAATATAGTG GCTCCTTATT GCAGTATTCA TTTTCGGAAG 60

CGGGTCAAGC TAAAGGGTAT AGACGTGTAC AATTAATGAT GGCATTATTA ACGATGTATT 120

TATTCCTCTT AAGCCACTTA GACAATTGGn AATTATCTCA GGCGAATATA ATGATGTTAT 180

TAATGAAAAA GTTCATGTGA AAAATAAAGA TAATTATnTA CATT 224

(2) INFORMATION FOR SEQ ID NO: 1763:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1763:

AGCAACCAAC GCCAGATAAA GCAGAAGATA ACGCATTTCC CCCCATCACC ATAT 54

(2) INFORMATION FOR SEQ ID NO: 1764:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1764:

ATTCCCTTAT CGCATTCTGT AAAATGATCT TCATCAGAAA TTGCTTCGAT ACGTTTATG 59

(2) INFORMATION FOR SEQ ID NO: 1765:

(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1765:

GATTCAATTC ATCTGTATAG ACGATATATC CTGATATGAA TTGGAAATGG AATA 54

(2) INFORMATION FOR SEQ ID NO: 1766:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1766:

ATCGCATAGA AGCATTAGAC TCAAACTATT TTCGGTTATG AGAATAACTC TGACATCCAT 60

ATGGATACTT AGTTTCCAAG TTAGA 85

(2) INFORMATION FOR SEQ ID NO: 1767:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1767:

CAGTACTGCT GAATGATGCT ATTGATTTTC TCATGAGACA TGGCGATAAC ATCG 54

(2) INFORMATION FOR SEQ ID NO: 1768:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1768:

GnCACTACTA ATCGTATCAG GATCACTAAT TAAGGCATCC AGCATCAGAT ACGAGCGCAC 60

GTCAGACTAA TCTACTGTCA TGATAAAGCA GCTGCTAACC TTGTAAGTTC GTGAAA 116

(2) INFORMATION FOR SEQ ID NO: 1769:

(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1769:

GTTCTATCCA ATATGGAAAT GAGGACATTA TGCGTGAAAG CTATGGACGA TGGACGATGG 60

TACACGCATG TTGTGTAAGC AG 82

(2) INFORMATION FOR SEQ ID NO: 1770:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1770:

TATCTGTATT GTAGTAATCC GCTTCTCCCA TCTATATAGG GATCTTTCGT AGATATTCAC 60

TTTATGCCTA GGATCCAAGA TGTGTAAGCA GCACTTTGCA TTATCTAATG CAAAGGGnAC 120

ATGCGGCTGT AAGCCCTGTT CTGATAATCA TA 152

(2) INFORMATION FOR SEQ ID NO: 1771:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1771:

TGGAGGCGAA GTAAATGAAA AGTATTACGT TTGAAGAACA TTATGTCATT G 51

(2) INFORMATION FOR SEQ ID NO: 1772:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1772:

nGAAACAAAT ATCTGATGAG ATATGCAATG ATGACTATAA GTAACATTAA AATGAAGCCC 60

CGTACACCAA TTATATCTTT GTGGnTGTTA TATTAAATCT ATATTATGTT CATTTAACAG 180

CATATGTTAA AAATTGACAG TTAACACATG TAGCTATTTG ATGTGAATGT GC 232

(2) INFORMATION FOR SEQ ID NO: 1773:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1773:

TAATGTCCCC CAGAATGTAG GCAAATGCAG AACCTGGTTT TAGGGTCAAC TGTTTnTTCT 60

CCAAGCAGAA ACAAAGTTCT TGTGTCAGTG CACTTTTGGT CCACCATT 108

(2) INFORMATION FOR SEQ ID NO: 1774:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1774:

CGCAATTGAA GGATACACTA TTTTAAGAGC TGCAAACATG CGGGTGTAAC GTGTGGTATA 60

CTGCAACTTT GGTnATTGGT TTAGTATAAG ATAAAATCAT CACAATGAAT C 111

(2) INFORMATION FOR SEQ ID NO: 1775:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1775:

CAGGTTATCA GCTAATAGAT ATGTTGAAGA GGCAGTTGCA GGCCAAATGA AACTGCAGAT 60

GTAGTTCAGT ACC 73

(2) INFORMATION FOR SEQ ID NO: 1776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1776:

TAGACACAGT GCAAAATCTG GTACAGCTTA TGGAATTAGA CGGGTAAAGC AAATTACTGA 60

GTACCCA 67

(2) INFORMATION FOR SEQ ID NO: 1777:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1777:

GTATGCCAGT GTCATTGCTG AAAACATCAA CCATTCCCTG CACCAAAATT TTTTGGTAGA 60

GTTTGATGCT GGCCATCCTC CAAGGGACTA AGGGTAATTT TGnTTAAAAA GAGCCAAAGG 120

CCCAATG 127

(2) INFORMATION FOR SEQ ID NO: 1778:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1778:

GAACCCAAAA ATTAGCAACA GTGGCTACAA TAGTTGGGCA CTGAAAGCCA GCCAAGTGGG 60

ATTTTTAGCC CTTGATTTGA AAGCGGGGTC CCCAGGATTA AAAAATTTAA ATTAGCCTAA 120

TAAGCCCAAA ATTCCCATTT GGAAAAGGAA ACCTCCTTAA ATTGGGTTGG AAAAAAGnTT 180

AAAAAAAAAA AGGCCCAGnC CTTGGAATTT TTTGGAATTG GAAAAAGGAA TTAAAA 236

(2) INFORMATION FOR SEQ ID NO: 1779:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1779:

(2) INFORMATION FOR SEQ ID NO: 1780:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1780:

GACGACTCGC TTCTATTTTA AAATCCGGCG TACTTgGTTA TATAAATATC ATAATGGTTA 60

AAATTAAAAA GCAATGTCAG TTCACACTAT TACTGACATT CTTTTAGTTA TGTGTATATT 120

ATTCATTCAC AAGCTTTTGG TCTATAAATC GAGTGATTTG CTTTGTTTGT ATATAACCAT 180

CTGCTACATA TTCATCGTTC ATTGTAATTA ATGGATAAAA TAGTTCATCn n 231

(2) INFORMATION FOR SEQ ID NO: 1781:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1781:

GTCTCCCTGC CCCACATTTA ACATTGTAAT TTTGTGATGT GAATTTGTTG GAAACGTTAT 60

TAATAATGTC AGAATAATTA TAGTCCAAAA CGTAACCAAT ATATATTTAC GTTTAGCCAA 120

TAACCAAAAT ATGTAATAAA CAGAAATTAT AAATACTATA AATATCCAAT CATTAAACTT 180

GGGAACAGAA AAATGTGATT GCTTGATTC 209

(2) INFORMATION FOR SEQ ID NO: 1782:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1782:

GTTAAACTTA GTTAGATAAA ATGCAAATCA CATTATTGTA GATAGTCTCT TTTC 54

(2) INFORMATION FOR SEQ ID NO: 1783:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1783:

TCTGGAATGT CTCCTTGTCT CTCTATATAG CTATAGTCCG TCGCAAGCGG ACGTAATGTT 60

CATTTTCATA ATGATTATAG TATGAAAGCG CTTTCTTGTA TATGTGACAT GTGCGTGTnG 120

(2) INFORMATION FOR SEQ ID NO: 1784:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1784:

CTACCATTTA CATAAAGACC GTCTAATTCT TCAGTTTCAA TGGCATTTTG GAGCAAT 57

(2) INFORMATION FOR SEQ ID NO: 1785:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1785:

TCATAACCAT TACCAAGTAT CCAAGCAGCT TTTAAACAAT ATGGCATAAA CATT 54

(2) INFORMATION FOR SEQ ID NO: 1786:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1786:

GGATGGGTGA TTTTAGCAGG TTTGGCTATG AGTACCGTAT TTGCATTAGG ACCGATTTCA 60

TTTAACAAAA TCATAATTTT GGGC 84

(2) INFORMATION FOR SEQ ID NO: 1787:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1787:

CCGGTTTACC CTTAAAATTA TTTTTTGGGG GGTTCCATTA AACCTTCCAA TTCCCAATTA 60

ACCCCnACCC CCCTGGGTTT TCCTTAAAAA CCAAAAGGCC CTTTTTTTTC CCAACCCAAC 120

CTTGGGGGAA TTGG 134

(2) INFORMATION FOR SEQ ID NO: 1788:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1788:

TATATCAACT AAAAAGCGCA TCTGCAACCG ACGGTTGAAA ATTTGGACAG GAGACAGATA 60

ATGTAATATA 70

(2) INFORMATION FOR SEQ ID NO: 1789:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1789:

AATATCCAAT TATACAAGCA GGTATGGCAG GAAGTACGAC ACCGAAATTA 50

(2) INFORMATION FOR SEQ ID NO: 1790:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1790:

TGATTTACTA GCTGAATCCG ACATGCTTGA TGATACACTA TGTGAATTCA 50

(2) INFORMATION FOR SEQ ID NO: 1791:

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1791:

CCGGACGCTT TACTTCCAAC TTTAGGTGGT CAACACAGGT TTAAACATGG CGATGTCA 58

(2) INFORMATION FOR SEQ ID NO: 1792:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1792:

CATCATCCTC TAATTTAGTC CAAACTCCTG GATGATATCC AAATGAAGTT CCAATTGA 58

(2) INFORMATION FOR SEQ ID NO: 1793:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1793:

CACAAGTTTT AGAAGGAAAC CAATAACAAA TGACGAGATT AATTGCCACA AACATTAACG 60

AC 62

(2) INFORMATION FOR SEQ ID NO: 1794:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1794:

AAGGCCCGGG GGGTTTAAAA AAAAAGGTTT AAAAAAGGnT TTGGCCCTTT AAACCCAAAG 60

GGAAATTTTA ACCCCAAAAA AAAAAAACCC CTTTGGGAAA GGG 103

(2) INFORMATION FOR SEQ ID NO: 1795:

(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1795:

TATCGATCGA TCATGTCGAA TCGATCTGTC GATCGATCGT ATCGATCGAA TCGCGTCGAA 60

TCGAATnCGT CGAATCGATG CTATCGATCG AATGCTATCT GAGTCGAATC ACGTCGATCT 120

G 121

(2) INFORMATION FOR SEQ ID NO: 1796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1796:

AATTCATGTT AAAATCCTCC TGATATTAGA TGGCCCATTT TTATTTTTTT CGTTTCCATA 60

TA 62

(2) INFORMATION FOR SEQ ID NO: 1797:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1797:

CATACTCGAC AATTTAGATG GTGAaTACTT ATCATTTAAG TCCTTTGaCA CCTCATCTAA 60

AATTCTAGGA CTTTTAACAA TTTCTTTATA CGTATTTACA AGTTGAATAT TACTTTGAAC 120

CTCTTGCGCC ATAAACTGAG GATTGTCACC CTTAGTTTGA TTCACTAAAA TTTGAGTATT 180

AGCTTGATAT TTAGGTGATA AGACGAAAAA TGTAACAATA GCGCTAATAA TTAAAAATAA 240

TAGCGGTAAA ATAATTAAAA TCTTCAAGTT TTTTTGTAAT ACTTCTTTAA TTTTTGTTAA 300

TTCTAATGTA CTTTCCATTA TTTACCTCCC TTAAAAATTT TCATTAAAAT TGGTATTATA 360

TATATAGTAT TTACATATTA CATATCGTTT AAACAAT 397

(2) INFORMATION FOR SEQ ID NO: 1798:

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1798:

CGGGTAACAG CGAATGGTGT GTCACCGTAT ATAACTTTAC TATTTAATAT TTGGCCTGTT 60

GCTTTC 66

(2) INFORMATION FOR SEQ ID NO: 1799:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1799:

GTTGCTAAGT TTGTATTACA ATTTAAATGA TTTTTAGCTT GAGTAAGTTT ATTTAAAGAT 60

GCAGTAATTT CGCTAGG 77

(2) INFORMATION FOR SEQ ID NO: 1800:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1800:

TAATGCTATT TAATTTTCTA CTTCCTAAGC TTCCACCCAT AACGAGTAAn ACTTTTTTAT 60

TTTCATTAAA GCCTGTTAAT TGATAACCAT TATGTGCATT ACCATTTTTT AAATCTTCTC 120

GAATTGTTGC TCCAATAAAA TCAGCTTTCT CTTTAGGTAA GTAGTTTAGC GT 172

(2) INFORMATION FOR SEQ ID NO: 1801:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1801:

AGTAAAATTT GTCATCACGA TCAGCAAAAG CTTTTGATTC TGACGTATCT TCCATAAATG 120

ATCTAAAAAT TGGTAGTTCG 140

(2) INFORMATION FOR SEQ ID NO: 1802:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1802:

ATCCCCCGTA CAGACTTCAG CTTACGTAAA CATGCTGAAC ACTCTAGTGA AGATTTCAAA 60

(2) INFORMATION FOR SEQ ID NO: 1803:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1803:

CAATTTAAAT GCATCTTTCC CATTAATTTC ATTTGTTGTC GCTTTAGCTG TGTTAATTAA 60

(2) INFORMATION FOR SEQ ID NO: 1804:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1804:

ACTTGATCGA AAAGGTTTCA TACCGGTAAA CGATAAAGTT GAAACAAATG 50

(2) INFORMATION FOR SEQ ID NO: 1805:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1805:

(2) INFORMATION FOR SEQ ID NO: 1806:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1806:

AAGAACTGTC TATGAATATT GGATGACGCT TTGATGAGAA CATTAGTAAG CCATTTGTTC 60

AAGGAGTACA 70

(2) INFORMATION FOR SEQ ID NO: 1807:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1807:

TAGCATTTCT AATGGAATCC AATCTTACCG AATGACAATT GGAATATAAC TGGTGATAAT 60

GTTGAATGGT CCTGTGA 77

(2) INFORMATION FOR SEQ ID NO: 1808:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1808:

CCCGGCCCAA AACCCCTTTT TTGGGTAAAA AATTTTTTTT AAAAAGGGAA AAATTTCCCC 60

TTTTTTGGTT CCCAAATTTT AAATTAGAAA GGGCCCCCCC TTCCCCCCCA AATnTTTCCC 120

A 121

(2) INFORMATION FOR SEQ ID NO: 1809:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1809:

AAGTTTGGTG AAGGAACCAC GTGCATGATG GTGTTCAAAC AATGCGTTAC GATGTTGACG 60

(2) INFORMATION FOR SEQ ID NO: 1810:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1810:

TGGTTGAGAA AACACAGCGT TAAAGTTGAG GTATTTCAAA AGACAAGTTG GAACATTA 58

(2) INFORMATION FOR SEQ ID NO: 1811:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1811:

CTTAAATAGC AAGTGGTTTT ATAACAACTT TGAGTTATCT CAATATAGTT ATCGC 55

(2) INFORMATION FOR SEQ ID NO: 1812:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1812:

TAAGTCTTCA ATTTTTTCAG TTGATACACC TAAGTGATAC AGCCATTCTT 50

(2) INFORMATION FOR SEQ ID NO: 1813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1813:

(2) INFORMATION FOR SEQ ID NO: 1814:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1002 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1814:

TGGTCATGCG GGAAATACTA GGACATGAAA ATTATGCTAA AGGCATCAAA GTAACTGAAA 60

ATAATGGCGT AGTGGATATA GATATGTACA TTATTGTAAG TTACGGTGTG AAAATATCTG 120

AAGTTGCCAA TAATGTACAA TCAACAGTGA AATATACTTT GGAAAAATCA CTTAATGTAT 180

CAGTAAATTC AATCAATATA TATGTACAAG GTGTACGTGT GAATAATACA GGCAAGAAAG 240

CTTAGGAGGA CAACTTGAAA TGATTAGCAA AATTAATGGT AAATTATTTG CCGATATGAT 300

TATACAAGGG GCACAAAATT TATCTAACAA TGCAGATTTG GTAGATTCTT TGaATGtGtA 360

TCCAGTGCCA GATGGtGATA CAGGAACAAA TATGAATCTT ACTATGACTT CAGGTCGCGA 420

AGAAGTAGAG AATAATTTGT CGAAAAATAT CGGCGAATTA GGTAAAACAT TCTCGAAAGG 480

TTTACTAATG GGTGCAAGAG GTAACnCTGG TGTCATCTTG nCACAATTAT TCAGAGGATT 540

TTGTAAAAAT ATTGAAAGTG AATCTGAAAT TAATTCAAAA TTGTTAGCTG AAAGTTTnCA 600

AGCTGGTGTT GAAACGGCAT ATAAAGCTGT TATGAAACCA GTTGAAGGTA CAATACTTAC 660

AGTTGCAAAA GATGCTGCGC AAGCTGCAAT AGAAAAAGCA AATAATACTG AAGATTGTAT 720

AGAATTAATG GAGTACATTA TTGTAAAAGC CAATGAATCA CTTGAAAACA CACCAAACTT 780

ATTAGCTGTA CTTAAAGAAG TTGGTGTTGT TGATAGTGGC GGTAAAGGTT TGTTATGCGT 840

TTACGAAGGA TTCTTAnAAG CGCTTAAAGG TGAnAAAGTT GAAGCCAAAG TTGCAAAGAT 900

AGATAAAGAT GAATTTGTAC ATGATGAACA TGATTTCCAT GGTGTAATTA ATACTGAAGA 960

TATTAATTTA TGGCTATnGT ACTGAGATGA TGGTTCGTTT TG 1002

(2) INFORMATION FOR SEQ ID NO: 1815:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1815:

GACAACGCTA TTATTTTTAG TTTTTCAATT CTATTATGTC ATAATTATGT CACTCAAAAA 120

CTGTTTTCCA ACATTGATTT ATTGTTGGAA AATCTCGAAA ATCTAGTCTA TTTCTCCAAC 180

AATCGAAGAr TTATGCCCTT TTTTCTCCCT TTaAATAAGT CATAATACGA GGCATACATG 240

CAACATTTAC AATAAAATAT GTTCCTACAT CGTATTATAC GAATGCTCAC ACTTATAGTT 300

GTTTAGTAAA CCCAGATGTA TTGCTAACAT ACCCATnAnC nCTATATAGT T 351

(2) INFORMATION FOR SEQ ID NO: 1816:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1816:

ATATCGTATC CCATGCGGGA AGGGCTTTAT TTATACTGTG CACGATGAAT GCGCACAACG 60

GG 62

(2) INFORMATION FOR SEQ ID NO: 1817:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1817:

AAAGGGGGGA AATTTTTTTT TTTTGGGTTT GGGGGGAAAA TTTTTTTTGG GTTTGGGAAA 60

TTTAAATTAA 70

(2) INFORMATION FOR SEQ ID NO: 1818:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1818:

CAAGTTCGGA ATGCGAACGC GTCTTAATCT ATATACAAGT GATGCACTCC A 51

(2) INFORMATION FOR SEQ ID NO: 1819:

(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1819:

TCGCCATACT ATCGACAGCT GCTAAAATTG CGCTCTTCTT GTGTCGCAAT CG 52

(2) INFORMATION FOR SEQ ID NO: 1820:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1820:

CAAATTGGGG AAATTACTAG AAATGAAGAT ATTTATAAAG ATGACTGGAC GTCAACTT 58

(2) INFORMATION FOR SEQ ID NO: 1821:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1821:

ACTGCTTCAG CACCTGTATT CATTGGGGAA AGCTTTATCG TTGACCGGCC AGTTTACA 58

(2) INFORMATION FOR SEQ ID NO: 1822:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1822:

ACCTGTTGCT CGTGTCATAA ATAGGTGACT ATAAATCTCT GTTCAATATA CTTTTCGTTT 60

TTCCAATCTT AAAGGTCGAT GTTCGTGAGT AATCTTATCT CTGGnCCAAT TTTAATGTCA 120

TGATATGTTC ATAGTATCAC CCCTTTGTTG TGTAATAATA ATCAGGTGGG TGGTTAGAAC 180

GGTGTGAATA 190

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1823:

AGCnTTAGCn TATGGTTTAG ACACAACTGn TAAAGATGCn AAGTTCTTGT 50

(2) INFORMATION FOR SEQ ID NO: 1824:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1824:

AAAAATTGGA AAAAAGGGGC CCAAAGGTTA ACCCAAATTG GAAAnAAACC CAAATTTTTT 60

GGAAATTAAC CCAAAAATTG GCCCCCAATT GGAACCCAAA AT 102

(2) INFORMATION FOR SEQ ID NO: 1825:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1825:

ACGTACCAAT GTCATAATCA GTCATTTTAC CACTCTTAAT AATCTGCTTC CGGGCAA 57

(2) INFORMATION FOR SEQ ID NO: 1826:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1826:

ACCATCTTGT ACAAAGTGGA TGTCATATGC ACCATCTTGT GTTTTGAGCT GCATTTAATT 60

G 61

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1827:

ACCGTTTCGC CAAGCCGACC TAATTTCTCA GCAATATTTC TTTCTACGCC ACCAAT 56

(2) INFORMATION FOR SEQ ID NO: 1828:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1828:

ACTTATAGGG CGCACTTATT TTTCGCTTCC ATAGCGAAAC TAGTGTCACT TATACGTATG 60

TG 62

(2) INFORMATION FOR SEQ ID NO: 1829:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1829:

GCTACACACG ATTTACCTTT CTTGTCACGT TTTGCGACCA TCATTGTGAT GATA 54

(2) INFORMATION FOR SEQ ID NO: 1830:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1830:

GTAATGACCA TCGCTGATTT ATGACATTGT TAGATCTCAT GTGCCATTTA GTCTGCTGAA 60

TCTTGGG 67

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1831:

ATAACTCTTC GnCAAACTCC TCAACAAACT TCTTGTGTTC CATCTTCTGG 50

(2) INFORMATION FOR SEQ ID NO: 1832:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1832:

AAACGTnAGA ATATTTAATG GAGCCAAGAA TGGTTTACAG ACGGAGAAAT GGGATATGTT 60

GAAGCGAGGC GTACGCGGAA AGCGTACTAG GCTAGAACAC T 101

(2) INFORMATION FOR SEQ ID NO: 1833:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1833:

TCGTCATCAT GTCTGTGTTA CCAACGTTTG ACGATTTAnT TCATGCnGAA 50

(2) INFORMATION FOR SEQ ID NO: 1834:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1834:

ATAAGTTAAT TGATTTATTG ATAAAGAGAA GCCAGATTTA AATATTATTA AACGT 55

(2) INFORMATION FOR SEQ ID NO: 1835:

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1835:

AAACAAGAAC CCCCATATGG TTAAGCTGCG CGTTTCAACA TACGGGGGGT TTTCATAT 58

(2) INFORMATION FOR SEQ ID NO: 1836:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1836:

TACGTTTTAT AAAAACAAGA ACTAAAGTAT GCAGTGTGAA TTGTTCACTT TCnTGGCGTT 60

GGAATTGATT AAAACGAGAT ATGGTGTTGT GGAAGTTGTT TGTGTTTGCA TATTTTAAAC 120

CGATT 125

(2) INFORMATION FOR SEQ ID NO: 1837:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1837:

AATCTACAAT CCTGAATCAC TCGTTAAGAT TAAAAGTATC GACAATGAGT ATCTGAACAT 60

GAGCTCATCT GCCGTTTTTA ATGCnAAAAA CCGGCGGCGG GATATTTTTG ACCACGGC 118

(2) INFORMATION FOR SEQ ID NO: 1838:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1838:

ATTTGGGGTT TTGGGACCCT TACCCAAAAA TTGGGGTTTG GTTATTAAAA AAAAGCCATT 60

GTCCCAGTTT TTGGGATTGC C 141

(2) INFORMATION FOR SEQ ID NO: 1839:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1839:

TCTGGGGACT AAGTATGTCT CAGGCTTTAT GCTGTTATGT TTGAAAATGA AAGG 54

(2) INFORMATION FOR SEQ ID NO: 1840:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1840:

ATTAAAAAAC CTTTTTAAAC CGGGAACCCA AGGAAAAATT CCGGGTTTTA ATTAAAACCT 60

TTTGTTAATT GGTTCCAAAC CAACCTTTTG GGTTAATTTT AACCAGGAAT TTTGGAAAAC 120

nGTTTTATTT GGA 133

(2) INFORMATION FOR SEQ ID NO: 1841:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1841:

AAAGTATGGA TTGATCGTGG AGAAGTTCTT CCTACTAAGA ACACTAGTCG 50

(2) INFORMATION FOR SEQ ID NO: 1842:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GCGTTTTCCT GGGATATGTT TGATGAATGG ATGTTGTAAC ATGTTAATAA ATCGTTGGTA 60

(2) INFORMATION FOR SEQ ID NO: 1843:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1843:

CTGAGATGAA TATTGTGTTT CGCCATACAT ACTGGGTAAT ATCCCAACCA TTGCTGTAAA 60

(2) INFORMATION FOR SEQ ID NO: 1844:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1844:

CATTACCTGT AAAAGGAAGC TAAAGACGAT GAGTATTTAT AGAAACCAAT TGCCGACCAT 60

TTGCAGCCAT TAGGAGGGTA GGAGGGCAAT CGCGnCCAAA GGTTATTAAC CGTCAATTAC 120

CTTGA 125

(2) INFORMATION FOR SEQ ID NO: 1845:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1845:

ATCCACCTGG GTTTGTTCTT AATTTAACCT GnTAATTAAT TGGGTTGGGT CCGGCAAAAG 60

TCCGGACCTG CAAATCGGAT TTTATCGTTA AATCTTGAAT TCTATTGCCC ATATTAAATC 120

GCAAAT 126

(2) INFORMATION FOR SEQ ID NO: 1846:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1846:

TTTTGGGAAT AAACCAATTA ATCATGGGCA AAAAATAAGC AATCCAAGTA CTTACTA 57

(2) INFORMATION FOR SEQ ID NO: 1847:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1847:

TGATAAATAT TTCATCTAAA GAGAGGGAGT CATTATGACA CTACTTACTG 50

(2) INFORMATION FOR SEQ ID NO: 1848:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1848:

ATCTAGGCAA TGAATGGACG GACTTAATAT TGATGTGCAA CAAGAAGAGG AGAAGCGAAT 60

CAATA 65

(2) INFORMATION FOR SEQ ID NO: 1849:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1849:

CGTGTGAAGT CATTACTTTT AATCCCATGA TGATGGTGAT GGATGAGACG ATATCTCTCT 60

GTCTTTAACA GTTAAGTCCA ATTCTTCCAA CGAAACTTTT CCATAGGTTG TTTTATAAGT 120

TGGAATACTT GCACAAATCA TaCCTAATTG CTTATCAATT TTCTCAAGAC TGTCATCAGT 180

TATAAGATCA ATTTTATTAA TAATAATCAT GTCACTTAGT TTCAACTGAT CTTCCATCAG 240

GCGA 244

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1850:

TTTAAAGGTT CCCGGAAAGG TTTGAAACCA AACCTTTGCC CCGGCCCCCC GGGAAAAAAA 60

AAAnTTGGTT TAACCCCCGG GGGGGGGGGC CCTTAAAAAA ACCCAA 106

(2) INFORMATION FOR SEQ ID NO: 1851:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1851:

TTTTTTAAGG CCCTTGGGGG GCCAATTTTC CCCCCCCCCC AACCTTCCAA AGGTTGGGGG 60

GCCTTTTTTT TTAAATTGGG GGGA 84

(2) INFORMATION FOR SEQ ID NO: 1852:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1852:

TCATGATTAA AATTCAACAA TTACAACATC ACTTTGGATC ACATAAGAGT AA 52

(2) INFORMATION FOR SEQ ID NO: 1853:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1853:

ATAAAACATT TCAAGATGCG CTTGTAATTG TATGTGATAC TGCCAATGCT CCACGA 56

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1854:

AAAAGATCAT GCGCATAATG ACATGGTGAT GATATGAGTA TGATGGTGGG TACA 54

(2) INFORMATION FOR SEQ ID NO: 1855:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1855:

ACAACAAATG GTAATGCATA AACATACAGC CAATAGCTAC AATTGCACGA CG 52

(2) INFORMATION FOR SEQ ID NO: 1856:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1856:

ACGGCTGCAC TCATCATGGT CTGTGGCGTG ATTGTTAATG TTTTAGTTGC CCGCTTC 57

(2) INFORMATION FOR SEQ ID NO: 1857:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1857:

GCAGATAACT TCCTTGATCC TAACAAAGCA AGTTCTCTAT TATCTTCAGG GTTTTCACCA 60

GACTTCGCTA CAGTTATTAC TATGGATAGA AAAGCATCCA AACAACAAAC AAATATAGAT 120

GTAATAnACG AACGAGTTCG TGATGACTAC CAATTGCACT GGACTTCAAC AAATTGGAAA 180

(2) INFORMATION FOR SEQ ID NO: 1858:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1858:

CGCTGCACTT CCTGAACGCA GTGAGACCAG AACGTGGTGT CACTTTCGGT CTATTCCGGT 60

TAAGTGTTGG TCTCGGA 77

(2) INFORMATION FOR SEQ ID NO: 1859:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1859:

TTTGGCGTTC GTGATTTTCT CTAGACGTAG TAACTTTCCC ACTCTTTGCG TCC 53

(2) INFORMATION FOR SEQ ID NO: 1860:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1860:

TTTCTCACTC GCGCATTTCA GTTTGTTTTG ATTTACCCGT CTCTTCTATT TGTCTTAAT 59

(2) INFORMATION FOR SEQ ID NO: 1861:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1861:

AATGAATGTA TGCACATTAA CATCATCAAT TAATCCTTTT AATAAATTGA GTTGTAATTT 60

(2) INFORMATION FOR SEQ ID NO: 1862:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1862:

ATTAATACTG AGCAAATGTG CATAAGACAT CATGAATTAG CACCAATTTA CAGG 54

(2) INFORMATION FOR SEQ ID NO: 1863:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1863:

TTTAACCATC ATTCTATGTC AAAGTTTTGA AATGATGGTT ATTTTTTATT GCTTAAATTT 60

ATTATTGCTA CTACTATACC AATGAAAGT 89

(2) INFORMATION FOR SEQ ID NO: 1864:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1864:

AAAGCTGGTA CGCCTGCAGG TACCGGtCCG GAATTCCCGG GTCGACCCAC GCGTCCGGAA 60

CCAAAATTGC ATCTGATGGT CTCAAGGGTC GTGTGTTTGA AGTGAGTCTT GCTGATTTGC 120

AGAATGATGA AGTTGCATTT AGAAAATTCA AGCTGATTAC TGAAGATGTT CAGGGTAAAA 180

ACTGCCTGTA CTAACTTCCA TGGCATGGAT CTTACCCGTG ACAAAATGTG TTCCATGGTC 240

AAAAAATGGC AGACAATGAT TGAAGCTCAC GTTGATGTCA AGACTACCGA TGGTTACTTG 300

CTTCGTCTGT TCTGTGTTGG TTTTACTGAA AAAACGGCAA CAATCCAGAT ACGGGAnGAC 360

CTCTTnTGCT GCAGCACCAA CAGGTnCCGC CAAATCCGGA 400

(2) INFORMATION FOR SEQ ID NO: 1865:

(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1865:

AAATGGCGTA TCTTTATGTA TCAACTAAGT AATCACCAAT TTCTTTCGGA T 51

(2) INFORMATION FOR SEQ ID NO: 1866:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1866:

GTGTTGCGGA TAATCCGTCG ACATTAGCGT CTGAAGGTAT CATGAGGCAA CTGCGCAA 58

(2) INFORMATION FOR SEQ ID NO: 1867:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1867:

ACAGCAACTG ACCCAGTTTA CTACCGTCAC TCAAATCACA CAGGTGGTAT CAAATCAATC 60

(2) INFORMATION FOR SEQ ID NO: 1868:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1868:

CAATCTCTTA CCATTTATCT CAGCTGGTGA AAACGGTCCA TTACACTTAG AATAAA 56

(2) INFORMATION FOR SEQ ID NO: 1869:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1869:

GCTATAGACT AGAGGTACAG CAAATTCATG TGTACAGTGA TTAGAAGGCG ATGAGCAAAA 60

GTAAT 65

(2) INFORMATION FOR SEQ ID NO: 1870:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1870:

GCTACTGGCG GGGGATAGTA ACACCCAATG TTACACGTAT ATACGTACGG CTTCTTGATA 60

AAAAGATGAA GCCnTTACAA GTAGAGAGCG TAAGAACGTG ATCATCTAAA TGGTAAGGGT 120

AGACTATCCC ATGCCATTGT GGGCGGTTGC ATAGGTACCA CGGCACATAG CGG 173

(2) INFORMATION FOR SEQ ID NO: 1871:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1871:

GCTGTGGGAT TGTCCTTTGG CATGGGGTTA GGGAGAGCGT TTCTAAGGGG CGTTTGAAAG 60

CCATTGATCC GTAAAAGGAC CATTGTTGGA AGCnGCCTTA AGAA 104

(2) INFORMATION FOR SEQ ID NO: 1872:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1872:

CCATTATCTC AAGAGGTTCT AGTAAGGGGA TGGCATTTGC TTCTTATGAA TTTGACCAGA 60

ATAA 64

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1873:

GACAACCTAT TGTTTCCCTA CCATACTGTT GTCCGGTTTG ACAAAACGGC GTTCCACAAT 60

CCATACATCG TGCACCTTGG ATAGAGGCAT CTTCTTTAGT AAATCGTTGT TGATATGCTT 120

TATGATGCTT CAAACGGTCT ACCAGTGATA ATTCACCTAA GTACTGTTTG TCATACTTCA 180

TAAATCCTTT AAATTCACCC ATCGTATCTC CCCCTTTCCT TAATACACAA CGGCTGGTTT 240

ATGTTTAGCA TCGATTGTTT TGACTGTnCA TCGTAAAATG CAGCTAACAT CGCTTCATCT 300

TCCATTGTCA TGTGAAGATT TTGTGGCAAA nGGAATTTTT TGCATCAATG AATnGGTGAA 360

CCTTTGGGGG TGACCTT 377

(2) INFORMATION FOR SEQ ID NO: 1874:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1874:

ATTATCTGAA TACGCAGCAG TTGCAGCACT TGATGGATCA GCAGTATTTA AAAGAGGTTA 60

ACACATTACC CAATAGTG 78

(2) INFORMATION FOR SEQ ID NO: 1875:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1875:

CTAAAAGAAG TTAAAGAGTG TGATGGTAGA ATTATATTAT TTATTGATGA AATgCCATAT 60

GCTTGTAGGT GsTGGTAAAA CAGATGGTGC CATGGATGCa GGCAACATGC TAAAACCAAT 120

GTTAGCACGA GGAGAGTTAC ATTGTATTGG TGCAACAACT TTAAATGAAT ATCGAGAATA 180

TGTTGAAGAT ACAATT 256

(2) INFORMATION FOR SEQ ID NO: 1876:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1876:

AGCGCGAAAT TGAGCAAGCG GAACATGCGA CTGATGAAGA AAAACAAGTT GCTTTAAATC 60

AATTAGCGAA TAATGAAAAA CGTGCATTAC AAAACATCGA TCAAGCAATA GCAnATAATG 120

ATGTnAACGT GTTGAAACAA ATGGCATTGC TACACTAAAA GGTGTACAAC CTCATATTGT 180

AATTAAGCCT GAAGCACAAC AAGCAATaAA AGCAAGTGCA GAAAATCAAG TAGAATCAAT 240

AAAAGATACA CCACATGCAA CAGTTGATGA ATTAGATGAA GCGAAT 286

(2) INFORMATION FOR SEQ ID NO: 1877:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1877:

ACTTCCAAAC ATGATAAAGA CAGACTACTT CACAGGTTTA AGGGAAGCAA CCACATTAGC 60

GGGATTCACC CTAT 74

(2) INFORMATION FOR SEQ ID NO: 1878:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1878:

TTTCATTAAG TTCAAAAAAT CTCAATAACT TTAAGGATTG GTCCGCATAT TA 52

(2) INFORMATION FOR SEQ ID NO: 1879:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1879:

ATACCCCTGA GATTAATTAC TTGTCCTTTT TTTAGAACAA CATCTCCTGG CTTTGTTTCG 60

(2) INFORMATION FOR SEQ ID NO: 1880:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1880:

AATATCATTA ATAATATCAT TGATGCAAGT CCTATTGTGC ACAACTGGGG TGATTGCCTT 60

(2) INFORMATION FOR SEQ ID NO: 1881:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1881:

ACAATGGCAC ATGGACTTAT GCCTGGGGTG TCCTGTTCGT CGCAGCATCA AAATGA 56

(2) INFORMATION FOR SEQ ID NO: 1882:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1882:

TGCAAAGCAT TGGCACATGG CCAGTCAGTT TTACAACGTC GTGACTGGGA AAACCCGAGA 60

nGCGACGTTG TAAAACGACG GCCAGTGCCA AGCTTGCATG CCTGCAGTCG ACTCTAGAGG 120

A 121

(2) INFORMATION FOR SEQ ID NO: 1883:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1883:

ACATTTAATG TATAACCAGT TTCAACATTG CCGATTTAGT GGCAGCAGTT GCAGGA 56

(2) INFORMATION FOR SEQ ID NO: 1884:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1884:

TGCATCCATT TGATTGAATT TTATGTTTTG ACCAAAGCCG GTTGCAATGT AC 52

(2) INFORMATION FOR SEQ ID NO: 1885:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1885:

TGAAAAGTGG TGGAATGGTG TTAAAAGTTG GTGGGTAATT TTAGAGAAGA G 51

(2) INFORMATION FOR SEQ ID NO: 1886:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1886:

TACACGAACC ATACTCACCA GGTTTTCGTG TCATGAGGCG ATATTTTTTG TCATTTTATA 60

TACATTTATC CAAATTCATC TTTTAAATGT TGAGT 95

(2) INFORMATION FOR SEQ ID NO: 1887:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1887:

GCTACCAAAG GCGTTTTACC TATTGCTAGT CACTGCAAGT GGCTTAGCTA TGCAGATCAA 60

CTGGT 65

(2) INFORMATION FOR SEQ ID NO: 1888:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1888:

GTGGGACCAA CTGGCCGGTG ACGGTGGTAA AGGTGCTTCA GTCGTATTGA AGTGGGATGA 60

(2) INFORMATION FOR SEQ ID NO: 1889:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1889:

TGTTGGAGAA ACAGTTAACG AGGTTTAATG TTAAAAAAGC AACGTATCAT GGGTATA 57

(2) INFORMATION FOR SEQ ID NO: 1890:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1890:

TGGGATCTGC TTGCAAATAC ACAAAACTTT CTGGATTTTA TTACAATTGC AATATAATCA 60

AACA 64

(2) INFORMATION FOR SEQ ID NO: 1891:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1891:

GGCATCCACT CAGATAAAAT AAAGATGTCA AAAAGGCAAA GATGGTGCTA AAAAAACAA 59

(2) INFORMATION FOR SEQ ID NO: 1892:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1892:

GGTATCTCAA CGATCCTTTA GGTTAATTCG GAAATTTCTA CACGTGAGTT AGCA 54

(2) INFORMATION FOR SEQ ID NO: 1893:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1893:

TTGTCTTGGC AATGGCAGAG CAACAGAAGT TTAAAGTGCT TGCTGATCAT AT 52

(2) INFORMATION FOR SEQ ID NO: 1894:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1894:

TAAACCTATA CCCTGTAAAA AGAAAAATCG TGGATCGAAA GAACATGTAT GTGGCATTTA 60

TGATTGATGC TCAAGCAGA 79

(2) INFORMATION FOR SEQ ID NO: 1895:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1895:

TTATAAAGGA GAGAAATCCT TAATTATGAA TAAAGCATCA TTTGATAAAA AAGTTAAAAA 60

GCAATTATGG TTTTTGAACA AGAAGGAGAA ACAAGCATTA GATCAACGAT TGTCTTCTAT 120

ATCTGATGAT GACAGCGTTA ACTTAAATAA GCCTGTTACC TTTGCTAATG CTTACTTAAG 180

ACAAAATGTA TTTCGAAATA AAGAAACAAA AAGTTATAGT ATGTTTGTTA CATTAGTAGT 240

GATGATGTTT GCTTATGTTG CTTTATTAGG TTTGTnTTTA TTTGGGCTAA TTACAAGTCT 300

ATCTGGCGTA CAATTTTTCG TTAGTCCTAA GGTAGATTTA TCTACnACTG TTGTTATTTT 360

AACAATnATT GGAGCGA 377

(2) INFORMATION FOR SEQ ID NO: 1896:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1896:

TTAGGATCCG TCTTTGCCGC AGCGTGGGTG TTCCGCGAGC GCTTCTTAGA GGTTTTGC 58

(2) INFORMATION FOR SEQ ID NO: 1897:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1897:

ATCGCTCAAA CCGAAATTGA AAATGCATCT ATTACTTCAT TAAGCCGTTT ACCAGACGTT 60

ATATTAGCAT TGAAAAGTGG AAAGGTTGAA GGTGCTGTAG TTGAAAAACC TGTAGCAGAA 120

GCATATTTAA AACAAAATCC TAAATTAGGA ATTTCCAATG TGAAATTTAA TGAAGAAGAA 180

AAAGATACAG TGATAGCAGT GCCAAAAGAT TCACCAAAAT TATTGTCACA AATTAATAAA 240

ACGATTAAGG AGGTTAAAGA TAAAGGATTA ATCGATAAAT ATATGACTAA TGCTGCAAAT 300

GCGATGAATG ATGACAGTGG TTTTATTTCT AAGTATGGTA GTTTTTTCTT GAAAGGAATT 360

AAGATTACAA TATTAATTTC ACTTATCGGT GTTGCATTAG GTTCTATTTT AGGTGCATTC 420

GTTGCGTTAA TGAAATTAAG TAAAA 445

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1898:

ACCTTTTCAA TGTTGCTTTG ATATAAATTC ACAAAGTTGA CTTTTnAATT CTTCAATAGA 60

TTCTCTACTG CGATAGCTGA ATTGCCATCT TTTCTACTAC T 101

(2) INFORMATION FOR SEQ ID NO: 1899:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1899:

TGCCCTGGAT GCCTTTAACT TGATTCATGA CCTGTGGTTT TATTTCAATT TAGATGAGCT 60

ACCTTCAAGA CCTTC 75

(2) INFORMATION FOR SEQ ID NO: 1900:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1900:

AGCAATACGG AACTGATGAA CGGAATTGTA ATACGAGAAT ATGAAGCATC AACG 54

(2) INFORMATION FOR SEQ ID NO: 1901:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1901:

AGTACCTGAG TATCGCAGAC CGGCTTCAGG TCGTAGAATT TCTATACGTG GAGCTAGAAG 60

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1902:

GTCTAACTAC AGCATGCCGG CTTATTGTTG CACTTTCTCA ATATTTCCAT A 51

(2) INFORMATION FOR SEQ ID NO: 1903:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1903:

GGATTnAAAC GTGCATTAAC GCGTGTnTTA AATAGTTATG GTTTAAGTAG 50

(2) INFORMATION FOR SEQ ID NO: 1904:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1904:

ATCGTATTTA TTTCAGCGAG TAGCGGTAGC CTTCAATACA CAAAGATTTT ACC 53

(2) INFORMATION FOR SEQ ID NO: 1905:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1905:

ATAAGACGCT AGATCTGGTC AATTTATTTC CGATTTTTTC AACACTATTC 50

(2) INFORMATION FOR SEQ ID NO: 1906:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1906:

TTCATCTGAA TCGTCGGCTT TCGCGATTAC TTCTTCGTCA GGGTTGCTAT C 51

(2) INFORMATION FOR SEQ ID NO: 1907:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1907:

CAATTGCTAA TAATCCTTTT AAGTCATTAA TGATTTGATC TTCCGTAATG TTGAA 55

(2) INFORMATION FOR SEQ ID NO: 1908:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1908:

TTGCCAAACA GACATGACTT AAATTTCAAT ATCTTCTTTG ACTGCATCGA TAT 53

(2) INFORMATION FOR SEQ ID NO: 1909:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1909:

TGAATTTCTA TACAATTATG GGGAAGGGTA TTGGTGAATT GGAATGGGCT CCTAAGTTTA 60

CAAGCCCCCA TTCGATGGCC GTTAAAGTTT TTAA 94

(2) INFORMATION FOR SEQ ID NO: 1910:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1910:

AACATGATCG TGGGGGGATG TTATGTTTGT TCATATATTT AGGAAGTCGT TTGTAGTTAT 60

TGTTTG 66

(2) INFORMATION FOR SEQ ID NO: 1911:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1911:

ATCTTCGCTC CACTTACTGC AATAAGGATT TGCGGCAATC CTAAACCGTT TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 1912:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1912:

AACAATCGTA ACGATACAAC GCAATCTTCG AAAAATAATG CAAGTGCAGA TTTCCGAAA 59

(2) INFORMATION FOR SEQ ID NO: 1913:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1913:

ACACCACACA CACACACACA ACACCCCACA CAACACACAC AAACACACAA A 51

(2) INFORMATION FOR SEQ ID NO: 1914:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1914:

TGTTACGACT TGGTCGACCT GGCAAGCGCT TCGCGCACGT TCTGCAGCnT CTCACTTATT 60

GGTATCGCGA TGCGACGTTA AGAAATTTCG GAGTTCTGGT CACCTTATGT T 111

(2) INFORMATION FOR SEQ ID NO: 1915:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1915:

TGGTCCGCTC TCAATCGCAT CTTCAGGTTT TACTTGGCAA AAGAGCGCGG TGCTCA 56

(2) INFORMATION FOR SEQ ID NO: 1916:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1916:

GCCGACAGTA AAATAAAGGT ACTTGATATA ACATATAACG GAAAGCAACA GTTACTGTCA 60

CA 62

(2) INFORMATION FOR SEQ ID NO: 1917:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1917:

ATGATATTTA TTTGATTGAA GAGATGTTGC TTAAACAAGA AGACGTACAA TTGATAnAAC 60

GTAAAGATTA TATTCAGCAC CCTAAAGAAA ATGGTTACCG CAG 103

(2) INFORMATION FOR SEQ ID NO: 1918:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1918:

CAGTGTAGCG TGTGTCATGC CGTTTTACCA CAATTGAAGA CTGAGCTCTA TCCCTGTGCC 60

(2) INFORMATION FOR SEQ ID NO: 1919:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1919:

TCAAATTAAC TTCCAACAAA AACAAATGCA AGGTGAAGAA ATTGCTGAAG AAGATTTACA 60

AAAAGCGCAA GAACAAGCGC AAGCAATTGA AAAAGATGAA AACATCTCTn CATTAAT 117

(2) INFORMATION FOR SEQ ID NO: 1920:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1920:

TGCCTAATGA AACATTTAAA AATATTTTTA AATATATCTA TCAACACATC GTTCTATTAA 60

TTGGGATTGT TAGTTTTCTC AAAGGATTTT TAGGATTTTT CATGGAAAAA AATGGAAGTA 120

ATTTATATTT TGTTTCATTC CCGTTTTCAG TAGTCGTTGG ATTCTTTATT GTCTTTTTAT 180

TTATATGGTT TAGTTTTAAA ACAATACAAC TGCAGTGTTT TAACAATTCA AATTGGATAT 240

GGATATTCAC CTATTTAGCA ATCATTCTAC TAATTGTAGG ATTTTTCTAT GTATTCTTTA 300

TTCCACAATC ATTACTTGCC TTTGGACCAT ATATTCAGGT AAGCAATTGG GTATTTATTA 360

TATTTTCATT TATAGTTATG CCTATnGGAT TACGCATTGA 400

(2) INFORMATION FOR SEQ ID NO: 1921:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCACAGTCAT CATTTnATTT TCGATTTTCA ATAATTGTAT TTTTAATTTA TCTTGATATT 60

CATTAAGATT TATACAAGCT ATCTTTAACA TTGCCTTATC TTTGATATAT TTCTTGCATT 120

CG 122

(2) INFORMATION FOR SEQ ID NO: 1922:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 410 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1922:

AGAAGATACC ATACACATTT aATTAGTTAC AGCATAAATC AATTTATACC CTTAATTATT 60

ACATTGTTTA TATTTTAAAT TCGGGGGAGT AATTTTAAGT AATATCTTGT TGCTGCTAAT 120

TCTATTGTTA ATAAATTGAT ATTAGATGTA GAAATTGAGT GTGAAAGTTA ATAATAGATG 180

ATTTAGCTAG TAACATAATT AATTCATATA TAGTCAAAAA GTTCTGTTAG ATACTGTTCT 240

TGATGAATAT TCTTTGATGT TAGGTGTTAG CTATTCTAGA TGAGTTTCTT AGATGTGGAT 300

GCCTGTCTTG ATGAAGTTAT CTATGATGTT AATATAATAC TTGATGTTGA TTCTTAGATG 360

TTAGTGCGAT TTCAAGATGC TGATTCTTTG TTGTTGCACT ATCTTGGTGA 410

(2) INFORMATION FOR SEQ ID NO: 1923:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1923:

TTTCTATGGT TTATCAGGTG ATTTTACGGA AAACAGTGAA GATTATGGCG TATACCGCTT 60

TAAACGTGGA TTTAATGTAC AAATCGAAGA ATTAATAGGG GATTTCTATA AACCAATTCA 120

TAAAGTGAAA TATTGGTTGT TCACAACATT GGATAAATTA CGTAAAAAAT TAAAGAAATA 180

GATGTAAATG ATGTTAGGGC TTATAGTnAT TGATACTATA GGCTCTTTTT TATATGTTTT 240

TTAATAAAGC CTCGAATAAT GATATATTAA ATGACAAGTT TAACAAGTGA TTGCAATAAA 300

TATAAATnTG AATTGCACAA CCGATTTGnA AATGATTGAG TTGAGGAA 348

(2) INFORMATION FOR SEQ ID NO: 1924:

(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1924:

AGGGCAGATT TAAGCTAACT TGGAATGTTT TCGAGTTTTT GAGTTAGTTC TCTATCCATT 60

TTTTCAGTTA CATGAGTATA TATGCGAATG GTTGnTTGTT CATCTACATG TCCTACCCTT 120

TTCATAATTG CTTTTAAAGA AACATTCATT TCTACTAATA AAGTTATGTG TGTATGTCTA 180

AATGTGTGCG TGGTAACTTT CTTATTCATA TTTAAAGCTT TTGTACGTTT TCTTAACGCA 240

CACCGGCCAT TTC 253

(2) INFORMATION FOR SEQ ID NO: 1925:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1925:

GGTATAGGTG CAAGTCCTAT CTTCCGCTCC ATGGTTTAAT GATAATGCGG GA 52

(2) INFORMATION FOR SEQ ID NO: 1926:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1926:

TGGTCACTGT TCCTGATGCT TACGTTAGAA TGTAAGATTC CCGATTTATC AGTTATATAC 60

TGTTTGCTTC ACTTTGGAGA TCTG 84

(2) INFORMATION FOR SEQ ID NO: 1927:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CTTTCTAAAT AATTCTAGTA TAGTTTTTAT TCAAATACGC TAGGCTCAGA GCTATT 56

(2) INFORMATION FOR SEQ ID NO: 1928:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1928:

GCAAATTGTC ATTAGACGGA GTATTATTTA GAATTTTCGG TGATATCCAC CGGCACAAGA 60

TCGATGTTGG ACAATATCTA ATATACTGAT ACGCATTTAA ATAGAAGAAG GGAATTAGAG 120

TTTGGTTnTG AATGCAAA 138

(2) INFORMATION FOR SEQ ID NO: 1929:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1929:

ACATCTTTAT ATGCTTCAAC ATCAAATACA CCACATATTG GTAAACAACA AA 52

(2) INFORMATION FOR SEQ ID NO: 1930:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1930:

TTTAATGTTC ACAACACCGG AATAATAATA ACTAAAGCGC CGCTAATAAA T 51

(2) INFORMATION FOR SEQ ID NO: 1931:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ACGAAAAATA AATAATCATT TCACCTTTAT AGCCAGTATT TTTAATTAAT ATATTTTCAT 60

CTATTAGCGC TTCTAAAAAT CTATTTGACT TTTGAACATA CTCTTTAGCT ATATTATTAA 120

CAACAGTATA GGATTCCTCA TAATTTAGTT GATTAAATTC TGAGTCGTTC ATTAATTCAA 180

CTAATCCTTT TATTACTTTT TGTACAACAT TAATATTTTT ATCAAAATCA AATTTATCTT 240

CCTTAGATAA ATTAATAnnn AAAGTCTTAA GAACATTTGT AAATAGCTCT GCAACACTTA 300

TAGTTTGGnC AAATTCCTTA AATTTATTTA CACAGTACTC ACACATTAGT TTTAAAAATA 360

ATGGATTGTT GAATTCTGGA TTTAATATAG GTAACTTAGG 400

(2) INFORMATION FOR SEQ ID NO: 1932:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1932:

ACTTGCGGAA nGACGCAACG TTTATGTACG TTGGAAGAAA AATTCAGGAC TTACGTTCAA 60

AACTACCATA GCAATATGCA TTGAAAGATG ACAGTATGCG 100

(2) INFORMATION FOR SEQ ID NO: 1933:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1933:

CGCTCTGCTT TAAGCGTTGG GACTTTGTCA ACGGTAGTGG ATGGGAAGTG GTTCTGCTTT 60

G 61

(2) INFORMATION FOR SEQ ID NO: 1934:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1934:

(2) INFORMATION FOR SEQ ID NO: 1935:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1935:

ATGTATTACG GTTTAATTAA GCCACATACC AACAAGATTG CATTTATGGT ATCTCA 56

(2) INFORMATION FOR SEQ ID NO: 1936:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1936:

TCGCACCAGA AACAAGGGAT TGTTAAAATT GCGTAAATCC TTAAATTTAT TTGTAAATAT 60

A 61

(2) INFORMATION FOR SEQ ID NO: 1937:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1937:

ATGAATAATC ATATTTCTAA TCAAAGTAAT AGCATTTATA TTGTGTTTAA A 51

(2) INFORMATION FOR SEQ ID NO: 1938:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1938:

TTGCTGAAGA TAGAGGCTTC ATGAAGGTGG AGAAGTTAGC TGATTTCTGG AACAGG 56

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1939:

ATCTCAATGT ATTCCTCTAG TGTAAGTTCT TCATAAATAA CCGGTGATTC C 51

(2) INFORMATION FOR SEQ ID NO: 1940:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1940:

CTCAGGTCGA CTCTAGAGGA TCCCCTGTTA AATAAAACTT CTTAAGCACA TACTTATTTC 60

ACTATGCCTT TTACGTTCCC CTTATACTTT TCTCACATCT TTCTCTTAGA CTACTCCCTT 120

ATACGCCCCG CTCAATATCT TTAATCATTT CATCTACAGT TATTTTCGCA CTCGTTAAGA 180

CAATAGGAAC GCCTGGCACC TGGATGCGTA CTTGCACCTG cAAAATATAw ATCTTTATAA 240

TCTCGCGATA CATTyTGTGG ACGATAATAA TTACTTTGCG CTAAAGTTGG GCATTAAACC 300

GAATGCCGAA CCAAATTC 318

(2) INFORMATION FOR SEQ ID NO: 1941:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1941:

CCGGGAAAAT TTTTGGAATT AAGTGGAAAA AAAATCCCCT TAAAATTCCC CTGGCCA 57

(2) INFORMATION FOR SEQ ID NO: 1942:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1942:

TGTTCTTCTT TTGAATCTGT TTTATTCGTT TGTTCCTCTT TTTTCTGTTC ATCTTTCATA 60

TTTCCACATC CCCCAATAAA AATGATTAAA AGTAATACAC TCATGTACAA AGCAATTTTT 120

TTTATATACT CCATCATTTC ACATCTCTCT GTTTTAATTT TATAAACATT TGAATATTTC 180

ATACAACTTA TTAAAATAGT GATTATTCAA CTTTTATGTT ATCAAACAAA ACTAACTTAT 240

TCAATTTAAT ACATGTAATT CATTTTAACT TTATTATTAA ATGTTCTAAC GTnATTTTTT 300

ATATTAGTAA TTATATTTAT TTATCCTCGC TTGGATTAAA GTAGATACTA TCTGTGAAGT 360

AnATATTTTC TGCCTTGn 378

(2) INFORMATION FOR SEQ ID NO: 1943:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1943:

AAGAAGAAGT CAAAATTCAG CTAAGTAAAA GCTCGAGTTA TAAAAAAGTC TAAATTGATT 60

CAACAGGAGT AGAAAAGGAA ATTAGTCTTG CATATTTTAG AAAATGAATA AAAACAGTTA 120

CTATATGCAA CTCAAGAATT AAATATTATT TAAGCCACAT ACCTATTAGA GTACAAAATA 180

TACAAGTTGT ACTTATATCT AGGTATGTGA CTTTTGATTT TAAGCGTAAA GTAAAAGTTT 240

TTATGTTTGT ATTAGTTCTA AATTATTTTG CACTTGGATG ACACGTATTT TTGAGTTTAA 300

GTGGTGACTC AAGTTCAATA AAATAAATAT CAGATAGGAT AATTTGAnAA TnATATGAAA 360

GGGTTATCTC CAAAATnATC TCCATATTAT AAGG 394

(2) INFORMATION FOR SEQ ID NO: 1944:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1944:

TATTCGTGAT GACGATTGTC GGTGACATGA AGTTCTATTT GCTGGCACTG AT 52

(2) INFORMATION FOR SEQ ID NO: 1945:

(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1945:

CGTTTAAAAA ATGATATCAA TCTTTATTGT GGATTGCAAC ATCCGTGTGC TCCATAAAAC 60

GTGTGGCGAG ACTTGGGAAA GG 82

(2) INFORMATION FOR SEQ ID NO: 1946:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1946:

GTATTATTGA TGAAGAAACA GCTCTCCAGT TGTAGATGCA TGCTACGTTC ACGTTACCAC 60

TGTATCAATT 70

(2) INFORMATION FOR SEQ ID NO: 1947:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1947:

TATCACCAGC ACCAAGGnTA ATGACATGCT GATCTTTTGC AGTTATGGTn 50

(2) INFORMATION FOR SEQ ID NO: 1948:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1948:

ATTGTATGAA TCTTTGGGGA ATGAACTTTn AACGAACGGA CATCTTGCAA TGACGCATCA 60

AAATGGTTTT AACACATGTA ATCGGCTCTC GGTACTATTC GTGTGATGTA CACATGG 117

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1949:

TTTGATGATT TCGGGATGGA TTGGTATTGT GGTGAATGAA TTTTTTAGCT CATCATCAAA 60

TTAG 64

(2) INFORMATION FOR SEQ ID NO: 1950:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1950:

CTCTAGTGGC CATTCATATT TGTCGCTGAA TGATGTTGGT ACATCCATTG CTGCTGT 57

(2) INFORMATION FOR SEQ ID NO: 1951:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1951:

CTGTCCTTCT GAAACTTGGG TATTTAATTA GGAATAGTTA AAAAAATCAT TCACAGAAAC 60

ATTTAATA 68

(2) INFORMATION FOR SEQ ID NO: 1952:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1952:

TTAAATTAAC CTTAAGGTTG GnATTTTTAA CCCCCAAATT TTTGGGGTGG TTAAAATTCC 60

(2) INFORMATION FOR SEQ ID NO: 1953:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1953:

GACATTTACA CCTGCTTCAA TCTGGTCCAG TGCAGCATCT AATTCTTCGA 50

(2) INFORMATION FOR SEQ ID NO: 1954:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1954:

ATTTGGCCAA CTGTTCAGCA CGGTATTGGT TCAATGCAAC ACTTTATCAT TGCTTCAGGG 60

CTATATCGGT GGTATGGGnT GTATCACTTC TTAGAACGTG GTATTAA 107

(2) INFORMATION FOR SEQ ID NO: 1955:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1955:

GAAGTGAATA TGAAGCTGCT AAAGACTCCG GAATGCTACC TCAGACAACT GATG 54

(2) INFORMATION FOR SEQ ID NO: 1956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1956:

ATGATTATTT TAGTTCCATT TGTTGAGTCG ACTGCTAAAG TTCCATTTAA ATGTTGTACA 60

ATAAGCAGTA ATTTATGATT GTTTACAGTT TTTAATTTAC CATGAACTTT TGAAGCATTT 180

GCATGTTTAA TAACATTATT TATCGCTTCA CGCGTAATCA TAACTAACAT AGATTGTTTA 240

GTAGGACTTA ATACTTGCGC TAATTCTTTA TTTTCAAATG TAAAATCAAT ATCAGCATCn 300

nTnAAAACTT TACGTATACT ATCAATCTCT TCAATAAATG ATGGTAATTT TACATCATCA 360

ATAAT 365

(2) INFORMATION FOR SEQ ID NO: 1957:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1957:

AAATAATGTC ACAAAAGTTA AAGATACTAA TATTTTTCCA TATACTGGTG TAGTTGCTTT 60

TAAAAGTGCA ACTGGATTTG TAGTTGGAAA GAATACTATT TTAACAAATA AACATGTGTC 120

GAAAAATTAC AAAGTGGGCG ATCGTATTAC TGCACATCCA AATAGTGATA AAGGTAATGG 180

TGGTATTTAT TCGATTAAAA AGATTATTAA TTATCCAGGT AAAGAAGATG TATCAGTCAT 240

TCAAGTTGAA GAGCGTGCAA TAGAACGTGG ACCAAAAGGC TTTAATTTTA ATGATAATGT 300

AACGCCATTC AAATATGCGG CAGGGGCTAA AGCTGGTGAG CGAATT 346

(2) INFORMATION FOR SEQ ID NO: 1958:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1958:

TTTTCCAGTT AATTTTTCCA GTTCACTAAA TACTTTATTG ACTGTACCAG ACCCAATAAT 60

AATTTGGTAT TGTCCCCCAG TAGAAAACGT CCCTTTAACT ACATCCATAT TGTTTAGCGC 120

CTCTTCATTT ACTAAACTTT CATCATTTAA AACTAATCGT AGTCTCGTTG CACAATGCGC 180

CATTGCATCT AAATTCTCTT CTCCGCCTAT CGCGTTCAAA ATTTCTTCTG CGGATTGCTT 240

ATAATTCATA TATTTAGCCT CCTAATTAGA ACCGGTTCCA TTTATTCCAC TTTATTGTAA 300

CCGGTTCCAA AAATATTTGC AACACTCTAT TATCATTTTA TATAAACACC TACACCATTT 360

(2) INFORMATION FOR SEQ ID NO: 1959:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1959:

GATTGCATAT AATAGTAAAA ACATTACATC TTGAACAGTA CTCGTTTTGT 50

(2) INFORMATION FOR SEQ ID NO: 1960:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1960:

AATTTGAACC AGACACTGAT ACAAGTCACA CCCAGAAACT TTTAAGGACG TAAATGT 57

(2) INFORMATION FOR SEQ ID NO: 1961:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1961:

AACGCTATAT TAGCGATATA CAATGATGCC ATTATCAATA nTACAnCTGn 50

(2) INFORMATION FOR SEQ ID NO: 1962:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1962:

TACAACGTCA GTTGGCAGAC ACCAGAAGAA GGATTCATAA GTATATTCAG GAACTTGTTA 60

(2) INFORMATION FOR SEQ ID NO: 1963:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1963:

AATTTTTCCC CCTTTTTAAA TTTCCCAAAA AAAAnCCCCC AAnAAAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 1964:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1964:

CAACAAGTAG ATGCATCAGA GAGTAGTGTT CAAACGTTAA TAGATGTGGC ATG 53

(2) INFORMATION FOR SEQ ID NO: 1965:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1965:

AGCAAAGGCA TAACTGCTAA TGACCATGTA AATGAGACGA GTCGATCGTG GCCA 54

(2) INFORMATION FOR SEQ ID NO: 1966:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1966:

CTCAAATAAC TGGCTCAACT CAACCGGTCT ATAACACCAT AACACCGCAT GCCACTCTAG 60

CATACTCAAT CGCTCTGGTA CCAGCnCTCA AATAACTGGC TCACGCCAAC TGTCTATAAC 120

ACTAACACGC ATGCACTCTA GCCTACTCAG AGCTCTGGTA CAGCACTCAA TAGCTGACTG 180

TCACAGTCCA CACACACTCA ATACTGGCTG ACACAGTTCA CACACnGCTT ACTCGCTCTC 240

(2) INFORMATION FOR SEQ ID NO: 1967:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1967:

CAGTTTAAAC TCGATGTTGT GTACTACTGT GCCAGCTGGA ATGTTTTATA ATGGTGATG 59

(2) INFORMATION FOR SEQ ID NO: 1968:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1968:

GTTACATGGC ATCACGCCAA ACCTGTCTAT AACACCATAA CACGGCATTG CC 52

(2) INFORMATION FOR SEQ ID NO: 1969:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1969:

ACAATTTTAA TTATATAACT CCAGGGGCTA CAGTAATACG ATTTCTCCAG ACTCCAAA 58

(2) INFORMATION FOR SEQ ID NO: 1970:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1970:

TGACGTATAA TGGATGAAAG TCTATTAAGT TTAAGAAGCT AATACTGTGA AATCTTTCT 59

(2) INFORMATION FOR SEQ ID NO: 1971:

(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1971:

TATCATGTTA TCTTCAATCG TTCACCAACA GTCATTTGCT GCATCAGTAA CG 52

(2) INFORMATION FOR SEQ ID NO: 1972:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1972:

TTGCTGGTGC CATAGACTAC ACTTGTTTGA TATCAGAAAT GGGATCTGTT CCATTACC 58

(2) INFORMATION FOR SEQ ID NO: 1973:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1973:

AGTTAAACCG AGTCCAACCC AAACCTCCAA TCCACCTAAT GGTTAAAATT CCAAACCATT 60

ACCAGGGAGG GACCAAAAAA CGGAATGGGG CCTATTGGTA GGGTACCTAT CCCATTTAAA 120

AATCCATCCA AAAGCCCAnA TTATCGGACC ATTTTCGCCA AAAATAATTT AAGCGGAAAT 180

TGAATACCTT AAAATTCTCn GGGCCCACT 209

(2) INFORMATION FOR SEQ ID NO: 1974:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1974:

ATCTGAGTAT TTATAACATA AATCACTAAT ATCGTTATTA CATAGGGATA GGGTAAAAGT 60

(2) INFORMATION FOR SEQ ID NO: 1975:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1975:

TTCCTGCATC CGAGTCTGAA TCGCTGTCGA ATCACGTCGA GTCGATCGCT ATCAGGTCGA 60

GTCGCGTCGA ATCGnTCGCT ATCGAGTCGA TCGCGTCGAA TCGAATCACG TCGAGTCG 118

(2) INFORMATION FOR SEQ ID NO: 1976:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1976:

TTGCAACnTT TGATCTAGAT ACTACCTTAG TTGGATTGTA CTACTTGATT CTACTTCACC 60

TTTAGTTGGT TTTGTAGCAG GCGTTTTGTC TTTACCTGAC TCACTAGATG CGTCATTTTC 120

TTTTTCAACA CTTGGTAATT GTTTATTGTC ATCTTTTTGG CTGTCTTGTT TTTGTGATTC 180

TTTTTCAACA GGTGATGGTG TTGGTTTGCT AGGCGTACTG GAGTAGCTTC CTTCTTAGCT 240

GAGTTATCTT GTTGTTCTTT TTTGTTAGAT TTATCGGTAT TGGCTTTTGT AAATGCTTCT 300

nTATCAACGA TTCTGACATG GTATTGTCCA TCATAATCAA TCGTTTTTAC GTGAACTTTA 360

ACGATAGCAT CATATAGAGT TTACCTTCAA CATATGGGAA 400

(2) INFORMATION FOR SEQ ID NO: 1977:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1977:

TAGACAAAGA CAGTAACAGT AAAGTACGCT TCAGAACTGA TGGCTCACTG CGAGTATAAA 60

AACTTGTAGT GTCC 74

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1978:

ACTCAAAAAC TCGGAAAACA TTCCAATTTA GCTTAAATCT GACCCTTTTT TTGACCCTTA 60

TATTTTTTAC AA 72

(2) INFORMATION FOR SEQ ID NO: 1979:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1979:

ATGTCATTGG CTTTGAACTT TATCTTCAAG CACCCAATCG TTTTAACTTT TCAAAATTTG 60

GCACCATAA 69

(2) INFORMATION FOR SEQ ID NO: 1980:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1980:

CAGAGAGTTG TCGCTCATTA AACGCCACnT GATGAGTTTT CGCTTACGAA GTGCCACGCG 60

GTATGGATAA TTTTCACCTG TTGCTGAGTC TTTGATAAGC CTCGACTGT 109

(2) INFORMATION FOR SEQ ID NO: 1981:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1981:

(2) INFORMATION FOR SEQ ID NO: 1982:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1982:

GAATCTGTTC AAGTTAGAAT TATCCCGGCA TAATGATAAA GGCGAGTAAA TGG 53

(2) INFORMATION FOR SEQ ID NO: 1983:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1983:

GnCTTTTGAA TAAAGAAAAA TTCATCAATA GAAAAACCGT CTTTATCGTC TATTTTTTTA 60

ACTAGTAAGT TCGGCGTTCT TAGAGACTCA AATATTGATT TTACGTTTTT CTTTGTTACA 120

CCACTAACAC TAAATATTCT TCCATCTAAA TCTACTAATT CTGGTACCGC AAAGACATCT 180

AAACCATGTG TTTTTTCTTT GTATTTATTT TCATCTTTTC CCAATAAAAA CACTTGGAAC 240

TTTTGATTTn GT 252

(2) INFORMATION FOR SEQ ID NO: 1984:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1984:

CGTGTTAATC AACTAATTCT TAGTTTTAAC TGTCGTAATA ATCAACTGAA CACTTTCAAT 60

CTA 63

(2) INFORMATION FOR SEQ ID NO: 1985:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1985:

TCCTAAAATG ACCGCTAATG CCTATGGATT GTTATCACCG ACCGCAGGGA CAGCACGACC 60

TAC 63

(2) INFORMATION FOR SEQ ID NO: 1986:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1986:

GGCATATAAA AATTAGAGAA ATTATTTCAA ATGAACAGAT AGAGGCACAA GATGAATTAG 60

TTAAACGATT AAACGATTAT GnTTTAAATG TCACTCAAGC AACTGTTTCT CG 112

(2) INFORMATION FOR SEQ ID NO: 1987:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1987:

TTTATCAATT TGTAACGAAC ATGAATTACA TGTTTCAGGA AAATATATTT CATCCCATTT 60

TTAAAAAGTA TAAGATTTTA TGAAAAATTA AACCAATTnA GTATAA 106

(2) INFORMATION FOR SEQ ID NO: 1988:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1988:

AATGGCGTAG TTACAGCATT TATGATTGTG TTAATCTTTT CTTCTGATAA ACATAATCTG 60

TTTGACCAAA AGTATTTAAG TGTTCAATTA ATTAGTTTTA TTATTTACGT CGTATGGCAA 120

GTTTTATTGA TAATGTTTTA TTATCATTCA AAACCAAAAA ATAATTCATT TTCAAAATTT 180

TGGTTAGGTG GACATCAGAT TCACTTCCAT GAAAGTAAAT TAATTGAATT TGTTGGTTTC 300

TTAGGAATTT CTTATGTTAC ATTCAAAAGT GTGCAGTTAA TTATGGAAAT TCGTGATGGT 360

TCTATCAAAG AAATTAAAGT ATGGAAATTA ATTCAATTTA 400

(2) INFORMATION FOR SEQ ID NO: 1989:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1989:

TTCAGCTTAC AATAATGAGC AGGTTGGGGT GGGCTCCAAC GCAGAGAATT TCGATAAGAA 60

ATTCCACAAA TAATACAAGT TGGCCCACTC CCATTCTGTA ATAAATATAG GAGGTCATTG 120

TTATGCAAAT AGAACTTACT GATGCAGCAG TAACTTGGTT TAAAAATGAA CTTGAGTTGC 180

CTGAAAATAA TAAAGTGCTC GTGTTTTTTG TAAGATATGG TGGCGAATTC CAACTCAAGC 240

AAGGATTTAG TCCTGCTTTT ACAGTTGAAC CAAAGGAAGA TGTTGATATT GGCTATGAAC 300

AACAATATGA CGATTTAAAT GTTGTCGTAG CGGAAAAAGA TTTGTGGTAC TTTGAAGATG 360

ACCACATTAT TGTAAATGTA GTTGTCACGA AGATGAATTT 400

(2) INFORMATION FOR SEQ ID NO: 1990:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1990:

CAATTTATTA TGTAACTAAT TATAGCATTG ATGAACAAGG CGCTCAACGT AATAnTACAA 60

TTAATGGATT GTTTCACAAG ATGGTAAAGC TAGGATGTCT TTTTATTAAG A 111

(2) INFORMATION FOR SEQ ID NO: 1991:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TAAACAAATT CATCAATTGT TAGTGGCATA TCCTAATGTA ATTAGAGAGG AGTT 54

(2) INFORMATION FOR SEQ ID NO: 1992:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1992:

GAACGATAGA TTGATGAAAA GTTTAAAAAA GTACGTATAT GTTTATTAAG TTTGAGTTT 59

(2) INFORMATION FOR SEQ ID NO: 1993:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1993:

CGAGACCAAA ATATTCGAAC GAATAATTTC AGTGTTTTGC TCCTTTATTA TAGATTCAAG 60

CTATGGATAA TAG 73

(2) INFORMATION FOR SEQ ID NO: 1994:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1994:

ATCCATACAA ATGTAACAAG CACAATTGCn GCCATACTTn GCATGACAGT 50

(2) INFORMATION FOR SEQ ID NO: 1995:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1995:

(2) INFORMATION FOR SEQ ID NO: 1996:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1996:

TCAnTTAAnA TTAATGTnCG TTGGGGCTCT AATAAAATTT GTTTACAACG 50

(2) INFORMATION FOR SEQ ID NO: 1997:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1997:

TCATGATTTG AAATGACTTT CAATGACTTG GGTGGGACAC TTGTTGCACA GCTGGATGTG 60

C 61

(2) INFORMATION FOR SEQ ID NO: 1998:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1998:

CATGCATTGA TGnTCTCAAA GAACATGATG AAACAGGTCA nCACATGnCA 50

(2) INFORMATION FOR SEQ ID NO: 1999:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1999:

GGTTCGCTAC TGATTGGGTA TACATCTGAT TTAGCAATCT TGCGCACTTG TT 52

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2000:

ATGTGGTTAG ATATCTGCAC ACTTGAACGT TATTGTGGGA TATACTTGGC CAT 53

(2) INFORMATION FOR SEQ ID NO: 2001:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2001:

ATCTCAGTAA GGGTAAGCGT CAAAGTCTGC ACGGATGCTA ATGTTTACCA GGTT 54

(2) INFORMATION FOR SEQ ID NO: 2002:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2002:

CTAAAGATTG TAATGCTTGA ACAATTGGTT CAGTGAATTT TTGGAAATTG TGGAAACTGT 60

TACCATCATC ATCTGTTATA AAACTAAAGT TTAAATTGCC AGTATCATGA TAAACAGCGC 120

CACCACCAGA AATTCTTCTT ACTACATCGA TGTTGTGAGC ATCGATATAT GTCTGATTTA 180

CTTCCTCTAT CGTATTTTGA TTCTTTCCAA CAATGATAGA TGGTCTATTT ATGTAAAATA 240

AAAAGTAACT TTCTTCTGCT GGTAAATTTT TTAAAACATA TTCTTCCATT GCTAAGTTTA 300

AAGTTGGATC TGTAATATTA TTATTACTAA TGAATTTCAT TACAATCTCT CCCTTATATC 360

TATATATATn CTCTACTTAT TTATGCCTTA ACTTTGCTCA 400

(2) INFORMATION FOR SEQ ID NO: 2003:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2003:

CCGAAATAGG ACGGGCAGTT GGATTTATTC GAAATGGGTG GCGTTAATAT ATACAGT 57

(2) INFORMATION FOR SEQ ID NO: 2004:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2004:

nAGTAGTTGA AGGCGACCGC GGTCCACAAG CTGCAAACGT TGTTAAACTA TAATTCTTAG 60

ATTTGAATCA TTGATTTTAA CTAACACCTT ACCAAGAAGT AAGGTGTTTT TA 112

(2) INFORMATION FOR SEQ ID NO: 2005:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2005:

AAATCTTGAC ATAGGCACAG GAATGTATAT TGATCTCGAT CACTTAAGTC 50

(2) INFORMATION FOR SEQ ID NO: 2006:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2006:

AAGGTGGGTT TAAATTTCCC AAAAAAAAAA GCCTTTTAAC CTTTTGGGGG GTCCCCTTTC 60

CTTGGAATTG GAAAGGGGCC AAAATTGGAA TAAGGGGnTT GGAAAAACCC AAGCC 115

(2) INFORMATION FOR SEQ ID NO: 2007:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2007:

TGAAGAAATA GCAAATGAAC TCAATATTTC TATTGAACGT CAATATTTCA ACCAATTATA 60

TCGCTTCAAT AATCAAGATT TAAAGCATCT TGAACAAGAn TTTGA 105

(2) INFORMATION FOR SEQ ID NO: 2008:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2008:

ATTGGCTACT AAAGTTAAGG ACATGATGGA TTGGATTAGT GGTATGCGCT TTGAAAAGAT 60

CAATTAT 67

(2) INFORMATION FOR SEQ ID NO: 2009:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2009:

TATAAATTAG CGTCCTTCAT ATCACAACGA TGATGCTCTG TGCGAAGATC TGATTTATTT 60

CAATGTGCGC ACG 73

(2) INFORMATION FOR SEQ ID NO: 2010:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2010:

CTTTGTTTAT GTTTCGTTTA ATTTGTAACC CTCTCTTTGG ATACCGAGGT T 51

(2) INFORMATION FOR SEQ ID NO: 2011:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2011:

TAACGACCAA GCTTAAAGAG ATACGCTCTT ATGCGATTGG ATAGGTCGTT AAAGTTAACT 60

ACAATACCTC ATAAGTAGAT TTAGAATC 88

(2) INFORMATION FOR SEQ ID NO: 2012:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2012:

GTCAACCCTT GCCAAGCTTA TATCACGATA CTGGGATGTG ACTTCCGGTG AATTAC 56

(2) INFORMATION FOR SEQ ID NO: 2013:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2013:

AGCTTATAGT ACTTGTGACT TCATAATGGA TGAAGTTGAA GTACCAAAAG AATTAACACA 60

ATTACACGAA TAATTTAAAT AGAGAGTGTG ATAGTAGGTG GAATTATTAA ATAGTTATAA 120

TTTTGTTTTA TTCGTATTAA CTCAAATGAT ATTAATGTTT ACAATACCAG CTATAATTAG 180

TGGTATTAAG TACAGTAAAC TTGATTATTT TTTCATCATA GTAATTTCGA CATTATCGTT 240

ATTTCTATTT AAAATGTTTG ATAGCGCGTC CTTAATCATA TTAACTTCAT TTATTATTAT 300

AATGnATTTT GTCAAAATCA AATGGnATTC nATTTTGTTG ATTATGGCTT CGCAGATTAT 360

CCATACTGGT GCCAACTACA TGGATATAGT TATATATGCA 400

(2) INFORMATION FOR SEQ ID NO: 2014:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2014:

TCTTTCGAGG ACAGTAGAGG GTCCACCCTA TTGGACGTGG TACTGTACTA CTTTTAAA 58

(2) INFORMATION FOR SEQ ID NO: 2015:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2015:

TCTACCTGCA GGCATTCAAG CTTGGCACTT GCCGTCTTTT TACAACGTCG TGACT 55

(2) INFORMATION FOR SEQ ID NO: 2016:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2016:

TACTCTTAAG CTAACAACGG CGGTTATGAG TCCTTTGACA AGGTATCGGA GGAAAGACCG 60

TAAAGC 66

(2) INFORMATION FOR SEQ ID NO: 2017:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017:

CCAATAAGCA CACTGCCATT ATTGAGGACG GTACATnTAC GGTTAGACCC AATTGTTCAT 60

GGCGGTGGGC ACATAGTGTT TGGCTTTGAG GAGGTTACCA TTGCC 105

(2) INFORMATION FOR SEQ ID NO: 2018:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2018:

CCTTCCAATA GTAATTGATT GATGTATGAG TATATTAGGT GTGAAATCAA GAGGATTC 58

(2) INFORMATION FOR SEQ ID NO: 2019:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2019:

TTTCCTCGTA GGTGGTTCTT CTTCATCTTC GTTGTTTTGT CCGAAGTTTG GA 52

(2) INFORMATION FOR SEQ ID NO: 2020:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2020:

ATAGTTTAGG TGAGGATGTT GnGGTACGAC AGGAAGAAAG ACGGCAAACA 50

(2) INFORMATION FOR SEQ ID NO: 2021:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2021:

TTGTCACAAT AATTTCTTCA GGATCATAGG AAAAATGATA ACGATTTTTG AAGTATTGAC 60

TAATTGCTTC GCGAGTTTCT AATAACCCTT TATTGTGAGA GTATGATGTC TTGTCATTGT 120

TAATAGCATC AATATATGCC TTTTTCACAA CATCAGGCAT CGGGAAGTCT GGTTGGCCAA 180

TAGTTAAATT AACACAATCA TCCAAATTAT TCATACGATT TGAAAATTGG CGATACTTGG 240

GTGGCTCCTA AAATAATTAG GAAATGAGGA nTTnAAGGAA GGTTTCCATT TnGTGGACAC 300

(2) INFORMATION FOR SEQ ID NO: 2022:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2022:

TCATCCAAAT TATTCATACG ATTTGAAAAT TGGCGAATAC TTGGTGCTCT TAAATATTTA 60

GAATTAGAAT TTAAAGAAAG TTTCATTTGT GACACCTCAA ATATAAATCA AATATTGTCT 120

AAAAATTTAG AAATTAATAA TATCATAACA TACTTTTAAA GCAAAAAAGG GTAAATTACT 180

TAAGCTTTAT TTGAAAAACG AAAAATGTCT AAATACACTG TAGTAACTAC TTTTCAAAAT 240

GAATAAAGTG GTTACAGTTA ATGTACTTAG ACAGTATAAA ATTATGAATC TTTAAACTGT 300

GATGGTCTTT GTAAATTAAT TATTGGATTT GTCCATTTAC AAACAAAGTT TGTAGATAAT 360

ACATATACGA TGATTACAGA TATACTTATT AAATAAAGAT 400

(2) INFORMATION FOR SEQ ID NO: 2023:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2023:

TTnAAATATA CCAATCACGT TCATCCACAG TGATCCTAGA CCAATCCAGA 50

(2) INFORMATION FOR SEQ ID NO: 2024:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2024:

TTTTTAATGG TTTAAAAATT CCCTAATAAA ATTTTGGAAA ACCTAAATTC CAAGGGGTTA 60

AATTCC 66

(2) INFORMATION FOR SEQ ID NO: 2025:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2025:

GTAAGAGCAA TGGCGCAAAA TGCCTGTAAT GATATTGTGA ACGTAATTGA ATCAGTAGAG 60

GACC 64

(2) INFORMATION FOR SEQ ID NO: 2026:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026:

CTGTCGCTGC GTGACTTAAT TCTTTTGCCC CGTTGGCATA TGAGGAAATG TCA 53

(2) INFORMATION FOR SEQ ID NO: 2027:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027:

CATTTCACTA TTATTGGTTT AGGGTTGTTC ACGTTCATCA TGACCGCACC ACA 53

(2) INFORMATION FOR SEQ ID NO: 2028:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028:

CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA 60

AACGGAATCG TCA 73

(2) INFORMATION FOR SEQ ID NO: 2029:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2029:

AATAATAATT CTGGAATAGT GTTTAATACT TATTnTCCGT TTAAGATTTC AACTTAATAT 60

GGTTTACAGC GCGTAGCTCG TCTAATTCAT CATCACGTGT AGAGTGCTCT GCCTTATCAG 120

ATCAGTT 127

(2) INFORMATION FOR SEQ ID NO: 2030:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2030:

GCAAGTGAAT TGAAGTGACA TGTGGCTGGT GCTTCATGGT AATGATAAAC CAACACCATG 60

G 61

(2) INFORMATION FOR SEQ ID NO: 2031:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2031:

ATAAATATCT ATTTAGATAT AAGTATTGAT AAGTTGCTTG AATTTATAAA GTGAAGGAGT 60

AGGTGTCATT AGTATAGT 78

(2) INFORMATION FOR SEQ ID NO: 2032:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2032:

GAATAGTGTT TATAAAATGT TGACACTGTA GTGGCATATT GTAAATTAAA TATTATTATG 60

TGATCATTTT GTTTAAATAT TAGTTATAAG AAGTGAAATA nTCATTTTAA AAGGAGACTT 120

AAAACTTGAA ACGATCAACG AATCAAGAAA AATTTCTTGA TACACTAATT AGACTTAATA 180

(2) INFORMATION FOR SEQ ID NO: 2033:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2033:

TTTTGTCATC TGTATAGGTA TGCGCGCCGG TGTCTTTATT CACTTTGAAC TGTGCGT 57

(2) INFORMATION FOR SEQ ID NO: 2034:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2034:

AAGGCATTGG ATATAAGACT TGATGTTGCA TGGCAATCAC ACTGCCTAAT CCTTGCATAT 60

AA 62

(2) INFORMATION FOR SEQ ID NO: 2035:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2035:

ATGGCAAATA CTATACATCG TCCAATTGAT TGAAAAATAT GGTTATTAAA GA 52

(2) INFORMATION FOR SEQ ID NO: 2036:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2036:

AAGGTGTTTT TATATGCTTA TTACAAATAC TTAACGCGAT GAGTTTCTCA ACCAAATTGA 60

(2) INFORMATION FOR SEQ ID NO: 2037:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2037:

TACCCACCCC CAAACCCAAG GTTTTAAAAA ACCCCTTCCA AAAGCCCGGA AAAACCAAAA 60

GGAATTATTT T 71

(2) INFORMATION FOR SEQ ID NO: 2038:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2038:

GAATCCCGGA AGTACAATTT GGTACGTGAA GAAAATGGTA GTGGAATTAC 50

(2) INFORMATION FOR SEQ ID NO: 2039:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2039:

CAGTATCTCT TGGTATTTTA ATTGGTGCTT TATTAAACGT AATTTTACCT TTATATATCG 60

ATGGAGCGAA GAGTATTTTC GTATACGTTT ATAGTGCGTC TATTTTACCA GGTATGATTC 120

CTTGGTTTAT GATTTTATTC AGTCATTTAC GTTTTAGAAA ATTACACCCT GAAGAATTGG 180

AAGGTCACCC ATTCAAAATG CCTGGTGGCG CAGTAACTAA CTATTTAACA ATCTTATTCT 240

TAATATTAGT ATTGGTTGGT ATGGTATTTA ATGTTGAAAC TAGAATATCA GTGCTTATTG 300

GTGTCATCTT CTTAACGATT GTAACGATTT ATTATTTTAT TAGATATAAT AAAAnTAATG 360

TAAAGCAnAA TAGTATGTTA TAAnGAGCGn TACTTATGAC 400

(2) INFORMATION FOR SEQ ID NO: 2040:

(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2040:

AAGCTGATTT TTCTAAATGT TGAAAATCAT AAACTGCTTA ATAATAAATA ACGAGATCTA 60

AGTAATAGTG CTCCATTAA 79

(2) INFORMATION FOR SEQ ID NO: 2041:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2041:

AATTGAACGG ATCGTTCCCA ACCGTTATCA ACCCAGACCG GTGTTTGAAC CCAA 54

(2) INFORMATION FOR SEQ ID NO: 2042:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2042:

AATGGGATTG GTTCAAACTG AAATGGGCTG TTAGTCCCTG TAAAACCAAG 50

(2) INFORMATION FOR SEQ ID NO: 2043:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2043:

ATTGGnATAA TCAAAGCATT GAATCATACA TAGTCACATT GATTGTTTCC TCAGAGTTTC 60

AACACTCTAT AACTCATTTT AGTAATTTGC TGATTGCGCA CTTCATGTG 109

(2) INFORMATION FOR SEQ ID NO: 2044:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2044:

TTTTATGGAG GTGATGAAGT GGGTGAAGCT GAAAGGAAGC AAAAGCTTGG 50

(2) INFORMATION FOR SEQ ID NO: 2045:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2045:

TTGGCCCCCT TCCAACCCTT GGAAATTTTA AAAGGCCAnT TTTGGGGTAA AACCCTTGGT 60

TCCAAGGACC CCCAAAAGTT TTTTAACCTT CCAATTATTA T 101

(2) INFORMATION FOR SEQ ID NO: 2046:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2046:

ACCCTTTCCA AAAAGCCCAT TTTGAATTCC CCAAAGGGAG CCAAATTTAA GATGGCCGCn 60

AAAAAGGACC GGGGGGTCCA TGTTTTAATT TAAGCCGGAC 100

(2) INFORMATION FOR SEQ ID NO: 2047:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2047:

GTTAGTTATG AGCAACGTAT TAATGAAATT ATTGAGCAGT AATTnACCAG 50

(2) INFORMATION FOR SEQ ID NO: 2048:

(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2048:

TACGTATTTT CAAATGACGT TGGTGGACGT CACACTCCAT TCTTCTCAAA CTATCG 56

(2) INFORMATION FOR SEQ ID NO: 2049:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2049:

TTTTCCCCCC CCCCCCCAAA TTGGGGGTTA AAATTTTAAA AAAAGGGGTT AAAGGGAAAC 60

CCCAATTCCG GTTAACCTTT TG 82

(2) INFORMATION FOR SEQ ID NO: 2050:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2050:

TCAGATGGAT GGCAGTTATT TGGTATTCCA TGGGTATAAA GATAGCATAT T 51

(2) INFORMATION FOR SEQ ID NO: 2051:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2051:

TGAACGGGAG AAAGATGTTG TTGCATGGTG TCTCGGAAAC GTTTGTGTCC ACGTA 55

(2) INFORMATION FOR SEQ ID NO: 2052:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2052:

ATACCTGGAT GCAAAGGCAA AGTCGCAATT TTCCCTGTTC TAATGTGTCT AACTTCTCTT 60

CTAAAGTTCA GGTT 74

(2) INFORMATION FOR SEQ ID NO: 2053:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2053:

AATCTTGTCT GATGTAATGT TCAGGTCCCT TGACCCTCAT ATGCATGAGG T 51

(2) INFORMATION FOR SEQ ID NO: 2054:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2054:

CATCGACTTA TAGCTTAATT ATTATAAAAA ATTTCTCCAG ATTTAACTTT CT 52

(2) INFORMATION FOR SEQ ID NO: 2055:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2055:

ACTGACACAT TATATTAGTG AATTATTAAA AAATGATGAG AAAATTAAAA TCATCATGAA 60

TGAATTCGGT ACTTTTGATA TTGATAGCAA TAGTATTTCA AATGAAATTG AAGTCCATTC 120

ATTGATTAAT GGTTGTGTTT GTTGCGATCT TAAACAAGAA CTTGTCTATG AACTAAAAGC 180

CATTGCTTTA AAAGGGGACG TTAATCATGT CATCATAGAA GCGACAGGCA TTGCGCATCC 240

TTATTTATGG TGTATTAGAT GCGACTCGAT TTTTAGAACG TCATCAATAT ACCGAAAAAT 360

ACAGTTTCGC TGGATGGGGA GGATCCAGTT GGAAACTAAn 400

(2) INFORMATION FOR SEQ ID NO: 2056:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2056:

TCAAAACTTT GAAGTTGTGC TTGCTTTGCA CCATTTTTAA AATGTTCAGC TGAGAGTATA 60

TCTTCCGCTG TAAAATTTAC TTCTCCTGGA CTTAAAGATT CAATTAACAA CCAAGCCGAT 120

AACGTATCAT TTAGCAATTG ACTCATGAAA TCCCACCTTG TTCCCTATTT GTTTTTTACT 180

TAATGCTATT TTAACAAATA ATTTAATCAT ATTAGTGTTT TTTCAAAAAT ATTCATATAT 240

TATCATTACC ATATTTATTC AACAAATGTT TGTAAAATCC TCACTAATAA AATTAATCGA 300

TATGACCATA ATTCATTATC CAATAAATGA CTATAAAAAT TTCTnCTATG CCTTCATTTG 360

CAACTAAATT TGGACATCAA AAAAGAGCAC TCCTGAATGA 400

(2) INFORMATION FOR SEQ ID NO: 2057:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2057:

TTGTTGTTGT GATTTCACAT TTTCAAAATT TTGTTGCATG TTGTTAACTT CATAAATTAG 60

TGATTCGACT ACATCATTCA TGAGGACGCC TCCTACATTT TTTAATTTAT CACAATATAC 120

TGTATTCGTC ATGTTTTAAC ACTCTATATA ATTTGATTTA ACTATTTTTT CAAATGTGTT 180

ATCTGTTAAA TCAAGTAAAT CTAAAAACTT CCTATATAAA TACAAAATTT TATCGTGTAT 240

GTTGTTATAC GATGAAAATA CTTTTAATCT AATAAAATCA TTTAAATCAA ATACACCTCT 300

GCTGATTAAC AACACATACT TGTACTTGCC TCAAAAATAA AAATTACTAA TCATGATTTG 360

ACTTTTATAA CAAAATTCAA AAATATTGTA ATGAGTATTC 400

(2) INFORMATION FOR SEQ ID NO: 2058:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2058:

TCTTTTTACT CGCAATTTTA GGAAAAATGG TTGGATCAAT TGATAAAACC GGAAAATTAT 60

TAACAATAAT CAATAAAATA TCAAGCATAA TAATTATTAT TGTTGCTCTG ATGATATTAC 120

AAAAACTTAT TCAATTATTA TTCTAAAGCG TTATGTAGTT GTATTTTAAA AGCGTTATAC 180

AAAAGACATA CTTGTGTCTA TGTATAACGC TTTATTTATT ATAAATTTGG ATCAATTAAC 240

TCAACAAATT TAAATGTTCC ATTGTCATAT TCAAATTTCA GGATATTACA ATTACCGATA 300

TTATGCTTTA ATGCTTCATC TAGTTTAAGG CAATATCTTA AAAATACCnC CCTTAnTGGT 360

CCATGACTCA CGACTAATGC ATTATTCTTT GGTTTGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 2059:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2059:

AAAACAACAC AATCAAAAAT ATTGGATACA ACTGAAAAGT TATCAAAGCT A 51

(2) INFORMATION FOR SEQ ID NO: 2060:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2060:

TTATCATGTT TAGTAGATTT TAAGAAGCTA GAACATTGTA GATATGATGA 50

(2) INFORMATION FOR SEQ ID NO: 2061:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2061:

AACGTCGTnA TATCAnCTTG CCAAACAAAG ATATTGTCAC CTTTTATCGG 50

(2) INFORMATION FOR SEQ ID NO: 2062:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2062:

ACCATGGTGn ATATGGTCAT GATGATCGTT TGTGCCGGGA GCTTGAGCTG 50

(2) INFORMATION FOR SEQ ID NO: 2063:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2063:

TTTCCCTTGG TTTTGGAATT TAACCAAATT TGGGAGGGAT TTGGGACCAC CCCCAGGATT 60

TTAAAAAAAA AAAATCCCAG G 81

(2) INFORMATION FOR SEQ ID NO: 2064:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2064:

TTTTGGGGAC CTTAACTGGG TGGGTCTGGA ACTGTTTCCC TTTCAAACAC A 51

(2) INFORMATION FOR SEQ ID NO: 2065:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATGATGTATT CAAAAGGTAT CTATAAAATA GCTTTAGTTG GAAAAGATGA GA 52

(2) INFORMATION FOR SEQ ID NO: 2066:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2066:

TTTCATCACT GGCATCTTGT AATTTCTTGG TCTCATATCT GGAATTAATA GGT 53

(2) INFORMATION FOR SEQ ID NO: 2067:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2067:

AACCATTAAG AAATTGGATA CACAGAGCAA ATATGGTTAT GATTAGGAAC CATGGCATTT 60

ACC 63

(2) INFORMATION FOR SEQ ID NO: 2068:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2068:

AAAGGCAGCG ATGTTACTCA TACCGAACCT GGTTATATAT GAGCGATGAT GCAATGTA 58

(2) INFORMATION FOR SEQ ID NO: 2069:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2069:

AACAGGA 67

(2) INFORMATION FOR SEQ ID NO: 2070:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2070:

CATTTAACCC ATCTTCTTTT TTTAATTCTT CTATACTACG GTTTAAAAAC TCTACAATAA 60

CTGCCATTTC ATCATCATCA AAGACT 86

(2) INFORMATION FOR SEQ ID NO: 2071:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2071:

GTTTCTTCAA AATATGTGTA TTACCTTTTT GTATGGTTAA ATCTTTTAAT TCTATCATTC 60

TTGTCTTACC TCTTTTGGTG TATCCTCTTT TTCAACATAT GTGATCGATA TGACATATTG 120

CCCTTTATGC TTTATTTCGA CATACGTTCT ACTAGGTGAA AATCCATTAA ATGTTAATTT 180

ATAATCAAGC TTTTCCCCTC TTTCACTATA AGCCGTAATA TTAACATATT GTTGCGTACC 240

TTTTGGCACT TTGGCATAAC TATACTCCGT TTTTAAGAAA GGATTAAAAC GATCAAGTAT 300

AGGATGATGT ATGAnTGTAA AAGCAATAGT AATGGATAAT ATTAATCCTA ATAATATTGC 360

AATGATAAAT TTCATAGTTA A 381

(2) INFORMATION FOR SEQ ID NO: 2072:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2072:

ATCCCCGAAT TGCTTCGCAA ATGTATCATC TTCGAGGCTA CGTTACTTAA AT 52

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2073:

CCAAAAACAG CATCACTGTG ATTATGGTTT TCATCTTCTA TAACTAAGAA TACATGTTTT 60

TTTGTAAAAA TTTTTTTGAT CA 82

(2) INFORMATION FOR SEQ ID NO: 2074:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2074:

TTTATCGCAA TGAGGGAAGA TAAAGGATCC CGAAAGCGCC GTATGGGTTG GCAAACATTG 60

GGGACCAAGA CCGTTCCCCA TA 82

(2) INFORMATION FOR SEQ ID NO: 2075:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2075:

CTTGGTTGCT CTTTATTTAT TTAATTGAGA CCTAGAAATA AGTTATTAAG CACAATCATT 60

CACTTT 66

(2) INFORMATION FOR SEQ ID NO: 2076:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2076:

(2) INFORMATION FOR SEQ ID NO: 2077:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2077:

TACGTTCTAT CATAGAGCCT GGAGATGAAA TTATAATACC GGGACCAATT TATGCAGGCT 60

ACATACCACT CATCGAAGTA CTAGGTGGTA AACCAATTTA TATTGATACA ACAGCAACAC 120

AATTTAnAAT TACACCTGAT GCATTAGAAA GTCATATTTC TCCAAAGACA AGAGCTGTCT 180

TGTTAAATTA TCCGACTAAT CCAACTGGCG TAGTTTTAAA AAGAaAtGAA GTTyTArATA 240

TCGTAAATGT ATTAAAAAAA TATCCGTTAT TTATTATTAG CGATGAGATT TATGCTGAAA 300

ATACATTTAG TGGTAAACAT GTATCC 326

(2) INFORMATION FOR SEQ ID NO: 2078:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2078:

ACCCCTTAAT TTAATTGATG TTTTGTTATT TTTAAAATGA ATAGTTGAAG AAAAAT 56

(2) INFORMATION FOR SEQ ID NO: 2079:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2079:

CACGTACTGC CATGTATGCA CAAGCCGGCA TTCATAAAGC CTTCCATGGC AGTCGTTATC 60

A 61

(2) INFORMATION FOR SEQ ID NO: 2080:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2080:

TGGGACAGGG CGTACCATTT CAAAATGATA GTTCTGAGCT GCTAATTAAT ATGCCTTCGA 60

AAAAGATGAG TTTAAATTTA GATGATGAGA CTGA 94

(2) INFORMATION FOR SEQ ID NO: 2081:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2081:

AAGACGACAT GCAAGACATT GCCTTATCTA ATGACAATGT TAAAGCGAGT 50

(2) INFORMATION FOR SEQ ID NO: 2082:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2082:

TTGTTCGGCT AAAAATAAAG TGGCATTGAC GTGACCGCAA GTTGACGTAC 50

(2) INFORMATION FOR SEQ ID NO: 2083:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2083:

CTTCCCAACA TTGCGCACTG AATGGCGATG GCGCTGATGC GTATTTCTCC TACGCTCTnG 60

CGTATTCAAC CGCTATGGGC ATCTCATACA TCTGTCGATG CGCTATTAAG CAGCCCGAAC 120

CGCACACCGT GAG 133

(2) INFORMATION FOR SEQ ID NO: 2084:

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2084:

GGTAGGGGCA CTATTTTGTA TGTAGAGGTT TTGTCGGGCA GTGTGAAATC AACGACT 57

(2) INFORMATION FOR SEQ ID NO: 2085:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2085:

CCCCCCCCAA AAACCGCCCC CCCCAATTTG GCCTTTTTCC AAGGGGGGTG TTTTAA 56

(2) INFORMATION FOR SEQ ID NO: 2086:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2086:

AATAGCGAGA GCCCGACCAT CGCCTCCAGA TTGCGACTGA ATGGCAATGC GCTGATGCGT 60

ATTTCTCCTA CCATCGTGGT ATTCAACGAT ATGGGCACTC TCATACAATn GCTC 114

(2) INFORMATION FOR SEQ ID NO: 2087:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2087:

AAGGGGGAAA AGGAACCCAA GGCCCCCTTC CCAAGGAAAT TGGGGGGTTG GAAAAAACCA 60

AAAATTTTTT AAAAACCCGG 80

(2) INFORMATION FOR SEQ ID NO: 2088:

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2088:

GGGGTAAGTG GTTGAGACAG GAACTTTACA AGAGGTGTTT CGTCATCCTA GAACGACGCT 60

TGCTCA 66

(2) INFORMATION FOR SEQ ID NO: 2089:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2089:

ATCAATGTAT TACGTATCGA AGGTGAATTA TATCATACTG CTAAATATGA CGGTTTCACA 60

TC 62

(2) INFORMATION FOR SEQ ID NO: 2090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2090:

GAATTCGCTA TCCTGAAATC CTGAGTCGCT GTCCTGAAAT CTGAAATCGC 50

(2) INFORMATION FOR SEQ ID NO: 2091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2091:

CGGGGTTCCC CCGTTCAATT CCCTTTGAGT TTTCAACCTT GCGGGTCGTA ATTCCCCAGG 60

CCGGAATTGC TTAA 74

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2092:

ATTGTTGGGT ACGGTGGTGG GTTAATAATC CAAACACGTT AAACTACCCG TTTTAGATAT 60

ACCTATACAA 70

(2) INFORMATION FOR SEQ ID NO: 2093:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2093:

GTTTTGGGTC TTGGGTATTA GTTTAATCTC CATCATGGTT AATTGGTATG GTATTGGTAT 60

TAGTAATCAT GTATGATGGG CTGGGCGG 88

(2) INFORMATION FOR SEQ ID NO: 2094:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2094:

TGGCCATTGA GGCGCATTAC GTACTACGGC TTGTCGTAGG GACAATTATT AT 52

(2) INFORMATION FOR SEQ ID NO: 2095:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2095:

AGTTGATGCA ATGAGTGATG CAAGGCGACT GAAAAGTTGG TATGAATGAC AAAACTTTAA 60

(2) INFORMATION FOR SEQ ID NO: 2096:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2096:

ACTTAAAATC TAATACGGTA TTTTCAAAAA CGAATAAAAG TTACCTCTTG TCT 53

(2) INFORMATION FOR SEQ ID NO: 2097:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2097:

AACTTAATAT TGCTACGATA TGAACGGCAT nAACATACTT AGCGnTGnTC 50

(2) INFORMATION FOR SEQ ID NO: 2098:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2098:

CAAAATAAGA AATTAATTAA GAAAATGCCA AGATGCCAGA TGCCATCGGC GGAAAGGAAA 60

TTGCACGTAC GG 72

(2) INFORMATION FOR SEQ ID NO: 2099:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2099:

CCACCCAAAC CCAAAAAATA AAGCCCAAAA AATTGCCAAG GAAGGAAAAG GAAAATTGTT 60

(2) INFORMATION FOR SEQ ID NO: 2100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2100:

CACCAATTTC TTCTGGnGCT GGATCTCGAC CTAAGTCCTG TAATAATTGA CGTTGAACAC 60

GAATTAATTT ATTAATTGTT TCTACCATAT GCACAGGGAT ACGAATCGTA CGTGCTTGGT 120

CAGCAATTGC ACGAGTGATT GCTTGTCTAA TCCACCATGT TGCATATGTT GAAAACTTAA 180

ATCCTTTGTT AAAGTCAAAT TTTTCAAC 208

(2) INFORMATION FOR SEQ ID NO: 2101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2101:

TAATGAAATT AAGTAAAATA AAAATTATTT CATGGATTGC TTCTATCTAT ATCGAAATAT 60

TAAGAGGAAC ACCAATGTTA GTTCAAGTAT TTATCGTATT CTTTGGTATA ACTGCTGCAT 120

TAGGACTAGA CATTTCAGCT CTTGTTTGTG GAACAATTGC ATTAGTTATT AATTCCTCAG 180

CTTACATTGC TGAAATTATT CGTGCAGGTA TAAATGCTGT TGATAAAGGC CAAATGGAAG 240

CCGCACGTAG TCTAGGTTTG AATTATAGAC AAACGATGAA AAGTGTAATT ATGCCACAAG 300

CAATTAAAAA TATTTTACCA GCTTTAGGTA ATGAATTTGT CACTTTAATT AAAGAATCAT 360

CTATTGTGTC AACAATTGGA GTTGGCGAAA TTATGTTTAA 400

(2) INFORMATION FOR SEQ ID NO: 2102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2102:

(2) INFORMATION FOR SEQ ID NO: 2103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2103:

TTTAAGGAGA AAGGTCATTG GTATAATCTT GAGAAAGAGT GGCAAGAGTT CTTAAACTCT 60

GGGAAAGAGG TGAAAAATAT TAAAATGGAA GTAAAATATA GCGGTAATAG TCAAAGACCG 120

ACTATATTTA AAGTTGAATA TGAAATTAAT GGTGAAAGAA ATATTAGAAG AATATTAAAT 180

AAGTAGAGGT GCCAACATGA CATTTGAAGA GAAGCTTAGC AAAATATACA ATGAAATTGC 240

GAATGAGATT AGCAGTATGA TACCGGTAGA GTGGGAAAAA GTATATACAA TGGCTTATAT 300

AGATGATGGA GGAGGTGAAG TATTCTnTAA TTATACTAAA CCAGGnAGTG ATGACTTGAA 360

TTATTACACC AATATACCTA AGGGTATAAC ATTCCGGTGC 400

(2) INFORMATION FOR SEQ ID NO: 2104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2104:

AACCATCATA AAATGTTATT AAACCGTCAT GGACCGCGTC ACCATTTAGT CCT 53

(2) INFORMATION FOR SEQ ID NO: 2105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2105:

AAGCACAAAT TAGCAGAGTG TTTTAATTTA AATGAACAAG TACCTTTACA ATTTTTGGAT 60

AATGTAAAAG TTGGTAAAAA TAATATTTAT GnTGCTTTGG AAGAGTTTGC CAACAA 116

(2) INFORMATION FOR SEQ ID NO: 2106:

(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2106:

AATTTGCAAA AGAATCATGG ACAATTGAAA GCAAAAAGGA TCATCATTAA AATTGAACTG 60

C 61

(2) INFORMATION FOR SEQ ID NO: 2107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2107:

GAACCAATGT TAAGCTAATT AATGGAATCC TAACAGCGTT AATCTATTTA AAAAACTTAA 60

(2) INFORMATION FOR SEQ ID NO: 2108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2108:

ATTTGAnAAT GAATCTGTGG AACATTTTGC TAATCATGAG GATAAAATCA TATGATGTTG 60

AAAGCGAGAA TGGGATTACG TTAAACGTGG GCGCTGCTAA TTTAAGCACC TTATTTAGTG 120

GAAGAT 126

(2) INFORMATION FOR SEQ ID NO: 2109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2109:

ATAATGTTAA AAAAACGGCA ACTAATCTTT TCATACTAAC AATGATTATA TGTACAATAA 60

CGTTAATAAT GCTAGATAAT TTTAAAAAAA TGAAAAACCG TGAATATCAA AAAGAAATAG 180

CAGAAAAAAA TAGACATATT AATACATTAA TTGCTGAACA AGAGCGACAT AGAATTGGTC 240

AAGACTTACA TGATACGTTA GGGCATGTGT TTGCAAGTTT ATCATTAAAA TCAGAATTAG 300

CTTATAAACT AATAGATGCT GATGTAGAnA AAGTAAAAGC TGAATTATTA GCAATTAATA 360

AATTATCTCG TGAATCATTG nACAAAAGTC GAGAAATTAn 400

(2) INFORMATION FOR SEQ ID NO: 2110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2110:

AAGATTTAAT ATCGGGGGTA ATGTTGATTT TCAAATATCG CGATGTGCTT GTACCACCAT 60

T 61

(2) INFORMATION FOR SEQ ID NO: 2111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2111:

TATACTAAAT TATGGCAACT TGGCTCATAT AGGTCGAGTT ACCAGACATA TTCGG 55

(2) INFORMATION FOR SEQ ID NO: 2112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2112:

CGAATAAGTT CTGGGCCTTT TGTTGTTCAT TAGCTTGTTT CTGTTTTGAT TGTTCTGCCA 60

TTTGAACTAC ACCAACCTTT TAAATTTATT CTAGTGACAG GATAACTAAA ATATATTTCT 120

TATGCAATAA TTTCCTATTG ATAAGCATTT TCAGATTTTA GTTGTAAATT TTGCCCTAAT 180

AATTTATAAA GAATAAATTC GTCTCCTCTT TGACCTATAA TATATTGAnC ATTATAAGCC 300

ATGCGATTCA TTCCAGACAC AGCCATAAAC TCTTGTTTAT CTATCATTTT AAATACCATT 360

TTTAATTTGG CTTAATGGGA CATTCCGTAT TAAATCATTT 400

(2) INFORMATION FOR SEQ ID NO: 2113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2113:

TGTTTTCAAA GCATGGTATA AATGCTTTGT AACATAGGTT TTGCCTACAT CAGTATTCGT 60

ACTTGTAATA AAAATCCTCA TAAAAAT 87

(2) INFORMATION FOR SEQ ID NO: 2114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2114:

TTTACAAGTT AAATATAnCA CTAAAAATTT TTAAGTCAAT AAGAATATAT 50

(2) INFORMATION FOR SEQ ID NO: 2115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2115:

TGTGCATAAA ATCCTTTTAC TTTTTGTAAT TGATTGTTAT CTTTAACAAT TA 52

(2) INFORMATION FOR SEQ ID NO: 2116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2116:

ATTTAnAACC CAATTCCCCA TTATTTTTTA AAACGGATTC CATGGGTGGA CCATTGGAAA 60

TTTTAAAAAA ACCATGGCCC CATTCCAAAA AGTTAGGATG GCCAAAAAGC CTT 113

(2) INFORMATION FOR SEQ ID NO: 2117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2117:

GATTTATCAA CTATTTCCGT ATTTTGATTA TCTCCATACA ATTTCCAATC CTCTGGCTTA 60

TCAATAAATA ATGATAATGG CTTATCTTTC GAT 93

(2) INFORMATION FOR SEQ ID NO: 2118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2118:

TGATTACCTT GAnACATGAC TTTnCCTGAn TGGTAAATAT TTACAGTTGT 50

(2) INFORMATION FOR SEQ ID NO: 2119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2119:

AGATATAAAA TATAAAAAAT TATTAAAAGC TATATCCAAT CAAGACTTTA AAGGGTTAGT 60

TCCAAATATC AATCAGAATG ATAATTATnC TGAAATATAT ATAATTAACA ATACTAAAAA 120

CTTAATATAT CATTTATATG ATGATAGAGG TCTATGGCTA GCTTTTAATA ATAATGAAGA 180

TTATGCAAGA TATnCTGAAA AATATAATGA TTTAATA 217

(2) INFORMATION FOR SEQ ID NO: 2120:

(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2120:

AGACTTAGTA AAGTTAGATC ATCTAAAGAT GAGCGTAAAA TTTATATTTA TTTAAATAAT 60

GGATGATATA TCTAA 75

(2) INFORMATION FOR SEQ ID NO: 2121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2121:

CACCACCTAC ATTTACTATA TAAAATGTAG GAATGGTAGA TTGATTTAGA TAAACTGGAC 60

GTATCACTTT AAGTGCTTTT TCAAAGA 87

(2) INFORMATION FOR SEQ ID NO: 2122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2122:

TGTTCTTTAG CTAAAGCTTT AGCTTCTTCA TCACTTTTAA CTTCATAAAA ATCTACACCA 60

GTAGCTTCTT 70

(2) INFORMATION FOR SEQ ID NO: 2123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2123:

TAnATCTAAA AGGAGAAATG CTGAAGATGA GAGAGGTATT TTTGAAATGT 50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2124:

TTAAAGGGTA ATTGTTTTAA AAAAAGATTA AACCGAGGAC TTTTAATTGT TAAAACCATC 60

CCT 63

(2) INFORMATION FOR SEQ ID NO: 2125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2125:

TGTAAACGAC TATTACATGA TCACAATCCA TTCAGCGCCA TTATATAAAG GTACTTAATA 60

TAGGACATCA TTCGCAGC 78

(2) INFORMATION FOR SEQ ID NO: 2126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2126:

TTTGGTCGTG TGCAAGACAG AAGTCGACAT ACTCCAATGA AACATCATGT 50

(2) INFORMATION FOR SEQ ID NO: 2127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2127:

TTTGTGTCGA TGCGCTTTTT CACTTCTTCT GAATGCTCGA AATCATTCGT 50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2128:

TGTCTGAAAT GATCATTAGG ATTGCTCCAG CTCAATGTCA GTnGnAATGA 50

(2) INFORMATION FOR SEQ ID NO: 2129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2129:

TCCAATTACC TACAAAGTGA GTGCTTTCTT GACCAAGTCA AAACGAACTT TTATATTTGT 60

CCAAC 65

(2) INFORMATION FOR SEQ ID NO: 2130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2130:

TTCCAAGGTG TCGCTGACTT TCAACACACT GAATATATAC CTGCCAGTCG GCTGGTCATG 60

C 61

(2) INFORMATION FOR SEQ ID NO: 2131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2131:

AGTTCTTCAG TCCAAATGCG GCATGTTGAC CCACCATAGG CGAGGGCATT TTCACCACGG 60

(2) INFORMATION FOR SEQ ID NO: 2132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2132:

CCCCTCGAGT TTTTTTTTTT TTTTTTTTTA CTGGAGCAAA ATGAATTTTT TTTATTGTAC 60

TTCAGGGCAA CAAGTCAACA GCTGCAGGAA AACAAAACCA GGTCCAATCT ATGATCTAAG 120

AGGAAGTCAG GAAAGGCTTG GAAGAGAGAT CCAAAGGCCA TCCTGGCAAG GGGAATCCCA 180

CATGAGAATT CCTGGGAGAG AGCAGGCCCC AGGCAGCAAG GTCATCTTGC CTGCTTCTCT 240

GTAAGTTAAT CCTTCACAGG GAGCCAAGGC TTCTCTTGAC TGCTTGGACA AGAGGGTAAG 300

GGCCCTGGTT GCAGGATTTG CCAGTGAAGT CATCCATGTC AATAGACCAG ATCATGGCTC 360

CTCCCAGGTT AAATTCCTTA AGAACTGAAC CTTGnCTCCA 400

(2) INFORMATION FOR SEQ ID NO: 2133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2133:

TTCATCATAC AACATTACAC TTTGTATGAC TAAACCCAAA TTAACGATAT 50

(2) INFORMATION FOR SEQ ID NO: 2134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2134:

GTGGCAAGCT TTTTTAAGGT CTGACTGCCA TCGACGGATC TATGTTAACA GGTGGATCT 59

(2) INFORMATION FOR SEQ ID NO: 2135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2135:

ATCAAAGTCA TCTnCATGGT CnATCACACC ACGCTTTATA TGGTAATTCT 50

(2) INFORMATION FOR SEQ ID NO: 2136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2136:

CGGGATCTGA GGTCGCTATC TGCAATCTGC AATCGCTATC TGCAATCTGG AG 52

(2) INFORMATION FOR SEQ ID NO: 2137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2137:

nCTCAACCAC CCACACAACA ACACAACAAG CAGCACCCAC ACACCACACA 50

(2) INFORMATION FOR SEQ ID NO: 2138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2138:

TGTATTGTCA TTGTAGACGT GTGTAGCCAA ATCATAAGGG CATGTGATTT ACGCATCCAC 60

CTTCTCGGTT TGTACCGCAG TACTTAG 87

(2) INFORMATION FOR SEQ ID NO: 2139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2139:

TTCACCGTTG CGCAACGTTC AAGTTTGAAG TTCGTTTGGC ATGTTGAAAT AAGCACCAGT 60

TACACCAAAA CGCCCAG 77

(2) INFORMATION FOR SEQ ID NO: 2140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2140:

ATCTTCTAAC ATTCACTTAG TAGCGTnATT TTTCGCTTAT AATGAAATGT TAAGCATATG 60

CGGGATTTAT ATTTTAAAGA GACCTTTAGA TACCATATAT ACCTAGGTTA TTGAAAATAT 120

GGATACCTTA TATAAGTGAT TTGCAATA 148

(2) INFORMATION FOR SEQ ID NO: 2141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2141:

GCTGGCACAT AGATGATCGT CAAGTCGATC TCGCCAGTCT GAAGTCAAGA 50

(2) INFORMATION FOR SEQ ID NO: 2142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2142:

TTGTTGTAAA TACTATCACT GTACATGGGT GCTATCAAAA TATTGTCAGT TCGTAAAATA 60

(2) INFORMATION FOR SEQ ID NO: 2143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2143:

GTAGTATATC TTATTAATTG TATCATGAAG CAATTTAAAT ATCATGACAA TTTAGTTTGA 60

AAAACACACT TTGTGTTGAC GTTGTGTTTT ATGGGATATA GnATAGTAAG GAATGTAAAA 120

TGAAGGAGTG AATGC 135

(2) INFORMATION FOR SEQ ID NO: 2144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2144:

TTTTAAGGTT TGAAGAAAAA AAGTTTTAAA AATTCAAGGA AACATTAAAT TAATTTA 57

(2) INFORMATION FOR SEQ ID NO: 2145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2145:

TTTCGAAAGT TTGATAGTCC ACCTTACATT CTCCTACTAT TTTCTGATGT CCCAATACTT 60

TATATTATTT AAAGTAATAT AAAAGCAATC TCTTTTGAAG ACATGTTAAC CTAAATATTT 120

TTATATATAA TATATATATA AAATATAn 148

(2) INFORMATION FOR SEQ ID NO: 2146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2146:

GTTAATACAA TACGGTTAAC AGCACCTTTA CGnTAGTTGC TTTnCTGCAn 50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2147:

AATCCCCTCT TTTCTCTATT TCCTAAATCA TAGAACTTTT AACAGTAAAA TTCAATCATT 60

AATACATG 68

(2) INFORMATION FOR SEQ ID NO: 2148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2148:

AGGTCCATTT GTAATTTATA ATGTTGACTA ATAACATCTA CAGAATTTAA CGTTCCCATA 60

CCTCGCCACT GATTGTAAAT AAACAAACCA TA 92

(2) INFORMATION FOR SEQ ID NO: 2149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2149:

ACCATCCATT AAATCAGGAT CTTCACTAAT AAGTGCTAAA TTAGCAGCGC CACGTTTAAC 60

GTAATCCAT 69

(2) INFORMATION FOR SEQ ID NO: 2150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2150:

TCAAAATATA TACGATCACC TTTCTGTAAA ATCACACTAT TTTTATTTGC CGCTTCTGGA 120

TGTTGTTTAA AAAATTGTTG GCCAACTTCA CCTTTTAACG TGGCAAATTG ATAATTTCTT 180

GGTAGGTCAT GTTGAATTAA CCAAATGACA TAGTTATAAC AATATATACA GTTTCCATCA 240

TAATATACGA TTGGCATAAT TTATTCGCTC CTTTAATAGT ACTTATAGTC ATTTTTCCTA 300

ATTTAAAAAC ATTTAAACAA GGTTGTCACT TGATAAGTCC TCGCGACACG AAATTGCCAT 360

AAAATTTATT TTTCAGnTTn ATAT 384

(2) INFORMATION FOR SEQ ID NO: 2151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2151:

TGTTGTTTAT CACTATATTT TAAAAATAGT CTATAAGGCT TATCAGATGA AGTAGCTGCT 60

GGCGTAACAC CACCAGTAAA TGT 83

(2) INFORMATION FOR SEQ ID NO: 2152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2152:

GTATTCGTAC ATTTTTCAGC AATTAACCAA GATGGTTACA AATCATTAGA AGAAGGTCAA 60

GCTGTTGAGT TTA 73

(2) INFORMATION FOR SEQ ID NO: 2153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2153:

CCCCCCTCCC CCCTCCCCnC CCCCCCCCCC CCCCCCCCCC GCCCCCCCCC 50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2154:

TATTTTAGGC TTAGCATTGA TGATGTTGCT CATTTTCAAT AATATAGGAA TTATT 55

(2) INFORMATION FOR SEQ ID NO: 2155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2155:

ATGCTTGCTG ATATAATGTA ATAGCGTCGT GATAACGTTG CTGGCTTATA ATATACATTT 60

GCGAGATT 68

(2) INFORMATION FOR SEQ ID NO: 2156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2156:

TAATCTTTGT CGTCGAAATA CAAACTAACT TTTGAGTTTA ATGATGAAGG TACGCATTGT 60

GTATCACT 68

(2) INFORMATION FOR SEQ ID NO: 2157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2157:

TCATTCATTT TCCTCTTTTC TTTTATTTAA AATGTTCATG GTTGTTTCTC TTAATTCTGT 60

AGATGCTAAA TGGTCAAATT GAATAATTGT TTCTAGACTC ATTTCATAAA TTTCGAAAAA 180

TAATTCTTCG GGATTACGTT TTTGTATTTC TCCAAATGTT TCATAAAGCA AATCAATTTT 240

ATCAGCAACT GAAAGTATTT GGCCTTCTAA TGAATCATCT TTACCTTCTT GCAGTCGTTG 300

CTTATAAACA TCTCTATATT GTAATGGAAT TTCTTCTTCA ATAAAGGTCT CTACCATTTC 360

TTCTTCAACT TGCGAAAATA ATTTTnnTAA TTCACTACTC 400

(2) INFORMATION FOR SEQ ID NO: 2158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2158:

TATTTTTTTC TTCTAGGCAG TGTTAATACT GCTTCAATTT GTTTTTTACT AAATTGATAT 60

TTCTCTATGA TTGAATTAAT CAATTGATTG TCCATTTACT TAACCCACAC TTTTTCTTAA 120

ATTTACTCAT TTATTTTAAC ATATTCTAAA ATACTTCTAT TAAGATATGA TACTTAATGT 180

AATTTTCACT TCCAAAACAT TTAAAACGAA TGATTAGGnC ATACTATATT nT 232

(2) INFORMATION FOR SEQ ID NO: 2159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2159:

CCGTTTTTCC AAAAACTTGA TCATAAACCC GCTCCTTTTT TCATCATAAC AAAATAAGAA 60

(2) INFORMATION FOR SEQ ID NO: 2160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2160:

CGATTTACTG CACGACACAT TGCCACATCC TGGATGGGCA ATCTTTTCTC TTACCCGTCT 60

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2161:

ATTAGTTGAA GTTTTTGAGC AATTGAAAGA TATTCAGGGT CAAATAAAAA CGACAAAAAA 60

AGAATATCAA CAGACCAACA AAGAACTTTC TGCTGTAGAT AAAGAAATTA GAAATATAGA 120

AAAAGACCTC AnTGATACAA AAAAAGCACA AAATGAATAC GAAGAGAAAT TGTATCAAGC 180

ATATCGATAT ACCGAAAAAA TGAAAACACG TATTGATAGT TTGGCAACGC AAGAGGAAGA 240

ATATACTTAT TTTTTCAATG GCGTCAAACA TATTTTGAAA GCTAAAAATA AAGAATTAAA 300

GGGTATTTAT GGTGCAGTTG CGGAAATTAT TGATGTGCCA TCTAAATTAA CTCAGGCAAT 360

TGAAACAGCA TTAGGTGCTT CATTACnACA TGTCATTGnA 400

(2) INFORMATION FOR SEQ ID NO: 2162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2162:

GTGCGTACCA TTGTAATCTT CGTAAACTGG GTAATTATTT TGTCTTTCTT CATCATAAAG 60

TAATAA 66

(2) INFORMATION FOR SEQ ID NO: 2163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2163:

AGAATGGTAA CATGGTAATA ATAAAATATA AACAGAATAC TAGTTAATAC ACTTTATACT 60

AGAAAAAGAT AT 72

(2) INFORMATION FOR SEQ ID NO: 2164:

(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2164:

CGATAATCTG TTTTTTTAAA TCTGTTGCTG TTAGATTTAG CACCGATTCG TTTAACTTCA 60

AATAATTTTT ATTACCTTTG GAAGAAAGTG GAACTATTGT AACTGTTTCT TTTCCTTTAT 120

TGTCTTTGTT ATCTAATATT ACACAAAAAT GATTACCAGA AAACTCACTT CCAATATTAC 180

TCCCTAGTTT TACATATACC ACTGTTCCTC TACnATATGA TTTATAATAT CTTTnTTTAT 240

TGCTTGTAAC ATCGCTATGT ATAGCAATTG GAATAAAACT CTAGCCAATG AGGCATGTnT 300

ATAACTTTCA TGTTTTTACT GTCGG 325

(2) INFORMATION FOR SEQ ID NO: 2165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2165:

TAAACCCCTT TTGGGTAAAA AAGTTTGGGA AAATTTCCCC GGGGGGAAAG GCCCCCAAAA 60

AATTGTGCCC CTCCnCGGGG GAAAATTAAA ATTTCCCCCC TTTTAAAAGG GTTTCCCCTT 120

T 121

(2) INFORMATION FOR SEQ ID NO: 2166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2166:

CGGACAGTTA AATGAACTGT TCAATGAGCC CAGGATGTTG TAAATGGTTC GG 52

(2) INFORMATION FOR SEQ ID NO: 2167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2167:

ATTACAGTAA AAAATGGATT AACATTACAA GCGTGTCTTG CTAGAGCAGC CAA 53

(2) INFORMATION FOR SEQ ID NO: 2168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2168:

AAAGATTATT TATTTGCAGT CATTAATTGT GATTTAATAC GGTCAGCTTT GTTTGAATGT 60

ATTAAATTAC nTTGAGCAGC TTTGTCTACT AACTTAACTG CTAAGCTTAC TAAT 114

(2) INFORMATION FOR SEQ ID NO: 2169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2169:

AAGGAACCCC CCCCCCTTAA AATTTTTGGT GGTTTTAAAA AATTCCTTTG GATTTATTAC 60

CTTTATTCCT ATnATTTTCC GTTTGGATTT TCCTGGATTA AATTTCCCCA TTAAGCCATT 120

TCCGCTTCCC TTATTTTATn ATTTTCCAAA ATTTCCAAAG GTTCCATTTG GGATTTTGGC 180

AATCCTTTTT TATTAAAATG GCCTAAAAAT TTTTT 215

(2) INFORMATION FOR SEQ ID NO: 2170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2170:

TATCGTTTTT AGAAATGGAT GTTCTCTCCA AAGATGATGG TATCTAACAT TATCTTATTG 60

GTATCATTAT GCAACCnTTA CAAAACATTT ACGCAAGATG ATACATTATC CAAC 114

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2171:

ATCACAGATG AGATAACAGA TCCACTGTAA CTTTACAATA AATAAATGGT ATCATAATTA 60

ACACGTAAAT GGTTTC 76

(2) INFORMATION FOR SEQ ID NO: 2172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2172:

ATTATCACAA AATGTTGACA CGCAAAAAGT TGGTCAGTTA TCAATATGGT ATATAAATCT 60

GAGA 64

(2) INFORMATION FOR SEQ ID NO: 2173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2173:

AAAGGCCAAC CAACCAAAGG CCAAAATTAA CCGGCCAATT CCAAGGGGTT AATTAAACCC 60

G 61

(2) INFORMATION FOR SEQ ID NO: 2174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2174:

CACCCCGCAC TCTCCCATCT TTTACCTACT GGCTTCTTTG CATTGCCCTG GCACCTCCGT 120

CCTCAGCCTC CCAGGCTGTA TTCATTCATT CCCTTACTGA GCACGCACCA TACACCAAGC 180

ACCATTCAAG GTGAACCAGT CAAATGAAGG CCTGGCTCAT TTTAATGGGG GACAATGAGC 240

ATTTTTGTTA CAATTTCATG GAGTGATGAG TGCTGTGAAG AACTAAACAG GTCAGGTGTA 300

AGTGGCTCAT GCCTGTAATC TCAGCACTTT GGGAnGCCGA AGCAAGTGGA TCATTTAAGC 360

CCAAGAGTCA AGACCAGCCT GGGGnnACAT AGTGAGAnTC 400

(2) INFORMATION FOR SEQ ID NO: 2175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2175:

ATATCGTTTA AACCATCAAC AAGATTTTAT AGATGCAACT TTTACTGCGC TGAAATCAGA 60

TAGAGCACGT TTAAAAGAAG TGCCAGTTCA TGTTGAACTT ATAAGTTATA TTTCTAAATC 120

AAAATAAACT GCTATCTAAA ACGCAAAGTT GATCAAAATA TCGATTTTGT GTTTTTTATT 180

GAGAAATTAT ATAGGAGTGT CAATCGATGA TTTATTGTGA ACAGAGCGTT TAATATTAAG 240

AGACTGGCAT GAAGATGATC TGTTACCTTT TCAAAAAATG AATGCGAATT ATGACGTACG 300

TAAATATTTT CCAAGTTTAT TGAGTTAnCG nCGTTCAGAA TTAGATATGA GACCTATGGA 360

TGCGGTTATn AAAGATTATG GCCATTGGGA TTATTGCCnG 400

(2) INFORMATION FOR SEQ ID NO: 2176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2176:

TAAATCAAGG AAAGACATTT TAAGGTACGA AGGTTGATAA CAAAAAACCA ACAGATTTAG 60

GGGTATCAGA G 71

(2) INFORMATION FOR SEQ ID NO: 2177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2177:

GTTGAATTAG GCAGCACGAT TATTGATGCT GAACTGTTAG AGTCAGATAA G 51

(2) INFORMATION FOR SEQ ID NO: 2178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2178:

TTAATTAATG GTATTTACAT ATTCATAACC AAAGGATAAA ATAATTGTGA AATTATTCAC 60

A 61

(2) INFORMATION FOR SEQ ID NO: 2179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2179:

CATTTTACCA TGCAGCAAAT AATACAGGTG GTGCCGTTAA CAAACGTGAn 50

(2) INFORMATION FOR SEQ ID NO: 2180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2180:

GCCGAACGAA TCAAATACCA TACCTAATTG ACTGCAGGCA TGTCCATATA GTGCAGTTAA 60

CTGTCTACAA GGC 73

(2) INFORMATION FOR SEQ ID NO: 2181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2181:

TACTTTTGGC GATATTCGGT ATCGTTATTA CAGTTATTTT ATATGCAATT AAATTGCCGG 60

GTTCTATCTT TATCGGTATG ATCATCACAG CAATCGTTGG TATGTTCACT GGATTGATTC 120

AAATGCCATC TGGTATTGTG GGTAAGATTC CAAGTATTGA ACCAACGTTC GGTGCTGCAT 180

TTGAAGCGTT TAAAGACCCA AGTCAATTAT TAACGATACA GTTCTTAATT GTTATTTTAA 240

CGTTCTTATT TATTGATTTC TTTGATACAG CTGGAACATT AGAAGCGGTT GCAnCnCAnG 300

C 301

(2) INFORMATION FOR SEQ ID NO: 2182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2182:

TTGATTCGCC TTGGCCAGAA TTACTTTTGT TTTGGGCGTC ATTGCAAGTT TCTA 54

(2) INFORMATION FOR SEQ ID NO: 2183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2183:

TTAGTnACAT TGGGACATTT AACTGATCCA CCAGTACTTT TGGCGATATT CGGTATCGTT 60

ATTACGTTAT TATTGCATAA TGCGGTCACT ACGAGACACC GCACTGAGTC CGATATCA 118

(2) INFORMATION FOR SEQ ID NO: 2184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AGATAGTTAT ATAAAGATTT CATCTTCTGT ATTACATTGA TATTTTTAGG TCCCTGTATA 60

TAAAAATCAT ATGCCTCATC AACAACATCA CTTTTATTTT TGATTGCAAT TTGATGTAAT 120

ATCTTTTGAC TAAAAACACG ATTAATCATA TTTCTATTAT CCATAGCTAC GCACCTCCTT 180

CAACATACAT TTAATGCTTA TCCTGTTAAT ATTATAAnCn ATTTTAAATG CCTATAGACA 240

TTATTTCTAT ACACATACGA TTATnAAATT GTATTGAAAC CAAATGATGG TTGCCAAACA 300

CAT 303

(2) INFORMATION FOR SEQ ID NO: 2185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2185:

CCGGGGTTTT GGTTAAACCC TCCCAAnATT TTTTTTAAGC CCAAACCTTG GAAAAACCCA 60

GGCCACCCGT TGGAATTTTT AAGCCTTGGA TTAATCCGGT TTGGTTAACC 110

(2) INFORMATION FOR SEQ ID NO: 2186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2186:

CCTATATTGT CACCCAACTT CATTACGGCA CCTTTACCGA AAGATTTCTC CATATTTTTA 60

ATTACTGTAT CTAAAGCTTT TTGACG 86

(2) INFORMATION FOR SEQ ID NO: 2187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2187:

TTTGCTAGAA AACATACCAC ATTTGCCAAT TATATTATTT ATTCTGATGT TTATTTTCGG 60

TATTTAGAGG TGATAAAATT TGTCAACTAT TACAAAGACT AAAATAAAAA TCTTTATTAA 180

TTATTTTATT GGTATATTAG CCTTGGCGTT TGCTGCTTAT ATATTATTTA AATAAAGGTT 240

AGAGTGAAAC GTGTTTATGA ACTAGACGTT CTAGTATAGT TACTACAGCT TTAGTCAGAA 300

GGTATCATTG ATAAGATCAT ATTAAATCAA AGAGGCATTG ATATACACTA AAAAGAGGCA 360

AGATTACCTG CCTCTTTTTA GTnATTAAAT ATACGTGTTA 400

(2) INFORMATION FOR SEQ ID NO: 2188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2188:

TTTTATAAAA TATCAGACAT TTTTGnTCAA CATACATCTC TTTCGATGTT TCTAATACTT 60

TATCATTAAC CATTACACCT TAAAGTTATG ATGTGGCATG TTTTCTTATA TTCATAACAT 120

CAATTTTATC A 131

(2) INFORMATION FOR SEQ ID NO: 2189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2189:

CGTAAAATAT TTTGATTTAA AATGGAGGGT ATTAATATGA AAAGGTTCAT GTAAAATCTA 60

GGGGTATTCC AATATTATAA GGCAC 85

(2) INFORMATION FOR SEQ ID NO: 2190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2190:

CCCGAGGAAT ACATGGCATT AAATACACGT TTAATATTTA TAAAGGTGAC TTAATTTTGT 60

ATAATTGTTT ATCAGTGATA AAATATTTGC AATAAGAAGA GAATGACTAA ATAATCTTAA 180

TTTTCAGAnA AGTAATTGTA ACCTTACTGG TCTTATGGTA ATAn 224

(2) INFORMATION FOR SEQ ID NO: 2191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2191:

AGCTTTTGTA GTTTTCTTAA GCACACCGGC GATTTGATTA TTACATAAAG GATTCCCTTT 60

TTTTGTTGTG AATATGAACC CTCTGTCAAC ATAGCTCGAA TTCCATCTTT TCAACATTTT 120

GTTTTCCAGT ATTATCTTTT TAAAAATTTC TACGGTTCTA GAATTGATGC TGATACTTCT 180

TTTTGAACTT ATAGTCTTTG TAGTGTCTTT GTATCCGAAT CCTTTCTCGT ATTTAATGCG 240

GTGAATTGTA CCTGTTATAT TGATAGTnTT GTTTAATAAA TCTATATCTT TTTCCTGCAG 300

TGCTTGTAGT TCTCCTATGC GCATACCAGT TAAAGCCTGT ACTTCTAAGA TGCTGGCAAT 360

TAAAATGCGA TTTCGCTTTT GTAACTTATT ATCATTTAGT 400

(2) INFORMATION FOR SEQ ID NO: 2192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2192:

GACGACTGAG AGGCCGTTGA ATTTGACGTT GCCATATnTT CAAATTTAAC 50

(2) INFORMATION FOR SEQ ID NO: 2193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2193:

GTTGTTTTCA TATCAAAACA CCGTAGAATA AACAATGAAT GGAATTACTT TTGCAATGAT 60

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2194:

CCAGTCACTG ACTACGTCTT CCTCGGTGCT GGCGGTGGAG CCATTCCCTT ATTACC 56

(2) INFORMATION FOR SEQ ID NO: 2195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2195:

GTAGGGAAAG GAAAAACTGC TTCCATTGGG AAATGTTAAA CCTTGTTCCT TGGTGATGCC 60

ATTGGATTT 69

(2) INFORMATION FOR SEQ ID NO: 2196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2196:

ATATGACACT ATATTTTATA AACATACATT TAATGATTCA TTATACAATT GCCAA 55

(2) INFORMATION FOR SEQ ID NO: 2197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2197:

GCCCTAGTTC AATCATATAA CCATCTTTAC GATACGATTG AATCTTTCCC CCCGGACGAT 60

TCGATGCTTC A 71

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2198:

AGTAGCACAA CAGCCATGCG GAGACAGAGA ATCGTTAGAG ATTAATGGAG ATCA 54

(2) INFORMATION FOR SEQ ID NO: 2199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2199:

GGCGGTTTTA TATTTATCGT TGCAGTTATG CAAATTGTAC TTGGTAGAAG TATAGATTCT 60

CGTGATTCGA AAAAAGTACT TTTAACGGGA TTGGGAATAG TAATCATATC TAGCTTTATT 120

TGTGCAGTGA CACATAACTT TATATTATTT GCTATATCAA GGTTATTTCA AGCAATTGGT 180

TGCGGAATTA TTCCTCTCGT GACTTTAACT TTATTAGCCA AACTAAGTAC AGATAATGGT 240

AGAGCTCAAG CTATGGCGAA CTATCAAATA TTTTTATCAT GTGCACCAGC TTTGGCACCA 300

ATCTTAGGGA GTACTTTAGG TGGCAAGATG GGGATATATT GGTATTTTAG TTTTTTGGCT 360

CGTTATATCT ATCGGTATTA TTTTTGGATA nCTnTnTTAA 400

(2) INFORMATION FOR SEQ ID NO: 2200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2200:

GGATATGCGA TGGATGACGC ATTGCTATAT CGGCAATTGn GAAGCTGCTG 50

(2) INFORMATION FOR SEQ ID NO: 2201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2201:

ATCGAATATC ACTACTATCT CTnTTnAAGT ATCTACAATC TCTCCAATCT 50

(2) INFORMATION FOR SEQ ID NO: 2202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2202:

TCGACAATCC TAATGCAATT GCTTCATGTG GnTGTGGTAG TTCATATTAG AACTGCAAAA 60

GTTGCAGGTG ATCCTGAAAA TTGCTAATAA AATAACTTTT TAATGGTTAA CCCAATTTTT 120

GGGATACAAA TTGATATCAA TAACGATTAA GGACATATTT GATTATGTCC TATTTTTGCG 180

TAAAGATATT TTGTTTTATT AAAAAGCTTA TTGAAAATTA AGAATCTGAC TATAAATAGT 240

ATTTTAAATG ATCGTGATAG CGGATACATT TTTAATCGAA ATCAGGCTAC GAAAAAATTA 300

ATTAATTTTT TCACAATCTG ACTGAATCTT GCTTGAAAAT ATAACATAAA AGCTATAGAA 360

TTAGTATTGG ATTAAAAATG TCTTTTTTGT GAACATCACA 400

(2) INFORMATION FOR SEQ ID NO: 2203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2203:

GCGTTGTCCT TTTCGTGACA TGAAACAATG TGGAAAACAT AATTAAATnn AGGGAAAGTG 60

TGAATAGTTA AAAAATTAGT ATTGTGTTAT AAAAAATAAT TAATACTGTT AGGATTTCAT 120

TAACTAACTT AACGTTGGTT CAAAAATAGT TAAAAAGAGG TTAATTCATA GCGCAGTATC 180

TCACTTATAT AATGATAGTA GATTGTTCGT ATTACGTAAT TGAATTAATC ATATAAAAAT 240

ATATTAAGAC AAATTTATAA ATAGATTGGG AGAnTAGTAC TGTGAAATTA AAAACGTTAG 300

CTAAAGCAAC ATTGGCATTA GGCTTATTAA CTACTGGTGT GATTACATCA GAAGGCCAAG 360

CAGTTCAAGC AAAAGAAAAG CAAGAGGGnG TACCACCATT 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2204:

GTTATTTTGT ATGGTTAGTC TTTAAAATAn ATATAGATAT TAAATATTTA TTTTACGAAT 60

TGTTAAGTAA AGAAAAAATA TTAATCAATC CGGGTTACAT TTATGGCAGT AAAGAAAAGA 120

GTATAAGGCT ATCTTT 136

(2) INFORMATION FOR SEQ ID NO: 2205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2205:

TTTTATTTTT TCGCAATGAA AAACAATCTT TCTGCATCTT CATTATGTTC ATCTATATTA 60

AAATCAGTAA ATGTTTCAAC ATGTTTAAAA CCAACTTGAG CTAACCAAGA CAAATATGTC 120

TTTTCATCAA ATGTTCTCTG AAAATGAGAC TCATCAAATC TTGAATATGT TTCATCTTCA 180

TGTCGAATGA AAAATGTCAT ATCATGATAA ACACTTAAAG GTAAATCTCC TTGCACAGCA 240

TCCCATGCTA AAAAAATGTC CCCTTTATCA TCAATATAAC TTTGATTATT AAACAAAGTC 300

ATCATTTTAT AAACAGTATG TACATCAGAA ATAAATACAC CTGAATCAGT CAGATGATGA 360

TAAACATTGA TGAATGTTTC AATCACTGCA GTTTCATCTT 400

(2) INFORMATION FOR SEQ ID NO: 2206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2206:

TTGAATATCA TATAAAAACA TCAGGTTCAA AGTTGACTAC TCTTAATAAT ATAAAAATAA 60

GAATTAAAAA CATTAAACGA TACTGCTCTG AGAACTTGCT TTTAAACAAA CTTGATACAA 120

GTCAACTCGG AGATATGAAA GGAGCnATTA AATATGCAGT TAAATTTTAC AATTATCCAA 240

ATGAATATTT GTTAACTAAT GTCAAAATTC CTAAAAGAAG AnAAACAATA GAGGATATCG 300

AAAAAGATGA ATCTAAAATG GTACCACTAT TTAGAAATGG AACCAAGTCC TACnGATACG 360

TGATCATATA CTAATGGAT 379

(2) INFORMATION FOR SEQ ID NO: 2207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2207:

CATCTTGGGA CGTTTTAAAA AGTAACGTAG CGAAGACTAT TGGAACAACA ATGAGAACCA 60

ATGCTAGAAG GATCAAAAAG TATTTTAAAA ATTTATTCAT GATTGATGCT CCTATATTAA 120

ATTTnTGTTA AATCATA 137

(2) INFORMATION FOR SEQ ID NO: 2208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2208:

GCGCCGCTCT GTTCATTTTA CCTAAATCCA ACGTTTCAGG AATAGATGTT TTCAAACCAC 60

TTTGAAATGG AT 72

(2) INFORMATION FOR SEQ ID NO: 2209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2209:

ATGTAGCAAC TAAAGATGAT AGTGGATAGC GACACGGTCA ATAAACTGCC TA 52

(2) INFORMATION FOR SEQ ID NO: 2210:

(A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2210:

TTTTTTATGT TCTTTTTTAA TAAGAGGGAA GTGAAGTTGT ATAAAAATGT ATTAAATATG 60

CACTTTTTAT ACATTAACGA TTCATATATG TCTATTATGT ACCAAATTTA TAATTTGTAT 120

AATTTTCGAA CTGGTTAAAT TCGAAAAATA TCACTAATAT ATnTAGATCG ATGTGTAACA 180

TTACGTTCTA nTAATTTAAT GTTGCA 206

(2) INFORMATION FOR SEQ ID NO: 2211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2211:

ACGATGTATT TTGATATCGT TACCAAAGTC TTTTAATAAC TCATTTTCAT CTAAATAAAT 60

(2) INFORMATION FOR SEQ ID NO: 2212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2212:

TGATAAGGTT TGTCCCATCG CTATTTGAAA TGATGCATTG TAAAAAACTA TCATTTGTTG 60

GTAATATCTT AGTTCGATGA CTTTCTTTCC AATCTTTCCG TGTCATAGAG ACAAGATTTT 120

TTGTAGCTAT CTTAGTTGCT TCTTGAATGT TCATTTGTTA TTCCTCCTTT TAAGATGTTT 180

GTnTTTCTTT AAATGCTAAA ATAATTGATT TCTTTTTATC ATTCGTGAAT ACGAAATTTT 240

CGTATTCATT ACCTAAAAAA ATATCATCAT ATTTAACATT AAAAGCACTC ATATACTTAG 300

AAAGTAAACT AACnTTAATG GnTGTAGAGT C 331

(2) INFORMATION FOR SEQ ID NO: 2213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2213:

AGCATAAACC AAAAGATGCG GATATACTTG AACGCGTCAA AGATATACTT AATAAAAAAG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 2214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2214:

TCTATTTGAG TTTACATTTG ATTAAATGAA TGACAATTAT ATGAACCTGA CTTGGT 56

(2) INFORMATION FOR SEQ ID NO: 2215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2215:

ATACCACTAC TATACAGTTA AATTAATATA CGTTAAAACT TTAATCCGAT ACATTGGTTA 60

AAATGATGTT CCTCGCTGGT GGATCGAGAC ATACTTCGCT CTGACTTCTT TAGTCAGTTT 120

TTTTTCAGCT TTTTAGGTGT AATCACTGAC TTTGTTACAT CACGTCAAAT TTACAGTCGC 180

TATTATCTTA ACTTATCnAC GCTTATCACA CATCAATTCA GATATTATAT TGCATTGGCG 240

nCTATCACTT TGAACCTGCT GTGACTGGAA CTACTGGCTG TCAnGAGCGA GGGCTGATAA 300

TGAGCATAAA GCAACATATA AGTAATACGG CCGAATATGT AAATTCGGCA GCTTTAGGCA 360

ATGCTGCCCG GGCATGACTA GnACATTCAC AAGAAGCTCA 400

(2) INFORMATION FOR SEQ ID NO: 2216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2216:

TTTTTAAAAA AGGGGTTAAC CAAAGTTTTG GAACCCCAAA AAATTCCGGA GTTAAAAAAA 60

CCCCAAAAAA TTAAATTAAC CGGTTATTCC GTTCCAGGAG CCAAATTTTT ATGGTTCCAA 120

TTnCCAAAGT GGG 133

(2) INFORMATION FOR SEQ ID NO: 2217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2217:

TACTCGTACC ATTAACCAGT CTGATTAACC ACAATACTAA GGTATTCAAT ACATCACTGA 60

CATC 64

(2) INFORMATION FOR SEQ ID NO: 2218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2218:

TATTCTATAG AATATGGATA ACGTTTAACA TGATGTAGAG TATTCATCAT TGTAACACGT 60

CAATTTGATA TGTGAGATTA AC 82

(2) INFORMATION FOR SEQ ID NO: 2219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2219:

TTTGACGCAA TGATTTAGCT GTAAATATGC AATCTAAAGG AAAGTACCAC TTATGAGATG 60

TATTAAAACG 70

(2) INFORMATION FOR SEQ ID NO: 2220:

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2220:

AAAAATTACC CCAAAGAATT GAAAATTTGT TGTTTGGGTT ACCGGGTTTA AGATTAATCC 60

GGTTGA 66

(2) INFORMATION FOR SEQ ID NO: 2221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2221:

GATCGCAACC AAAATAATGG TCTTCCTGGA TTATTACTTT ACCAGCTGGC ATAC 54

(2) INFORMATION FOR SEQ ID NO: 2222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2222:

GTGTTGCTAC AGCTAnCATT TCATATTTAA CGnGTTGTGG TATTTCTAAA 50

(2) INFORMATION FOR SEQ ID NO: 2223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2223:

AATGGGGGnA CCCAGCnTGA GTTATGTCAT CATATCGGTA TGTGATACAT 50

(2) INFORMATION FOR SEQ ID NO: 2224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2224:

GTAGATGCGC CCTCATATGG ACAAAGATAA AGTATCAGCA GATTGGACGC TTTA 54

(2) INFORMATION FOR SEQ ID NO: 2225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2225:

CGAGACTTCA CTTTGACTAA ACGCGTTAAG AATTTAGATT ATGCTTACGA TGAAGAAGAA 60

TTA 63

(2) INFORMATION FOR SEQ ID NO: 2226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2226:

TGGCCATTTT TAATGGGGGG AAACCTTAAA AAGGGGTTTT TAATTTTAAA CCAAG 55

(2) INFORMATION FOR SEQ ID NO: 2227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2227:

TCCATTTGGT TGCCTTCTTT AAATAAACCT TGGATTATGC CTTTCCTCCG GTTAATTAAT 60

GGGACCAGGG GCCAAAAATA CCCCCTTTTA AATATAnATT CCCAAAATCC ATAGTTAAAT 120

AATCCATTTG C 131

(2) INFORMATION FOR SEQ ID NO: 2228:

(A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2228:

CCATCTGTGC TTCGTTAGGC GCTTTCGGCA TCACGGTGAT GGTTTGCGAC AGATCCGCCA 60

TCCGGCTGAA TGGGAAGCCC GCGTTAnAAA GGCGCGTAGA TCCGGCATCG GGATGAAGTG 120

GTAATACTTC GAGAAGTCGA TGGTGGAGTC GTCACCAATC ACCACATGAT TCTGCACCGG 180

CTGGAAGGTA ATACAGTTAT CCACCGAACC GCCCGGCATC GGGTTCATAT ACTCAAAGTC 240

GAAGCGCACT GGnTTTGGTC GCGCCCAGTT TCAGCGCCGG AATAGAGACA TCTGTTTTGC 300

CATCCAGCAA ACCTTGTAAT ACCGGAnTCC GCAGCAGCAG GCGGTTTCGC 350

(2) INFORMATION FOR SEQ ID NO: 2229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2229:

AACTAAAAAT ACTATATAAA AAAGGTTGTT ATAATTTAAT GGATATAAAT AAAAACGA 58

(2) INFORMATION FOR SEQ ID NO: 2230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2230:

GGGCGAAAGC TGGACGGAGC CAACGTCGCG TGAGTGGATG GAAGGTTCTT 50

(2) INFORMATION FOR SEQ ID NO: 2231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AGCCATACGT GGTAAGCACA TGCTAAATTT GCCAGCCTGA AAATGTTTAG 50

(2) INFORMATION FOR SEQ ID NO: 2232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2232:

TGTATCATTT TGGCAAAATC ATAATCTTTA TCGTCGAATA CAACTACTTT TAAGTTTAAT 60

GATGAAGGTA CGCATTGTGT AATCACTTCA TCTAACTTTT TTAAATCAGG TGTCATAGTT 120

GAACTTGGnG GT 132

(2) INFORMATION FOR SEQ ID NO: 2233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2233:

GATCTTGAAG CAGTTGAAAC ATATGTATCA GATGCATTAA GACAAGTACA CTTACAATCA 60

GACATTTTTG CTGTATCA 78

(2) INFORMATION FOR SEQ ID NO: 2234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2234:

TTTAGGCACA GACGGTAATA AGCTACAATT TTCATAAAAT CATCTCCTTn 50

(2) INFORMATION FOR SEQ ID NO: 2235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2235:

ATCCTGGAAA ATCTGGTAAG ATATCTTGGA AATAACTAAT ACCAATTCCT AAAA 54

(2) INFORMATION FOR SEQ ID NO: 2236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2236:

GGGTGATGGT CATTGACAAA GTCAACTTGT GATAAGCCAT GGATATTTTT CGTT 54

(2) INFORMATION FOR SEQ ID NO: 2237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2237:

TTATTTACTT TAAATTTCTC AATCTACAGT GTAATCTTAT TTCTTATTAT 50

(2) INFORMATION FOR SEQ ID NO: 2238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2238:

CCTTAATGGG TTTTGGGGGG GGGCCCCCCC GGCCCAAAAC CTTTGGCCCA ATTGGTTCCT 60

GGGTTAAGGA AAAA 74

(2) INFORMATION FOR SEQ ID NO: 2239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CCACCCATGG CGCTTGACAA AATATGGATG GAACATAACC ACACCGTCCA AGTTCACTGT 60

TAGCACCGTG T 71

(2) INFORMATION FOR SEQ ID NO: 2240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2240:

CAGCTAGGTA GTTAGGGATT CGACTCGTAA AACGGATTAA TAGGTTTTAT AAGAAGGGGG 60

TTTG 64

(2) INFORMATION FOR SEQ ID NO: 2241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2241:

CTTGACACGT ACATCTAATA CGACAGTCTG TGCGTTTAAA ACCTTTTGGG TCAAACTG 58

(2) INFORMATION FOR SEQ ID NO: 2242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2242:

GACTCATCAC CGnTTGTTAA GAnATACAAT TTATTACCCA GCAnTTAACA 50

(2) INFORMATION FOR SEQ ID NO: 2243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AAATTTGGAT TGGTTGGAAA TTTACAGTTA AAATTTAAAG GGTGGATGGA AAAATTTTAG 60

GAACTTCTAA G 71

(2) INFORMATION FOR SEQ ID NO: 2244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2244:

GGGGGCCCCT TGGGGGTTTG GGTTTTGGGG GGCCCCCCTT TTAAAAAnTT 50

(2) INFORMATION FOR SEQ ID NO: 2245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2245:

TTATAATTTT TGAAAATAGA AGAGGGAAGC CTTAAATTAC CAAATGGATT TA 52

(2) INFORMATION FOR SEQ ID NO: 2246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2246:

ATTAGTTGAA AAGTACAATA TTCCGCAAGT TACCAATCGA TACAGGTATT ACAAG 55

(2) INFORMATION FOR SEQ ID NO: 2247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2247:

(2) INFORMATION FOR SEQ ID NO: 2248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2248:

GGGAAGGTAA AACTTCCTGC TTTTTTTATA AGTATTCATA CTCTATTGCT ATATTAGTAG 60

AAACCGTAAA ATCAGTCATT CACATACATT nTGAAACATC TAAATAG 107

(2) INFORMATION FOR SEQ ID NO: 2249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2249:

GTTGGATACC TGnAACTAAA TAACTATTCT TTAAAAGTTA AAAACCAACC ACTAGTGGCC 60

ATTGGGGATT AAAATTCCAA CCTGGGCCGG TCCATCCCCA TGGTGGGTAA AATGGGGGAG 120

GGAAAATCCT TATTAGCCAA AGGATTCCTT ACCTAATAAT AGGGGGAA 168

(2) INFORMATION FOR SEQ ID NO: 2250:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2250:

TTTAGTTGTG ACATACTGAG AACTGTAGTA CTTAGTGCnA TACCAAAGGG 50

(2) INFORMATION FOR SEQ ID NO: 2251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GCAGAACATA CCACGTGTCG CTGATTACCA ATACAGTAGA TCAAGATGGA CTCGATTGC 59

(2) INFORMATION FOR SEQ ID NO: 2252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2252:

GTTTGTGTTT TAATTTTAAG GGGAAGGGAT TTTTTTACCA AATGGGAATT TT 52

(2) INFORMATION FOR SEQ ID NO: 2253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2253:

AGTGTAATTA GAAAGGCAAG TACACCTGTT TAAAGTTTAT CTTCTAAGAT TTGTTTACTT 60

TAGAACTATA GCAGTTAATC 80

(2) INFORMATION FOR SEQ ID NO: 2254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2254:

GTAAATGACA GAGGAAATAT AACAATGATT AATAATGTTA CAGCATTTAC TGCAAATATC 60

TACTAT 66

(2) INFORMATION FOR SEQ ID NO: 2255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ACATGTGTTA ACTCTTTGGC AATATATCCT GTTTCTTCTT CTAATTCACG 50

(2) INFORMATION FOR SEQ ID NO: 2256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2256:

AATCTTTTAT AGGAAAGAAA GAAGAAGATG TTATCAGTTG CGATTATCGG CCCAGGCGCT 60

GTCGGTACA 69

(2) INFORMATION FOR SEQ ID NO: 2257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2257:

TAGCGGGAGA TAGAAAAACC ATTCCGCATT AGCTTTGGTC AAGTTGGGAA TGGGTAAAAA 60

AATA 64

(2) INFORMATION FOR SEQ ID NO: 2258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2258:

GGTTAAGGTA TGGCGAAATA TCTCCAACAA CACTTCAAAA GGTTCAAGAA AATAGAAGTC 60

GACTGAACAA TGTCATTCAC ATGTGTGCGT CATGCACACC nTATGT 106

(2) INFORMATION FOR SEQ ID NO: 2259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2259:

CGGAATAACT GACTATGTAT CATTTGATGT TATTAACATC AATATTTTTG GTTAAATGAT 60

ATGCTAGAAA TAAAGCATA 79

(2) INFORMATION FOR SEQ ID NO: 2260:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2260:

GCTGGnTGTT AnTGGCAGAG CATGTGAGCT GGATAATCAG TTGGAGAGGC 50

(2) INFORMATION FOR SEQ ID NO: 2261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2261:

nCCATTAATG ACCGAGATTA GTGAGCATGC ACAAATTGTT ATGGTAGGAT 50

(2) INFORMATION FOR SEQ ID NO: 2262:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2262:

AATGAACCAC ATAATGACAA CTTGAATGAC AATATGAATA TGATGTCAAC A 51

(2) INFORMATION FOR SEQ ID NO: 2263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CATTAGGTGC TTATATAAAT TACTTTGTGG TGGCTCCAAA ACTTCGGGTT AAAAC 55

(2) INFORMATION FOR SEQ ID NO: 2264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2264:

TTTCnTCCCC CCCCCGGGGT TTTTTGGTCC CTTTTTTTTT TTAAATTTCC 50

(2) INFORMATION FOR SEQ ID NO: 2265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2265:

TCATTCATAG AGGTGTAAAG ACATAAGGGG AGCTTAACTG CGAGGACCTA CA 52

(2) INFORMATION FOR SEQ ID NO: 2266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2266:

AGATGATGCA ATAATGGTGC AGTATAGAAG TACTGAGCAA TGCAAATTTT AGACG 55

(2) INFORMATION FOR SEQ ID NO: 2267:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2267:

GTTCATCACA TTTATTACAT TCAGCGTTGG AATCAGTACT GGGTTATCAT G 51

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2268:

CTGTTGACAA CAAATTAAAA ATGACAACAT GTCGTAGTTA TAGTTAATTG ATTG 54

(2) INFORMATION FOR SEQ ID NO: 2269:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2269:

AACCAAAAAG AAAGCAAGGT CAAGGAAATT TCAGCGnGAC GTATCTTTAG TTTTGAATAA 60

GCATATTAAT ATGGTGATAA TATGCAAGAn AACCTGTTTA TTCGATTCAA TGAAATTATA 120

TTATTAATAT ACTTAATCAG TATCATTTGC TATTTTTATG ATTTTGTACA AAAAAGTCAT 180

AAGATTAGAA GTTTAGGCAT ATATTTATTG GGGATTGTTT GGGTTTTACA AACAATCTCT 240

TTATCTATTT TTATTATACA AACTAGACAT ATTCCATTAG GGnCTATTTC AGATGTATTC 300

TATACTTTAA GT 312

(2) INFORMATION FOR SEQ ID NO: 2270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2270:

GTTGATGGAT TCTCTTGGTT TGGTGTAGTC ACAATTTCTG AACTGGCCCT TGTTTACG 58

(2) INFORMATION FOR SEQ ID NO: 2271:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2271:

CGTTCAGACG CTAAATCAGG CACCAGGTTG TACAATTGTC CTGGTTCTTC 50

(2) INFORMATION FOR SEQ ID NO: 2272:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2272:

CAGGTGTTGG TAAAACATTT GAGATGCTTT CAAATGCCAT TGAACTATTT CAAAGTAA 58

(2) INFORMATION FOR SEQ ID NO: 2273:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2273:

TTATAAATTG GTGTAACAAT TTCATACACA TGATCATTCT TTGATTGAGG TAAAAATGAT 60

TCTACTAAAC GTACACGTTT ATGCTTCTTA TATTCTTTCA TCAATAAATA TCTATGATTA 120

GCTAATGATA AATTTAGTAG AAGCTTGTTA TCTCCATAAA CTAAATTCAC GATATTAGGT 180

ATATTGAATT GTTCTTGATA TTTCAAAAAT TGTTGATCCC ATTCTTCATT TTTAGGTAAA 240

GGTAATACCA TCTCGTTAAT TTTCCAATAT GCTGGTTTAA GAATGACATT TTTATATCTG 300

ATTCGTGGTG AATAACTAAA TGAATCAATA CTCACATCAT TCATAGGTTC AATGCATTTC 360

ACAGATTCCA TTGAAATTTC TCGTAACAAT CGATATnAAT 400

(2) INFORMATION FOR SEQ ID NO: 2274:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2274:

GGGTACAAAT TTGTnGATGA TAGAAAAGTT CGTATCGCTA GAAAGTCTGG 50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2275:

TGATTTACCA GTTGATTACG ACAAAGAAGA ATTTTCAAGA ATTGTTGAAG CATCAAAACG 60

CATTA 65

(2) INFORMATION FOR SEQ ID NO: 2276:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2276:

ATGGCGTTCC ACCAGCAGTC AATAATCCTG TTGGGATAAA TGCCAATACT GTCGA 55

(2) INFORMATION FOR SEQ ID NO: 2277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2277:

TAATAAATCA CGTGCATTTA CGCTCACTAG CTTTCATCTC CTCATTTTTG CTTTTCAAAT 60

TTATTAAGTA TGAATA 76

(2) INFORMATION FOR SEQ ID NO: 2278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2278:

GTGGCTTTGT CTGTGTTATT GTAGTTTTGT TTCGCTGCGT CCAGCTTTGC TGCTTTTCCC 60

(2) INFORMATION FOR SEQ ID NO: 2279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2279:

TTAAGTGCCA AAGTCCTTGG TAGCCAGAAT GAACCACCAA CCTCCATTTT TCCAAAAATG 60

GTCTTACCT 69

(2) INFORMATION FOR SEQ ID NO: 2280:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2280:

GGATGGAATT GGGTTAAGAA TAAAAAAGGT AATAATTGAG TTTATGATAA TAATAATAAT 60

ATTGAGA 67

(2) INFORMATION FOR SEQ ID NO: 2281:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2281:

TTGTTACTTC GGCACGGATA AATCCACGTT CAAAATCAGT ATGAATGATA CCAGCACATT 60

GAGGTGCAGT CATACC 76

(2) INFORMATION FOR SEQ ID NO: 2282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AACCCAGAAG ACTTATTATT AGAATCTTAA TCCACAACAC AAAATAGTTT ACTATTCCTA 60

AAAGCGGGAT TAAATCAATA ACAAACAGCA GTAAGATTAT TTCCTAGTCG AAATATCTTA 120

CTGCTGTACT TTATTTn 137

(2) INFORMATION FOR SEQ ID NO: 2283:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2283:

ACAAAGATTT ACTATTTAAC TAATTTATAT GAAGAATAGC TTTCCCTAAT AA 52

(2) INFORMATION FOR SEQ ID NO: 2284:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2284:

ACTCCTGCAT ATCACAACTA GATTAAATAT ACATCAAACA GATATAGTAA A 51

(2) INFORMATION FOR SEQ ID NO: 2285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2285:

CTAACATGTG TGAACGATAT GCAAATTCAA TATCTCATTC ACGCTTTGCA CTTTATTACT 60

ACAATCAACG TAACTAT 77

(2) INFORMATION FOR SEQ ID NO: 2286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2286:

AAACCTGTAT TTTTAATAAA CAATCGCTTG GACCTATTCA CTGCAGCTCT TCTGGGAC 58

(2) INFORMATION FOR SEQ ID NO: 2287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2287:

AATTCATAAA ACCAATAAAT AAGAATTTTA TAGTAAAAGG AAATGGAnTA GAGTTGGCAG 60

ACTTATACAA TATTAAAAAC AAAGAGCTTT TCACGATTAA AAGAGGAATT AATACATCTT 120

TATCTCTTTA TAGTCTAGAA CAGGAATATA ATAACAATTA ACGCCTTAAA ATATCCAGAA 180

TCATATAATT TTGAAGAATT AATA 204

(2) INFORMATION FOR SEQ ID NO: 2288:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2288:

GCTCGTAAGG CGTCAACTGT GGCCTTGGGT GCTACATGTA AAGGTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 2289:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2289:

TCGCTTCGGT GGTAAAAATG TCGTGGAGGT CCCGTTGCAG ATGGTTTTAA ACG 53

(2) INFORMATION FOR SEQ ID NO: 2290:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2290:

TTGGAGGTCA ATGTTCGGCG TAATCTTCAA TGTTTCCGTA CACAATTGCT GCGGTTGACA 60

CACATACG 68

(2) INFORMATION FOR SEQ ID NO: 2291:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2291:

TTCGACGAAT TAAAACAAAT CCTTTTATAT GTTGAAGTGT ATTCGAGATT AAA 53

(2) INFORMATION FOR SEQ ID NO: 2292:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2292:

ATCAATTGTC AACATCTAAT ATTCACTACC AATTATATCG CCACATGTTT TTTAGCAGTA 60

ACA 63

(2) INFORMATION FOR SEQ ID NO: 2293:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2293:

CGACTCAGGT CCATCAAGAG AGACACATTT CGACTACAGG TTATTACTTC TTTGA 55

(2) INFORMATION FOR SEQ ID NO: 2294:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2294:

AAATTTTGGT TAATTTTAAA ACCAAAAAAC CTTGGAAGGA AATGGCCCTT TTCCCAATTT 60

T 61

(2) INFORMATION FOR SEQ ID NO: 2295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2295:

AATCTTAAAA CCTATGGCGT CTATTACATT CCCAAAACCT ATTTTCAGnA ATGTTACCAA 60

TTAAACTTGC CGGGGTATGG ACCAGGGTAC CAGGCTAAAA ACTGGAAGAA AGGAAGGAAT 120

TTTAGAAAAT AATTTATTAA CATGGACCAG GTAACTAA 158

(2) INFORMATION FOR SEQ ID NO: 2296:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2296:

TGTTCCAACG ATGAATGTTT GCATGCTTTG TTGCACTGAA ATTGATGAGT TGCTACTTGC 60

AATCCTAG 68

(2) INFORMATION FOR SEQ ID NO: 2297:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2297:

GTAGGGATTT TTTTTAACCG GGATAGCCCA ACCAAAATTT AATTAATTTT GGGTTTTTGG 60

ATTGAAGGAA TT 72

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2298:

AAAAATTnTA CCAGGTGAAA AATTATTTTG GTAGGATTTA AATnTAATGG TTTAAATGGT 60

GGTTTATTAC CTAATTTAAA AATGGTTAAA AGGGCCTTTA CCATTTTTAA AATTTAATCC 120

GCCTTTTGGG AGGGGGATTT TAGGGATGGT CCAGTTAGGA CCCCATTACC ACTGGAAACC 180

AACTTAAAAT TTGACCAAAT TTCCTGGAAA AAA 213

(2) INFORMATION FOR SEQ ID NO: 2299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2299:

TATTTTTAAA GGAGGGTAAT AATCTTAATT TAAGTTCATT ATTTTTACTT TCATTATAAA 60

TATTTAATGT TACTTTCTTA TTTAGATAAC AATAAAAAAA TATAATCTCT nAAAACCCAA 120

TGAAACAGCT GCTCCAAACA ATTAGTTCTT CTAATTGAA 159

(2) INFORMATION FOR SEQ ID NO: 2300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2300:

ACAAGGTCAT TCGGATTTGA CTTTGTTTCA ATTGTTAAAT TTTGCTCCAT CAATTGTCTA 60

ATTCT 65

(2) INFORMATION FOR SEQ ID NO: 2301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2301:

TTTATTCTTA TTTAAAAACC CAnTGAAAGT AnTCTTTnCA TTAnTAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 2302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2302:

GAGATATATG CATGAGCTCT ACGACTTCTT TAGGTTTCAT GGCGACTATC CTGGCAGGGA 60

TG 62

(2) INFORMATION FOR SEQ ID NO: 2303:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2303:

ACCAATCCCG TTGTTTTGGT TTTTTAAAAA AAGGAAATTC CAAAAATCCC CCATTT 56

(2) INFORMATION FOR SEQ ID NO: 2304:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2304:

TTTAAAACCC AACGGGTTTG GTTAAAATGG CCTGGGCTTT TCCAAAACTT GGC 53

(2) INFORMATION FOR SEQ ID NO: 2305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2305:

CGAACAGGTT GCCACTGTAA GATCTGGTGG CATTTAATGG CAATCGTATT TTATTTGGAG 60

(2) INFORMATION FOR SEQ ID NO: 2306:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2306:

CTTTATAATG GCGGCGCACT TGGCATCTCT GCATTCAGTT ACACGCGGTG GCAACACAAA 60

ATTTAGGGAA TTCT 74

(2) INFORMATION FOR SEQ ID NO: 2307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2307:

TGTCCATGCA CAGCTTTATT GGAATTTACC TTTTTACAGG CAACCGCTAA AGA 53

(2) INFORMATION FOR SEQ ID NO: 2308:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2308:

TAAATGATTA TGGGAATATC CAAAATTATC GAGATCTAAT ATGAAGTGAC TGCACACATA 60

TCAGCTCTGA ATGAAT 76

(2) INFORMATION FOR SEQ ID NO: 2309:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2309:

TCCTCAAAAT GTGAGTTAAT AGTCGAGTGG AAGCTGTGAC TTGAGCGACG ATACATCATC 60

AnACTATCAA TAATGTTTGC ACATCACTTT TACTACTATC ATTTGATGTA TAAATAC 117

(2) INFORMATION FOR SEQ ID NO: 2310:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2310:

AAACTCATAT CGCTTCCGAT AACCAACCCT GCTGCTGTTG GTACAAATTG TC 52

(2) INFORMATION FOR SEQ ID NO: 2311:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2311:

AACACTGGAG TCCTAATGTC ATCAAACATC TACCTATAAG ACCTTATATA ATCGTC 56

(2) INFORMATION FOR SEQ ID NO: 2312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2312:

GATAACATCA TAGGCCATAA CTTCCATTTA GGCCATCAGT TATAGCATGC GGACGACATA 60

CTGTGCCATA TG 72

(2) INFORMATION FOR SEQ ID NO: 2313:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2313:

CATCTAATGG GAACGTGTCG ATCCTAGTCA GTATAGTCAT CGGCAGGTAC GA 52

(2) INFORMATION FOR SEQ ID NO: 2314:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2314:

TAAACTGAAA TTTAATTTTC GGATGGTATT GTTATTAAGA AATAGACATA ATTTGTGCTG 60

GATA 64

(2) INFORMATION FOR SEQ ID NO: 2315:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2315:

CTAGTTTAAA TTTCTTAAAC TTCTACATCA GTAAAAGGCC GCTCTGGGAC CATACAATC 59

(2) INFORMATION FOR SEQ ID NO: 2316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2316:

GCATAGTAAC TTAATTGATA GGAGATGAAA ATCCGCAAAG TCATTGGAAG GATT 54

(2) INFORMATION FOR SEQ ID NO: 2317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GTATATGCTG GAAAGATAAA GTATGGAnAA TGCATGGCGA ACATTTTGTA AGCAGAATGA 60

GCTATAAGCG TTGAATGGGT TTGAACGTAA ACAATCGAAC AATGATATGT CAGACATACT 120

TGCTTTAGAG CACATTTAGA GAGCGACATG 150

(2) INFORMATION FOR SEQ ID NO: 2318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2318:

AAATCATCGA TGTTAAATAA TTTAATGACA AGGATTAATG AAAGACGGAT TG 52

(2) INFORMATION FOR SEQ ID NO: 2319:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2319:

TTAAGGAAAC CTTGGCCAAG GTTAAGGAAA ACCGGGGGTT CCAAGGTTTT TA 52

(2) INFORMATION FOR SEQ ID NO: 2320:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2320:

ATGAAGTTGA TTTAGGATGA AAATTAATCT TGGGATATTT AATACTTTGT 50

(2) INFORMATION FOR SEQ ID NO: 2321:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CTAACGCTAA GGGCGACGGA TGGTGGTnAT GTCAAAGAGA CAAATAGGAT 50

(2) INFORMATION FOR SEQ ID NO: 2322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2322:

CGTGGTGATT AATTTTTCGT CGCGTTTTGT TTCCTTTCCC CAGTCATGTT TTATCATTGT 60

GGGCATCATT GCACCTGGGT TCCATATTAT GACGTCATTT TTTAnAAT 108

(2) INFORMATION FOR SEQ ID NO: 2323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2323:

GTCACCGAAT TTCGATTTAT ATTATCACTC AATTTATTAT CTTGAAGCAC GCGTTAAATC 60

GTCTTTAAAT TGnAACAGTT GCTACTTTAT TGTCTTTACC ATTGATCTGA ATTTGATCCG 120

CTTTAAGTCC ACTATCTTTT ACAACTTGCn CTACCTTTTG TTGAGTAATT GCTTGTTTAG 180

ATTGGAAATC TACGCGTGTA CCACTTGAAA AA 212

(2) INFORMATION FOR SEQ ID NO: 2324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2324:

TCATTTGTTT TTAATACGTT GTCAAAATTA CCAACAAATG ACAAATTAAA TTTTGCAATA 60

CATATCAAGG TGTTATTTTT TTCCTATTTT AATTATGTAT AACGCATTAA AAGTGACGTn 120

AATATTCAAA GGA 133

(2) INFORMATION FOR SEQ ID NO: 2325:

(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2325:

ATGAACGACC GTGGACAGAC AATATTTAAA GCATTTAAAA ACAGCGTTCC CAGAAAGACA 60

ATATATAACC AATATTAACA AAAGCAATGC ACATTACTTC ACAAATGAAA TCAAAGCAAC 120

ACACATATAC AATGCAATAA GCGGGCAACA ACAAACAGAT TTCAACACGC CTGTCATACA 180

GCAATATCGT TAACAAATGA CAnCCGCCnT TTAGGC 216

(2) INFORMATION FOR SEQ ID NO: 2326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2326:

TGACCATATG ATTGAGGAAG GTTTTATTGA TCCTAAGTAT CGTGCTCTTG CACCGTTATG 60

CGACACTAAG GAATCATTAA TTGAATCAAT ATTAAATTTn AAACCTCTGG GTACTCGTTC 120

ATACGATTAA TCATTCTAAG G 141

(2) INFORMATION FOR SEQ ID NO: 2327:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2327:

TGAAACTGCA GCGTGGCCGA GTGGGGGTTG TGCCAGGTGA CCCCAGATGG GCGTG 55

(2) INFORMATION FOR SEQ ID NO: 2328:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GAAGCCAGCC TAATTGGATA CCACCGGAAG TAACTTTTGA CCAGGGCCGT CGCA 54

(2) INFORMATION FOR SEQ ID NO: 2329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2329:

GTTCCCGGGT CCAGGCCGTT GTCTTGTGCC GGGGTGTTTG GTCCTTGGTT GTGT 54

(2) INFORMATION FOR SEQ ID NO: 2330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2330:

TATATTATAT ATTTAACTGC TGTGATGTAT TCTGAAAAAA TAGTAGTATT GCCTATAATC 60

ATCTATGCCA TTGTGTTTGT AATAATTGGT ATCACTTATA TCTTTATAGG CGACAGCTAT 120

GATCAATTAA CAAATTTCAA TGTGATTTTG TATATGGGGA GTTTGTnTTA TGCATGGATG 180

GCTATTAGAA 190

(2) INFORMATION FOR SEQ ID NO: 2331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2331:

TTTTCACCTC GTGTTTTAAA TTCAATTGAA TCTAAACTAA AAGTACCTTT AAGT 54

(2) INFORMATION FOR SEQ ID NO: 2332:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2332:

TTCTAAAAAT ATTAACGAAT TATACAACTT TAAGAGTTTT TAGTATGTAA ATATTCTTTT 60

CATATTAATA CAATACACCC CTATATATGC TCACTTGTTT GAATTAATAA ACTTTAGCAT 120

TCTGCAAATA ATATTTTAAA AATAACTATA CTTTTTATTT ACCTATTGAA AAATAGTGTT 180

ATCATATTTA TTAAGAAGCT ATTTTTATAC TAGTAGGTGT CAGTCATGAA TAACATTTTG 240

TTAAAT 246

(2) INFORMATION FOR SEQ ID NO: 2333:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2333:

CCTTCTAACA TCTTTTTACC ACTCATTGAA ACATGTGATC CTAATAACAT AA 52

(2) INFORMATION FOR SEQ ID NO: 2334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2334:

AGAAAAGAGA CTGAAACAAC AAATTCAGGC AACTTTTGAA CAACAGAGAC ATCGATTAAT 60

(2) INFORMATION FOR SEQ ID NO: 2335:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2335:

CCTCAATCAG CTCCTAAAGA ACAAAATAGC GACTCGATTG ATGAGGAAAC AGTAACGAAA 60

AAAGAACGAA AAAGTAAAGT AACACAATTA AAGCCATTAA CACTTGAAGA AAAGCGGAAG 120

TTAAGACGTA AGCGACAAAA GCGAATCCAA TACAGTGTTA TTACAATnTT GGTATTGTTG 180

(2) INFORMATION FOR SEQ ID NO: 2336:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2336:

CCTACAGTCC CAACACTGTC AGTACACTGC CGATACCCAA CCTCTGGCCG GTCCGGCA 58

(2) INFORMATION FOR SEQ ID NO: 2337:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2337:

ATATTTTTnA TTTAATGGTT TTACTACTGC TACAACTATC ATAGGTGGCA 50

(2) INFORMATION FOR SEQ ID NO: 2338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2338:

CTCCTGTAGA TTTAAAATCT CCTAAATAAC AAACGAATAA TCGGCCATCT TTATGTATTT 60

TGATTGCTGC AGGATTCGCT TTGTGACTTA CAAAAGGTCG TTTGATTTCC TTCGTTTCAG 120

GATTGATTTT GAAAATATTG CCTTCGAATA CATCCAATAA AAAGAGTTGT CCCTGCCGAT 180

CAAAGTTCAA TCCTTCTAGT TGCAATCCTT TTTTGGAAAT TTCAAGCCAT GGTTCAGCTG 240

TAATTGTTTG TAATTCACTT TCAGATATAA TTGGAACAGC ACTATTGGAC TTCCCGCnAT 300

AAAATAATGG AGGGnAAAnC TGGTGGGGAC ATCCATGAGC CATTCCTTTC CATTCCATTC 360

GGTTTTAACT AACCAATT 378

(2) INFORMATION FOR SEQ ID NO: 2339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2339:

ATGAAAATAA ACTGTGTCTC CnGATGTATA CGTCCCTTCA AGCAGACTTC 50

(2) INFORMATION FOR SEQ ID NO: 2340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2340:

TATCCATATG TGAAAAATGT CATATATGAG TCTAGTTTTG TATAAATGGA GACTCGAAC 59

(2) INFORMATION FOR SEQ ID NO: 2341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2341:

ATTGATAAAA TATGATTAAG CGTTGTTGCA AATGACATTT TCTCAAAAAG CGCTTCACTA 60

TCAATTGGTA CTTGTGTGTn AATTTCAGCC AGTCGCTTCG ATAAATATAG TTCATCTAAA 120

TTGTCATTAA TCTTATTACG TTGCCCAGCT GATAATGCAT CAATGTTTTC AACCACATTT 180

TCAACGCTT 189

(2) INFORMATION FOR SEQ ID NO: 2342:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2342:

ATCAATTAAA ACAAAGCATA CAACAATTTG TTGATGTTGA ATCTAAATCA ATTTTAGAAC 60

AACAAATGAT TCATCAGCTT CAACAAATGG ATCGTTCTTA TGTAGAGATG ATTACAGAAT 120

(2) INFORMATION FOR SEQ ID NO: 2343:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2343:

CTTAACCCCC CTTTTTTCCC AATTTTAATG GGGAAAAATT GTAATTAACC TGGGC 55

(2) INFORMATION FOR SEQ ID NO: 2344:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2344:

GACAAATAAA CATGACCTGG ACAAAGAAGA ACAATAAACA AGCCTGGCAA 50

(2) INFORMATION FOR SEQ ID NO: 2345:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2345:

GTATTGCGAT GATGCATACG GGTATTGTTC TGATTAAATA ATATTTCATA TTTAATGTTG 60

ATAAATGTTG AATAAACAAT CCGCAAAGnG CACTTGATGA TAGTGCTAAG A 111

(2) INFORMATION FOR SEQ ID NO: 2346:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2346:

GCAAACAGTT TCCGTGTCCG TTTTCCAATT AAGTTAAGGA ACCCAAAGAG A 51

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2347:

TCGTAGGTGC CATAACACAC GTTACCTGGG ACTCATATGA AGTATTATGT CGAGACGACC 60

(2) INFORMATION FOR SEQ ID NO: 2348:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2348:

GTTTTTAATA GGCTCTTTAC GTATCTAAAA ATAATTGCAT TATTGGTGTG CCTTGATGTA 60

ATTGAATTAA AGTACCGTTT GGTTGTAACG TTTCAGGTAT ATCATTTTCA ACnATAAC 118

(2) INFORMATION FOR SEQ ID NO: 2349:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2349:

ATGACAGAAA GCAAAATCCC AATGTTGATA TACCGTTTTT GACACCACTT GATTATCATT 60

ATTTTTTCTT TAGCGATGGA TTTTATATTA CGATTTCAAT TCTTACTATC GTTGCATTAT 120

TGTCATTCAA ACTGTATCGT TTTTACTnTT ATAGACTTTT CGCAATAGTA ACATGG 176

(2) INFORMATION FOR SEQ ID NO: 2350:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2350:

CTACGACTGA CATTAACTGT GCAGATGTAC CTGGATTCTA TTTTTTCAAG AACAAATTGT 120

AATAATTGAT AGTTATATGG TGCAATGTCA CCTTCATCCA TTGAGCGCTC AATAATTTCA 180

GCTGCnAGAG CGGCnTGACT G 201

(2) INFORMATION FOR SEQ ID NO: 2351:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2351:

ATCGCTATAA CCTATCAGTG ATAATATTTG ATTGCATGGT GCACCATTTG AnATTTCACT 60

TAGAATGGTG GTACCTAATT GCTTATTTTT ATATGTCATT TGAAGATTTA AAAATTAAAA 120

ACTTTGATAC AGAGTGAAAC CATATTTCAA CAAATTAC 158

(2) INFORMATION FOR SEQ ID NO: 2352:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2352:

TCGTAATCAA AACATTTTGA ACAGGATTAT AGTAAGGGAA TTTTTGGATT TTAACTTGTG 60

TTTGTTCATT TTTTAATAAG AGTCGAGCTA AGTCTTGCAA CATCATTACT TGCTTGGCAT 120

CTAACTGTTC GTCATTAAAT TTTATGAAAC GATCACTCAT GTTTTATCCC TCTTTAAAAG 180

TTTAGTTCTA CAGCATTATA TATTGCTTGT TGTTCACGTT CATCTTCCAA TTTATCAATA 240

ATTGTACGTT TAATTGCACG TTCAACTGGC ATTACAGTGA TTAAATCACA CAAGTCTAAT 300

AATGCACGGG ATACTAGCGG CTTCTTCAGA AATTTGTCCC TGCTTAGACA TAGTACGTAA 360

ATCTTCATTG AAACTTnAAT AATTTGGTTC GATTTGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 2353:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2353:

ATTAATGGGG TTAAATAACA TTTTGACTGC GAAAGATTTA TTCTTTTCAG GTAAATCATT 60

GATAGATGTA TATAGTCAAT TTGCTGGATT AGCTGAAATG ATAAATGTnT TTGCGAATGC 120

ACCATTT 127

(2) INFORMATION FOR SEQ ID NO: 2354:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2354:

ATCTCGCTGT TTTTATGAAA GAAAACTACA TTTTCGAGAG AATAAAAAGA TTTTTCTGAA 60

ATTTAATCTA TCAATTACAT TGATTTACTA ATATAATTAG AAAGTAAATT TTATTTGATC 120

AAAGTAAATG GGGGAAGTAC TGTGATAGAA AATAAGAAAA CAGTTGAAGA TACATATTCA 180

ACAGGCGCAA TTGTTGATTC AATATCATCT TCAGTnCAAA TGn 223

(2) INFORMATION FOR SEQ ID NO: 2355:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2355:

ACACTTGTTC AAACACTCAC AATGATAAAG CATATTATCA GTATTGTAGT GTGTGGAAAA 60

TGACAGCCAT CTAAGGAGAA AAATGATGAA AAGAATATTG GTAGTATTTT TAATGTTAGC 120

AATTATATTG GCAGGTTGTT CTAATAAAGG TGAAAAGTAT CAAAAAGATA TTGATAAAGT 180

GTACAAAGAA CAGAATCAAA TGAATAAAAT TGCCTCGAAA GTACAAAACA CTATTAAAAC 240

AGACATTAAA CAAGAAGACA GTAATACACA TGTTTATAAA GATGGTAAAG TCATTGTTAT 300

TGGTATTCAA TTATATAAAG nTCGTGAAAA AATGTATTTA TTTCGCATAT GAAnTAAAAG 360

GTGGTTAAGG CCAGAGGATT TAATCAGnGG AAAnTAGACC 400

(2) INFORMATION FOR SEQ ID NO: 2356:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2356:

AATTTACTTT GTGCCACAAG GTTATCAATG TCTTTTGAAC CACCAAACAT TCTAGCGATT 60

AAGTGACCTC CATCATCGTC TGGTAATCTA TCCTCTCCCC CCACAGTTCT TTGTGCATGG 120

CTATTACGAT CCCCATCTTT TAGAGAGAGA TTGTCTACAT AAACTTCTTT TATGCGACCT 180

TTATGATCGG TTCGATATAT GTGACCAGTA GGTGTTGTGT ATTCAATATT CGCCTTTAGT 240

TTCTTAGGTn CTAAGTCTTG GCATAGTGTT CTCCGAATTC nAACCTTGGT GTTAGTTTGG 300

TGATTCAACA TACTTTTGAT GGAATTCATT TnCATGGGCT ACTT 344

(2) INFORMATION FOR SEQ ID NO: 2357:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2357:

TATGCGCCCC TGCTTGATCT TTCATTTGCG TCCACTCAAT TAGTTGTTTG CGC 53

(2) INFORMATION FOR SEQ ID NO: 2358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2358:

ATTTTTTCAC CTTCTGAAAT TGATAAATCT AGGTTATCGA ATATAGTCTT ATCGGCATAA 60

GATTTATTTA AATGTTCAAT TTTATATGCT TCCATACCCA TCTTCCTTCT TCTGTTGAAA 120

TCTCTACGTA CTTAAATCAG TTCTATACAT TATACACCTT TTTGAAATCA AAAGAAATCG 180

ATACCGTTAA GTGTCATAAT TTAATATATT GTTGCTTCAA CTATAAATAA AACTTGTTAA 240

GGCTTTGATG ACTATGCTAA TGATCTTTAT AATATACCTT TTTATCAACA CATATAATGT 300

AAAACATAAT ATAnAAGAAC ATAATAAAAA CCCGGATTGA TATTTTATCA ATCCGAGTTC 360

GTGTTTAGAT ATTATTTTTT AGAGTTTGCT TTAGGTCCTG 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2359:

TTAATGTCGC CATTTTTTGT TAGGTAGACG TATAAATCTG GACCTTTTGA TGATTTGTAG 60

TTAGTAAGCA TTAATTTACC ATTTTTAATC TCAGCTTTAC CTTCAACAGT TTCACCGTTT 120

TTAGAACTGA nTGTACCTGT TAGGTGTTTT GTTT 154

(2) INFORMATION FOR SEQ ID NO: 2360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2360:

ATATGTCTTG TGATTTTTCA GGTGTAAGTT AGTATGCAAG TGATTATGAT TGATAGT 57

(2) INFORMATION FOR SEQ ID NO: 2361:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2361:

GGCATCAAAT TAGTAGCGAC TCACACGTGA TGCATCCTGT GTTTTGGATC TCATTTCT 58

(2) INFORMATION FOR SEQ ID NO: 2362:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2362:

TGTTATTATC GnAGAGGCTT TTCGCTTTGG AATAAGGTAT TACGTGAATG 50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2363:

CTCTTCTGGT CCCTGACATA CATAGGAGAA ATAGCnCCAT GTACAACGTG 50

(2) INFORMATION FOR SEQ ID NO: 2364:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2364:

ATTGCCAATG TCGTTAGTTC GTGAGGCTGT TGGTGAAAGT TGTGTTTGAA 50

(2) INFORMATION FOR SEQ ID NO: 2365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2365:

CCATGATTTA AATCATTGAT TAATGGTGCT TGTTCTACAT CTGTGTAAAA TTCATACAAT 60

TCTTTAGCAT CGTCGAATAG TTCATCACGA CGTTGGnTAA ATTCTTCTTC T 111

(2) INFORMATION FOR SEQ ID NO: 2366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2366:

TAATGCTGAG CGTGTTACTT TAGTTGGATC AACGATACCT TCTTCTAACA TATTAACCCA 60

CTCnTTTGTA GCAGCGTTAA AACCAACACC CGGCTCTGCG TTTTTCAAAC GTTCTACAAT 120

(2) INFORMATION FOR SEQ ID NO: 2367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2367:

CCTGATTGCA AAGTACAGCA AGCACTACAG ACGCCTAAnC ACTnACACTA 50

(2) INFORMATION FOR SEQ ID NO: 2368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2368:

AAAATGGTAT TGCAATTAGT AATGTTACAA CAAGTGTTGT AATAGCTGCA TAAAT 55

(2) INFORMATION FOR SEQ ID NO: 2369:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2369:

TATAGGATGA AAATCCTGCC AAAAGATTAA GGGGTGGCCT AATGAACCAT G 51

(2) INFORMATION FOR SEQ ID NO: 2370:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2370:

TTGCTCGAGG TGGTAAATAC GCAAAGTTTA TTTGGTTGTG CTAAGAGAGA AA 52

(2) INFORMATION FOR SEQ ID NO: 2371:

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2371:

TAATTTGAAT AAGGTGGAAG TGATAAACAG TGCTTTGCGA ATCTAGAGTC ATTAATCAAA 60

ACCCTA 66

(2) INFORMATION FOR SEQ ID NO: 2372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2372:

AGACAGGTAC TGTCCTACGG TATGGAGCAG AAGCGGGAAA GCTGCCCAGA GCCAACTGTA 60

GACAA 65

(2) INFORMATION FOR SEQ ID NO: 2373:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2373:

TTGCAGTGAC GGCTTATAAT CATTCCAAGC GAACAATTAG ACATTCCATA TAAAATATAC 60

AGATGGCTTT CAGTAGAGTA GTGGATTCGG ATTCACGAAC TATACTGGAA GCTTTTTATT 120

ATAAATGAAG AGAAGTTATA TTTTTAGCAT GTATAGTTGA ATACTGGGTT AAAATACCAT 180

ATTAATAATG AAGTAAAGGT ATGAGTGATT ATGAAAGTGT TTTGAATGAA ATATATTTAA 240

TTGGTGATGC TTTTAATTGA AAAGATTAAC AGGATTCAAC TTGGTAAATT GTATTAAATG 300

TGAGAAAATA AAAGTATATT CATTGAGAGA TATATGAGTC AATGATCGTT TTAAACAAGA 360

TAAGTGTATT TTAATATGTA AAAGTTATGT AATAAATATT 400

(2) INFORMATION FOR SEQ ID NO: 2374:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2374:

CCTATCATGC CTCTCTCTCA CTGAATCCTT TAGATCCCCT TCCCTCCCTC TCCCCCCTCT 60

TTTCCCCTCC 70

(2) INFORMATION FOR SEQ ID NO: 2375:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2375:

CCAAGTCAGA GCAGCAGTTC AGTTCGTCAG CnGTTCAGTT CAGAGCnGTC 50

(2) INFORMATION FOR SEQ ID NO: 2376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2376:

GTTGGTGAAG CTGTTGCCGA nGGAGAAGCG GGTATGGATC CTGACGGTGn 50

(2) INFORMATION FOR SEQ ID NO: 2377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2377:

AATTGCAGGA CAGGTCAAAG GCAAATGCAC GTATTCAGGT CATGCTCATG TGCATGTTG 59

(2) INFORMATION FOR SEQ ID NO: 2378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2378:

TTTATCATCG TATAAATCTA TATCTAATTG ATTAAACTTC GGGTGCTTAA CTAACTCTCT 60

CAATACACTT ACACCAGCAG TTCCCATGCC TATTATTGCT ACACGCATAT ATCATCCATC 120

CTTTTGTAAT TCAAAATATT ATATTTAAAC TATTACCTAT AATTATAGCA ATTTGGTATT 180

TCCAATAAAA TTTATnAAGG TAAGCnATTA TTTCACTTTC ACAACCATT 229

(2) INFORMATION FOR SEQ ID NO: 2379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2379:

AGTTTTTTGT TTGACGTATT TAATTTACTA TTTGCTTGAT TGATATTTTT AGACATTAAA 60

TAGTGTTCTC CTAATCAATT TATTCTTCTT TATnTCAGCA TTATTCGCAC TGACAT 116

(2) INFORMATION FOR SEQ ID NO: 2380:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2380:

CAAATCTTAG CGGATGATTG GCATGTATAT TCTGCTGGTA TCGAAnCACG CGGTGTTAAT 60

CCCAAAGCGA TAGAAGCTAT GAACAGAAGT CGGCGTTGAT ATGTCGAATC GTACGTCAGA 120

TTTAATCGAT AATAAT 136

(2) INFORMATION FOR SEQ ID NO: 2381:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2381:

TTAATTGATA GCTTTTATCT GTAGGAAAAG CTATTTTAAA GATTTCTAGT GTATCTATAA 120

CTTTTTTGGG ACGATATTGA ATATTACAAT CTTTAAATGC CTTTTTAATA AAATTCAAAT 180

CAAAATCTAC ATTATGAGCT ACAAAAATGC AATCTTTTAT CTTATCGTAG ATTTCTTGTG 240

CAACTTGATT AAAATATGGC GCTTGTTGTA GCATATTTTC TTCAATGGAT GTTAACGCTT 300

GAATGAACGG CGGAATCTCT AAATTTGTTC TAATCATAGA ATGATATGTA TCAATAATTT 360

GGTTATTGCG CACAAACGTT ATACCAATTT GAATGATATC 400

(2) INFORMATION FOR SEQ ID NO: 2382:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2382:

TATTTTGTTA ATAAAGTTAA TATATGTTTG TTGTACAGAT AGTTCAGGAT ACA 53

(2) INFORMATION FOR SEQ ID NO: 2383:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2383:

CCCGAGCTTG CCCTCCTTCC CCCCTCTTCG CCTCCAGACG AAGTGCCCTT CTGTCCTTG 59

(2) INFORMATION FOR SEQ ID NO: 2384:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2384:

AGCCAACATC CCnGATGGTA CTTGCATTAA TGCATAACCT AGAGAGAAGA ATGATGCCAA 60

TAAACCAAAT TGTGGTTTTG TCATCCCTAA ATCATCCATC ATTTGCTTAG 110

(2) INFORMATION FOR SEQ ID NO: 2385:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2385:

TGAAAGTTCT TTTAnGCATC AATTTTAAnA CTACGAGCGG ACnCTAATAT 50

(2) INFORMATION FOR SEQ ID NO: 2386:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2386:

GGCAATTTAT TGACACAATG CTTGAGCnAT TGATAGCAGG ACAAGAAAGA ATACTTGATG 60

AGTTAATACC AAAAATGGAT GCGACTGAAA AATTAACGCT TTATTTAACT AGTCATTATA 120

AACAGATAGA TTATGAATTT TTGTATCTCC TTTCAATGGA TAAATTGTTT GGAAATAAAA 180

GAAATAGATT AACATTAATT GATTTAGAAA ACATATTGGG AGTAGGAAGA GTAAAAATTA 240

GTnGT 245

(2) INFORMATION FOR SEQ ID NO: 2387:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2387:

CACAAAATTC GAAATCGTCA TCGGTGATAT GTTTAATACT TGGGAAAATA TAAAACGCGC 60

CTTCAGGTTG AGCGGTAATC TCAAAACCTA ATTTAGTTAA TTCAGATACT AAATAATTTC 120

TTCGTTCnAC ATAAGCTTCG 140

(2) INFORMATION FOR SEQ ID NO: 2388:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2388:

ATATAACATT GTAGGGCCTA ATAATTTATT TTATGTCTCA GACTCATACA ATGGTTATTT 60

AACTTATTTA CCACAAATTG AGCACTAAGA CTCACTATTA TCGATTCTTC TATTGAACAn 120

(2) INFORMATION FOR SEQ ID NO: 2389:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2389:

TCTAAATCCA GCATGATCTA CATCAAAGCT GAATTCACCT TTTTCATCGA CTTGCAAATC 60

AGGGAATTCT TGACCTTCAC CTAGT 85

(2) INFORMATION FOR SEQ ID NO: 2390:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2390:

GGTGTTTATA AAGCAGGGGC TGAGCCTCGG TCAGGACTGG ATACACAGGC AGTACGGGTG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 2391:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2391:

TAAAGTAACC ACTTTAGATG ACATTTTAGA AGTTATGGGC CGAATGCAAA C 51

(2) INFORMATION FOR SEQ ID NO: 2392:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2392:

GGTCGGAnTC CCGGGTCGAC CCACGCGTCC GCATCAACCT AGnAGAAGCn 50

(2) INFORMATION FOR SEQ ID NO: 2393:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2393:

ATTTCCAAAC GAATTGAAAA ACGGACGTAA ATTCTTAACT AAAGGCGATA AATGT 55

(2) INFORMATION FOR SEQ ID NO: 2394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2394:

ATAGGTTGCT ACTATTTATA TCGACTCATT TTCACTTACA AATATGACAT TGTCTCTAGA 60

ACACnAAAAT TAATTTGCGT CATATCTGCT ACAGTTTTGA GTGTGTTATC AAGTGTATTT 120

(2) INFORMATION FOR SEQ ID NO: 2395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2395:

TGGACCATAG TAAAGCATTA CGGTCGGTTT ATTATTTTCT AAGGAAGTAT GTTTATATAA 60

ATCTATGCTC ATTTGTTTTT TAGCGTCTGT TTGACCTATT ATTTTAGAAC CAGCCATCTG 120

CTCTTTATAA AAATTTATTA CATCATCTTT TTTTAATGTT GTATATTCAT AGTTTATTTC 180

TATTATnTCA GAATCGTGAA AACTATTTAG TGATTGAnAT ACTCTTTTTG GAGGATTCTG 240

AATATAGATT TTCTTAATAT T 261

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2396:

GTTTTGAATA TAGGGGCTTT TATCACTCTC CGAAGTCTnT TCTAAGTTAG ATTTGGAAAA 60

TAACACTTTT TTAGTTTCAT TCAAGCGAGT CGAGTGACTC CAGA 104

(2) INFORMATION FOR SEQ ID NO: 2397:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2397:

GATTATCGAT CACAGTATGA TTTACGTAGC AATTTCTGGT ACATATACGC CTAT 54

(2) INFORMATION FOR SEQ ID NO: 2398:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2398:

GCTTCACCTT GAACTAGCAA ATAAGGATAA AACAAGCATT CTTTACATGT TTCTTTTAAA 60

TACGTTTGAT ATTTTAATAA TACTTTTTCG ATTTTACTCA TATAAGTTTG AAGTTCTAAT 120

TTTTCATTCT CACTTATTTT GTATATATTA CATTCATTAT GTTCTGTCAG AAAAATATAA 180

GGGTCAATAT TAATTTCGTC TATCAATTCA TAAATTTCAC TTAAGTATTT nTnCT 235

(2) INFORMATION FOR SEQ ID NO: 2399:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTTGATGCAC TTATTTGTGT AATGACATCT TTACAGTCTT TTCCTTCCTC CATCATTTTA 60

ATAATTCCAT TTAGTTGCCC TTGTATTCTA TTAATACGAT TAATCATTTT n 111

(2) INFORMATION FOR SEQ ID NO: 2400:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2400:

AAATGCTGGC TGAGTTTTGG GCCACCCGCA AAGGCACTGG ACCGGTGCGA AACC 54

(2) INFORMATION FOR SEQ ID NO: 2401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2401:

AACCACTCAT CACTACTAAA ATGATACTTA AAAACAAAGT CTTAATACAC TTTTTCATAA 60

TATCAACTTC TTTCTATATT TAATACATTA ATTATACATC TTTnTnAAAT AAAAATATGT 120

GTAAAATTTT AAAACTTATT TAATTGATGT TTTAATAATG TATTATAGAA ATTATTGACA 180

TATGATTAAA AACCCTTAGG ATAGT 205

(2) INFORMATION FOR SEQ ID NO: 2402:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2402:

AGATAATCAT AGAGAAAGTC CACAGTCGGT AGAGGTGGTA GCTGAAAACA ACATACTATT 60

AATTATGAAG TGCTTTGTAA CTTGTCGAGA CGTTTGCCGC GAATCTATCA TGATGGTGAT 120

CAACGTTTTG TnACAAATGA 140

(2) INFORMATION FOR SEQ ID NO: 2403:

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2403:

ATTTAACCAC TCCTCCAATG ATAAGATTGA AAGGCAAGAT GACCTTCCAA TCTTATTT 58

(2) INFORMATION FOR SEQ ID NO: 2404:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2404:

CAGCTTCTAC AATACGGCGT GCTATAGCAA GCATTAATGT AAATCCTAAT TCTGCAGTTG 60

T 61

(2) INFORMATION FOR SEQ ID NO: 2405:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2405:

AATAATCATT TTAATACGGT CTTCAGGAAT TGAAGTGTCT ACAGGTACAT ATCCACATCC 60

TGCTTTAATG GGCACCAATC ATCCCAACAA TCATATATGG TGACATGTGA CCGAnTAAAA 120

TCATCGGGTT TCTnACTACC TTGTAATCGA TGTGGCTAAT TTACTAGACT CATCCATTAA 180

CTGTTGATAA GTTAATTCCA TCAGTTGTGT GTCTAAC 217

(2) INFORMATION FOR SEQ ID NO: 2406:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2406:

GTAGTATCCA ACGTATTTCG GATTGCATCG AGTTGATTTT TATTATTTTC TTCAATGCTA 120

TCAAGCGCAn CTGTATTACG TCTTACTTTA GGTTTTATTT GCTCTATTGC CTTGATTGTT 180

TGATnTCTAA CATCAGTAAC AGCAGCATCT TGATTTGTAT TGTCTATT 228

(2) INFORMATION FOR SEQ ID NO: 2407:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2407:

CCTTTCGTCT CGCGCGTTTC GGTGATGACG GTGAAAACCT CTGACACATG CAGCTCCCGG 60

AGACGGTCAC AGCTTGTCTG TAAAGCGGAT GCCGGGnAGC AGACAGCGAT 110

(2) INFORMATION FOR SEQ ID NO: 2408:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2408:

GGAGACCCCA AAAATTTTGT CGTTGAAGAT GCCTTTTTTT AAGCGTTATT TGGCTATATC 60

AGTTTCTAAC TGT 73

(2) INFORMATION FOR SEQ ID NO: 2409:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2409:

AAATCATTAG AGAGGAATAG TTCCCTTTGT TACGCCAAAG ATTCGATATT GAC 53

(2) INFORMATION FOR SEQ ID NO: 2410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2410:

CCATATGATT GTATAGGATC CATGACGTCT CCACTGACCC CTGACTCTAG TATC 54

(2) INFORMATION FOR SEQ ID NO: 2411:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2411:

GTTCCTCTTC AATTGTTATA TGTATATCAC AAAAATTATT TCATTATTTT ACCATTATTA 60

TTTTACAAAT ATTATCCCAA GAATACAATT CAAGAAATGA TTAACTTTAC TTTAGAATTG 120

TACCTTATTA CATTATTTAT GAAAGTACTC TCTCAATTAT AACnAAAAAG AAGGTGTTCA 180

ATACATnCAT ATTTAGTCTT ATAT 204

(2) INFORMATION FOR SEQ ID NO: 2412:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2412:

CAGTGGCGCA GAAACATAAC GCTCAGGGAA GCACAGCACC TCATTATGCC AAAGCT 56

(2) INFORMATION FOR SEQ ID NO: 2413:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2413:

TCGCTGGCGG GTCCCGCGCG CCTAGCGTGC TCATGTGCGG TGTTCTAGGT GTTGGGGTTG 60

CAGTCA 66

(2) INFORMATION FOR SEQ ID NO: 2414:

(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2414:

GGATAGAAAT GGGAATCCAC CCATCGGTGG GGGTACCAGG CTCTTCATAT GGCCTTGTGG 60

ACTTC 65

(2) INFORMATION FOR SEQ ID NO: 2415:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2415:

TTAAATAGAT AGAATAGAAT TAAAGAGACG ATGATAGGTG CTGCTATCGT CTTAAAAACG 60

ATGATAAAAG GATCAAAAAC ATATGATACT TTTTCGAAAA TAAAAATAAC AATACCCAAC 120

AATACTAGCG CTATTAATGA GAAGACTAAA TCATTCCCAC CAACAAACTT CATATACCGT 180

GATTCGGTAA ATTTTnnAAA ATTCTTTCTT ATATTCTTTT CATTTTCATT CAATTATAGA 240

TTCACCACCA CTTAAAATAT TCATAAG 267

(2) INFORMATION FOR SEQ ID NO: 2416:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2416:

TTAAACAAAT GAATATAGTA GTTCCATTAT CCTCACTTTT AATCGTTTAT 50

(2) INFORMATION FOR SEQ ID NO: 2417:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTTGCTGGGA GTTGCATTAA GAAAATATAC ACATTTACTT GACATTCAAC TTGATAAAAA 60

ATTAGTTATT GCCATATGTT GCATCACATT TATAGGGATT TTAATATTTT ATGTACGCCT 120

AATTAAAAAA TCATCTTTAA ATATTTATAA TACTAAAAAT AAAAGGTCAA AAATnTT 177

(2) INFORMATION FOR SEQ ID NO: 2418:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2418:

AAAATGAAGC GGTCGCAAAA TATAATGACG TGAAAGCATT TTATACTCAT GGACATTTAT 60

ATCAAGTCAA TCGAACAAGA GATTTATTAG CTGAAAAAGG ACTTGAATTA GGTTGTTTGT 120

TTGCATTTTA TGGACATACA CATGTGGCAA AATATGAGTA TATTAATGGT GTTCATGTTA 180

TTAATCCTGG AAGTATATCT CAATCTAGAA GTTCAATGGA AGAAACATAT GCTGAAGTTA 240

TTATTGATGA TCAAACTTTA CATGGCACCA TCAATTTCAA AAATCGACAT CACGAAACAA 300

TCAGTCATAC TACTTTTTAA ATAGAAnTAG CTATGGCTTT TTTTAGTTTA TAGACTGATT 360

TAACTAGGAG GTCGTGTCAT CCAATGTTTG TTTAAAAGTA 400

(2) INFORMATION FOR SEQ ID NO: 2419:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2419:

AGGGTGCCGA GTTAACCAAG AAAGGCCGTT GGTTGCCCCG GGTATTTTCC CCC 53

(2) INFORMATION FOR SEQ ID NO: 2420:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2420:

(2) INFORMATION FOR SEQ ID NO: 2421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2421:

ACCAGAAGAC AATAAGTGTA ATGATGCCTG TTCTAATACA GAATCTTTAC TTTTTATTGC 60

CTTTTCAAGT CGTTGTTCCA CTTTCTTAAT TTCATTGTTC ATGTTTAACT TTGCCAnGTT 120

AATCACCTTT GGTATTATCT TTTTCTTTAT AG 152

(2) INFORMATION FOR SEQ ID NO: 2422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2422:

GTACGTTTTC ATTAGTTGTT ATATTTCCAT CTTGATAATT TTTTAAATCT TTAAAATCAG 60

CATACTGACT AAAAAATTTA AAATTTTCAA TTTTTTGTnT AAGTTTTTGT CTTCTACATT 120

ATCCAAAAGA ACAATCTnAT TATTTTTTAG TTCAACACGA TATTTTTTCT CATTATGATT 180

TTTGCTAATA TCATCATAAA CTTTATTTAC AAAATAATAA CCTGTTGCCT TTTTGGTATT 240

TCTATTAAGA TATAACACCA TGCCTTCATC ATCTAATACT CCTGGTTTGT TACTTTTTGA 300

AAAACCn 307

(2) INFORMATION FOR SEQ ID NO: 2423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2423:

ATTGTGTTGT ATTTTAGACA AGACCTTCAA TTTTGGAGAT TTCACGATTT ACCACC 56

(2) INFORMATION FOR SEQ ID NO: 2424:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2424:

AGTCCTTTGG ATCGTCAAGA TTTCACACAT TTACAnTTAT TAnCTCGTGA 50

(2) INFORMATION FOR SEQ ID NO: 2425:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2425:

ATGTAATATT ACAATTCAAT TAGnAAAGAA CTTTATCTTT AATTGCTTTT CGATTTCATT 60

CATGTCATCT TCTGAAATTA TTATCGTTCC AGTAGGATCA GAATCATTTA TTTTGCTTAT 120

ACGTCTTTTG CTTATTGTTG TAATTGCTGA TATATTAACG TATGTATCTT TCCCTTTGTG 180

CTTGGAATAA ACACCTATCA CTCTATACAG TTCATTAGCT TTTTGAnTTA AGTTAGACAA 240

AAGCTTTT 248

(2) INFORMATION FOR SEQ ID NO: 2426:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2426:

CCTTATTATA TGACAGGTTG CCTAAACAAG TGCCTAGAGA AAAAACTAGC CCC 53

(2) INFORMATION FOR SEQ ID NO: 2427:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2427:

TATCCACTAA AATGATTTGC GCGTATTGTA ATATTAATCG TTCTACTTTT TATGATTATT 120

ACAGGGAGCA ATTTGATTTA TTGGATACCA TCAACTCnAA GCATAGGTGG AGG 173

(2) INFORMATION FOR SEQ ID NO: 2428:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2428:

TACTTATGTT TATGTCGCAA TAATTAATGT TCGAnTTAGT GGAATTGAAC 50

(2) INFORMATION FOR SEQ ID NO: 2429:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2429:

AGTCATCATA TTATCAATAA TACGCCGCGT TAAATCTGAT AAATTCATAT AGTCTGTATC 60

TAACTCTG 68

(2) INFORMATION FOR SEQ ID NO: 2430:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2430:

TGAATTGAAA ACGGTCGGTG AAGCGCTAAA AGGTAGACGT GAAAGGTTAG GAATGACTTT 60

AACAGAATTA GAGCAACGTA CTGGAATTAA ACGTGAAATG CTAGTGCATA TTGAAAATAA 120

TGAATTCGAT CAACTACCGA ATAAAAATTA CAGCGAAGGA TTTATTAGAA AATATGCAAG 180

CGTAGTAAAT ATTGAACCTA ACCAATTAAT TCAAGCTCAT CAAGATGAAA TTCCATCGAA 240

CCAAGCCGAA TGGGACGAAG TAATTACAGT TTTCnATAAT AATAAAGACT TAGATTATAA 300

GAGTAAATCC AAAGAGCCAA TACnATTATT AGTAATCATG GGnATTACAG TTTTAATAAC 360

(2) INFORMATION FOR SEQ ID NO: 2431:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2431:

TGACTTCGTC CAAGTACAAC TGCAGTCAGT ACCTACGAAA TCAAGATCAG CATGGAT 57

(2) INFORMATION FOR SEQ ID NO: 2432:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2432:

ATTCTTAATC GCATCATAAT TAATTAACGG ACGCATAACA AATCCGATAA TACTATTATC 60

TTTCCAAGTC ACTGACACTC CAAATTGATT TGCTTCnTCT ATCCATATTT GCTCAATAGT 120

ACCATCATTT TGAGTACACA CTTTTAATTC ATGTACATCA GACTGCCTTG TATAAGATTT 180

GAAAAGTTTC CTAAACTGCC AATAACTGnA CTCTCGCTTC AAATT 225

(2) INFORMATION FOR SEQ ID NO: 2433:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2433:

CGGCCTGACG TTACATTTCT TCAACTTCAC GTCAAAATTG CTTCGCAATA ACCAGGA 57

(2) INFORMATION FOR SEQ ID NO: 2434:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTAAACGTGT CTTTAATGTG GAAGTTGAAA TATTAGTCCG TAAAAAAATG AAACTTAAAA 60

AAAAATAATA TTTATATTTG TCGTACAAAG ATGAAAGCGA nAGA 104

(2) INFORMATION FOR SEQ ID NO: 2435:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2435:

TTTGCTAATC GTTTCACGGA TTGTGGGGAT GGGTAAAGAC TTTGCTAGTG G 51

(2) INFORMATION FOR SEQ ID NO: 2436:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2436:

AAAnTTAATT TTTGGGGGGC CCTTTTTTAA CCGGAAAATC CAATCGGGGC TTTTAAGGAA 60

TGGTTTTGGT TAACAGGCTT TGGAATTTGG TTTGGCAAAA CAATCCTTGG TTTGGGGTTT 120

CGGTCCGGAG GGTCCTAATT 140

(2) INFORMATION FOR SEQ ID NO: 2437:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2437:

GAAGCGGAAC CACCGTTGTT TTTCTTTTCA GGTCCAATTG AATAAATGTT ATGAATAGAA 60

TGGATAAAAA TATAATTATT TAAGTGTTAA AGTAAACCAA ATCATGATTT AAGATTATAA 120

GAAAGAAAAA TTGACTAATG TTAAAACCAA CAATCATATG GGTTGTAACG TTTATACAAT 180

CATCGTAAAA CTCAATATGC TTAATTTATT CAAAATGTTC GTCAATAAGT ACAATGAAAA 240

GGAGATTGAT TTTTGAATAA AAAATATCTT ATGATTGTAA TTATAATTTT AATATGATTC 300

AAGATACGAT TTTGAGACCA TGTGAAGGGA TTAAATATAG 400

(2) INFORMATION FOR SEQ ID NO: 2438:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2438:

TCTGTTTTGA AAGTTGCAGT TTGGACAGCA CCCGATGATT AGGTGAGTCT TTTGGTTTA 59

(2) INFORMATION FOR SEQ ID NO: 2439:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2439:

TTGGTnAAAC CGTTACAGTT GCAAGTTTTG AAGTGAGTTA TTTTTTGGTT 50

(2) INFORMATION FOR SEQ ID NO: 2440:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2440:

ATTAAAAATA AATTAAAnGT TCCAGAACCA GTTAACCAGA ATATTTACGA 50

(2) INFORMATION FOR SEQ ID NO: 2441:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2441:

TGCTGTTTTG GCGGTTTTTC TCCGTTTGGT TGAGTATGTG GTGTACCTTT TGTC 54

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2442:

GTTGTTGGGT GTGTGGTTTT GGGTGTTGTG GGTTTGGGGT CTGGGTTCGT TGGTGG 56

(2) INFORMATION FOR SEQ ID NO: 2443:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2443:

GAGACAAACT AGTCGTCCAG AACGGAATTT AAGTAATCAT AATAATTACG GAAGTGCACT 60

TTTGTTTTTG ATTTATCATT GATGGAAATT AGAACAATTT ATCGAATGAT ATTAAAATTA 120

CATAACATCA TGTTGAATGT GAAATTAGGA TTGAACATTA CCTGTnTATT TGAAAAACCT 180

TCAGTTTTTA AATCACTAGT ATCACAAATA AAGCGACTTA AATTCGATTC GTTAATAATA 240

GATAATGCAA ATTTAnGTAG CCCT 264

(2) INFORMATION FOR SEQ ID NO: 2444:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2444:

CCGTCTTTAG TACGTACGTT GTTTGCGGGG CTTGGGGTGC TTTCTGGGTG TTGGTCATTG 60

TATTGGG 67

(2) INFORMATION FOR SEQ ID NO: 2445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2445:

AGCTGCATTT CTCGTGCAGG CTATCAGCAT CGATATCTGT ACCATTTAGT GATCATGC 58

(2) INFORMATION FOR SEQ ID NO: 2446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2446:

AACCAAAACA AACATTTGTT CGTTAAAATA TTGACACAGA ACATAAGTTC TGA 53

(2) INFORMATION FOR SEQ ID NO: 2447:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2447:

CACAAATTAC ACCCATTGTT AnTACTAATA CTTnCCTnTT CATTTGTTTA 50

(2) INFORMATION FOR SEQ ID NO: 2448:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2448:

GCACAAACCA AACGCACCTT AACTGCTTTA AATGGCTGGA CGGGGGGTCA ACTGGCCTTA 60

ATGACACTTG AATCG 75

(2) INFORMATION FOR SEQ ID NO: 2449:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GCAGCCTTCA AGTGTTTGCT ATTTGCTTTG GTGTCACAAG CCATTATCTA CGGTCCCGCA 60

ATTTAGCCCG C 71

(2) INFORMATION FOR SEQ ID NO: 2450:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2450:

TGGCGTGAGG AAAAATATCA TGTATTGTTA CACAGTCAAC AGTCTTACCA AATGATAAGG 60

AATGCTTTAA AAACGGATTT ATCACTTCAT CAAGTTCAAC AAATGATTGA TGTTGCTTTG 120

TTAATTGAAC CGGGTATAGG AAGTGTATGT AATGCTTTTG ATCATATGTG GGGATATTTA 180

AAAAAATGTG CGAATGAAGA AGGAAAGACA ACAATCAAAA CTACTTAAAA GCTGATTTTA 240

TTTAATGGnA AAAATCGACA CCCCAACTTT ATTAGATTTT TTAGCAGAAC TTGCCTAATA 300

AATATGGAnG TCAATATTTA CTACAAAGCC GnGTTTTTAA ACCCCAAAAA G 351

(2) INFORMATION FOR SEQ ID NO: 2451:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2451:

GTGTACCGCC TCGGCTGGCG TTCGCGGTGG GTGGTGCGGT CGGTGCGTGT CTGG 54

(2) INFORMATION FOR SEQ ID NO: 2452:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2452:

TGCCATTCCA ATGTTACCAT CGTCTTGGTA CTACTATATA CTGCGGCTAT 50

(2) INFORMATION FOR SEQ ID NO: 2453:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2453:

AGACGTGTTT CCACGGTATG GGATAAATGA AGCACCGACT GATAAATCAA TATAGCCTCG 60

TGTTTTTAGT TTACCCGAAC TATCCCTTGA TAATGATTGT GACATCTGCG GATAATATTT 120

CATTTTCTTA GATATCGTCG AAATATCACC GATTACTTGA AGTCCATCTG TCGTAAACAA 180

TTCAATTCTG CTTTGTTTGT TTTTACTTGG GGCGTATGTC ACTTCGGCAA TATATCGTCT 240

AACTTCAGGT GTCATTTCAG ATAACGCCTT AATCATATCA TCTTCTTTTG TACCTTTGAA 300

ACCATCCATG ACAGGTGCAT CATTAATTTT GACATCATTT GAACCTTTAA GCAATTTACC 360

ATTTTCTAAT AAAGGTAAAT ATTTACCTTT ATATTTCACT 400

(2) INFORMATION FOR SEQ ID NO: 2454:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2454:

AGAAAGAAAT ACCATTTGGA GATAGAGACT CGTGTTATTT CTTAGCGATG GGAGATTTTT 60

ATAATAAAGA AGATAGnAAG AAAATTATCA AAGGTTATGA AAATAATTAT GGTAGAGGTA 120

TTAATATTCC TCGAGCACAT AGTATATATT TATATG 156

(2) INFORMATION FOR SEQ ID NO: 2455:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2455:

ACTTAGGTGA TATGAAATGT GGTCCGCGAC GATCGTCAGT AACAAAATAA CAGGCAGTCA 60

TTGGATTATG TTTAACG 77

(2) INFORMATION FOR SEQ ID NO: 2456:

(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2456:

AGTGAAATCG CTAAAGAAAA AGATGGAACC TCGGTATCTA ATACACAACT TCTTGAACGT 60

TTTTA 65

(2) INFORMATION FOR SEQ ID NO: 2457:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2457:

TATCAATAAT TGCCACTTGC AATGACTGAT TAATTTGAGG TGCACATAAG CCAG 54

(2) INFORMATION FOR SEQ ID NO: 2458:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2458:

AATTTTATTT CGAGATTCTT CAATATAGAT GTTTCTTCAT TAATTTGATT CTCTAACTCT 60

TGCTTACTAC CTAATAGTTT ATCTAATTCA GCTTTAGCTT TTTCATTTTC TTTAATTATA 120

TTAATTTCAT TATTTATGTT CGTnATCGTA TTATTTAGTT CGATAA 166

(2) INFORMATION FOR SEQ ID NO: 2459:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2459:

CCAATGATTA AGCAATACAA TCGTCACTAA AATTACACCG ATAATCTGAA TCATCGTCAT 60

(2) INFORMATION FOR SEQ ID NO: 2460:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2460:

AAATCAAAAA AATGTATAAT GAAAAGAAAA AGAAATTTGG AAAAAATTGG GAAGACGCTC 60

AAAAAGCTGG AAAAGCTGTA GGTGAAGATT TGAGTGTnAA TGG 103

(2) INFORMATION FOR SEQ ID NO: 2461:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2461:

TTTATATCAG AATAGAATAG TAAACTAAGG CATTTGGAGA ACTTATTCCA TG 52

(2) INFORMATION FOR SEQ ID NO: 2462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2462:

CAGCAGCGAA TTTTTGACGT CCAGTGTAGA ATGGATGTGA ATCAGATGAA ATATCTAAAC 60

GAATAACTGG GTATTCTTTT CCATCTTCCC ACTCCATCAT TTCTGAAGAn GTT 113

(2) INFORMATION FOR SEQ ID NO: 2463:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2463:

CTAACATAAT TGTTAACACT AAAATATTTA CTACTTTTAG AACTGTGCGA TTAAATACAA 120

TTGTCAGTAT TGTTATGACT AGGCTAACGA TACATAAAAT AAAGAAACCG TTAAAGACTA 180

AAATTAAGCG ATCGATTCCT TGTTGTAAAT CATTGATATT ACCCAAATTA ATAnTTAATT 240

GGATGCATTT nCCAA 255

(2) INFORMATION FOR SEQ ID NO: 2464:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2464:

TATGCGACAA TTCGAAACAT TTTATATGCA AAAGGTTATA CAACAGAGAA TGTTGATT 58

(2) INFORMATION FOR SEQ ID NO: 2465:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2465:

TGAATTTCAT TACCACATAT CGGACATTGA TCTCCAATAT TTACAGCAGA TTTAATTTCA 60

CTTAT 65

(2) INFORMATION FOR SEQ ID NO: 2466:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2466:

CGTGACCTTC AAAGACCGAA CGAGAGAGTT GAAGAGCATT TGCGAAGGCC A 51

(2) INFORMATION FOR SEQ ID NO: 2467:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2467:

AGTTTGTTAA GTTTTAGTTT ACTAACTTTT CCATTAGATA TTATTAATGA AAAAC 55

(2) INFORMATION FOR SEQ ID NO: 2468:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2468:

TTGTTGGTAA GGCACTTCTT AAATATCAAC AACGCGATGA TATTTTCATT GGTACAAAAG 60

TAGGCAATCG TTTAAC 76

(2) INFORMATION FOR SEQ ID NO: 2469:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2469:

CTTCTATAAT AAAACCATCT GCAATTAAGT CTTCAATAGA CGATGGATTT CTATTATGTA 60

TCAATGCATA C 71

(2) INFORMATION FOR SEQ ID NO: 2470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2470:

CTTCGTCATT GTATTCGAGC GCCTGTATAG CTTGCTCAAA TGATGCATAA AT 52

(2) INFORMATION FOR SEQ ID NO: 2471:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2471:

AGAGGTTATG TTGATGTGCT TTATTTTCAT CAATGTCATT AACACAATCA TATTTCTTCT 60

GTTAATGCAC TGTATTATAT TCAAACGCGC TATCGACAAT TAATTTGn 108

(2) INFORMATION FOR SEQ ID NO: 2472:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2472:

GTCCCCAGTT GATATAGGAT CACAGTTTAA TATACTTGGT GAGATAGTAA TACTATTATT 60

AATTCAAATA GGTGGTCTGG GTATCGTGAC CGTAACCCTA TTGACACTAG TATTTTTAAA 120

TAGAAAGATA TCAATGAAAA ATAGATTCTT GATTATGGTT ACATGGAATA TTGACGAACC 180

TGGTGGTGTT ATTAAGCTAA TTAAACACTT GGCTATTTAT AGTTTAGTCA CTGAATTAAT 240

TGGTATGATT TGTTTGTGTT TATCTTTTAT ACCAAAATTT GGTATAGGCA AAGGTTTATT 300

TTTAAGCTTA TTCACATCAG TATCAGCTTT TAATAATGCT GGGATTTGCC CTTTTTAAGA 360

ATAACTTAAT AGATTATTCT AGTGATCCAA TTGTCATTAT 400

(2) INFORMATION FOR SEQ ID NO: 2473:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2473:

CTTCAAATAC TAAATCAGCG TTGCTAAACA TACCGTATAC ATTTGATGGC GTTGATAACG 60

CGTCCTGCGC TTCTGTTAAT AACTTTTCAG TTTCAGCATC TAAnATATGA GGACGTTTTT 120

CATTAATCAA CTTCAAATCA AATGCGA 147

(2) INFORMATION FOR SEQ ID NO: 2474:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2474:

CTTTAGGTGC TTGTGGTAAT TCTAATTCAC AAGATCAAGG TAACAAAACT GAACAAAAAA 60

CA 62

(2) INFORMATION FOR SEQ ID NO: 2475:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2475:

CCTTTAAAAT CATCTAGAAT ATCTCTTGAG AAAAATTCGA AATCTACAGT 50

(2) INFORMATION FOR SEQ ID NO: 2476:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2476:

ATAGTGGTTA GTCAATGTAA TTAAATGAGA ATAGAATGGT GATTTCATCT TAGCTTGATA 60

ATTAGCAGAA TCTTTAAAGA AAATTTTGTC TTnCAAGCCT AAGTTTACAA CGT 113

(2) INFORMATION FOR SEQ ID NO: 2477:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2477:

CGTAACTAAC TCAATTTACT GAAAAAATCG CTTGCGATGC AATAGCATTT G 51

(2) INFORMATION FOR SEQ ID NO: 2478:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2478:

TAGTTGCCGC TACGTTTATA CTCGTATTAA TGAAAAAAAC TAGCAAAGAA TCTAAAAAAG 60

(2) INFORMATION FOR SEQ ID NO: 2479:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2479:

TCGGACATGA TGGTAAAACC GTATTGGGTA TTCGCACTGA CACCTTAAGG GA 52

(2) INFORMATION FOR SEQ ID NO: 2480:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2480:

TTCCTAATTA AGGATTAAAA AGGGTTTCCT AATTAGATTA nAATTCCGGG ACCTGGATGG 60

AAAAAAGTTT TTAACTTTTC CATCTGGTCC CGTTTTTTGA TTTTCGATAT AAAAAAAGCG 120

CAATTATCTC TAT 133

(2) INFORMATION FOR SEQ ID NO: 2481:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2481:

AAATGTTTTG GAAGAACGTA AGAnAAATCA ATCTGAAACA AATGCACGAT ATGAAGAAGA 60

ACAAGAAAAT TTAATGGAGC TTTTAGAAAA TATATCAAAT GAGATTTCTG AAGCTCAAGA 120

TACTTATAAG TCTCTGAAAA GTAAACAAAA AGAACTCAAT GCTGTCATTC GTGAACTTGA 180

AGAACAACTA TATGTTTCAG ACGAAGCACA TGATGAAAAA TTGGAAGAAA TTAAAAACGA 240

TACTATAGAA GAGAATGAGG CTAAAAAATC CAGACAGGTT CTCGTTAGTT GGAGTTTTGA 360

GCCATTGAAA GTATTCnGGG GGCCAATTAA AACCGCCAAA 400

(2) INFORMATION FOR SEQ ID NO: 2482:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2482:

AAGGTGCATA GTCAACAACA TTTACAGCAT CATTTGATTC TGAACTAACC GAAACATTAT 60

ACTTACCG 68

(2) INFORMATION FOR SEQ ID NO: 2483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2483:

ATGAGCCnAC ACAGTGGTGA GGTAATCAAC GGTACAGTGG TTAGTGTGAT 50

(2) INFORMATION FOR SEQ ID NO: 2484:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2484:

CGGAACTCGT CGAATAACTT TTTAGATTCT TCGTTAGCTT TTACATTAGC GAATGCTTCT 60

nTGATTGCTT TGTATTCTTC GCTTTCTCTT AAAGCTTGTT CTAATTGATT TGCATAATCA 120

TATAAATTTA CTGCCATGGT TATAGCACTC CTTGGTnGTG ATGTTTATTA AAACGTTCGA 180

TATTACTTTA CCACATCTCG CTTTTTTAGA CAA 213

(2) INFORMATION FOR SEQ ID NO: 2485:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2485:

GACCAAAATT ATCTTTAGCA CTTATAGGTA TCTTTTTAAT ACTTTGTGAG TTTTTCTATG 60

GCATTCCTTT TTTAGGTGCA ACGTTTATTT TAAGTTTTGG ATGGCAGCCT TTACTCTTTA 120

ATGCATTACT TTATCTAATT CTTACTATTA TATTATTAGT GAATAGACAA AATGCGATTA 180

GACCTATAGC GATTATTCCA ATATTTGGTA TAGTAGGTAG TTTTTTAGCT ATTATCCCCT 240

TCTTAGGAAT TTTGATTCAT TGGATTTTAT TTTTCCTAAT GATTCCAnTT GTCCTAGTTG 300

GATTATCAGC GCCAACCTAT ATACCCAATA AAAATGCTCG TGnCnTTTTA CACACAATAC 360

AAAGATGGAC CTAGAG 376

(2) INFORMATION FOR SEQ ID NO: 2486:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2486:

TTGACCTTGA CGGAAACTTT TTTCCAAGTT CTAAAAGTGG GCCAAAATCT T 51

(2) INFORMATION FOR SEQ ID NO: 2487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2487:

GAATTTTGGC ATACACATAC ACTTTAAAAG ATATTATTGA AATTACAGGT GTAACTAAAA 60

GAACTTTACA TTATTACGAT GAAATAGGAT TATTAGTTCC AGn 103

(2) INFORMATION FOR SEQ ID NO: 2488:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2488:

AATTACATTA GCACCAATCC ACACATCATT TTTAATTGTT GTACGGCTAG GTTGGTCATT 60

AAAGTCTATA AACGTTTnCT TTAAGTTAAA TGGATTATTA TTTAGA 106

(2) INFORMATION FOR SEQ ID NO: 2489:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2489:

TGAATTTGCT TGAGTCGTGC TGCTGATAAC AATAAAATTG CACATGGATA AAGAATGACG 60

C 61

(2) INFORMATION FOR SEQ ID NO: 2490:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2490:

GCTCGTATGA TACAAATTCA TAATCTGAAA CTTCTGTCGT TTGTCGAACA TGTGGTAACC 60

AATTCTTCAA GATGCTGTAT ATTTCTGCGT AATTTTCGTC ATTCCTGAAT AACCTCAACT 120

TTAAAATGTC ACCTTGTTTG ATATAACGCA TTAAAAAATA TTGATCTATA TCTCCCTTAT 180

CTTTAAGATG TTTTACAAAT GGATACAAAT TGTCGATGAT AAATGTATCT TGCGATGGCT 240

TATCGATATG AATATGTAAT GCAAACCAGT CTTTGTCATA TTCAATATCT GTATTTTTAT 300

ATTTTGGAAT TTCGATTTCG GGTCCTCGAT AAGATGATTT TTTATAAATT GGTGTAACAA 360

TTTCATACAC ATGATCATTC TTTGATTGAG GGAAAAATGA 400

(2) INFORMATION FOR SEQ ID NO: 2491:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GACTGTTTTA TCGCAACTAT TTACACCTAT ATTATCGTTA GTAGGACATC TCGTCGG 57

(2) INFORMATION FOR SEQ ID NO: 2492:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2492:

CATTGAACTT GCTTTTGACG TACACCAGTA ATCAATGCCA TAATACGATC CGG 53

(2) INFORMATION FOR SEQ ID NO: 2493:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2493:

AATACAACTA ACATACACTT ACCCATGTCC GAAGTCCnTG TTGAGGAATG 50

(2) INFORMATION FOR SEQ ID NO: 2494:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2494:

GCTGTTTAGC TTGCTCAAAT GATGCATAAA TATCTGATGC AACTATCATA TCAGCTAGTT 60

CATCA 65

(2) INFORMATION FOR SEQ ID NO: 2495:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2495:

ATTAAGCTTT CTAAATCATT GATGTTAGGA GCTAATGTGC TCGATAAGCA GAGTAAAGAA 120

GAATTGCTTA AACAAGCTAA ACATATAACA GGTTTAGAAA ATCCTAATAG TCCTACACAG 180

TTATnGGCTT GGTTAAAGGA TGAACAAGGA TTAGATATAC CTAATTTACA AAAGAAAACG 240

GTTCAGGAGT ACTTAAAAGA AGCAACAGGA AAAGCTAnAA AAATGCTAGA AATTAGATnG 300

CAAATGTCTA AAACCAGTGT GA 322

(2) INFORMATION FOR SEQ ID NO: 2496:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2496:

ATCAGTGTTA ATTCGCACGG AATTTCCTTC CATTAAACTA ATCCGATCAT ATAATGGAT 59

(2) INFORMATION FOR SEQ ID NO: 2497:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2497:

CTAATTAAGC CAAAAGGGGA AGGGTCCACC AACCCTTGGT TTCCCCCCAT TGCCCGGAAA 60

CCACCAGnAA GTTTAAAGCT TCCCTTTAAG CCGTCCGATG GGTAGTCCGA ACTTTACCGT 120

TCCCGC 126

(2) INFORMATION FOR SEQ ID NO: 2498:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2498:

CACTTTGCGC CAGTTTTCAG TTGAGTGGCA TAGAGTCTGC TCATCAGTTC CTTGCTCC 58

(2) INFORMATION FOR SEQ ID NO: 2499:

(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2499:

TCATGATGCA GACGCAACAG CATTTGGTTA TGAATATGGA CAAATACCAC AGATGCCGGT 60

AGCATTTCAA TCAAGTAAAC CTTTAATAGA 90

(2) INFORMATION FOR SEQ ID NO: 2500:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2500:

TGCTCAAAGT CGTGTAGACA GCCAACTAAT GCATTTTCAA GATCAGTGAC ATCTCCGACA 60

CCAAAGAAAT CACCGAATAT TTTTGCATGT TCGATTTTAC CTCGTTTAAC ATCAAACTTA 120

ATTTGTACAA ATCCTTTTTC AAATTTTTCC TCGCGTTCAA AGTTATATTT AGGGTTTCTA 180

CCATAATTCC ATTCCCAAGT TCTATATTTG TCGTTACTTA ACTTTTCAAT ATTnTCCCAA 240

TCTTCATCCG TTAATTGATA TTCTTCnACT TCAGTTTCGC CAAAGATAGT TT 292

(2) INFORMATION FOR SEQ ID NO: 2501:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2501:

GGTGTGTGTA GAGGTCGAGA GTTGGGGGGG GAGTAACGTG GAAGTTGCCC GGACAGCA 58

(2) INFORMATION FOR SEQ ID NO: 2502:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATACGGGAGG TATCAGCACG TACGTGCAGT CGGTAATGGA TCnAAATACG 50

(2) INFORMATION FOR SEQ ID NO: 2503:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2503:

ATCCCCACTC TTTTTTAAAT GATTTAACCA TATTTTATTT TTAAAATAAA TATCCATCAA 60

AGTGTATCAA TAAATTTATC ACATGTCAGA AAGTATGCTT CATCTGAATA CACCAATACT 120

CTCATGAAAC TTATTAAAAA TTACTCTCTC AACGTAAAAn ACCATTCAAA TTCATGAATG 180

GTTTGGAAGA ATGATTCATT GTTACGCTAT TTAATCACTA CATCTTAATT ATTGTTGCTC 240

TAAACGATTA CGCTTACCAT TTAAGAAAGC ATAAACGAGA CCTACAAAAA TACCGCCACC 300

GACAAAGTTA CCTAAGAAAG CAAAAACGAT ATTTTTTAAA ACGTGTAACC ATGAAACTGC 360

ATCAAGGGTA AAGAATACCA TACCTGCATA TAGACCTGCA 400

(2) INFORMATION FOR SEQ ID NO: 2504:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2504:

ATTATCTATG AATAAAATTT ATAATAAACA TATATTGAGA AATTCTCTAA TACCTATTAT 60

TACATTTTTA GGTGCTGATA TTGTAAGTAT TTTAGGTGGA GCCGTGATTA CGGAGACTAT 120

CTTTTCATAT AACGGTATCG GTAAATTATT TTTAGAATCG GTAATAGGCC AAGACTATCC 180

ATTAATGATG GCATTAACGT TATTTTTCTC ATTTTTAGGT TTACTGGGTA ATTTGATTTC 240

TGATATTACT TATGGATTTA TAGATCCAAG AATTAGAAGT AACTAGGGGG GATTAGAATG 300

CAAAATAAGT CAAAATCGCC TTTnAAAATT GCATTTTCTA AATTnATTCA TAnTA 355

(2) INFORMATION FOR SEQ ID NO: 2505:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2505:

CCGTTAGTTC CATACCATAT TTTTTTCTAT AAAATAATTT AACATCTAAT TGCCTTTCTA 60

ATTTTTCAAT AGGGGTAGAT ACAGTTGACT GTGAATAGTT AAGTAACTCT GATGCTTTAG 120

TAAGGTTCTT TGTTTCACTA GTTACTAAAA ATGATTTTAA AATGTTTAAG TTCAAAGTAG 180

TACCTCCTTT AGGGTTCCCT TTTATCGAAT CCTGAATTCT AAGAATTCTG ATTTAATAAT 240

AATATATnAn ATAT 254

(2) INFORMATION FOR SEQ ID NO: 2506:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2506:

AACTCCACCG TGTAGTTGCG CTTCATCGCC TTGAGGATGC GATTGGCGCC GTGCTGCGCG 60

GCACGTGCAG ATAGTGCGAG CACTTGGGCA GATCGCGCAC CGCCTCCAGC AGGTCGTCGG 120

TCATATCCTT GGGATAGTTC GTTACGAnTT GGATCCGGTC GATGCCGTCG ACATCCGAGA 180

TGCGGCACAG CAGGTCGGAC AGTCGCGTTG nCCGCTGGCA GTGTCGTAGT GGTAATGTTT 240

CACGGTTTTG ACCTAGCAGC GTTCACCT 268

(2) INFORMATION FOR SEQ ID NO: 2507:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2507:

AAAAGTGGCT AATATCATCA GCAGAATGTA TAACATAATC GAATTGCAAC CAGCGATTAT 60

ACCTTT 66

(2) INFORMATION FOR SEQ ID NO: 2508:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2508:

ACCTCCGCTT CAAATGTCAT TGATAGACAT TTAAAGCGGA GGCATGTACA TGT 53

(2) INFORMATION FOR SEQ ID NO: 2509:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2509:

ACCCTATGAn AGATGAAGTn ATTAACCAAA AACCACGTGT TGTAATATTA 50

(2) INFORMATION FOR SEQ ID NO: 2510:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2510:

TTAACCTATT ATATTAATTT TAGTATCAAT TCTTTCTCCA GTTCCTGCGT CATTTTT 57

(2) INFORMATION FOR SEQ ID NO: 2511:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2511:

ACGTGTTCAT AACCCATAAA GGCGAATATG GTAACACCGA ACATCATGAC A 51

(2) INFORMATION FOR SEQ ID NO: 2512:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GTAnAGCGGT CCGCGCTTAA AGCGCTTGCT AACTTCGAAC AATGAATCTG CGGAACATCT 60

TGCGAATCCA CGAGATGATC TCATATGACG GGCAGCGAGG T 101

(2) INFORMATION FOR SEQ ID NO: 2513:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2513:

GGGTAATGTA ATAGTATTCA TCTACATCAT CTTGATCATC GTAATGCTGA TTGTACCCTT 60

CTAAATC 67

(2) INFORMATION FOR SEQ ID NO: 2514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2514:

CCCGTCGTTT TCGTGnTTTT CGCGGCGTGT CTCCTGTTCG CGCCTCTACT 50

(2) INFORMATION FOR SEQ ID NO: 2515:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2515:

AAGAAAATAT CTCTTGAATA CTGATCGATT GCCATCGAAA AACACTGTTA AATCAAGTTG 60

CCCAGTCCAT TGTTGTTCAT CCATTATGAT AATCCTTTGA GTAAAGTGTC GCGTTCAATC 120

CAATCGATAA CTTCATCCAA ACCTTCGTCG GTTTTTAAGT TAGTAAAAGT AAATGGACGT 180

TTACCACGAA ATACTTTAGT ATCTTCAGCC ATTTGTTCTA ATGATGCACC TACATAnGGA 240

GCTAAATCAG TnTTGTTAAT TACAAAGACA ATCTG 275

(2) INFORMATION FOR SEQ ID NO: 2516:

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2516:

CTGCACCACC AATAACGTAA ATACTGTATA TACTAGTAAT CGCTAATACA CCGATATTA 59

(2) INFORMATION FOR SEQ ID NO: 2517:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2517:

TCTGCTACTA CGTATACGAT AGAATGGATT TCTTTTTGAA CCTAAACGTG TTAAACGAAT 60

TTTAACTGCC ATTTATAAAA TCTCCTTTAA GTCATGTTTT AATTTTTATT TTCTACAnG 119

(2) INFORMATION FOR SEQ ID NO: 2518:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2518:

ATTTCCTTTT AAGTTTTTAA AAATCCAAAA TCCTTGTGGT AGGGCCATGA AAGGGTTGGG 60

(2) INFORMATION FOR SEQ ID NO: 2519:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2519:

ATAGAAGTGA AGCACGTAGA TTGAAACGAT GGTTAAATAA CGAGAGACAT TTAGAAAACA 60

ATAAAAATGA GGAATAATCA ATGATACATG GAATTGGTGT AGATTTAATC GAAATCGATC 120

GAATACAAGC GTTATATAGT AAGCAACCAA AATTGGTTGA GCGGATTTTA ACTAAAAATG 180

GGTTTGCTAC AAAAGAAGCG TCAGTAAAGC ATTAGGCCCC GGCCTnnGGA AACA 294

(2) INFORMATION FOR SEQ ID NO: 2520:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2520:

TTTTAGGCCG AAGAnGTAGT AATTTCCGGT CCTTTAAGGG GCGGGTGGTT AACCATGGCA 60

ATTAATCCCA GGGATGACCT TACCTAATAA CCACCTAATA ATTACCCGGA CCAAAGGTGG 120

AAATAATCCC TCCGGTCCTT CCCGG 145

(2) INFORMATION FOR SEQ ID NO: 2521:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2521:

TTTTAGTCAC CAAAATTCTC GCATTTAACT GATACGAATG TGCAATAACT AAAAATCGAT 60

CTAATAATTG CGTTGAAAAA TTTGGCTCGA CAGCACTCAT TACAATTACn AGTGTATCTA 120

TATTACTTAC AGGTGGTCTT TTCAACTCAT TTTCCCGCTC AAACACTTG 169

(2) INFORMATION FOR SEQ ID NO: 2522:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2522:

ATCCAGCCTT TCAACAAATA AATCTGAAAT TCGATGTTCT AAAATTTCTG CTTCTTGATG 60

TACTTCTTCC CAATTATATT TCAATATT 88

(2) INFORMATION FOR SEQ ID NO: 2523:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2523:

CAGTAACATC AATCTGTCCT GTAAGCTTGT GGTACTCCGA TACAACCATA AGTCAACGCA 60

CCACCAAAAA CGCCTTGGAG CCGTTCTACT TATTAGTCCA AGTTTAGACA TTGAAATACC 120

AACAACTTTG CAnTCCATAG TATCTGAAAA TGTAGACATT GCCTGCAATA AATTTAACnC 180

ATCATTTTTA TTATGTGGCA TTACTGCTAA TTTAACGTAT TCTGGGTT 228

(2) INFORMATION FOR SEQ ID NO: 2524:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2524:

CTCATCCATA GCGCTGGTAT TAGTATAGGT GTCAAACCAT TAGCGTATAT CATATCTTCT 60

GGATGTnCTC ACATATTCAT AGATGCACAT TTTACTTCTC TCGTACCTTA GTACTGGGA 119

(2) INFORMATION FOR SEQ ID NO: 2525:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2525:

TACCAATATT AAATTTGAAC ATTATAGTTT GACCATCATA ATCTATCTTC TCTATTTCAT 60

TATAACTAAT ACTTCTATAA TAAAATTGGC CATTCATATC TACATTCATA ATTAATCTTT 120

CATTTGTTGC TATAAATGCC CCTTCAAATT CATTCTCACC TTGAACTTGA TACTCAATTA 180

TTCCTAGCAC TGACGGACCC TTTTTTTCAG TTGGAAATAA ATCATTTGGA TTCACATTAT 240

CTAAAATCAT AATATCCCTC CCACTTAAAA CTATAAACTA TTCTTCATAG GTATATGAAA 300

TACAAGTGAT TAACTATTnA TnATnAAGCT TAACTTGTAT TCCCTTTTCA AGATAAT 357

(2) INFORMATION FOR SEQ ID NO: 2526:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2526:

CACGCGTCCG GCCACCTGGA CATGGCCGAC CTAGAAGCCA AGCTGCAnGA GGCCCAGAAG 60

CATCGGCTGC GCCTGGGTGG CCACTGATGG GGCCTTTTCC ATGGATGGCG ACATCGCACC 120

CCTGCAGGAG ATCTGCTGCC TCGCCTCTAG ATATGGTGCC CTGGTCTTCA TGGATGAATG 180

CCATGCCACT GGCTTCCTGG GGCCCACAGn ACGGGGCACA GATGAGCTGC TGGGTGTGAT 240

GGACCAGGTC ACCATCATCA A 261

(2) INFORMATION FOR SEQ ID NO: 2527:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2527:

CTnTAGAGGA TATGAGTTCC TCATCATAAG AATTTCTGGA TCCTTAATAG ATCTCTTGCT 60

ATATATAATG TAATAGAAAC ATCTTTTAAG GATCCAGAAA TTCTTAGA 108

(2) INFORMATION FOR SEQ ID NO: 2528:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2528:

TTTTAAAATA CTTGGTAGAA GTTGGAATGG ATTAATCATT AATTATCTCT CAAGATGTAA 60

TGACTGTTCA GCACACTTTT CCGATATGAA AAGAGATTTG AAnACAATA 109

(2) INFORMATION FOR SEQ ID NO: 2529:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GATTAAAATTT GTTATACCTG GCTTGTTGTC ACGATCAAAT TTAATAATAC CATCTGAATC 60

AGTTACTGCG CTTTTAATTT TTTTAGCTGC AACATTCGGC TCGTCTAATA ATGAAATnGA 120

GTTTTTAGCA TTATCATCAC TCTTACTCAT 150

(2) INFORMATION FOR SEQ ID NO: 2530:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2530:

TTCTTTTTGG CCAGTGGCAG GAAGTACGGT CTTATTTGGT GTTATGTTAA GAAGGTATTC 60

CCATTTATTT ATCGTTAAAT ATGnATATAG TATAGTAATT TTAATTTGTT GCATCATAAT 120

ACTAGGT 127

(2) INFORMATION FOR SEQ ID NO: 2531:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2531:

CACATAATGA TTCGAATTAT TGTTTTAATT AAACCTTTTT CACATATGTA TAAATTTTAn 60

AGAGCGCATG CGTGAATATT TTCATTTGAT TCAAAGGCAA AAGATAGCCT TATACTCTTT 120

TC 122

(2) INFORMATION FOR SEQ ID NO: 2532:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2532:

AAATAATAGA GCAATTGGCA CATGTAAGAA TGCAAATTGA CTATGGCATC CAGTATTTTG 60

GTCACAAATG GGTTGTATAT GAGCATGTTG AAAAATAAGT CTTATGnTAA ACACTTAGTA 120

(2) INFORMATION FOR SEQ ID NO: 2533:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2533:

GAGAGCGGCC GCGTGTAAGG AGAGCGGCGT TCGTTCGCGT GACGCGAGTG TGGTTCGCGA 60

GAAGnGGACC AGAGTTCCCG ATCGAGGCTG TTCGGGTAAA T 101

(2) INFORMATION FOR SEQ ID NO: 2534:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2534:

TTGCTCATTA AAGATTATCC CAATCAATAT CATCTATATT TGTTGTACCA CTATTATCTT 60

TTTCTCTTTC TCTTACTTTG TnCATTGTAC CAGTAGATTC AAGATATATT GT 112

(2) INFORMATION FOR SEQ ID NO: 2535:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2535:

ATAACGAATC CAAAAATATA GAGAATGACA GTGAAACTTA AATAGGACTC T 51

(2) INFORMATION FOR SEQ ID NO: 2536:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2536:

(2) INFORMATION FOR SEQ ID NO: 2537:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2537:

GGATGTACCA CCAGCATAAT AAACAACTTC AAATGGATTG ATAAAGAAGA nACCAGCAGA 60

GATAGGTAAT TCATTACCAT GTTCTTCTTG TAGACGTTTA CCTTCTTCAA TCTTTTGCTC 120

ATTTGCATCA AGTTGTTGTT GTAAGTTATC TCGCTTGT 158

(2) INFORMATION FOR SEQ ID NO: 2538:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2538:

TATATTCATT AAATCCACAA AGCGGTCCCG TATAAACATG GGTTTCCATT 50

(2) INFORMATION FOR SEQ ID NO: 2539:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2539:

AAAGTATACA TATCACTCAA CTAATCAATA ATCATACTTA CCTTCAACAA ATTCTTTAAC 60

ATGCAGTGTT ATCCCTTGAT AATATGGATA TTTnGTTAAT CTA 103

(2) INFORMATION FOR SEQ ID NO: 2540:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CAATCAATTT GTCTATCTGT TGAGTGGCAA CCTCTAATAA GCCTTTTATA TTGTCA 56

(2) INFORMATION FOR SEQ ID NO: 2541:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2541:

TGGAAATAAC GAAAGTATTA TTAATTTAAA GCATCTTTCT CCCAATACTT TAATGAGTGA 60

TATTGTTTAT ATACCGTATA AAACACCTAT TTTnGAGGAA GCAGAGCGCA AGGGAAACCA 120

TATTTA 126

(2) INFORMATION FOR SEQ ID NO: 2542:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2542:

ATCAGTTTCT TCAAAAATAA CTGAAGTATC TGATGCTGAA AATTGGAATA GTTGATGGGT 60

CGGGnTATTG ATTTTTATCT GATGTAAAAA TCCATAAGTG CCATAAGATG TATATAGTTT 120

CTTCATATGA AAGGTCCCCC TTATGTnTTT ATTTATTATA CGATGATAAA CTAGTCATTA 180

CCACTATTAA TAATTGATTA A 201

(2) INFORMATION FOR SEQ ID NO: 2543:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2543:

GAACTTTATT ACAGGAATAG ATAAGCACAG TCGTGTTACA CAGACGCTAA ATGCGCGTTC 60

GTATG 65

(2) INFORMATION FOR SEQ ID NO: 2544:

(A) LENGTH: 102 base pairs
(B) TYPE: nucl ic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2544:

AGCTATTAAT GGCGCTATAA TTGATACAAT AGTTATGATT AATAAAAAAA TAACCGATAA 60

CATTGCAATT TTATnATGAA TAAATTTAGG AAATGCAATT TT 102

(2) INFORMATION FOR SEQ ID NO: 2545:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2545:

AATCTACATC CAGCATGATC nACATCAnAG CnGGATTCAC CCTTACTTCA 50

(2) INFORMATION FOR SEQ ID NO: 2546:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2546:

AACCATTCAA CACACGACAC TAAAGTGCAG TACAATCCTA CAAAACGATT GTTTTTATCG 60

GGTGGTCTAA CCATTGAATA AATAATGAAT AATGGTAAnA 100

(2) INFORMATION FOR SEQ ID NO: 2547:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2547:

ATTGAAAATC TTTTATCATT TCATACGTGT GCATAATTAA AAAGGTGAAA CCTCTTATTT 60

TGAGATTTCA CCTTTTTTAT TGTTAATTTA AATTTAATTT TAATGATTAT TTTGTTTCAC 120

(2) INFORMATION FOR SEQ ID NO: 2548:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2548:

AAAGTGAAAA TTGGAGGTGT AATTTTGACT AGAACTTATA ATATTATTGG TATCCTTTCT 60

TGTCTTATAT CTTTTATTAT TATGGCGTTA CCAATnATTT GGTACACAGC TTCAGCATTA 120

TGGTTCTTCC CAGGTGCAAT CA 142

(2) INFORMATION FOR SEQ ID NO: 2549:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2549:

CCCAACCCTA CnAACGACAT TACACAATCA GTAACAGATC GGTATTAAGA CTGGATATCG 60

TGGCATCTGT TGAGTTAATA TCAACAGTCG TCCAGAACTC G 101

(2) INFORMATION FOR SEQ ID NO: 2550:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2550:

TGTAACCATG ATTTAGATGA CTAAACGTGC TTGCCAACAT GCTTCATCCA ATGCCGAATC 60

CTTTAGCTAC AT 72

(2) INFORMATION FOR SEQ ID NO: 2551:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2551:

CAGTAAGAGG ACAAGGCTAT AAGGTGGAGA ATCATGTTTA AAACACTCTA TGCTAGAATT 60

GCGATTTATT CCATTACGGT TATTTTATTT AGTGCATTAA TAAGTTTTGT ATTAACAAAT 120

GTTTACTATC ATTATAATTT AAAAGCATCT AATGACGCGA AAATCATGAA GACGCTTAAA 180

GAAGCAAGAC AATATGAACA ATCAGCTAAA CCAACGCACA TTCAACAATA TTTCCAnACA 240

TTTAGGGTCA AATGGAATTA CCAAATAATG ACCATGGATC CATAAAGGTC nTnAGACCTT 300

TTT 303

(2) INFORMATION FOR SEQ ID NO: 2552:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2552:

TTTACTTTAG CCTTTATTGC ATTTGTAATT TATAGAACTG CGAACAGGTG ACTACTGTnA 60

ATTTATGTGA TTAAAGTTTC AATGATATTT GATTTATTAG ACCATTGCAA AAGCGCAAGG 120

TTCTCATGTG CTGCTACAGT TTGCGGTCTT 150

(2) INFORMATION FOR SEQ ID NO: 2553:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2553:

GCACTCGTCA ATAAAGATGA AGCAGCATTT AATCAATATA CGGCAGAATA CAAAAATT 58

(2) INFORMATION FOR SEQ ID NO: 2554:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2554:

AAAATCGTTG AATAATCAAT CATAGCAGTA AGCTATGTnA TATATTTTTA AAAATTGA 118

(2) INFORMATION FOR SEQ ID NO: 2555:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2555:

ACAACTTCAA AGAAATCATG TCACAAAAAA AGTATTTGAT TTTAATCATA nGTGGCGACA 60

ATCCGCATAC CAAAGCACAA CCTTTAGTCA ACCAATTCAG AT 102

(2) INFORMATION FOR SEQ ID NO: 2556:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2556:

AGATGCATTA GCAGCATTAG ACGTTAAACC AGTTGGTATT GCTGATGATG GTAAGAAAAA 60

ACGTATCATT AAACCAGTTA GAGAAAAAAT TGGGGATTAT ACTTCTGTAG GTACACGTAA 120

ACAGCCAAAC TTAGAAGAAA TTAGTAAATT AAAACCGGAT TTAATTATCG CTGATAGCAG 180

TAGACATAnA GGTATTAATA AAGAATTAAn CAAAATTGCA CCAACATTAT CATTAAAGAG 240

TT 242

(2) INFORMATION FOR SEQ ID NO: 2557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2557:

TGCACTCATA ATCATCGGAA TATGTATAGA ATCAACTATC ACTTTGCCGT GTTTATCTGT 60

GTTAAATGTG TAACCATAAC AGTGTGTCCC ATTTGGATTA TGAATCTCAG AATAATCATC 120

AAAAATATCC TGAATTTnCA AATTAATTTC ATTATAGCGG nAGCAATGTC TATAAAATTT 180

TATTTCAA 248

(2) INFORMATION FOR SEQ ID NO: 2558:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2558:

TTTGGGTCGT GATTGAAAAA ATCTAAGGCT AATAAACCAT GTTGTTCTGC GCTTAATAAT 60

TGTTTGAGTA TACGGTTAAT AATTAACTCT GTATCATGAG GGTTGACGCG AAAGTCAGAG 120

CGCATATAAG TCATATAATT CTCGAAGATT TCTCTATCAG TATTGCTTAA TCTTAATGAT 180

TTAACATTAT TTTCTTTTGT TAATTGCGCA GTACTTTTCA TTGTTACTTA AGCGCTCCTT 240

TAAAAATGTT TAATTCCAAA TTAAAATGGA AATGATTTTA TAGTATTAAT AAGGTCAATC 300

ATATCATATT AAACGCATAA ATATAACGAT TAATATTGGA GAGGAAAATG AGGACACTTA 360

ATAAAGATGA ACATAATTAT ATCAAGCAAA TAGCTAATAT 400

(2) INFORMATION FOR SEQ ID NO: 2559:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2559:

AAGGGAAATT TAAAAGTATC ATTTGATTAT ATAGATTGGA TTAAATTAGG TTTTGGCCCA 60

TCAGGAAAGG AAAACTACTA TATGTACAAA AAATTTGGTA TTTTACCAGA TATGGAATAT 120

GAAATGGAAG AAATTCGAGC AGTAGAGAAG TATGTTAAAG AGCAAGAGTA GCAGACATGT 180

TATAAAAGAC TGTGCAAAAT CACCCTCGTT TTACATTTGA TTCAAAGAAG AAGGTAAAAG 240

ATAAGAnTAT TTGCAACTTA AAAAGTCAAT nAGCTTATCG GTATCCATAC ATCATGGATA 300

AATGAGTnCA ACTAATTAAC AAATCACGAT ATA 333

(2) INFORMATION FOR SEQ ID NO: 2560:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2560:

GTAAGACATT CACATTTATC ATTTCACCAC AATGGGTTTA CCAACCATGG TTTAACGAAT 60

CCAAAACTTT GATGCTCGTA TGTCTCA 87

(2) INFORMATION FOR SEQ ID NO: 2561:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2561:

TTGCATTTTG ACGTAAATGA TTAAACAAAT CGTGATTATC TCTTAATTTT CTAACCGCCT 60

TTTCAATTTC TAACGGCGTA ACTTCCTTTA GAACAATGCC AAATTTATAT TTnTCAT 117

(2) INFORMATION FOR SEQ ID NO: 2562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2562:

AAGTCAAACA AAATAAGCAA ACAGACTGGT CAGAAGATAA GTTGAATAAT ATAGCTTTGA 60

(2) INFORMATION FOR SEQ ID NO: 2563:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2563:

AAGTGTTATT ATTGTGATCA TAAAGTGAAG TATTACCTTT TTTATTCGTA ACCCGATTCC 60

ATGCGCCTTC AACATAAACT 80

(2) INFORMATION FOR SEQ ID NO: 2564:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2564:

AGACATGGGC TTATCAGATA AAGTAAAAGC ATTACCTAAA GGGGGAGGCG GTAAGTCATT 60

ACCG 64

(2) INFORMATION FOR SEQ ID NO: 2565:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2565:

GTTTGTTTAT AGTACCCTGG ATTTTCTTTA TTTCCATCAT GTGAAACTGT GTCAGTGAAC 60

GCTGAT 66

(2) INFORMATION FOR SEQ ID NO: 2566:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2566:

TTAATTATTT GTGACGTATT ACACGCATTA CTTTAGAAAG TGATTCCCAA AGCGAATTAT 60

CTTTACGATA AACTA 75

(2) INFORMATION FOR SEQ ID NO: 2567:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2567:

ATATTATTAT ATTGCTTTTT TTCAGTTTGC CGTTGTTACT TTCATAACTT 50

(2) INFORMATION FOR SEQ ID NO: 2568:

(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2568:

TTTTAGGATT TGTAGTAGGT GAGCGACGTA TTnnGGATGC AATCCAGAGA ACAATAAATA 60

TTGAGAGAGA GCAATTCATA ACGCAGTTGA AATACATGTG TTACGAATTG CTTTTATGTT 120

AGTTTTTATC ACACAAGTTT TTTGATGCAA CCCCGTGATA GCGAAACTCA TATGTAGATA 180

ATACAGCTTT TTCAGCATCA TCTACATGAA TTCCAAAACA TCA 223

(2) INFORMATION FOR SEQ ID NO: 2569:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2569:

AATAATGCCA TACAGTGAAG ACCATGCGCA TCAATCGATG TCTAGTGTGT ACTACGTC 58

(2) INFORMATION FOR SEQ ID NO: 2570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2570:

CGTTTCATTA GTTTTAAATG ATCCCCAATA CTTTTTGTAC CTTCACCAAC TATCGTTCCA 60

ACACTATCTA CAGCTTTTTC TGTGGTATTT TTAAACAGCG TCTATTTAAT GTCTTATCCA 120

ATTAGTTTTA TCTCTTAATC CAAATTTATT AGTATGAAAA GTCCAATTTT TAAGAATTGT 180

CTAAACAGAT TCCGCAACAA AACCAGCTAn AAACCGTCCA TACTATTGGA ATnAAAACGC 240

CAATGTTATA 250

(2) INFORMATION FOR SEQ ID NO: 2571:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2571:

AGCTCCTTTC TTTCTAGTTA ATATCATTnA ATCTTGTTTT TCAGTGTCAA AATTACCTGT 60

AAAAACAACA TTTTTATCTT TTAAAATAGG GATTACACTT TCCACTTCTA TTTTATTAAT 120

CTCAGATATT TTCATATGAA TTTTTTGAAA TCCTGAATCG AAAAGTTTAG TTGG 174

(2) INFORMATION FOR SEQ ID NO: 2572:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2572:

CATGCGGTAG GTATTTCTAA TCTATGGACA AATGGCGGAT TTATGCCAAA TGGTATTGTT 60

GGTTTCTTCT TTGCATTATC AATTGTAATT GGTTCATACC AAGGTGTGGA ACTGATAGGT 120

ATTACGGCAG GTGAAACTAA AGATCCTCAG AAAAATATCG TTAAAGCAGT GAATGGTGTT 180

ATCTGGAGAA TTTTAATTTT CTATTTAGGC GCTATTTTTG TTATTGTTTC AGTGTATCCT 240

TGGAATCAAT TAGGAGACAT TGGAAGTCCG TTTGTTGCAA CATTTGCTAA AATCGGTATT 300

ACATTTGCAG CTGGATTAAT TAACTTTGTT GTAnTAACTG CAGCAATGTC AGGATGnAAC 360

TCAGGGnATT TGCAGTGCGA GTCGTAATGA 390

(2) INFORMATION FOR SEQ ID NO: 2573:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2573:

TAGAGTACAG AACATACGCA AGGAACTCGG AGTTTACTCA CGGGACTTnT 50

(2) INFORMATION FOR SEQ ID NO: 2574:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2574:

TACAATTACA AACGCATCGT GAGATGTTTT AAGCATCAAT GAGAATCTAA CTCTCCAAG 59

(2) INFORMATION FOR SEQ ID NO: 2575:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2575:

GACACAACGT ATGACGCATG AAGAGTTGCG TGTTGACAAT CAAGATGATC ATAGCCAAGT 60

TAGTCTAAAT GGTTACACAA AGGGGTCTGA GAAAGATCAA GAAGCATTCA CTAATAATAA 120

GGATGAGGAA GCAGTTGCTG CTAAAAATCC TGAATCAGAA GAATATAAAG TGAATGAAAA 180

AATAAAAAAA GAACATAAAA ACTTTATTTT TGGTGAAGGT GTTTCAnGCG GTAAAATATT 240

AGCGGCATTA TTATTCGGTA TGTTTATTGC GATTTTAAAC CAAACATTAT TAAATGTTGn 300

TTTACCAAAA ATTAATACGG AATTTAATAT TTCTGCGTCA AnAGGGCAAG GTTGATGACG 360

GGATTCATGT TAGTAAACGG TATTTTAATA CCAATTACGG 400

(2) INFORMATION FOR SEQ ID NO: 2576:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2576:

TTTAAATCGT ACCTTAAATT TGAAAGTAAT AAGACACACC AATTACCTTC TAACTCTATC 60

GATAGTTTCA AACAAGAAAT CGnTAGTACA TTCAGTTATT TAGAACGCGT TGATTACCAG 120

CT 122

(2) INFORMATION FOR SEQ ID NO: 2577:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CACATTGAGG TGCAGTCATA CCTTGTTTAA ATGTCCAAGC ACGTACTTCT T 51

(2) INFORMATION FOR SEQ ID NO: 2578:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2578:

AATTATGACT ACAGGTCTGA CTCCCCCTTG TTCAGATCCC TGTACTGGTG ATAAATCTGC 60

TAAATAAACA TCTCCTCGTC TAATCATTCA TTCGTTGAAT TAGAAGATAA ATATGTTTCG 120

TTGCAATCGC ATGCTTCACA CTCTATCGGA AAAGCTTCGT TCGCTAGGGA GAGATTTAAA 180

TCAGCCATTT GTGAATATCC TTCTTTTAAA GATTGTTCTA AGCTATGACT TCTATTTTGA 240

CTAAAAGATA ACATATGAGA ACCTCCAATT GATTCCAAAA GTTATTAAAT GACCTTTAAT 300

TACTCTAATG ATAACAAATT TTATATGCAC TGACCATATT ATTTTAACAA TTCATTTGTT 360

ACAAAACGGT GGATCACCCA TCATGGATAG AGTCGCGGGn 400

(2) INFORMATION FOR SEQ ID NO: 2579:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2579:

ATAAAAACCT AATTGACTCA TAATCTTCTA ACGGTATATC ATCCACAATC ACAGTATGAT 60

TAGGATTATC GTTAGATACA TCTnTCACTG CCTTATCTAA CCCCTCATCA CC 112

(2) INFORMATION FOR SEQ ID NO: 2580:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2580:

CATGAnTnTA ACGGATTCAT TCCATATATC AATTGCGTTT GTTATTTTAA TAATGCTATT 60

ACTACAACTT CGATTTAAGC TATATTTATA AAAAAATGCG CCTACTCATA ACATTCTTTG 180

GCTATTTAAC TTTAATAAGC TAGGGCCAAG TTTGTCATAA GATAAGCGCA C 231

(2) INFORMATION FOR SEQ ID NO: 2581:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2581:

ACTTCGTAAA ATTTATCTTG AGTGGTTGTT TCTATATTAA GATTCATTTC ATTACACTCC 60

(2) INFORMATION FOR SEQ ID NO: 2582:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2582:

GTCAAATGCT GAGTTCTAAT AATGATGTTG GCCACCATGC ATACAAAAAT GCTAAAAGAG 60

AATTACGCAA GATTTTAGAT AGCTATCTCG AAAATGGTAA ATTAAAATAT TACGATATTA 120

TCGTTACAAG CAATTTAGCT ACTAAACATC CGTTTTTCGA GTATGCACGT TCATTTGATT 180

TTATCATTGT TTCAGATATC GGTTTAATAA ACGTTGATGT AAAAAGCTGG GGTGAAAAAA 240

CATTTTATCA CTTTGATGTA CCTGATGAGC ATGATACAGA nAnA 284

(2) INFORMATION FOR SEQ ID NO: 2583:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2583:

GAGTCAGTCG AAGTTTGTCG TTCGACCCGT AGAAGTGTAA AACGGCATTG TGAATG 56

(2) INFORMATION FOR SEQ ID NO: 2584:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2584:

TCGACTAATG TAATGTAGGC ATTGGACGTC AAATGTAATG TGGGGCAATC CGACGAGATG 60

ATGGTGC 67

(2) INFORMATION FOR SEQ ID NO: 2585:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2585:

CGTAACCGCC CCTTGTCCGG GCCCTCCAAG CCTTTTAAGG GGACCCCCCG GA 52

(2) INFORMATION FOR SEQ ID NO: 2586:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2586:

ATTAGCAACA ATGTCAGATA ATCGATACCA ACTAATTAGG CGAGAAGCGG TTTCTCATGG 60

TCTTAGTGGC CTAGAAATTG ATGTATTTGA TTTGCATTCA AATAAGTCTA GACATATTAG 120

CTCGTTATCA GGTGGAGAAA CTTTCCAATC GTCGCTTGCA nTAGCTTTAG GGTTAAGCGA 180

AATTGTACAG CAGCAATCAG GAGGTATTTC ACTAnAATCA ATATTTATTG ATGAAGGA 238

(2) INFORMATION FOR SEQ ID NO: 2587:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2587:

ACTGGAAAAA ACCGCnAACA CGACATTGTC AAAACGACGG CCAGTGCCAA 50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2588:

GnGCAATTAT ACCACTATAT TTATTTCTTA TACTCCATTT GATTTATAGT TGTATTAATA 60

CATTGACTCA AAAACTAATT AATCAAATAT GTTTTTTAGA TT 102

(2) INFORMATION FOR SEQ ID NO: 2589:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2589:

GCATAATATC GGATATGCGn GTGTGTCAGT CnCATAGTCG nTGGATTGCG 50

(2) INFORMATION FOR SEQ ID NO: 2590:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2590:

TTAnAAATTG CCTnTCCAAT TnTAAGAATC CTTTTTCCAA GGTAAAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 2591:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2591:

CTTCATCCCT TACTTTTAAT TGTCACGTCA AATAATATTT GTCTTTAACT AGTAATAACT 60

CCAAATATAT TTAGTTTGTG GTGCTAGCTA TAAACACAAA TGAnTCATAA CACTATATTT 120

TGATTTTnAA TTATTTATAT 200

(2) INFORMATION FOR SEQ ID NO: 2592:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2592:

TGCATTAATC ATCTTGGATA CTCTTTCTAC CAAAGTAATG ATTGCACTAC CATGACGACG 60

ACCAGCAATA GTAT 74

(2) INFORMATION FOR SEQ ID NO: 2593:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2593:

CACCTGCTCA CCTCTATTTT CAAACAATTA TGATTGAATT GAATCATTCT AATTTTTGTA 60

AAGTTACTTG TTTAATTTAT TATATTTATT AACTCTATGA TAACAAAAAT ACTGTTTGTG 120

TATAACAATA AATTGAGATA CTCAATAATT TGATAATGTG AAATTGATAC TTTTCAAAAT 180

AGTTGAATAT GACAATTAAT GATTAGTTTT GCnATGGTGC TATAAnCAAT ATTTAGCAGT 240

TATC 244

(2) INFORMATION FOR SEQ ID NO: 2594:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2594:

ATATGGTATG GAACTAACGG AAGAAGGCTT AGCATACGTT AAATATGCTA AAGTGATTTT 60

AGATAGTAAT AGCGAATACG AGAGAGAnAT AAAAGGACTT TACAATAAGA AGGTAAATAT 120

AAGTATTAAC ATGCAAGAnA GTCAGTATTT GTATCGCTAC TATAATAAGA TTAGTGAATG 180

(2) INFORMATION FOR SEQ ID NO: 2595:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2595:

AAAAAGTATT AAAAATTGCA ATTCTTAAAC TGTTATTCAT ATTAATATTT CTAGCAAATA 60

ACATTGTAAA ATAAAGAAAA ATAATTAnAG TATTGCACTT TATTGAAATT TATATTACGA 120

TAGTAATGCA GAAATTTATA TATGCAAAAT ATTATA 156

(2) INFORMATION FOR SEQ ID NO: 2596:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2596:

TGATCCGCAA ATCGCTGAAC ACGTTCTTCT ATTGGAATCC CTCCATTCAC TTTTAGCTAG 60

AC 62

(2) INFORMATION FOR SEQ ID NO: 2597:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2597:

TTACCTTTAG nTTTTAAAAC CTGACCCTCC AACCAGCCTA ATTGGTTAAA TGGGGATCCA 60

TTTATATAAT CCCAGGCCTA ACCTTCCAAG GACCAACCTA AGGGATTAAT CCCCCCAATG 120

GCCAAAGTGG GATGGGTAAT 140

(2) INFORMATION FOR SEQ ID NO: 2598:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2598:

ATTAATTGGG GAGTTAAATT AAAAAAAAGG GGTTCCTTCC AACCGGAnCC ATTCCCATTT 60

TGGATTAAAA ATTCCCGCCT TTGAAAAAAT TGTTTGCCGA ACCGCCCTTA AG 112

(2) INFORMATION FOR SEQ ID NO: 2599:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2599:

ATACCGCCCC CAGTTCAATA AGAAGCCCTG GATCAGACCT GACCCTGGTA TGGGGGGAAT 60

CCC 63

(2) INFORMATION FOR SEQ ID NO: 2600:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2600:

ATACTATGGA ATGCCTTAAT GGTGGATAAT TTCACCAAAT TAATTTTAAA AAC 53

(2) INFORMATION FOR SEQ ID NO: 2601:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2601:

AACTAAAGGT TCTAAAGATA CAGTAAAAAT TGAAAATAAC TATAAAATGC GTGGCGAGAA 60

AAAAGATGGT AGT 73

(2) INFORMATION FOR SEQ ID NO: 2602:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2602:

CGGTTGCCAG CCAAAACTTG GCAnCCAAGG CAATTATAGC AAGGCACCCA CCTAAATTTG 60

CGGACCACCC GGAATGCGGC CACCAAAGTT GGTGGGAGGC CATTTTAA 108

(2) INFORMATION FOR SEQ ID NO: 2603:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2603:

AAGCTTATAA CTATTTGTGT TTGTGATCGA GATAGGTTTG CCTGTAAAAA TGGCCATCA 59

(2) INFORMATION FOR SEQ ID NO: 2604:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2604:

ACGTCCAAAG GGCCGTTCGC CCCAGAnGTG CTGGCAAGGT TCCACAACGn 50

(2) INFORMATION FOR SEQ ID NO: 2605:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2605:

GTCCAATGTC ACATTAATTG ATTGGTATAA GCGATCACAA GGnCATAGTG AATATTTTGC 60

ACCAGACGGT GTACATTTAG AGTACAAAGG AGTCCTAGCT TTAAAAG 107

(2) INFORMATION FOR SEQ ID NO: 2606:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2606:

GTTTAAAGCA ATTTGGAAGG ACATTGGTTA AAGGATGGGA GTGGCAAAAT CTGG 54

(2) INFORMATION FOR SEQ ID NO: 2607:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2607:

GTTTTAGCTG AAGTTAATGA TGAAGATATC GGAGCTATGG TAATTAAACT AGTTAAACTT 60

ATTTTCATGC TTGATTATGT TTTATTTCAT TCAATTCAAA AAAGCTATAC AACACATATG 120

AATGAGCTTA AAAATTGTTT CGATTACATA GCTGAATTAG ATAATCATTA TGCATTAGCA 180

ATGTATCGTA GAACGCTAGA ATGTTATACT GAACCACAAA TTGATGATTC AAATGATGGC 240

ATAGTATTCT CTGAGTTAAC ACATCCACTC ATAGCAGATG GCAGTAGCCA ATGATTTCnC 300

ACTATCACAn AATATACTGT TAACTGGGGT CGAATGCTTC GGGnTAAATC AACATTTTAT 360

GGAAAT 366

(2) INFORMATION FOR SEQ ID NO: 2608:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2608:

TTCTTAGACG TCAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT 60

TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGTA TAAATGCTTC 120

AATAATATTn GAAAAAGGAA GA 142

(2) INFORMATION FOR SEQ ID NO: 2609:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2609:

GGGTCGTCAA TTGAnGGCAG GTAGAGCATT AAGTCAGAAT TGTAGTAAAT 50

(2) INFORMATION FOR SEQ ID NO: 2610:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2610:

ATTGGGTGAT GAATTTTGAC GGTATTGTCA AGTCCAGTGG CTAACTTCCG G 51

(2) INFORMATION FOR SEQ ID NO: 2611:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2611:

ACAAACTTCG GACTGCCAAT TACATTTACC TTGGGGGGTC AGAAACAATG GGTGCATAAA 60

GGCCCGTGTT TCGAAACGGG AAAAAGCCCA GCA 93

(2) INFORMATION FOR SEQ ID NO: 2612:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2612:

ATGATGTTTT TCGGCTAATT TTTATACTGA ATTTAGTTTA ATTAACTTAT GATATTTT 58

(2) INFORMATION FOR SEQ ID NO: 2613:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2613:

TTCTCACCAT TAACTATGCA TACTCACTTT ACACATAAAT TTGCTTAACA TGCAGAACGG 60

AAATAAATCA TTACCACATA TAGATCCCAT CATATATTTA nA 102

(2) INFORMATION FOR SEQ ID NO: 2614:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2614:

TGAACTACAA GACGCTTATA TCATTGACGC ACATTTCTCG CAGTGAAAGA AACACTTGCG 60

TA 62

(2) INFORMATION FOR SEQ ID NO: 2615:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2615:

TGGAGCATTT CACATACATT GGCAACCTCA TGGAGCTTAT CATTCTACCT TGGGGnACAG 60

ATATAACAAC ACTAACGCAA CATGGATGGT GTCGTTGATA ACTTTCAATC TATAGAATTA 120

(2) INFORMATION FOR SEQ ID NO: 2616:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2616:

CTGTAGTAAA TTGCCAGAAT CCGTATCAAT ACCAGTCTGT GACTGCGTTG GCC 53

(2) INFORMATION FOR SEQ ID NO: 2617:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2617:

ACATATGATA TGAGTATATT AACGTTTAAA TTATGGATAC TCTAAAGACA GGCGATTTTG 60

AnAAATCAGC AAAAAGTTAT ATGATGTAAG TGGGACAGAC ATACTAGATG TAACACATTA 120

ACCAAGTG 128

(2) INFORMATION FOR SEQ ID NO: 2618:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2618:

CCTAACCGTG TGTGTATGTA TACCTACAAA AAAATTTACA TTGTGACACT GCGTACGTG 59

(2) INFORMATION FOR SEQ ID NO: 2619:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2619:

GCCCATGGTC AATCAGACAC ACGGATTGAA CGTTAACAAT TTATGACTTT AACA 54

(2) INFORMATION FOR SEQ ID NO: 2620:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2620:

ATCATTGTCA CATTGAGTAG CCGTAAAATG GTCAGACGAT CAATGCGAAC TGA 53

(2) INFORMATION FOR SEQ ID NO: 2621:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2621:

CTAAGTGTCG CCCGAATAAC CGTCAATCCA CGGAGCACAT AGGATCTCCC ATG 53

(2) INFORMATION FOR SEQ ID NO: 2622:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2622:

TGGGACCGAT AATCATTCGC ATGAACACCT TCCACCGTCT CTTACTCACT ACCTACGGC 59

(2) INFORMATION FOR SEQ ID NO: 2623:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2623:

ATTAAATTGT TATTTCGTCA TTAGGTGACA ACTTGTATGT AGATATTTTA ACATATTTTA 60

TGCT 64

(2) INFORMATION FOR SEQ ID NO: 2624:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2624:

CCGTCCCAGA ATATCATATG ACAAATGTTA AGAGACTTGA ATGATCATAC ACGTG 55

(2) INFORMATION FOR SEQ ID NO: 2625:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2625:

GTGGTCACCA GGTACGGGGG ATACAGGGGG TTAATCCCAC CTTGGATAAG TGGAAAACGG 60

ATTTCC 66

(2) INFORMATION FOR SEQ ID NO: 2626:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2626:

CCACCAATGG GTGGGGGATG GAATAACCCT TAATGCGGTG GTACCCGGGT AATGGTAGCC 60

CC 62

(2) INFORMATION FOR SEQ ID NO: 2627:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2627:

CATGTTTTTT CATTCCTTGA TGACGACACT AGAGGTTCCC GTGTTCATTA TTAA 54

(2) INFORMATION FOR SEQ ID NO: 2628:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2628:

TTGGCCAATG GGCGATACAC CCTCTCAATT CGATACATAA CTCAAGGCTC AGTCAT 56

(2) INFORMATION FOR SEQ ID NO: 2629:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2629:

TGTCGCTAGG TAACCGTGCA TCGTTCACAG GTACnTATGA TTTCACCnGA 50

(2) INFORMATION FOR SEQ ID NO: 2630:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2630:

GAAGGnCCCA AACCAGGCGT TAAAGGCCGA TTGGGTTTAA ACCAAAGGTT 50

(2) INFORMATION FOR SEQ ID NO: 2631:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2631:

CGCGAGTGTA TCCGTCGATA TGTCGAGAGG AAAGATTGAA GTGTGGAAGA GTGTTGAGTA 60

ACCCT 65

(2) INFORMATION FOR SEQ ID NO: 2632:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2632:

TGAAAGAACT TTAGCTAGAC GTTCGTAAAG GTCTTTTGAC ATAAAGCTAG AGA 53

(2) INFORMATION FOR SEQ ID NO: 2633:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AAAAGCCAAA AGGAATTAAT TAACCCCGGG GTTTAATTTC TAATGGGAAT TTG 53

(2) INFORMATION FOR SEQ ID NO: 2634:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2634:

GGTGTTCACA TTCTGAAGGT TTAGAGAGTT AAGATTATAT ATATATAAGT TTTGGGGTGA 60

TAGATATG 68

(2) INFORMATION FOR SEQ ID NO: 2635:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2635:

CCAATTTCAC TTGGTGCTGC CATTTCGGTC TCTCGTGTAC TTGTGATTGA GGTGCCATTG 60

TTCCCGTAGA TGGTTCACAT 80

(2) INFORMATION FOR SEQ ID NO: 2636:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2636:

CTTACACCCA ACTTATTGAC TTATAATCTA TTAAAGTGCC ATTTTACAAT CTGAATCCCT 60

TAATATAGCA ATAATTACAA CTTCCGACAA ATGACTTGTT TTATGTGCGT GATTCATCAA 120

TGAACATCGT AATGCGACnT AATA 144

(2) INFORMATION FOR SEQ ID NO: 2637:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2637:

TAATTCGGCA ACTAATATCA AGATCATGAT CAAATACTAC TGCCATTTTC TTATACCTCT 60

TAATGTGAAA TCACTGnCAA CACATAACAT CTTAAAACTT TGAC 104

(2) INFORMATION FOR SEQ ID NO: 2638:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2638:

CATTCATCCG TTTTTTTGGT TCATGTACAT ACCATTGTTT TGTACACAGC GAAGTCAGTT 60

AACCTTATAT CCTTGTATAA CAGTTGAAAT CGGCAATATT AAACAGTACT TTCCCAATTG 120

CTTTCTTCCT CAATTGTGCG ACGGACTGTA n 151

(2) INFORMATION FOR SEQ ID NO: 2639:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2639:

AAGATCAACT GAAATTCATG TGTTGCCCTT TATTAAGATC ACATGGAAAT A 51

(2) INFORMATION FOR SEQ ID NO: 2640:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2640:

TTAGCTAGTT GGTAGGACGG CTACCAGGCA CGTCATAGCG CCTGGAGGGG TC 52

(2) INFORMATION FOR SEQ ID NO: 2641:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2641:

CAGGCTTAAA CCTGAGTTAG TGCCATTCAT AATTGCAATC CCAAGCGACG GAA 53

(2) INFORMATION FOR SEQ ID NO: 2642:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2642:

ATGTTTGTCA TCTGGAGCnA TAGAACAGGG TTCATCATGA GTCATCAACT TACCTTCGCC 60

GACAGTGAAT TCAGCAGTAA GCGCCGTCAG ACCAGAAAAG AGATTTTCTT GTCCCGCATG 120

GAGCAGATTC TGCCATGGCA AAACATGGTG GAAGTCATCG AGCCGTTTTA CCCCAAGGCT 180

GGTAATGGCC GGCGACCTTA TCCGCTGGAA ACCATGnCTA CGCATTCACT GCATGCAGCA 240

TTGGTACAAC CTGAGCGATG GCGCGATGGA AGATGCTCTG TACGAAATCG CCTCCATGCG 300

TCTGTTTGCC CGGTTATCCC TGGATAAGCG CCTTGCCGGn CCGCA 345

(2) INFORMATION FOR SEQ ID NO: 2643:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2643:

CTTATACGGA TGTATAGGTC GGTCCAAACA TTTGATTTTA GTGGAGAGCA GCCTTTCACA 60

AATTATGTTC AATGT 75

(2) INFORMATION FOR SEQ ID NO: 2644:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TACCGGTTAA TTAACCAGGG CCCCGGTAAA AAAATCCCCG GTATTCCCCA TTCCAAC 57

(2) INFORMATION FOR SEQ ID NO: 2645:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2645:

AAAGCAATTC GCCCGATAAG AGTAGAGACG AATTGCTTTT AAGGTTAAAA CAAAGTGAGT 60

TCAATT 66

(2) INFORMATION FOR SEQ ID NO: 2646:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2646:

CAGTATAACT TGTGACCTAT TTAGAGGGGC ACGGTTGGTA CAATGAGTCT GAAACCGTAT 60

CAA 63

(2) INFORMATION FOR SEQ ID NO: 2647:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2647:

TAGAACATGG ACCGGTATTT TACATCCTGT ACGCCTAATC TGTTGTAAGT ATCTTTAGTG 60

AACCGTTGCT CTGGAATAAC CGCGATTCTG GGCAAACAGT GTGTAAACCG ACTnTATGGG 120

GATGTGTGAG TAATCATTGT GnACTGTTGA TTCTGTTCTG GAATCCCATT TCACAACACG 180

ATCTTGGAAG TGCTGTCATT TTAGATGC 208

(2) INFORMATION FOR SEQ ID NO: 2648:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2648:

TTTTAACCTA AAGAATACTA ACACTAAAAG AGAATGATTC TGTACCGCTT TCCTTTTTCA 60

CTCAATAACT TTATATTTAG TTATCCTTAT AATTGTAATT TATGTTAGTT GGTAAATnTT 120

TACATATATG TATTTGATAT GCTTGTAAAT 150

(2) INFORMATION FOR SEQ ID NO: 2649:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2649:

AGTTTAACTG ACATCGAGTG GTACACAATA GCAATGGTTG TGTGTAAAGT CCTGGTGACA 60

ACATATGAGA GTAACATTTG TAGTGATTAT CTTGTACTGA GAGAATTGAC ATCTATGnAG 120

TTTATCACGT GCAAATAT 138

(2) INFORMATION FOR SEQ ID NO: 2650:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2650:

TCACAATTGC AAACTTCTGG CACGCACTCA TCTGCGATTT CACAAGCTAC AT 52

(2) INFORMATION FOR SEQ ID NO: 2651:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2651:

GAGTCAAATT AAAATGCCTA TTGGCCATTG TGATGTATAA TCACTTAGTT CACATATACT 60

(2) INFORMATION FOR SEQ ID NO: 2652:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2652:

GGGCGGTAAT TGTCACCATC ACAAATTGCT ACGTTGAAAC ATCGAGGATT CAAGCTGGAC 60

AGCAGAG 67

(2) INFORMATION FOR SEQ ID NO: 2653:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2653:

ACACATCTTA TATGTCTTAC TGATTTAAGG AAAGAATCAG TGGATCAAAC TG 52

(2) INFORMATION FOR SEQ ID NO: 2654:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2654:

CAAGCTGTAA ACCAAGAATT CCAGCATTAA ATATCTCTCn TGGTATCGGT TGAGATAAAT 60

ATTCCGTGTG CTCATTAAAT GTAGTAATCT TTATTGTAGT TCCTCAACCT ATGACACGAA 120

TATTGCACAA TATTAGTATA GACAAATATT TCCTTTATAA TCTCATTCAA TTTTCTCCTT 180

TAATTATGTA TCATACATTG TATATTCTCA TATAGACGTT TTGnCATATT CATAGCTTCA 240

ATATTAGTGC ATTTATGTAT T 261

(2) INFORMATION FOR SEQ ID NO: 2655:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2655:

AATCCTATTA GCACTTATAA TGATCATGAA AAGATGTCAT CGAGAATCAC CTAGTACACG 60

(2) INFORMATION FOR SEQ ID NO: 2656:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2656:

CGCCGAAAAC AATAAATTCT CGGAACATAG AATTTATCAC ATACCACGCT TGGATTATCA 60

CAATGGACTG AGTCG 75

(2) INFORMATION FOR SEQ ID NO: 2657:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2657:

TATTAAATAT GCGGTTGCAT ATATCTACGG CATGATTTAA CCGTGAACCA TGAATCATTT 60

TAATCGGGCA CGCGTAAAAT GCTCATTGAT CCGCAnATAC CACTATATAT CTAATAGCAA 120

GCGTCCAGGA TTCTGTGTTT TATAAATTTA AACTAACTGA AACGTGTGTA TCAGTTCACT 180

CCGnTCGATT ACCACACTTC AA 202

(2) INFORMATION FOR SEQ ID NO: 2658:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2658:

CGTACATGTG CATCATGTAT CTACGTCAAT AAGATGATGG GGTCACATGA TTGGACCATT 60

(2) INFORMATION FOR SEQ ID NO: 2659:

(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2659:

CTAATCATGT CATGTCTACA ATTATTTGGA GTATTGCTGA CGAAATGCGT TGTACAACTT 60

TTTCATTCTA GCACCTTGCG GGGGCCCACA AAnGAATTGG TCCATTCTCA nCATCAGTGG 120

GGGGCGCGAA TAATTTCGAA ATTATTCTGC CACTCCCACT TCATCGATTA AGTTGTAACT 180

CTACATTACA TTTGTCTTAA ACCATTG 207

(2) INFORMATION FOR SEQ ID NO: 2660:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2660:

TTAATTATGT ATAATACTTA ACAAGATCAC CTGATAGATG TCTAAATATT ATCT 54

(2) INFORMATION FOR SEQ ID NO: 2661:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2661:

ATTAAAAAAA AATGGGGTAA TTTCCGCCAA ATCCCGTTTC CCCCTTGCCA AGGCCAAATT 60

TAACCACCCT TGCCAAATnA TTAAGCCAAA TTTTCCGATA TTTGTTTCCG TAATGTTTCT 120

TTAATTAATA 130

(2) INFORMATION FOR SEQ ID NO: 2662:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AAAGTAAAAC CAGTCTATTC AAAAAGGTGA AAAATGGTGA CGCAGCGTAA ATAAnTGGTC 60

TCTGGTAGGG TAAATCGCGT TGTGGGTTTG TCACATCAGG AACT 104

(2) INFORMATION FOR SEQ ID NO: 2663:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2663:

AAAAAGAATA AAAGGACTCG AAAAACTCAA AACTTATTnT AGATAGTCAT CGTGACAAGA 60

AACAAACATT TAACTAGACT AAGAAAAATG CTTCGATTAA AAGGCAGACT CATCA 115

(2) INFORMATION FOR SEQ ID NO: 2664:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2664:

GCATGCGCCA CGGTGTCTCA GCAGAGTGAC TGCCACCTTG TGTGCGCAGA GTCTGCGCCT 60

AGTACAGTCA GGGTGAAACA CnCTATACGC ATTAGGTACA GTACTTCCTG TCTCCGACTT 120

GAGTAGAACG TGACATATCT ATCAGCATTC ACTCGAAAAA GGGA 164

(2) INFORMATION FOR SEQ ID NO: 2665:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2665:

AATTACGCAA TnTCCCTGTC TTAnTGAAAG GAATTGACCT GTTAATTCGT 50

(2) INFORMATION FOR SEQ ID NO: 2666:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2666:

ACAATTCAAT AGAATTTACC CGTAACAGCG TTGCACTGCA CTCAAGACGG CTGACGTATA 60

GCAC 64

(2) INFORMATION FOR SEQ ID NO: 2667:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2667:

GTAGAACCAG CGACGGCGCG GCGGCTGAGC AACATCTGAC TACCTATCGG CCGCGC 56

(2) INFORMATION FOR SEQ ID NO: 2668:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2668:

GGATCGATTG ACTACATGAC GTGGnGACGC AATTATACGG ATAGTCCACT 50

(2) INFORMATION FOR SEQ ID NO: 2669:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2669:

GCAAGATCGA ATTACAATCA CGACGATCAA CGCACGTAAT CATCTCTGAT CACAGTAA 58

(2) INFORMATION FOR SEQ ID NO: 2670:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2670:

ATACCAGCCA GACTTCGATC AACAGTGTTC AACTGCATTG CCCAGTAAGT TGGATAGCTC 60

GCACATAGTG CTACAAGTTA ACATATACAn CGAGTTTGTA TCTCAAGCTT GAAGCTTGAC 120

TACC 124

(2) INFORMATION FOR SEQ ID NO: 2671:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2671:

CGCTTACTGC ATAAAAGCCC CTAACACCGG GGCACTACGC TCGTTCGCCG GCTT 54

(2) INFORMATION FOR SEQ ID NO: 2672:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2672:

TCAGCGATTT AACACTAATT CTTCTAGCTA TTCTCTGTAT TTGGACGACG A 51

(2) INFORMATION FOR SEQ ID NO: 2673:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2673:

GATAAGTTGT ACCATATTTC GATGCAATTC AATGGACAAT GAGGTCACCT GGCTTGT 57

(2) INFORMATION FOR SEQ ID NO: 2674:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2674:

TCCTTTGGCC AATTTTTCCA AGTTTTAACC CAAACGGCCC GGGTTGGGTC CCCAATTCCA 60

ATCCAAAATA ATTTTA 76

(2) INFORMATION FOR SEQ ID NO: 2675:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2675:

TCCGGGAACC TTACCCAGTG GCCCTACCCT ATGGGTTAAC CCAACCAGTG GGGCCA 56

(2) INFORMATION FOR SEQ ID NO: 2676:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2676:

TGCGGGGTCT CGTGCCGCCG TCTGCGGTGG TTGTTTGTCC GGTGGTGTGT CGGAGTCTTT 60

GCCAGCT 67

(2) INFORMATION FOR SEQ ID NO: 2677:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2677:

GGACAGAGGC CTTGACCCCC CCACAATCCT GATTCACCGT AAGTTGCTCT CCCCC 55

(2) INFORMATION FOR SEQ ID NO: 2678:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2678:

AAATTGGGGC TTCCATCCCC ATTCCAAATT ATTAAAACCG TTTAGGGGCC TTATTGGCAC 60

CATGG 65

(2) INFORMATION FOR SEQ ID NO: 2679:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2679:

ATTTTGGGAT TAAACCCTTA ATTAAAATTG GCCGGGAAAA GGAAAAGGCC GGTTGGGAAA 60

AGGCCAAGGA AAAGACCTTG GGAnACATTA AAAACCTTGG GCCAAGGCCT TCCAAAAACC 120

GGTTGGTTTT TATTTTGGGA ACCAAATTGG GGGGCCGGGA TTGGGCCAAA ACCTTG 176

(2) INFORMATION FOR SEQ ID NO: 2680:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2680:

GCCCCAAAGA ATTCAAATAA CCnTTCGGAC CCGGTAATGG CCACnTAATT 50

(2) INFORMATION FOR SEQ ID NO: 2681:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2681:

TGTGCATTTA TTGCATAACC TATATATGTG TGACCGATAT TTAGTGCGCA CTTCAATGGT 60

GCG 63

(2) INFORMATION FOR SEQ ID NO: 2682:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2682:

TTATCCAAGC TTCCGGATAG TTTCAAGAGA AACCAATGAA ATCCGTTATG GGACCAATGG 60

GT 62

(2) INFORMATION FOR SEQ ID NO: 2683:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2683:

AACAGCATTC AAGTGAGTTA CTGGGGTTTA TGCACCATCA TTGGATATCT GCACAAGGAA 60

TTTCAACGTG 70

(2) INFORMATION FOR SEQ ID NO: 2684:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2684:

CTTAAAATTC CCCAGTTTCC TTCCTTTTAA ACCCCATGGA ATTATCCCGG CCAAAAATGG 60

ACCATTAT 68

(2) INFORMATION FOR SEQ ID NO: 2685:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2685:

TTTTAACAAA ACACCTAGAT ATGTTCGCTG ATCAGAGATG CCTGGTGACC GGTGATCC 58

(2) INFORMATION FOR SEQ ID NO: 2686:

(A) LENGTH: 87 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2686:

ATCCATCCTT ATAGGCATTC ATCCTTTAAC ACCAACGATT TACATTATGG ATATAACGAC 60

TTGAGGGGGA ACGTGGGGTC CATCCTA 87

(2) INFORMATION FOR SEQ ID NO: 2687:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2687:

ATGGCTGGGC GCTTTACGTG GCCACATTAG GATTATGGCA CTGAAGCGTA 50

(2) INFORMATION FOR SEQ ID NO: 2688:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2688:

AACGGTCGTA GGCAAGGGAC TCCCCCCnGG nGCTAnATGA ACTGGTCGTA 50

(2) INFORMATION FOR SEQ ID NO: 2689:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2689:

GCTAGCATCC ATGGCTCCTA TGCCGAAGCT GAGTAGACTT AGGTGACGGG TGCGTGACAA 60

(2) INFORMATION FOR SEQ ID NO: 2690:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2690:

ACTTAAAAAA GGAAGATTAG AAAATTCATA AAAAAATTTT GCTGGGGATT CTTGATCCCA 60

TGGGCCCATn TCTGGATTTA GGTTATTGGG TTGGCCAGCC AGGTTAGCGG GGCCCCCATT 120

CTTCCAGGCT CGGTTTCTCC CAGGAC 146

(2) INFORMATION FOR SEQ ID NO: 2691:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2691:

ATTGGTGTCT AGATCATTTA ATACTAAACA TACAACACGA CTAATTCCAT TCA 53

(2) INFORMATION FOR SEQ ID NO: 2692:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2692:

TATTGAATTC AAACTATGTA CTATTTCCTA AATAATACAA TAAAAACGAC TACCATACTG 60

GCCAGAAATA TATTTTATTT GTTACACATT AATTTCAnTC CTCCATAATT TGC 113

(2) INFORMATION FOR SEQ ID NO: 2693:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2693:

GACTTATGTC CGTGTTCCGC TGAAGGCACG TCACGTAAAC TACCCGGTAC AGCT 54

(2) INFORMATION FOR SEQ ID NO: 2694:

(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2694:

CTTCAGCATG AAGAAGTCGC GTGATATACA TCATATCGAT ATATACCGAT TATATCATCA 60

GAACATTCTC CTGGTATCAT TAGATAGATG ATAATTTGAC ACAGTCCACA ATTTGTnACA 120

ACGCCGAGAC TCAATGGCAT CCTGTACnTG ATCTATGCCG GAAAACACTA GTCTATATGC 180

CCGCAGACGT CCACTATATG CATC 204

(2) INFORMATION FOR SEQ ID NO: 2695:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2695:

ATAACTCTAA TTTGAATTAT CTCTCACTAT TAAAACGCGA GCTGTGTAAT AACGAACGCT 60

GACATAATCT TGTATTGTCG CATCATTCGC TGGTATTATC ATAnTGCGGT TA 112

(2) INFORMATION FOR SEQ ID NO: 2696:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2696:

TGGCAAAATT AGATGTCTGA ATAGTTTTAT TTACAAGTAC AAACCTTGTA CCATTTTAAC 60

GTAAACACAA TTTACTTATT GAAAAGAAAA TAAATGTATT CATGAAnACA CACTTTCCAT 120

AGCACTCATC TATAGTACTC AAATTCAG 148

(2) INFORMATION FOR SEQ ID NO: 2697:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2697:

CCTATAATGC TAAACTTCAT ATATCTCTTT GGCAACTATC TCCCTTCTAT TACCAAAGTT 60

ACGATAGCAA nACAATAAAG CAAGCATGTC ATGCTTACTT C 101

(2) INFORMATION FOR SEQ ID NO: 2698:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2698:

TTGATAACAT TTGAAAAGCT GCTCCGATAT CAGCAACCAT TTCATCGACC ACAATATACG 60

ACATAGTCAC AAAACTGATT AGAAGACACC AATTGCTGAT TATCAAATCA CAAATTTAAG 120

nTGAGATTCA A 131

(2) INFORMATION FOR SEQ ID NO: 2699:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2699:

GATAGCGGTT GTTAATCAAA CGATGGTACA TGCTTACATG ATGCGCCATG TTTGATAACA 60

GCTCTCTATG ATTACGATGG AAGAATGGTT TATTTCATCT CAATTATTCC TATTAAATGn 120

AACATGCCCT AGCAAACGGA TACAACACAA TCACAACATC ACTTTGAAAT TGTTAAACCT 180

GAGAACCACA TACGCGnAAC AC 202

(2) INFORMATION FOR SEQ ID NO: 2700:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2700:

TTCGAATTTA ACAAACGTAT CACGCCATAA AGGTTGTATA TGTTGTTTGT AAATTC 56

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2701:

TATTGCGGGC TTATTAGTAC ACGATCTATA TGATGGTCAA ACTTATGTCT TTCATATTCA 60

AGTGTGACAT TGTGCGGTGA TTATATTTAC GCGTCGTTAT CTACGAACGC CACATTAAGA 120

TTCGAAACTG ACAATCAACT CATAACGCCA TGGTCCTAGA AAn 163

(2) INFORMATION FOR SEQ ID NO: 2702:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2702:

TAnACAATCG TAATCGAGTC AATGATGTGA ATTGCCCACG TGAGCGCTAA GAATGCGACA 60

TTCCACACGA TAAGGCAGTG CGCATGCGCA CTGACCTAAT AACACTGAGG ATGAGTACTA 120

(2) INFORMATION FOR SEQ ID NO: 2703:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2703:

CTGCTTGATT AGGATCGTAT TTATATGAAG ACTGTGTTCC ATAATGATGT GCGTTTTGGC 60

TGAAGTCCCT TAAATGTACn TGTGTATAAA TGCTATAATT TAG 103

(2) INFORMATION FOR SEQ ID NO: 2704:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCTATAACGC CTCTCATCGT TTGGTCACAT ATTACCATTA TTCATTTTAT GTTCTCGATA 60

ATTGTATGCG nTGTTTCTCA CTGTCATCAC ATTGATACAA CTCATTGTCA CTTTATACGA 120

TTCACACACC TCGATACGAG TGATGATATA TGACAAAGCT 160

(2) INFORMATION FOR SEQ ID NO: 2705:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2705:

TTATTGTTTA AGATGGTTAA ATGTCATCAT ATAACAnTTA ATTTTTAGCA ATTCGATATG 60

CCTATAACCT ATAAATTTCA CGTCAACAGA AAGTGACAGG CATACGGATG TGTGAA 116

(2) INFORMATION FOR SEQ ID NO: 2706:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2706:

TTACACCTGC AGTGTATGGA CTATGGCTAG ATACAATAAT TTTAGTCATC AAnCTACATC 60

ATACAAACTT ACGACTTACA CATATCTGCT TCTAnATCTT CTAACTGATT AAAGCTCGAC 120

ATCGGAAGCT ATTCTAAATT ATTATCATAT ATCTAACTAA CTGACCTAAT ATATACTACC 180

ATAAATAACC CGCCTCAAGG TTCGCATCCG CATATAATGC TTAGAAGTC 229

(2) INFORMATION FOR SEQ ID NO: 2707:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2707:

TCCATATCAA TCCTGAAAGT ACACATATAT CGTACACCAT ATGGTACAAT TTCCTATAnT 60

ACACATCACG CATCTTTCAA GACACATGTT AGGCGCTGGT CGGTGTATCT CAGAAATGCA 120

(2) INFORMATION FOR SEQ ID NO: 2708:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucl ic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2708:

GGAACTTTTC TGATTAAGTG TTCACACGCC AACCATAACA TGTATTCATG CACACAATTG 60

TTGCTAAnCT CACTAACAAC ATACGACCAT TTTACTTTCA ATACATATGA TCCGTATAAC 120

TCGAATTCnC TGCTTATAAA TGACCATTTT GACGTTCACA ATGTTAAACG ATTGGAAATT 180

TTAAAGTTAG CATGTCCACA TCCGAGCAGT AACTATGCCG TACCATTTGT ATA 233

(2) INFORMATION FOR SEQ ID NO: 2709:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2709:

TTGTACCTAC CAACGAGGAT ACAATGGATG TCACACGAAA ATTGGGATAT AGATGTCCCA 60

GT 62

(2) INFORMATION FOR SEQ ID NO: 2710:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2710:

CTTTAAAAAG GATAAATGAT TGAGAnAAAA ACCCATTCGA AAATCATGCT GCTCATGCTG 60

TAGACTTATC GTTTGGACAC TCGCGTAAGA GCGAGCAGTG AAAT 104

(2) INFORMATION FOR SEQ ID NO: 2711:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2711:

GTCCAGAATA TTAATCTGAC ACAACCATTT TAGCnGGTGG ATTAAATATA TACGACCTCA 60

CCGCAAGAAT CTCTATTTAA CTTAACCTAT CATGAATAAA CTGGCGCTTG TGATATCATA 120

TGAAGATTAG CGAAAGATAG C 141

(2) INFORMATION FOR SEQ ID NO: 2712:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2712:

TGGTATTGAA TAGCAAAATT TTGACACTAT TTGCATACTC AATGATACAT CATATCGTTA 60

TATGGATTTT TATGGTCATT AATGGTAAGA ATTTGATACG GAATATTGGC AGGTTTGGAA 120

ATCAAATAAT ATGAGAAATT GTATTAACnA TTAGTCAAGT TAACGCTCAT AAATAGACTC 180

ATCnCGCGCT ATAACGCTTA CC 202

(2) INFORMATION FOR SEQ ID NO: 2713:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2713:

TTGAACTGTC TAAGACTTGG ACGCTAAATG AATGCGTTGA TACAAACGGT GAATCC 56

(2) INFORMATION FOR SEQ ID NO: 2714:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2714:

CATGACCGAC ATCAGGTGCA AACTCCCTCA TTAATCTGGG AAAACTGTAT CCCGGTAGCT 60

(2) INFORMATION FOR SEQ ID NO: 2715:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2715:

CCTATAACTA CTCAATATTG CAATTACACA TCCTCACTTT TGTCAATTGT TTGACAATCn 60

AATACACGTT ATGCACAACT CCATTTTAAC GGAATGGAGA GCACATATGG ACAGTAAATT 120

AAAT 124

(2) INFORMATION FOR SEQ ID NO: 2716:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2716:

GGAATATGTA CTATTATCAT TTGATGTTAT TACTCATATT TTTTGTAATG AATGCTATCA 60

CCTACAAAAA ATTTACTTGA AACAGTAATA ATAATTAATT ACCACAAACC ATGATAAATT 120

TAATAnCTAA TCTAAAATAT CGCATGTTCA nAGCCACAAG ATATAACGCG TTCCGTAGAT 180

GGAACTAGAT AGTATAAGGC GCCGTGGAGC CTGGCCT 217

(2) INFORMATION FOR SEQ ID NO: 2717:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2717:

ATGACATACG CGCATATACA TGCTATCCCG AACTAATATT GATGCGTATT ATGTAATTGG 60

AGCGAACACT CA 72

(2) INFORMATION FOR SEQ ID NO: 2718:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2718:

CATATCATCA CTATATCCAT TGCGTAATAG TGATGATATT GATTGGCATA ATGGTATATG 60

GCAGATACGA TAACATAACn AACACCTCGG ATAATTGCTA TTAGCTGCGA AGTTATCGTG 120

CCTGATTTAA CGATGTAGA 139

(2) INFORMATION FOR SEQ ID NO: 2719:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2719:

CTCTATCATA TCTAGCCATA TGCATGAGAT TATCGTTTAT CTCGACACGC TCTTAAAAGG 60

CGACACCGGC ATATGATGT 79

(2) INFORMATION FOR SEQ ID NO: 2720:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2720:

CAATCACAAT TGAAATTACA CAAATACAGC CCATTGCATG ACACAGACCA ATC 53

(2) INFORMATION FOR SEQ ID NO: 2721:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2721:

CGCCCGAGGC TACCATTTTA CCATAAAGAC CGGTCTAAAT CCTTCCGGTT TCCATGGGCC 60

ATTTGG 66

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2722:

TnCCTCGCCG AAAATGACCC AGAGCGCTGC CGGCACCTGT CCTACGAGTT GCATGATAAA 60

GAAGACAGTC ATAAGTGCGG CGACGATATC ATGCCCCGCG CCCACCGGAA GGAGCTGACT 120

GGGTTGAAGG CTCTCAAGGG CATCGGTCGA CGCTCTCCCT TATGCGACT 169

(2) INFORMATION FOR SEQ ID NO: 2723:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2723:

CCGGGCCAAG CTGGTGATCA CCGATGTGGA GCGCCAACAT CGCATCGAGG AAAT 54

(2) INFORMATION FOR SEQ ID NO: 2724:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2724:

ATCGGTGATC ACCAGCTTGG CCCGGGACAA CTGCAGAGCG TGCAGCAGGA ATTC 54

(2) INFORMATION FOR SEQ ID NO: 2725:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2725:

AAAACCATTG TCCACCTTTA GAAAGCTTTT GTTTTGGGAA TACCTAAACC GTGGTTAATG 60

(2) INFORMATION FOR SEQ ID NO: 2726:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2726:

TTTAGGCCCT GTAACnGnTT GCCGnTTGGn CCGTGTGTAT ATCGGGGGAA 50

(2) INFORMATION FOR SEQ ID NO: 2727:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2727:

GGATCATTAA ACGTGTATCA CCATCCAGTT TGCAAGACGG ATAAACTGCT GCAACG 56

(2) INFORMATION FOR SEQ ID NO: 2728:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2728:

ACCCATGGAG AATTAAATTT AAAAACCGTA TTCCGGGTGG ATGCTGGGTG GGTAAGTTGG 60

CCATACTGGG 70

(2) INFORMATION FOR SEQ ID NO: 2729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2729:

ACCACCTTCC CCAATAAGCT GGCCTAAAGC CCCATAATGG GCCATGGTGC GGCC 54

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2730:

TGTTTGGGGA CCTTAAATGG TTCCAAATTC CAACCACCCA CCAAAAGAAT TCCAGTTTCC 60

AATTAAGCCA GCCA 74

(2) INFORMATION FOR SEQ ID NO: 2731:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2731:

AAGTTGGGGA TTAAGGCCAG TTATGGAAAG GATGGATGGT CCATTTGGGC TTATTAGAAG 60

AGCATT 66

(2) INFORMATION FOR SEQ ID NO: 2732:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2732:

TTTGnAAAAG CCnGTAAGAG TATTTGATTT TGTTGGAGGC CAAACCAGAA 50

(2) INFORMATION FOR SEQ ID NO: 2733:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2733:

AGTACCAGCG GACAATTCGG ACCCAACTTG GCAATTTGnG GTTTTGGACC AGGAAATAAA 60

(2) INFORMATION FOR SEQ ID NO: 2734:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2734:

CCAGGCTGGC AGTTTTTCTA AAATGGTGGT AGGAAAATTA nCCAAACCAT TTAGGATGGC 60

ATGGTCTTCC ACGGATGGCG GCCGTTAACC CCAAAAAAGG CCATTCCATT T 111

(2) INFORMATION FOR SEQ ID NO: 2735:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2735:

CGTATGGGAT GGCCATTCTG ATGACACACA ACGGTTAGGT TAGCAACGTT GTCAAA 56

(2) INFORMATION FOR SEQ ID NO: 2736:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2736:

CAATCCGGGT GTGCGGGCGT GTGTACAAGA CCCGGGACGA TTACCGACAT 50

(2) INFORMATION FOR SEQ ID NO: 2737:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2737:

TAACATTTAT TGTGGAGAAA GTnAGGTATC GTGGTAGTGA GGATTGTGTT 50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2738:

TAAATTTAAA CCCGTCCCGG TTTCCCAAAT TTGGAATTTT TTGGAACCCC TGT 53

(2) INFORMATION FOR SEQ ID NO: 2739:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2739:

ATACCCACCT TGGATTCTTA ATACCCCAAA AAGGCCGGGG CAACTTGGCT TAAAAAACTG 60

GCTTGTTTAA ATTGGATTTC CGGCT 85

(2) INFORMATION FOR SEQ ID NO: 2740:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2740:

GGAAAGTTTA GTAGTTTAGA GTCGAAAAAT TAGTTTTCTA GTGTAACGAA TCCGGACCCA 60

AATTTTTTTC 70

(2) INFORMATION FOR SEQ ID NO: 2741:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2741:

CGCGCCAATT TACCTGGCGC AGCAGACGCT CAACGAGGAG CACGGCAGCT GCG 53

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2742:

TGAAGAAATC GCACACACTA TCGAACGCAG ATCGCACATC GAATGCATCA GAATCAGCTC 60

(2) INFORMATION FOR SEQ ID NO: 2743:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2743:

TATCACCTCT TTTGCATATT ATTAGAATAT ATAATGATCT TTATAGAAAG GAAAGAAGAA 60

GAGTTATCAT nGCGATATCG CCCAGCGCGT CGTACACTAT GCCATGAATT ACACAATCAT 120

GCCTC 125

(2) INFORMATION FOR SEQ ID NO: 2744:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2744:

GAATTTCCCC CGAAACCGGG AAAAATTTTT CCCAACCGGT GGCCTTCCCC CGTTCCCGT 59

(2) INFORMATION FOR SEQ ID NO: 2745:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2745:

TTTTCCTTAA GTTAGTTTTT TTATTGGGCC AAAACCGGCC CCAGGAATTG A 51

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2746:

TAATTTGGTC ATAATGTTGT TTCAGATGAA ATGCTAACAA TACACTGATT ACAGT 55

(2) INFORMATION FOR SEQ ID NO: 2747:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2747:

ATGGTGGAAT GGGATTTAGG TGGATGGCCC CCCCAACCAG CCGGTCCTTT TTAAGGAACT 60

TTGT. 64

(2) INFORMATION FOR SEQ ID NO: 2748:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2748:

AACAAGAGTT ACATTGGTTG TGGAAATCAT CGGTTTTAAT TAGTCCAAAA GGATGGATTC 60

AATCGGTAGG GGGGTAAG 78

(2) INFORMATION FOR SEQ ID NO: 2749:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2749:

GCAAGTGGCG GAGTCACACT TATAGACAAG AAGTACGACA TCTTGTATGT GGTG 54

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2750:

TATTTAGATT CAAAGCATCA AATTGGTTTC GTACCCTTTT GCACATCGGT TGGGATAA 58

(2) INFORMATION FOR SEQ ID NO: 2751:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2751:

GGAAAACCCC CCAAATTTTC CCCCCCCGTT GGGAAAAGAG TTCCCAAAGT TGGAATTAGT 60

TCCCAAACCC GGGAGTTCC 79

(2) INFORMATION FOR SEQ ID NO: 2752:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2752:

AGAACCGAGA GATAGTGCCG AGAGAGCGAG AGGTTTTAAT AGAGATGTTT GGCCGTACTA 60

GTTAGCCG 68

(2) INFORMATION FOR SEQ ID NO: 2753:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2753:

ATAATCTATG GGGGGACCGT CTGGTAAGGA ACCTGGTTGC CCTGCCAATG AAGCCACCCT 60

(2) INFORMATION FOR SEQ ID NO: 2754:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2754:

ACAAAGGTTT TACGCCCAAA TTGTTCACTG GCTAACTGGG CGATGGTTAG TATTGGCAGC 60

GCAAAAGTGG CAGGGG 76

(2) INFORMATION FOR SEQ ID NO: 2755:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2755:

ACCTCAGGGA CAATTAAAAG TTTTTCTTCG GAATGAATGA CAACAACAAA T 51

(2) INFORMATION FOR SEQ ID NO: 2756:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2756:

ACGTATTCCC TCGTTCTTAG GTCTTCTAAA CATAGGTGAC TTTTTGGTCG 50

(2) INFORMATION FOR SEQ ID NO: 2757:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2757:

AAATGCTTCG TATTAACGCC TATTTTAGCT CCGTTATAGA CACAACTTAC ACA 53

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2758:

ACACGGCAGC GAATACTCGT TTGGTGAGCC TGTACACATC TAACACGAGA A 51

(2) INFORMATION FOR SEQ ID NO: 2759:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2759:

GGGAAAACCA ATTAAGGATT TAAAGGTTnA TTTAAAGGGG CCGCCACCGG GTTGGGGATG 60

CCCTTTGGGC ACCTTAAGAA AGCCCCGATG GAAAGGGACC GGTTACCTTA ACCGG 115

(2) INFORMATION FOR SEQ ID NO: 2760:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2760:

TTTGGCCAGG CCAATTAATT CCTGGTGGCC AATTAAATTT AAGGGGACCT TTGGGGGAAT 60

AAGGTTTAAA ATTGGAAAAT GGTCCAATTT GGACCTTTTG GCCAATTGGA TTCCCGGCTT 120

AAAAAGATTT GGACCGGTAA ATCCCTTTTT AAATTACCTC GGGCCAnGGC CCAACCAAGC 180

CAAACCAATT TAAATCCGCC TGGAAACCAA CCCATAnTTC CTTTACC 227

(2) INFORMATION FOR SEQ ID NO: 2761:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ACACTATTGT GCCAGCGCAC CTTCGAGGTA TCTTGCATCA CTCAGCTGTT TTTTACTGT 59

(2) INFORMATION FOR SEQ ID NO: 2762:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2762:

TTATCCTGTT CCTAAGCCCG ACGGCTCGGC CACACGATTA ACCTTTAACG CCATCTTGTC 60

CAACCTGT 68

(2) INFORMATION FOR SEQ ID NO: 2763:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2763:

TGGAAAGTAC CATATAAGTA ATGGTAGTCG TTTCAGAAAG ATATAAATCG TTGGGAAAAG 60

AAGAAATGAC AnATTAATGT AAATATTTGT TCATGTACAA ATAAATATAA TTTATA 116

(2) INFORMATION FOR SEQ ID NO: 2764:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2764:

TTGTTACAGT GGTGTAGCGG ATCGCACGGC CTTCAACTAA GTGGTTCAAT GCTTGATACC 60

AGTTATGAGT GTTGGTGC 78

(2) INFORMATION FOR SEQ ID NO: 2765:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2765:

ATATATTCGT ATGCACCTTT TGTAAGGCTT TGTAATACGA AAATTATCAC TACAATGATT 60

GCTGTAACGA GTAACGACAT ATATGGCACA CCGTTTTTAT TnGTTTTACC AA 112

(2) INFORMATION FOR SEQ ID NO: 2766:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2766:

TATTGAAGAT TTTTTCGAAG ATAAAGGTGA CACATATTCA TGTCATGTTT AATATCGTTA 60

CCTTACGTAA CCATATAAGA CTGTAACTTG TGTCATATCA TTCGTAGAAC nTTTGGAAAT 120

GAT 123

(2) INFORMATION FOR SEQ ID NO: 2767:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2767:

GTCCGCGCCA CGGAATGGCC CACGGGACGA TAAGTGAGGG CACCGACGGC CGAACCCAAG 60

(2) INFORMATION FOR SEQ ID NO: 2768:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2768:

GTACGCGGAG CACGAATTCC GCGGATCTGG GAGCATCTCT AGGTAAnTTT 50

(2) INFORMATION FOR SEQ ID NO: 2769:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2769:

CTTAGGTAGC TCAGTGTGTT ATTGAGAGGC CTGTTGGCAG GCCCCGGACG ATC 53

(2) INFORMATION FOR SEQ ID NO: 2770:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2770:

AAATTGATAG CGTGCACAAA CCAGGTCCAT CCACGAACAT GCCAATCCAG CCCAGGAAGT 60

AATTGCCCG 69

(2) INFORMATION FOR SEQ ID NO: 2771:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2771:

ACGATCATCT GGATGGATAT ACAGAACAGT GTGATTGTAC GTGGTGGGGA AA 52

(2) INFORMATION FOR SEQ ID NO: 2772:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2772:

TTAACAGTAT GATATTATCA CACGTGAATA GGATATGCCA ACACTGGCAT CGTTGGGGAT 60

AGCGTAATAC 70

(2) INFORMATION FOR SEQ ID NO: 2773:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2773:

AACATTGTAT TCGTGATTAA GACTTCGATC GGTTCAGTAT TCGGCAGATC CACATGTGAC 60

CATGCTT 67

(2) INFORMATION FOR SEQ ID NO: 2774:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2774:

CACCCTTGTG ATATCACATT TGTATGTGTT AAGAGGGAGC CCCTTTCCCG ATCAACTGGC 60

GATAAAAACA GTTGAnAAGT GGGCGGGGGT TATTATTTCT GATGACGGCG GGGTTTTTTC 120

(2) INFORMATION FOR SEQ ID NO: 2775:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2775:

AACCGTTGCA GGTnAAGCTG GGCnCACCAT TCTTCTCTAT TAATGGTTCA 50

(2) INFORMATION FOR SEQ ID NO: 2776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2776:

CATGTACGGT GTCCACACAA GAAGTATTTA GGTGGTTGTT CCCGGATTTA ACCTGGC 57

(2) INFORMATION FOR SEQ ID NO: 2777:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2777:

AACGACCCCG GGTTCCACCG GGGTCCATTA AGCCAAGGGC CAGGGGACCC C 51

(2) INFORMATION FOR SEQ ID NO: 2778:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2778:

TTGTTCCGGC CTAAAAAATT TAAATTGAAC CCAAGGGTTG CCTTGGGTTG GGTAATCCAT 60

TTTTTGAATA AACCTTTGnC CCTAATGAAT TTTTCCGCCA TTTAAAGGGT GTCCGCCAAT 120

CCGG 124

(2) INFORMATION FOR SEQ ID NO: 2779:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2779:

GTAAATTTGG GAATTACCGG AAAATTAAGG AAAGGCCAGT AAGGGGTTTC CAGGCCAA 58

(2) INFORMATION FOR SEQ ID NO: 2780:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2780:

GCACTCCAGC CTGAGCACCA GGGTGAGACC CTGTCTCAAG AACAAAAACA nCAACAnCAA 60

AAAACTTGTT CAAAACTCAC TTCCTGCAGT AATCTTTCCT TGAACAAACT CACCCTCTAA 120

TTCCCACCTG CAATTGTGTG TAGAAATCCA TTCTCGTGTG TAATTTTGGG CTTATATGCA 180

CACATTGAAA ATCCAAGAGC CAGAAAGAGC TCTAAGGAAT TATCCAGTCC AGCTCTGTGC 240

AGCCTGGGCT AGGACCCAGA TCTTTCCCAT TTCCCTGTTC CAAAAATTTT nGGCACAGGG 360

TGGCCACCCT G 371

(2) INFORMATION FOR SEQ ID NO: 2781:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2781:

GGGGTTGCCA AAGGGGTGTT AAATTTAAGT CCGATGAAAA TTAAGnAAAA AAATCCCATT 60

TTCCCTTCCG GGTCCGTTGT TGGGGCCTTA ATTTCCCGCC AATCCAAGTT TGGTGAATGA 120

AATTAATTAC CGT 133

(2) INFORMATION FOR SEQ ID NO: 2782:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2782:

GTTCAAGTTG ACGCTGGATC ATCTGGTACA CACGTATCCT GCATACTATA GATGTCAT 58

(2) INFORMATION FOR SEQ ID NO: 2783:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2783:

GCTAATTATA GGCCGTCAGG CATTACGnGA TCGAATCTGG CAACTCACAA 50

(2) INFORMATION FOR SEQ ID NO: 2784:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2784:

GCCnCnCTCT GTGACACTGT GTATATACAC CCGCGGGAAT ATCTCCAACG 50

(2) INFORMATION FOR SEQ ID NO: 2785:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2785:

CTTTGTCTGA CATATTGGGG CAGTGATTTT TGGGACGGTT CTACATGTCG AGTACTTTAG 60

TCAGAGTTGT GAGTAGCGGA CGGGTnTACT TGATATACCC TTAATGTGTA T 111

(2) INFORMATION FOR SEQ ID NO: 2786:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2786:

CATGATGATA CTTGCATGTA CGTTGTACGT GAACGTACAG TTACGTTGTC 50

(2) INFORMATION FOR SEQ ID NO: 2787:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2787:

TCAGCAAGTA GTAAGGATAT CAAACTATGA TCTATTTGAT GTTATGCCAT AA 52

(2) INFORMATION FOR SEQ ID NO: 2788:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GCATCATGGA ATATTAAAAC AGCTGATATG TTTGAGTAAT GATTGATTGA CGAGATATGC 60

GGCA 64

(2) INFORMATION FOR SEQ ID NO: 2789:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2789:

TGAGAGAAGT CACAGTCGCC AGCGGCAAAG AACCCGnnAA GATGTGnGCA 50

(2) INFORMATION FOR SEQ ID NO: 2790:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2790:

CAGTGTATGG AATCTTGTTT GAGTGTGAGA GTCAAAGACT TGGTGATTGA ATGGAAAAAT 60

TGAA 64

(2) INFORMATION FOR SEQ ID NO: 2791:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2791:

ACAAnGGGTG AAGTTCTCCC ACATGCTGTA TACCGTGGGA TTATTTTTAA 50

(2) INFORMATION FOR SEQ ID NO: 2792:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATTCCTATTC AACAACGGAT ACATAATCTT TTATATCTTC CTTCTAGTCA TATGATACTG 60

GAATAAGTGA TATTTCTTAT AAT 83

(2) INFORMATION FOR SEQ ID NO: 2793:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2793:

CATATGTCAT CGTACGTAAT CATCGATGAA ATATCAACAT CTCGACTTAA TAGGTCAACA 60

AGAT 64

(2) INFORMATION FOR SEQ ID NO: 2794:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2794:

CCCTACTCCG CGCAATAACC GCATTACCAG ATGCGCTTCC ACTGAGGAAC GACGGAT 57

(2) INFORMATION FOR SEQ ID NO: 2795:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2795:

AGATAAAGTG TCATCTATAT CCATCTATCA ATATAGATAT GTTTACGGCC GATTTCAATC 60

CGCAA 65

(2) INFORMATION FOR SEQ ID NO: 2796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2796:

TATACGCCTC ATTACACCCA ATTGGACCCT TTACGTATGG AGTACATTAT AGAATCGA 58

(2) INFORMATION FOR SEQ ID NO: 2797:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2797:

nGCTAAGAAT TTATAAGAGG TTTCGGCAGA TATATATACG CAAGTATCTG 50

(2) INFORMATION FOR SEQ ID NO: 2798:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2798:

AAGCAGTCTT TCACAAAAAG TGAATAATCA CTAGTTCATT AATTTGCATT TGAACCTTCA 60

TATAATGCAT ATTACTTAAT GTACAAGCAA AGATGTATTT ACCTATCAAA GAATTTnC 118

(2) INFORMATION FOR SEQ ID NO: 2799:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2799:

CCATAGAACC TGTGAATACC TATACATATC ATACTGTGGA ATTCGTTACG AGG 53

(2) INFORMATION FOR SEQ ID NO: 2800:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CCAATTCAGA CTGTTATTCT CTCTTCGTGA TAACCCGTGA TGTTTGTCTG C 51

(2) INFORMATION FOR SEQ ID NO: 2801:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2801:

GGGGGnGCAT ACCGCACCGA AGCATCAGAC GATGTGAGCG ACCTACCTCC 50

(2) INFORMATION FOR SEQ ID NO: 2802:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2802:

CCGTAGCGCA CATATGACGA GACCAAGGAT AACGTGCAAn GnCATATTGT 50

(2) INFORMATION FOR SEQ ID NO: 2803:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2803:

CACGTCATGA ACGTGCATTC AACACAATCA TTTACGAGAT GGACCAAGAC 50

(2) INFORMATION FOR SEQ ID NO: 2804:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2804:

TATGGTGTTT ATTTTAGCGC TnGTTGTGCT TTGTCTTCAG CATCTATAAC CTAGTGCGAT 60

CTATTG 126

(2) INFORMATION FOR SEQ ID NO: 2805:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2805:

AAAAGCGCAT ATGGTGTTTT TCTCATATCA CTCCAGGACT CAGCAGCTGG AAGGAGTTAA 60

GAAGTAATAA GGTGCCACCC TAAATCCA 88

(2) INFORMATION FOR SEQ ID NO: 2806:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2806:

TGGATCCGGT ACCAAATAGG GACTACCGGG AATGTCCCGG GGGGCCTAAT GCCGAATGGG 60

GCAACG 66

(2) INFORMATION FOR SEQ ID NO: 2807:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2807:

CCCGCTAACG TGGGGAAAGT TTTGAAGTTA AGAAGGAATG GATTCCTAAC GGGGCGGGGT 60

CCAAAC 66

(2) INFORMATION FOR SEQ ID NO: 2808:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2808:

ACAAAGCAGT ACTGAACTGG TTTCGTTGGA GCCCGTGTTG CTGTTTATTC ACGGCA 56

(2) INFORMATION FOR SEQ ID NO: 2809:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2809:

AGGGGGCGTA CAACATAGAT TTGCGAGATA CTCAGCATTA CACTTCCATT TAACTTATTA 60

TCC 63

(2) INFORMATION FOR SEQ ID NO: 2810:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2810:

TTAGGCGCCT GTTCCAACCG CACCCATATA AGGCGGTCGG CTGCACGCAC GACGTATG 58

(2) INFORMATION FOR SEQ ID NO: 2811:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2811:

AAACCCCCAA GGAATTAATT TTCCGGTTTT CCAACCCCTT AAAAAGGGAA AGGCCAAT 58

(2) INFORMATION FOR SEQ ID NO: 2812:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CATCATTAAG GCAAAAACTT TCACAAAGTC ATGAGGCGCA AAAGGTATTA TTATAACACA 60

TCCCGCGTTG GG 72

(2) INFORMATION FOR SEQ ID NO: 2813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2813:

CCATTTAAAG CGGTACGGGG CTTGGTTCAG GAACGTCGTT AGACAAATTC GGT 53

(2) INFORMATION FOR SEQ ID NO: 2814:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2814:

TAGTACCCAA TTTCCAGTCG AACCAGGATG GGACCAGAAG CCAAACCAAC GTT 53

(2) INFORMATION FOR SEQ ID NO: 2815:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2815:

GAAAAAAAGG CCTTGTTTAC CAAAGGGGCC AATTTTTTCG GTTCAAGGTC CAAACCTACC 60

TT 62

(2) INFORMATION FOR SEQ ID NO: 2816:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCTGAATGAC GCCGAAATCC CATCTGAATT CATGGGATTT TCCACTTTCA 50

(2) INFORMATION FOR SEQ ID NO: 2817:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2817:

CGTTACTAAA GCTACATAGT GCGTCATTTA AGATTATAGC AAGTAGCATA T 51

(2) INFORMATION FOR SEQ ID NO: 2818:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2818:

CATTCACCAT AATATTCATT GTTCCATTAG CATATCAGGC ATGTCACGTG CACA 54

(2) INFORMATION FOR SEQ ID NO: 2819:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2819:

GTGTATCAAA TGAGCATGTT nCAATGGTTC AnCATGGCGT TTATGGCACT 50

(2) INFORMATION FOR SEQ ID NO: 2820:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2820:

ACAATTGCGG CTGCTCATTG TGAGCACGAC TTTATCATGG TTGGGTTCAG 50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2821:

CAGTAGTACG TAAAAATGAA TCACTTGAAG ATGCGTACGT AGATTTTAAA CGTCAGTTCT 60

AAAAAGTGGA CAATCCAAGA GACGTAACGG AATTTnCGAA AA 102

(2) INFORMATION FOR SEQ ID NO: 2822:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2822:

GAGTACTTAA TCCGGCACCG TTTACTTCTG GGGGCATCGA CTAAGTGGGG CGGCC 55

(2) INFORMATION FOR SEQ ID NO: 2823:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2823:

ATTGGTTTCT CATAAACACT TTTCTATGAA TTTGTATGTA TTTGTTTATT AAAATCTCTA 60

ATTCTTATGG A 71

(2) INFORMATION FOR SEQ ID NO: 2824:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2824:

CCATTGAGTG TGAGTATATC ATCGATCAAT ATGCAACATT TATCAGGTGC ATGTTGCTTA 60

TGGATAATTG AACA 134

(2) INFORMATION FOR SEQ ID NO: 2825:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2825:

CCAGAATGAT GAGCTACAGG ATCAGCCCAG ATATGCAGGT AAACGGGCCA ACCATTG 57

(2) INFORMATION FOR SEQ ID NO: 2826:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2826:

CAATAATGCT GAACAGCAAC GCATCTCATT CTAAAATCGC TCAGAATCAC ATCCCATGCA 60

CACATAATAA GTGGCACTTA GCTTAAAAT 89

(2) INFORMATION FOR SEQ ID NO: 2827:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2827:

CGGATTAGTG GTGTAAACTG GGTGACCCAT ACCACACCTC GCGTGTTGTG AAAAAAGGAC 60

TTAA 64

(2) INFORMATION FOR SEQ ID NO: 2828:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TATACAGAAA ACAGCGTGCC GTTATCCATT ATCACATGAC ATATGTAGTC C 51

(2) INFORMATION FOR SEQ ID NO: 2829:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2829:

GAGATACGGT CTTCGTATAT GATATGTGCA TATTTAGATA GTCATTTATG AGAGAACGTG 60
GACGTGAG 68

(2) INFORMATION FOR SEQ ID NO: 2830:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2830:

TGATGATTGT TTATGATACG ATATGTAAAT GATAATCATC CAGGAGGTCT AGCATGGT 58

(2) INFORMATION FOR SEQ ID NO: 2831:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2831:

CCTAACAAAC ATAATTAAAC CCATAAATGC ATCCAATGCG GTTAAACCAT GAAA 54

(2) INFORMATION FOR SEQ ID NO: 2832:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2832:

(2) INFORMATION FOR SEQ ID NO: 2833:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2833:

GTCTGCTACC CTTTCAGAGC AACATGCTGA GTGTATAATG CCGTGTATAG GGGACAATGC 60

CATTCACTA 69

(2) INFORMATION FOR SEQ ID NO: 2834:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2834:

AACACCAGCT GGTAAGTATC ACGTTACATT TTGTGTCTTC ATGATTAATA AAAAC 55

(2) INFORMATION FOR SEQ ID NO: 2835:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2835:

AGAGCTTGGA TGTCGTTCGT AATTGATGCT CTAGCTCCAT GGGGCCCATG 50

(2) INFORMATION FOR SEQ ID NO: 2836:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2836:

TTTCGTCACT ATTGCTCATG CATAGACATT TGCAATACCG GCAAATGACG ATGGnATATG 60

TTAATGGTCA ATACAGGG 138

(2) INFORMATION FOR SEQ ID NO: 2837:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2837:

GTTGGCAACT TCAGTCGCTA CTTTAACGCA TCTCACAGTC CTCCTCCCAA AGAGAACGTA 60

T 61

(2) INFORMATION FOR SEQ ID NO: 2838:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2838:

ACGTGAATCC CGTGAGGCCA ACAGTGATTT GGATAATTAC ATGGATGTTT GACTAATGGT 60

CATTCACACC CAGATCAG 78

(2) INFORMATION FOR SEQ ID NO: 2839:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2839:

ACTTAAAATC TCCTCTTGCC TAACTTCCAC ATTCTTATCG ATATGAATAC ACCATACGTT 60

TTATAGATAA GTTGATGTTG ATGCATATGT 90

(2) INFORMATION FOR SEQ ID NO: 2840:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2840:

TATATTTAGT CTGTTATACA AGGTGTATCA CAGCGGTAAT ATGCCTCTAC ATGGCCATAT 60

G 61

(2) INFORMATION FOR SEQ ID NO: 2841:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2841:

GGGCCCCGGC GGCAGGGAGG AAGGGGGCAA GGGCGGCGCC AAGACCACGA CCGGCACC 58

(2) INFORMATION FOR SEQ ID NO: 2842:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2842:

TGTACAGGTG CAGTTAGACC GCCTGACGGA ACGAGACGTG CAATTGCCAG CAACGCACAA 60

(2) INFORMATION FOR SEQ ID NO: 2843:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2843:

AAACATGTGA AGTGATCGAG GTATGGACGG AGTAATGATC GCACAAGACA TAGCATCCCC 60

GT 62

(2) INFORMATION FOR SEQ ID NO: 2844:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2844:

ACGATTTAGT TTGAATTTCT ATTAGGGTTT GGTGATTCTA CTACTTCTGA TA 52

(2) INFORMATION FOR SEQ ID NO: 2845:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2845:

GATTATCACA ATTATGCAAA GTTGTCTAAT CGTTAGACCA ATTTCTGTTC AAACACCACA 60

ATC 63

(2) INFORMATION FOR SEQ ID NO: 2846:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2846:

CGTTATATAA GAnCGACATG GAAGCATGAT GAAATATTGA ATACATCATA 50

(2) INFORMATION FOR SEQ ID NO: 2847:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2847:

CCACAGGTGC ATCCGCCTGG TATGGAGCCG GCCAGTCTTC ACTGCTTTCA C 51

(2) INFORMATION FOR SEQ ID NO: 2848:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AAAACTGTCC CAAGCTGTTT TTATTTAGAG CAACCAATCC AATTTAAACC CCCCACCATT 60

ATTTTAAATA ATACCATTCC AGCGAAAGCC CTTTCCAnGG TTTTGGAATA TAA 113

(2) INFORMATION FOR SEQ ID NO: 2849:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2849:

CATCTGGAAC TTTTTAATTC CAGAAGGGTT CCAGAAGGTT TCGAAATCCC TCCTAATGGG 60

CTCCATTAAC GGATTTTAAA TTTTTTAATA ATTTTAGGCC AAAAAATTAA TTTCCAGGAA 120

AAGTAAGTTT CCAACCCGGG TAAGAAATTA CCnAA 155

(2) INFORMATION FOR SEQ ID NO: 2850:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2850:

CACAAACTAA CATAGAAGGG CCATCATCAG GTGCTATTAA ATATCTACGC TAGATTGTAA 60

ATCA 64

(2) INFORMATION FOR SEQ ID NO: 2851:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2851:

AATTATTCAT CAATAGCTCT TTACGATTCA CAAATCTAGG TACTTTTCAG ATCT 54

(2) INFORMATION FOR SEQ ID NO: 2852:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2852:

AAGCCCCTTT AAACTGGGCC TTTAAGGAAC GGTGGCGAAA ATCCCCAAAT TCCGGGCA 58

(2) INFORMATION FOR SEQ ID NO: 2853:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2853:

AAAGGTTTCC ATTCGGTCCC ATTAAGATTT TTTTGGAAAT TCCATGGAAG GATGGTTGGT 60

CCTTTAGGCC TGGTAGGTTA TCCTTTTTGn AGGTGGTATC CAG 103

(2) INFORMATION FOR SEQ ID NO: 2854:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2854:

GGCCACGGTC ATTCCTCCAA GCCAACCAGT GGACAAGATG GGTGGAAGGC GCAGG 55

(2) INFORMATION FOR SEQ ID NO: 2855:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2855:

TATTTGGCAT TCAAATAACG TAAACGGATT TTGAAGTAAT TTACATAAAG AGG 53

(2) INFORMATION FOR SEQ ID NO: 2856:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2856:

ACAATTTGAC AATGACTGGG ATGCTGACAC TTGATATGAA GACAATTGAA GAT 53

(2) INFORMATION FOR SEQ ID NO: 2857:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2857:

AACTGCGTTA CATGCTTTGC TTTTAACTGA ACCCAGAACA ACGGTTTCGG 50

(2) INFORMATION FOR SEQ ID NO: 2858:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2858:

CTTTnnTAnC TTCATCTCTA TTATTATTGT CCGAATTACT ACGTGGACAA 50

(2) INFORMATION FOR SEQ ID NO: 2859:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2859:

TCCAGGTCGA ATTTATTGCC AATTAGCCTC CCGGGTTAAA AGGGTGGGTG TCGGGTAAAA 60

TCGTAC 66

(2) INFORMATION FOR SEQ ID NO: 2860:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGTATCCAGT CCCCCGGAGG GGTGACAAAC TTCCACGCCC AGTGGGGGGA CTACCGTTTT 60

GGACCAAAGC CC 72

(2) INFORMATION FOR SEQ ID NO: 2861:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2861:

AGTGTCGAAC AATTAAAGAT ATTGAGTGAC AGGATTGCTT AAGGGCCGGT CGGAACAG 58

(2) INFORMATION FOR SEQ ID NO: 2862:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2862:

TTAGCGGTAA ATCCGAAGAA CTAAGAAGAC GTCAAGAAGG GGATATACGC 50

(2) INFORMATION FOR SEQ ID NO: 2863:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2863:

GCAAAAnTGA GAGCTCAAnC TGCAnnAAGC AAATCAACGA AAGATTAGGT 50

(2) INFORMATION FOR SEQ ID NO: 2864:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2864:

AACTATTCTG GATTTGTGCA GTGGCTATGG GGATGAGTGC GTTCCCCTCT TTCATGACGC 120

AGGCGAACGC CAGCAACGCA ACCACTGATC AATGCTGAGC CAGCTGTAGC CGCCCAGACG 180

GAACAAAATC CGCAGTGGGG GCAAGTGATG CCGGGCGTGC AnGGCGCTGA TGnCAGTTCG 240

TGGCAG 246

(2) INFORMATION FOR SEQ ID NO: 2865:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2865:

ACAGATGATA CCTCTTGATC ACTTGCCAGA GATCGTCTAA GTCGTCCTTG 50

(2) INFORMATION FOR SEQ ID NO: 2866:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2866:

AATACCACGC TGACCTTAAT AAGCCATCAT GGGGGAAATC ATGACCGCAA T 51

(2) INFORMATION FOR SEQ ID NO: 2867:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2867:

CAACTTGGTA AGTGGTCGTT TTGGGCCCCA CCCTACCCGT TTGGACCTGG 50

(2) INFORMATION FOR SEQ ID NO: 2868:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2868:

CCCAACCCGG TTCCGGGCCT TAATTTTTTn CCTTTTAAAG GAAAAAAAGG AAAAACCGGT 60

TAATTCCGGC CCAAAAAnCC CGGAAGTTGG AAACCTTTTT TTAATAAAAA TAATGGACCG 120

TCCCAACCTT TGTTGCCAAA AGGTGGCCTA AAGGTTTAAA AAAAACCGTT AAAATCCATG 180

GCCAGGATCC AGCCTAAAAT TGAAACCATT ATAATTGATA AAC 223

(2) INFORMATION FOR SEQ ID NO: 2869:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2869:

TGGACCTTTG GTAATATGAA TTGAATGGTG CTTTGTGGAA ATCGGGAATT CGCCTCGTGC 60

CTTGTA 66

(2) INFORMATION FOR SEQ ID NO: 2870:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2870:

AAnAGCCAnG ATCATGGTAT ATCCATTAAG AGACGAGAAG ATCGATGCCC 50

(2) INFORMATION FOR SEQ ID NO: 2871:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2871:

TTATTTGGAC TTACAAGGAG AATAGTCAnT TCTAGGAAAG TGGTGCGAAA GTCACTTACC 60

AATATACGGG GATTATTCAT CCATCGTCGG TCGGTCATAT GATACGGAAT TAACACGCCA 120

CTCCG 125

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2872:

CAACACCTGA CGTGTATAGA ACTCATCTCT TCAATAACGT CGCTGTCAGG TTACGAAGTC 60

GA 62

(2) INFORMATION FOR SEQ ID NO: 2873:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2873:

TATACATTCC ATTTAACACC TTAACACATG CAAGTTACTT CCTCCTCAAG CATC 54

(2) INFORMATION FOR SEQ ID NO: 2874:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2874:

GCTGAAAGGA GACTTCTGCA GGTGTGATCA CAAACTGCAC ATCTACACAA GCCATT 56

(2) INFORMATION FOR SEQ ID NO: 2875:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2875:

AGCGCGACCG CGAGAAGGGA GGGGGAGCCA GAGCAGCAGC AGGCCCCAGG GCGAAACCCC 60

CAAGAGGAGC GAGnAAGAAG GAGGGAAAGC CCAGCAGGGG CGCCCAGGCC AG 112

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2876:

GnGCGTTnnA nCGGTCGCGT AGAGATGTCG GGTCTGTAGT AGATCTGGGG 50

(2) INFORMATION FOR SEQ ID NO: 2877:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2877:

ACCTTGACTT TGCAGACGAT GATGCTTTTG GCTGGGATCT TCACCATCTG GCAACTGAAT 60
ATGGTTGG 68

(2) INFORMATION FOR SEQ ID NO: 2878:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2878:

CTCCACCTGA TGCATGCCCC CATATCAGGA AAATGATAAC CTCGGACACC TTC 53

(2) INFORMATION FOR SEQ ID NO: 2879:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2879:

GGGAACTTTG ATCTGCCCTT GAAATCCTGA AAAATGTTTG CAAACGGGAA TGATCTTGTG 60
CCTTGCTTTG AATGA 75

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2880:

AGAGAGGCCG AGATGGCAGA TGAGATTGCC AAGGCTCAGG TCGCTCGGCC TGGTGGCGAC 60

ACGATCTTCG GGAAGATCAT CCGCAAGAAA TACCAGCCAA AATCATTTTT GAGGATGACC 120

GGTGCCTTGC TTTCCATGAC ATTTCCCCTC AAGCACCAAC ACATTTTCTG GTGATACCCA 180

AGAAACATAT ATCCCAGATT TCTGTGGCAG AAGATGATGA TGAAAGTCTT CTTGGACACT 240

TAATGATTGT TGGCAAGAAA TGTGCTGCGG ATCTGGGCCT GAATAAGGTT ATCGAnGGTG 300

GTGAnTGAAG TTCAGnGGTG GACATCCGTC TATCACGTTC A 341

(2) INFORMATION FOR SEQ ID NO: 2881:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2881:

GCGGTTACTG TGTAATGGCA TTAAATATGA AACGAGCCGA TGGAGCGTTG 50

(2) INFORMATION FOR SEQ ID NO: 2882:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2882:

CTCATCATTT GTAGTTGGAA AGGTTTATGT ACATTTGGAA AACACCGACA CATGACGTAT 60

CTCCATTGCA ATTTACACAA G 81

(2) INFORMATION FOR SEQ ID NO: 2883:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2883:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 60

TTTTTTTTTT TTTTTTT 77

(2) INFORMATION FOR SEQ ID NO: 2884:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2884:

ACGGTGTGCT TGATGCACTT GGAACTGTGA GTTTGGGTGT GACTTTGCTT TGGCTTGCTT 60

GCTGAATGTT TTGACTATGC ATTGCGTATA TGACTTGnAG CGCG 104

(2) INFORMATION FOR SEQ ID NO: 2885:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2885:

AGCAACGTGT CTGTCAACGT GGTGTCATTG GAAAAGGCGT CATGTATTGn CCGGTGGGAT 60

TTACGTGTAG TCACACATGT GCCCAATTAT TGTTTTGAGG CCAACTTGAG TAGGTTGATG 120

GTTATGT 127

(2) INFORMATION FOR SEQ ID NO: 2886:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2886:

TGAGCGAGTG CTGTGTGAGC GCGAGGTTGT GAGAGTTAGA ACCTTGTGAG C 51

(2) INFORMATION FOR SEQ ID NO: 2887:

(A) LENGTH: 63 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2887:

TTGAAACCGC GAACCTGAGT TCTGGTTAAC TACAGTCTGG TATACACATT GAGGGAAACT 60

TCG 63

(2) INFORMATION FOR SEQ ID NO: 2888:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2888:

AGTAnCATAC nCAACTATCT CAGCATACAA TATTGGnCAC CTCGCAGCTT 50

(2) INFORMATION FOR SEQ ID NO: 2889:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2889:

AAAnATAATC CCGGTTTTAT CCCCCTACCT AATTAGTGGG AAAAGTACCA ATTGCCAATT 60

GGTAAAATAG GTTGCCATAA CGGCCTCCCA AAAGTAAATT CCCTTTTTTG GTTTA 115

(2) INFORMATION FOR SEQ ID NO: 2890:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2890:

AATCGGTCCG TTATACTCTT CATAATATTG TGGCGCAACC ATTTCAACTT TATCTTTTCT 60

TATAAATAGC ATCATCGCAA TAnTAAAGAA TAATATCGGA ATGATTAAAG TAACGATAAG 120

(2) INFORMATION FOR SEQ ID NO: 2891:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2891:

AACACAACAA GTTGTTAAAG ATGCATTTTT ATCACAACAT AAATCTATTG GACGTAAAGC 60

TCAAGAAGCA TACTTATCAT ATCGTTTAGA ACAAGAGTAT AGTAAAGATG ATATCTTCCA 120

AGTATATCTA AACAAAATTT ACTATTCTGA TGGCGTAACA GGTATTAAAG CTGCTGCTAA 180

GTATTACTTT AATAAAGATT TAAAAGATTT AAACTTAGCG GAAGAAGCTT ATTTAGCCGG 240

TTTACCTCAG GTTCCAAACA ACTATAATAT TTATGATCAT CCAAAAGCTG CTGAAGATCG 300

TAAAAnCACT GTTTTATACT TAATGCATTA TCATAAACGC ATTACAGATA AACAGTGGGA 360

AGATGCTAAG AAAATCGATT TAAAAGCGAA CTTAGTAAAT 400

(2) INFORMATION FOR SEQ ID NO: 2892:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2892:

CCTAATTAAA CCTCCATCCA TCCTTTTGAA GGGGGATCTT TAATAAAnCC GGAAAGTTTG 60

GGGGAAAAAT CCTCCATCCT TTGAAGGGGG GGGCTTTCCA ATGGCCTTTA AGAATGGCCT 120

TTTCCAAGCC AACTTTTAAT TCCCCCGGT 149

(2) INFORMATION FOR SEQ ID NO: 2893:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2893:

GCCCGAAGTA TTCTTGTAAG TATTATGATA CTCGGTnCTT TTTATGATTT ATGTTAATTT 60

TTATGTTAGT 130

(2) INFORMATION FOR SEQ ID NO: 2894:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2894:

GATGAGACCT GAATTGATTG CAACCCAAAT CGGCATATGC AAATTGCATT AAAGTTGGTT 60

CAACG 65

(2) INFORMATION FOR SEQ ID NO: 2895:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2895:

CGCACAACAC ATTTAGCGAC TCAGATGTCG CGCGAATGGA CCGATATGGC GTGTCTACAC 60

ATTGTCATAT TGTACGAATA GATGAGAAAT TnCAAAGACC GA 102

(2) INFORMATION FOR SEQ ID NO: 2896:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2896:

ATTAAGTGAT GGGCTAATGT TTACGCCCCA ACCAAAGGTT TCCAAAGAGC CCTTGTTGGG 60

CCTGTGTTG 69

(2) INFORMATION FOR SEQ ID NO: 2897:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2897:

ATTGAATTAA TGTCCCAACC AAACGAATGG TTGCCCTTTT TCCATCCAAA GGGGGCTAAT 60

TGGGAAGGGT ATTGGTTCCC 80

(2) INFORMATION FOR SEQ ID NO: 2898:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2898:

CAAATCCTGG AGATGAGCGT AACCAAAAAT AACGTTGAGA AAATGACCAC ACA 53

(2) INFORMATION FOR SEQ ID NO: 2899:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2899:

ATCGTGAACC TCTCATCCAA TCACTCATGT GAGTGAATTG GATGACCTGA A 51

(2) INFORMATION FOR SEQ ID NO: 2900:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2900:

AGCTTTCAGG GCTATATCAG ACCCACGCAT TCATCCACGT GAATGAAACA CG 52

(2) INFORMATION FOR SEQ ID NO: 2901:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGTACTGACA GAGGGACAAG GTGGAAAGGn TGCCAATGTA AGAATACGGT 50

(2) INFORMATION FOR SEQ ID NO: 2902:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2902:

TGTCTGGAAT TCAGGTGAAT TGATGCGGAG ATTTAGGTGA TTAAGGAGTG TTGATTATGA 60

AGATGACCAC TT 72

(2) INFORMATION FOR SEQ ID NO: 2903:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2903:

CATGCCAAAG CAGTAGGCAA GCCGCTTAGC AAGCCAAAAA CGTCAGCCCA 50

(2) INFORMATION FOR SEQ ID NO: 2904:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2904:

TTGATGTTAC CTGATCGCAA TCTTGACCAC CTGGCAGGGT CTCATTGTTG GGTATCGA 58

(2) INFORMATION FOR SEQ ID NO: 2905:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2905:

GCGGTCTAT 69

(2) INFORMATION FOR SEQ ID NO: 2906:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2906:

ATTCCATTAG GTTCAATTAA AAATTAACGG GGTTATGGTT CCGGTAATTC GGG 53

(2) INFORMATION FOR SEQ ID NO: 2907:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2907:

AAAGCTAAGA AAGGAGGATT AGCTGGTAGT GGAGGAATGT TAAGTGAGGC TGGTGAT 57

(2) INFORMATION FOR SEQ ID NO: 2908:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2908:

GGGAATGGCG CATGAACGTG CACATCAAAT GACACTGCAG GAAATCAATT AGCACGGATA 60

TGGCATAAAG ACAATGGTAA AAGTGG 86

(2) INFORMATION FOR SEQ ID NO: 2909:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2909:

(2) INFORMATION FOR SEQ ID NO: 2910:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2910:

GAATTTGTTC CGAGGTATCG AGGACTACGC TTATAAGGTG CTTACAGATA CATTTAnCAT 60

TAATGGCGTG TGCTGCTGTA TGGGTTATAC TGTTCACAGG TTTAAGAGA 109

(2) INFORMATION FOR SEQ ID NO: 2911:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2911:

TTGTCCCCAT AGGGAGAAAT AATTCCGCCT GGGCAAAACC AAATCCACGA GCTTCTAAGG 60

(2) INFORMATION FOR SEQ ID NO: 2912:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2912:

TAGATGTATC CAGCTGACAT TAGCTATTGG TAAGGTAACG GCTTACCAGG CAACG 55

(2) INFORMATION FOR SEQ ID NO: 2913:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2913:

GCCATGAGGC CCACCCATCC ATGTTTATGG ATGGTGGATT GGGGAATTAC TTGTTTCAAA 60

TCA 123

(2) INFORMATION FOR SEQ ID NO: 2914:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2914:

ATCCGTAATT CTGGCCTACC AAGGGTTTAG GCCAATGGGC CATTCTTTTA TTTAACCC 58

(2) INFORMATION FOR SEQ ID NO: 2915:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2915:

TGGTGCGACA GTGGTAGGCT TTTTACGGTn TGCnGGCGAG AGTTCTGTAG 50

(2) INFORMATION FOR SEQ ID NO: 2916:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2916:

CTGTTACGCT ATGCCCCCCA GTTGTATGTT GAGTGGAATC GTGTTTTTCG ACCTGCCTTT 60

GCTTTTTT 68

(2) INFORMATION FOR SEQ ID NO: 2917:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2917:

GGAAA 65

(2) INFORMATION FOR SEQ ID NO: 2918:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2918:

AAATTCCAAT CCTGGGAATG GGATTCCATG GTnTTCGGAA AAATCCGCCA CCCCAAAAAA 60

ATAAATGGGT CCCTTCCCTT GGAAATATTA CCTTTACCAG G 101

(2) INFORMATION FOR SEQ ID NO: 2919:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2919:

TAATAAATCC ATGACCACCG TCACGACGAT CTGACTGATA AACTAATGAC ATATGACTGG 60

TGTACACACC GTATG 75

(2) INFORMATION FOR SEQ ID NO: 2920:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2920:

CTTGGATTGA CCATCATTAG TTTTGGTCAC TCTAAGTTGT ACTGTCCGTT GTACAA 56

(2) INFORMATION FOR SEQ ID NO: 2921:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GCTCATTGCT TGTATATTAA TCCCTGAAAT TGACCGTGTA TATCCCGTCG ATCTATCTTG 60

TCCTG 65

(2) INFORMATION FOR SEQ ID NO: 2922:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2922:

GCAATATTCT AATCTGTATG TTACAGCACA TGGATATAGC ACATCCGGGC 50

(2) INFORMATION FOR SEQ ID NO: 2923:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2923:

TGTGATTTAA CAGGATTACA CAGGTGTACC AGCCGATAGT TGATTAAGCT TCTT 54

(2) INFORMATION FOR SEQ ID NO: 2924:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2924:

ATCCTGGGAA GTGCTGAAAA ACCACTnCAC TAAAGGCATA GGAnCCACAC 50

(2) INFORMATION FOR SEQ ID NO: 2925:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2925:

(2) INFORMATION FOR SEQ ID NO: 2926:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucl ic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2926:

TTGGTCACAT TTATTCTCGT GTTGTGCCGT TCTTCTTCAG TACTAAAGAC AAGGTGATTC 60

GG 62

(2) INFORMATION FOR SEQ ID NO: 2927:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2927:

CAAAAGGCTA TCCCACCTGA TTTGCAAAAG GAACTGGACT GCAAGGGAAG TCTCAG 56

(2) INFORMATION FOR SEQ ID NO: 2928:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2928:

TGATCTTGCT ATTTAGTTGC GGCTTGGATT CATTTGGCAT GGTTAAGATT AAATTAGATG 60

CTTCATTCAT TCAAGATTTC TTCATGTTAG CATTCTTTAC GACAATCGGT CTTGGTGCAT 120

CATTGAAATT ATTTAAATTA GGTGGCAAAG TCTTGCTATT ATACTTTATG TTTTGTGCTA 180

TCATTTCAGT CATTCAAAAC ATAGTTGGTG TATCACTAGC AAAAGTATTA AATATTAAAC 240

CTTTGTTAGG ATTAACAGCA GGTTCCATGT CTATGGAAGG CGGTCATGGT AATGCTGCTG 300

CTTATGGTAA GACAATTCAA GATTTAGGTA TTGATTCGGC ACTGACAGCG GCTCTTGCAG 360

CTGCAACTTT AGGTCTTGTA TTTGGAGGGC TATCGGTGGT 400

(2) INFORMATION FOR SEQ ID NO: 2929:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2929:

CTGAACCGAT GGCGCACTTT GCTACGCCAC CTACAGCAGA TCCCAnGGGG GGnGAAGCTT 60

ATACTGAAGC TCTACGTTCA ACATTTTTCC ATTGGGGATT CCATGCTTGG GCTGTTTATG 120

GTGTTGTTGC GTTACGTTTG GCATATTCGC AATTCCGTAA AGGTGAACCA GGTTTATTAT 180

CTAGAACTTT ACGTCCTCTT TTAGGTGATA AAGTAGAAGG TCCTATTGGG ATTTTTATTG 240

ACGTTTTATC TGTATTTGCG ACAATCGTTG GGGTAGCCGT TTCGTTAGGT ATGGGTGCTC 300

TACAAATTAA TGGTGGTTTA CATTACTTGT TCAATGTTCC AAACAATACG TTTGTACAAG 360

CGATTATCAT CATTGTTGTT ACTATCTTAT TTATAGCAAG 400

(2) INFORMATION FOR SEQ ID NO: 2930:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2930:

ATGTAGATCT ATATGATGAC TTTTTACAAG ATCCATCATC TGTACCAGAA GATTTAAAGT 60

CTTATTCAGC ACAATTAAGA ATGATGACTC AATTGTACCA GCTTTAAAAA GTACAAGTAG 120

TCAnAATAGC GACGGCACAA TTAAGCGTGT CATGCGTTTA ATTGATAATA TTCGCCAATA 180

CGGGCATCTT AAAGCCGATA TTTATCCTGT AAATCCTCCA AAAAGGAAAC ATGTACCTAA 240

ATTAGAGATT GAAGACTTTG ATTTAGATCA ACAGACTTTG GAAGGTATAT CAGCAGGAAT 300

TGTTTCAGAT CACTTTGCCG ACATTTATGA TAATGCCTAT GAnGCAATTT TAAGAATGGA 360

AAAACGTTAC AAAGGnCCAT TGCATTTGAG TATACCnTAT 400

(2) INFORMATION FOR SEQ ID NO: 2931:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGTTATACAA TCTAGAATCG CATGATAATT TAATGCTACA AATCGATAGT ACAATATATC 60

TACCGTGAAT AACTGTGCAA ATAGTGACGT TGTAGCCGCC ATACGCATTT CATTTTCATC 120

AGTTCTGCCA TAAATCAATG CATAGTCTGC AATTTGAGCC ACTGGATTAT TAGCTGTACT 180

AGATATAGTT ATGATGGGAA TACTGTAATG TGTGGCCACC TGTGCAATTG ACTGCAATTC 240

ACTATGGACT ACCTTGGATT CGTCACAAAA ATCATGCAAT CTCTATCATC ATGCGTCGCA 300

AATGTTGACA CAAGTGAAAT GCGTTTCCAT GTAATAACCT GACATTTGAA GCCATACGAG 360

ATAACTTTGG AAAAAGATCA CCAATAGnCC AACTCGATGG 400

(2) INFORMATION FOR SEQ ID NO: 2932:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2932:

CTTTCAGTAG CAGCTACAAT TGTCTTTAAC ATTTAAGTTT AAAGCTGTAT GTGTCAACCG 60

CAAATACCGA TAGCCATTCA CTAATGAAGT TTCAACTAAT TTAGTACGAT CTGACAATAA 120

CTTTTTGTAA TCTTGGGCTG CTTCAGCTGA TACAGCAATA TTTCTCATTG TTTTAACAGC 180

TTCTTCAGGA TATAAACCAG CAGCAGTTTC ACCAGATAAC ATTACTGCAT CTGTACCATC 240

ATAGATTGCG TTGGCAACGT CACTAGCTTC TGCACGTGTA GCACGTGGGT TACGTTGCAT 300

AGAATCTAAC ATTTGTGTAG CTGTAATAAC TGGTTTACCT AATTTGTnAC ATTGTCTGAT 360

TAAATCTTTT TGAACCATTG GGACTTTnTC AG 392

(2) INFORMATION FOR SEQ ID NO: 2933:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2933:

TGACTATGGT ATCGCATGTT GTGTATCAGC GATGACAATT GGTAAACAAA TGCAATTCTT 60

CGGTGCACGT GCGAACTTAG CTAAAACATT ACTTTACGCT ATCAATGGTG GTAAAGATGA 120

AAAATCTGGT GCACAAGTTG GTCCAAACTT CGAAGTATTA ACAGCGAGTA TTAGAATATG 180

ATTAAATGTT ATTCACTACA TGCACGATAA ATACAGCTAT GAACGTAATT GAAATGGCAT 300

TACATGATAC AnAAATTGTA CGTACAATGG CAACAGGTAT CGCTGGTTTA TCAGTAGCAG 360

CGGACTCATT ATCTGCATTn AATATGCACA AGTTnAAACC 400

(2) INFORMATION FOR SEQ ID NO: 2934:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2934:

AAAATATGCC ATGACTGGCA TGACAAGAAT TGGACGTTAG AAGCATCTCA AACTGGTACG 60

TTCAGAGGTC GTAACTnTAA CTTCAATGGT GAAGGATTCT CACGTCAAAC ATTTAAAGTA 120

AATGCCGTTA GTCAAAAAGA CTACGACAAA TGGGTGAAAG AAGTTAAAGG TAAGAnAACG 180

TTAGATCAAG ATACATTTGA TAAACAATTA TTACCAAGCA CACCTAATAA AGCTTTAGAA 240

TTTAATGGTA CACATATGGC GTTTGTTGAT CCAGCAGCCG ATCCAGAATA CATCTTCTAT 300

GCATATAAAC GTTTCAATTT CGGATTGAAG GTCCCAAACT TCACTAGTGA GGAAAATATG 360

TTTAAGGTGT ATCAGACAAA CCCTTAATAC CTGCTCGTGA 400

(2) INFORMATION FOR SEQ ID NO: 2935:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2935:

ATGGAGTATA CAACTACTTC GGCATTGGCG CTTACGACAA CAATCCTAAC TACGCAATGA 60

CGTTTGCAAG GAATAAAGGT TrGACATCTC CAGCAAAAGC AATCATGGGC GGTGCTAGCT 120

TCGTAAGAAA GGATTACATC AATAAAGGTC AAAACACATT GTACCGAATT AGATGGAATC 180

CTAAGAATCC AGCTACCCAC CAATACGCTA CTGCTATAGA GGGTGCCAAC ATCAAGCAAG 240

TACAATCGCT AAGTTATATA AACAAATCGG CTTAAAAGGT ATCTACTTCA CAAGGGGTAA 300

ATATAAATAA AGAGGTGTGT AAATGTACCA AATAAAAGAT GTGAAACGAG AATTAAAAAT 360

GATGGTGTTG ACTTAGGTGA CATTTGGCTG TCGTTTTACA 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2936:

AAACAATACA AACAAAAGAA AGTCAACCAA GGATGGATTC CTATTTTAAT CCTTGGTTGA 60

CTCTTATTTT ATTTAAATTG TAGAACCTAG AAAATAAAGT TTAATTAAAA GCACCAATCA 120

TTTCTACTTT GAAATCTAAG GTTTCTAAAA TAGCAATGAC TTTCTTTATA TCGGTTGTAA 180

TTGCAGAATC AGCCTGAACG AAAAATCGAT ACATACCTAA TTGTGTTTTT AAAGGACGAG 240

ACTCAATCCA GGGTAAATTA ATATTAAACA AAGCAAATGT ATTAAGCACA CTTGCTAACA 300

ACCCGGGTTA TCATGCATTG GTGTAATTAA AAACATCAAT GGTGTCGCAT TTTGATCAAA 360

TGCTGCTGAT TTTTTATAAC TAAAAACGTG TCAGGTATGT 400

(2) INFORMATION FOR SEQ ID NO: 2937:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2937:

TTATTATCTT GATACATTGA GTGTATATTC CATTTTCCAT GAGGCGTTAA ATAACGCATA 60

CCAAAGCATC TGTACCACCT TTAATTTTCT TATCTCTATT CCCAAATACC ATTGGCGGCA 120

ATGTCGGTTT ATATACTGGT AAGCTCTCCC CAAATTGTTG GAAAACTTCG TGATCCACAT 180

AATAACTTTG GACGTCCTGT TAATGTTCTA AAAGGTACTA GACGTTCTAT ATTCGTTGTA 240

AATGGTGGAA TATCGTCGAC CTTGTTTATT TGAACCGGGG AATACTGCTG TCGGTATTAC 300

TTCTCGTGGT TGTGGAAGTT ATATTTAAAA ACGGAAATTT TCTCAGCAGC GnTTTCGTTA 360

GGAAATATCT TTTAACGGGC ATTCCAGTTT GTTCnTCGGG 400

(2) INFORMATION FOR SEQ ID NO: 2938:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2938:

TATCTCTTAA AGCCGGTGAT GGTGGTAATG GTATTACCGC ATACAGAAGA GAAAAATATG 60

TACCATTTGG TGGACCAGCT GGCGGTGACG GTGGTAAAGG TGCTTCAGTC GTATTTGAAG 120

TGGATGAAGG TTTAAGAACG TTATTAGATT TTAGATATCA ACGTCATTTT AAAGCAAGCA 180

AAGGTGAAAA TGGCCAAAGT AGTAATATGC ATGGTAAAAA TGCGGAAGAT TTAGTATTAA 240

AAGTTCCACC TGGTACAATT ATTAAAAATG TTGAAACAGA CGAGGTTTAG CAGATCTTGT 300

TGAAGATGGT CAAAGAGCTG TAGTAGCGAG GGCGGTCGAG GTGGCCnAGG TAATTCACGT 360

TTTGCAACAC CTAGGAAACC CTGGCACCTG GACTTCATGG 400

(2) INFORMATION FOR SEQ ID NO: 2939:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2939:

CTAACCTCGA GTTCGTATTA TGCCCACCAC ATGTCTGCTG GCTTGTCGTA AATATTAACA 60

GATTTCAAAG TTTGACAAGC TTTTTGGAAA CCTTCTTCTA CTGACATAAT AGGATCTTCA 120

TGTTCAATAC TTAATACATA ATCATATCCA TTAATAATAA GTTGACTTAT GATATCTGCC 180

CATACATATG GACTATGTCC TAAGCCAACT GTACGGAATG TCATGCTCTT GTCGCAACGT 240

TACCATATGG TTGCATATCA GTTAGACCAT ACATATTTAC ATTTTCTTGG ATTAATATAC 300

GTATCTTTAG CATGGAAGTG ATGAATTGCA TTTGCTTGGn CTAATATGCG AATCGCAGCC 360

AATTGGGTCA ATAnCnTGGC CACC 384

(2) INFORMATION FOR SEQ ID NO: 2940:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2940:

TTTCATATTT TTCTATTAAT GATTCATATT GTAGGGTGAT TGCAATGTCA TCTAAGCCAT 60

TTACAAGTTT ATTCTTCCAA GTTTCATCAA TTTCAAAATG GAAACGCTTG TCTGGTGATG 120

CACTTTTTTC TAAAACGATA GGCAACATCG CATTTTTAGT GCAATTCATA TAAAATATGT 240

CACTGAAACT TCCTGCAATA ATAATATGAA AACCATAGTC CTTAAGAGCC CAAGCAGCAT 300

GTTCACGACT TGAACCACAT CCAAAATTAT CTCCAGTnAT TAAATnGGAG GCCCCTTTAT 360

ATTGTGGTTT GTTAGGGTTG AATCAGGGTT TnTnGGAACC 400

(2) INFORMATION FOR SEQ ID NO: 2941:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 409 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2941:

ATCATAATCC ATCGTGCGTC CAAGAAGTAC TTGATTATTT AAAGTTTGTA TTGTGAATCC 60

TGTGCACATT GTTCTCACTC CTCTGTACCT TCATTTACTT TAATCACTTT CAAATAAAGC 120

TGTTTCACTT AAACATACTA TAAAAAATCA ATTATACAAG CAATTAATTG ATATTCATTC 180

TCAATAACTG TGGTATGATA TGTAAGGAAA TCATGACTTA TGTGTGAGTG AACGATCATC 240

TATACATCCG TTCACTTCAT CTCATGACTT TCTATATTTA ATTTTTACAA GGgAGTGACA 300

TCTGTGAATa ACACACAATC TTCACCACGC gTAaTaTtAT TaTTGCGATT ATGTTGTCTG 360

CATAACATAT GGTTGTTGCA CAATCATTAT TAnTATAGGA CCTCCGTTG 409

(2) INFORMATION FOR SEQ ID NO: 2942:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2942:

ATGAAGTGTC AAAAGGTTTA AAAACATCTG AAAGGGGTTC GCACATGTTT TAAACTTTAA 60

AAATAAAGGT GGATGTCCAA AATGTCGACC AGCAATCAAC TATTATTTAA ACATGGTTTA 120

TCCACATGAT CATGAAGATG AAAGAGAATC AAGATTTGCT AACGAACGTT ACCATGCGAA 180

TATTCAAAAT GATGGTACAT TTTCTGTTAT ACCTCAAATG CGTGGGGGTG TTACAGATGC 240

AGACCAACTG ATTCGTCTAG GAGAAGTGGC TAAGAAATAT CATGTGCCAC TAGTTAAAGT 300

GACAGGTTCA CAACGTGTTG GTTTGTATGG AGTTAAAAAA GAAGATTACC AAATATATGG 360

(2) INFORMATION FOR SEQ ID NO: 2943:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2943:

ACCTGGAAAT GTATGTGCCA TCTCTTTAAG CCAATCAGTA TCTTGAATAC CTTTCGTTCC 60

AACTATGCAA TAATTAATCC CTGCGGCAAA GTAGTCCATG ATTGTGACTT CGTACGAATG 120

CCACCACCTA CTTCAATATC TTTGGTTGTT AATCTCCTCA ATGACTTAAT ATAATCAAAC 180

TCTCGGGCAT GCTGTGCCTT AGCACTCATC AAGTCGACGA TATGAATACG ATTCACACAT 240

TCAAATTGAC TATAGTAAGC AATACTTTCT TCAGCCGAGC GTGGACATTT TTTCTTCACT 300

ATCATATTTA CCCTCTGTTA ACCTCACACT TGTTGACCCA ATCAAATCAA TCGCTGGGCC 360

ATAATTCAAT CATTTnATAA ATCCCCCTTG TATTGGCCTG 400

(2) INFORMATION FOR SEQ ID NO: 2944:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2944:

AACAAAAGGG GTCTATCGTC AATCGTTTCT TGAATAGTGT TGAAAAAATC GGAAATAAAT 60

TGCCAGATCC TAGCGTCTTA TTCTTTTTAA TGTGTGTGGG CTTAGCCATT ATGACATGGG 120

TTATCTCATT ATTTAATGTA TCTGTTAAGC ATCCAGGTAC GCATCAAACC ATTTATATTA 180

AAAATATAAT TAGCCATGAT GGATTTACGA TGATAATGAA TGATACGATT AAAAATTTCT 240

CAGAGTTCCC AGCATTAGGC TTAGTACTAG CAGTGATGAT TGGTATTGGT GTTGCAGAGA 300

AAACAGGATA CTTCGATAAG TTAATGATTT CTGTTGTGAA TCGCGCACCA CGTTTCTAAA 360

TTTACCGCTA TAATATTAAT GGGnATTTTA GGGAGTCAGA 400

(2) INFORMATION FOR SEQ ID NO: 2945:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2945:

ATTTTACAAG TAACGGTGCA TCACCAGATT CTAATTTAAT GTCATGCTCA GCAGCATTTT 60

GATAACCCAA CTTTTCAAAG TAGTCAAAAC AATGGTCTAC AACAACCGTA CTATACTCTT 120

GTGCTTTGGC CGCTCTTCTA CTGCTTGAAC CAAGCCACGA CCTAATTTTT GTCCACGTAA 180

TTCAGGATGA ACTGATAAAG AGGCAATCGC CAAACCATAA TACGTCTTAT CATCACTATT 240

AATTTCTACT TCAATTAATA AAACGTGTCC AACGACATCG TTATTTTCAT TTTTCGCTAT 300

TACTTCTAAT TCAAAATTAT AGCAAGGAGA TTTTCTTAAA TGGTTTACTT TCGGCACGTG 360

CCTGGCCAAC TCGTTTTCAG GATTATCATC CAAACTTTCC 400

(2) INFORMATION FOR SEQ ID NO: 2946:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2946:

GGAAATAATT ACTTGAGCTA GATAAGTTGA CAGCTGTGCA ATTATTTTCA GCAGCTAATT 60

GTAAAATTCG CTCTAATCTT GCTGATGAAT GTTCAGGCCC TTGACCCTCA TATGCATGAG 120

GTAAGAATAA TGTTAATCCT GAACGTTCTC CCCATTTTGA GCGAGAACTG AATAAGAAGT 180

TGTCAAAAAT CATTTGTGAC ATATTTGGCA AAATCACCAT ATTGTGCTTC CCAAATATTG 240

AAGCTTTTTT TGTTTTCCAC ATTATAGCCG TATTCAAAAC CAACTACTGC TGCTTCTGAA 300

GCGGAGAATT GTGTATATCA AATGTCGCTT TTTGAnCAGG AGCATGATGT AAAGGTGTAT 360

ATGTTnCACC nGTTTGCTCA TCATGTnACA CGGCAGCCGT 400

(2) INFORMATION FOR SEQ ID NO: 2947:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2947:

AAGTGGCATA AAAAAATCAC ATGACGATAC ATTGTCGTCA TATGACTTTA AATATTATTC 60

TTCAATTGTG TCACCGATTT TTAATACATC TTCCACTTTT TCAATTCTAT TTTTTGAAAT 180

TTGTGAAATG TGAAGCAACG CATCTTTACC TGGGAATAGG CCTACAAACG CACCGTATTT 240

TTCAATACGT TTAACAGTGG CTTGGATAAG TTTGACCTAC TTCCGCTTCA CGTGTAATTT 300

CCTCAATGAT TTCACGAGCA CGATTTATCA TAGCTTGATC AACAGCACCC ATAAAGATAG 360

TACCATCCTG GnCCATATCn AATTTAACAC CnGGnTCCTC 400

(2) INFORMATION FOR SEQ ID NO: 2948:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2948:

TTTTTCAAGT TTTGCTGAAG GCTTTACACA AGGCTATTTA ACAATGGATG CCATTGCAGC 60

AATTGCTTTT TCAATGATTG TTGTTAATGC AGTAAAACTA ACAGGCATTA CTAAAACAAA 120

TCAAATATTC AAACAAACTT TGACTGCTGG TTTAATTGCA GCCGTAGCTT TAATTTTCAT 180

ATATATTTCA TTAGGTTATA TTGGTAATCA TATGCCAGTA AGTGACATGA CGTTAGATCA 240

ATTGAAATCC AAAGATCGAA ACATTGGGAC ATATTTATTA ACGACAATGG CTTCAACAGG 300

ATTTGGTCAT CCGGAAAATA TTATTGGGCA TCATTGTGGC GCTGGCATGC TAACTACAGC 360

ATGCGGGCTA TGGTGCAGTT CCTGAATATT CCATAGATCG 400

(2) INFORMATION FOR SEQ ID NO: 2949:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2949:

CATGGCTTCA GATTGTTTGA ATTGAATGGA CAATTTTGGn TTCTGTCCAA AATTCTTACA 60

AAATCTTCTA CCGATAAACT ATCAAGTTCA ACTCTAATCG GAAAAACGAC CTTGCAATTC 120

TGGTATCAAG TCACTCGGCT TAGATACATG GnAAGCTCCA GCACCTATAA ACAGCATATG 180

TTCAGTATTC ACAGTACCAT ATTTGGTTTG AATAACGCTA CCTTCAAGTA TAGGTAAAAT 240

ATCTCTTTGA ACACCTTGTC TTGAGACATC TTGACCACTA TTATGATTAT TCGTCGCAAC 300

GTTAGCGCTT TCTTGATCAn TTAGTTCATC CGCATAACTA 400

(2) INFORMATION FOR SEQ ID NO: 2950:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2950:

TTGACTTTGT AACTAAACTA CTCACTCGAC CGACTCAACT GTTTAAATGT TTCAGATGGT 60

TTAACTCTAA ATACTACGTA TAAATCACCA GCAGGTCCTC CATTCACGCC TGGAGAGCCT 120

TCACCAGCTA ATCTAATTTG TTGTTCATTG TCGACACCTT CAGGTACTTT CACTTCTAAT 180

TTAACTGTTT TATTTTCAGT ACCTTTTCCG TGACATGTTG GACAAGCTTC TTCAAATTCT 240

TGACCACTTC CATTACATTT AGGACAAACT TGTTCAGTAC GAACTCTACC TAAAATTGTG 300

TTTTGTTCTA CAGCTACATG ACCAGCGCCA TTACAGTAAC TACAAGTCTT TTTACTTGTT 360

CCAGGCTTTG CACCATCACC ATGACATGTT TCGCATGTnA 400

(2) INFORMATION FOR SEQ ID NO: 2951:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2951:

CAATGATTTT AAAAGATGCA ATAAAACCAA ACTTAGTACA ATCAATTGAA GGGACACCTG 60

CATTAGTTCA TGGTGGACCA TTTGCGAATA TCGCACACGG TTGTAACTCA ATTTTAGCAA 120

CTGAAACAGC ACGTGATTTA GCTGATATCG TTGTAACGGA AGCTGGATTT GGTTCAGACT 180

TAGGCGCTGA AAAATTCATG GACATTAAAG CGCGTGAACA GGATTTGATC CGGCAGCTGT 240

CGTTGTTGTT GCGACAATTC GTGCGTTAAA AATGCATGGT GGTGTAGCGA AAGATAATTT 300

AAAAGAAGAA AATGTAGAAG CAGTAAAAAG CAGGAATGGT TAATTTAGAG CGTCATGTTA 360

ATAATATTAA CAATTCCGTG TAGAnCCGGT TGTTGCCATA 400

(2) INFORMATION FOR SEQ ID NO: 2952:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2952:

TCAAGTAGCA AAAGAAACAG GTGCTTCAGT TATCGGTATT GATATTGGTC CACAAGCCGT 60

TGACCTAGGG CGCAGAATCG TTAACGTCTT AGCACCAAAT GAAGATATAA CAATTACGGA 120

TCAAAAGGTA TCTGAACTTA AAGATATCAA AGATGTGACG CATATCATAT TCAGCCGACA 180

ATTCCTTTAA AGTACAGCAT TTTAGAAGAA TTATATGATT TAACAAATGA AAATGTCCGT 240

AGTTGCAATG CGCTTTGGTG ATGGCATCAA AGCAATATTT AATTATCCGA AGAAACAGCG 300

GAAGATAAGT GGGCCATGTG TGAATAAACA TATGAGACCA CAGCAAATTT TTGATATAGC 360

ACTTnATnAA AnAGCCGGCT ATAAAGTnGG TATTACGGAT 400

(2) INFORMATION FOR SEQ ID NO: 2953:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2953:

CGCAATTCAC AATAACATTA AATAATTTTT GGTCTCATAT TTTCAAAAAA CATACTGTTA 60

TTATCCCATG GGnTTAAAAA TATCATTAGT ATATAAACGA AACACTTTAC GATAAATGAT 120

ATCTGCAAGC CAAGCTGTTA CAAATGGTAC AACAAAGAAC GCTACTACAA TTAGTAAGAC 180

ACTCAACCAA GCAGAATCAA CCTCCATAAA TTTAAATGCA TTAATCGGTC CTACCATTCC 240

TATAAAACCA AATCCAGCTG ACTCTTTCGT TCCATGAATA CCTACTAATG CTGATACCAA 300

ACCTGATACA ATGGCTGTCG TAnGGGCGGG GnGCATAAGA ATTGGATATT TCACCATATT 360

AGGTATCATC ATTTTAACGC CTCCAAAGAA GACCGGATAA 400

(2) INFORMATION FOR SEQ ID NO: 2954:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2954:

AACACTTTAA TGGAGATTTA GCAGGCACTG TTACACTGAC AGCAGGTTTA GGTGGTATGG 120

GTGGTGCGCA ACCGTTAGCA ATTACTATGA ATCATGGGGT AGCAATTTGC GTGGATGTTG 180

ATGAAACACG TGTTGATAAG CGAATTGATA CGAAATACTG TGATGTTAAA ACAGCTGATT 240

TAGATGAAGC ATTAAAATTA GCAGAAGAGG CGAAAGAACG TGGGAGAAGG ATTATCAATC 300

GGGTTAATTT GGAAATGCTG TAGACATCCC ATCCAAGCGG ATTCTAGGAA AAAGGGTTTT 360

AAAATTGGAC ATTAATTACT GGnCCCAAAC CAAGTGCCCC 400

(2) INFORMATION FOR SEQ ID NO: 2955:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2955:

TTCAGAATAC GAGCAATGTC AGTTGCAGTG TTTAATAAAT TTTGTTCGCT ATTTTGTAGG 60

CATCTTCTAA AGTGCTAGGT GAAGAGATTA TAGAATAGGC ACTATCAATA CCGAAATCGT 120

AAACATGTTG ATAATTTTCG CCTAGACTGC CACAAATCGC GATGACAGGA ATATGATATT 180

GTTTTGCAGC TAACGCAACG CCTACGGGTG TTTTACCAAA GATGGTCTGA TAATCCATGC 240

GTCCTTCTCC AGTAATAACG AGGTCTGCAT CTTTAATTCT TTGATGAAAA TCTGTAATGT 300

CAAAGACGAC ATCAATACCT TTTGTTAAAG TTGTCTCACA AAACGnTAAT AATGCTGCGG 360

CCATACCGnC AGTGCACCAG AACCTGGTAT TTGGTTnACG 400

(2) INFORMATION FOR SEQ ID NO: 2956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2956:

AATACGTCCT TTATATAATG TTAATAACCA GTTAAACAAT TTCACACCAG TTGGAATACC 60

AATCAGCATT GTTGAAATTG AGAAGAATGA GTTGATTAAC GCACCATTAC CCATTGTGAA 120

GAAATGGTGA ACCCAAACTA AGAAACTAAG GAACGCGATA CCGGCAGTTG CCCATACCAT 180

ACTTTGATGT CCGAATAAAC GCTTACGAGC GAATGTCGGG GATAATTTCT GAGTAAATAC 240

CCAAAGCATT GGGCATACCG CCATGTGGCA CTGTGGAAGA ATGCTGTGTC CAATATTCCG 360

nTCATTGGTn CATTAATGGC TAACGCTAAC GGTTTAAAGG 400

(2) INFORMATION FOR SEQ ID NO: 2957:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2957:

TAGTAATTAA TACGATGTCA GCACCTACTG ATTTTGCTTT GTCTGCTAAT AATCTTAAAT 60

GTTCCGTGGA CCTGAACCAG AGATAATTAC AAATACATCA TTCGACTTAA TCGCAGGTGT 120

CGTTGATTCT CCAACAACAT GTGCCTGTTT GCCGAGCTGA TTTAAGCGCA TTGCAAAACT 180

ATTCGCCACG AATCCTGGAA CGTCCTTTGC CAGCTACAAA TATATGTTCA GCATGTAGTA 240

TTTTGGGATG CAAAAGTTGG AAAACTCCAT CCGnTTCAAC ATGTGACAAA GTCATCTTTG 300

AATTCATCTA GAnTTAATTG ATAGTCACTA AnTTTAGCCA TATTACTTAC CTTCGGTTGC 360

CAGCGCGACC ATTGTTTCGC AGCTTCTTAC TGGG 394

(2) INFORMATION FOR SEQ ID NO: 2958:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2958:

AATTATTCTA CCTATAATTA AAAATGCTGG CAAAGGTGTA ATGATGATGA GTAATGAACC 60

TACAACATTT AATATCAATC CTACATAAGT AATTTTGACG CGACCAAATT TATCAGCAAC 120

ATCACCAGCA CCTACGATAA ACAAACCAGC AAATAAGGCA GATAAGCTAA CAGCGATTAT 180

TTATCGTTCC AACGTCACTA CTATATGTTG ATTGTAATGG GACAACAAGA TTAACAAGTG 240

ACTGCGCGAA TAGCCAAAAG GTAATAACCC CTAAAACGAT ACCCAAAnGC AATCGGTTGT 300

TCACCTCTTA AATTGTTTTG ATGTGTCCnT GGATTAGGAT AAGCCTCCTA TGTTTAGGAA 360

AAACAATTTT TAATATGGTA TATTAAGGAn ACATTTCCTT 400

(2) INFORMATION FOR SEQ ID NO: 2959:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2959:

CTTCTTTCTC AACATCAAAG AACATATGGT TTTGTTTCAA ATATTCTTTT ACTAGCGCGA 60

TATGTTCGTC TGATCTACCA GTTAACTTCA TATATTTAAG AGATTCATCA TCAACTGGGA 120

AGAATCCGCA AGTTGCTCCA TACTCTGGTG CCATGTTTGC AATTGTAGCA CGGTCTGCTA 180

GTGGTAAATG TTGTACACCT GGACCAAAGA ACTCCACAAA TTTACCAACA ACACCTTTTT 240

TACGTGGCTC TTGAGTTACT CTTAACGCTA AATCAGTTGC TGTTGCGCCT TGTGGTAATG 300

AATTTACTAG TCGTACACCA TTAACCTCTG GAATTGGGGA AATAGGAGGG TTGTCCAGGC 360

ATTCCAGCTT CAGTTTCAAT ACCACCAACA nCCCTCCTAG 400

(2) INFORMATION FOR SEQ ID NO: 2960:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2960:

ACGTCAAATG TAATCACAAT CGGAAAGTAT CGTGACAATG CATATATAAC AGGGAGGGTT 60

TAAATATGAG TTACTAAGGG GATTTTTAGA TTTAGGTGCA CTGTTTATTT TACCGGTTGT 120

CATATTCTTG CTTGGCCTAT TCTTTAGGCA GAAAATTGGA GCGGCATTTA GGTCTGGTTT 180

AACAATAGGT GTGGCTTTTG TAGGGATTTT CTTAGTCATC GATTTATTAG TTAAAAATTT 240

AGGGCCAGCA GCACAAGCGA TGGTTAAAAA TTTAGGCGTC AnTCTGAATG TGGATTGATG 300

TAGGTTGGCC AGCAACATCA TCTATCGCTT GGGCATCATC TGTnCGCnCC ATTTTATTAT 360

TCCACTCGGG ATTCATAGTT 380

(2) INFORMATION FOR SEQ ID NO: 2961:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGCCATTGGT CGAACTTACG AAGAATCATT GTTAAAAGCA ATTCGATCAC TTGAGTATGG 60

TGTGCATCAC TTAGGATTAC CAAATGGTGA AAGCnTCGAT CTTGATTATA TTAAAGAACG 120

TATTTCACAC CAAGATGATG GACGATTATT TTTCATCGGC GAACAATTAG AAGAGGCACA 180

ACAGTAGAAG AAATTCATAA TATGACTCAG ATTGATTACT TCTTCTTACA CAAGTTCCAA 240

AACATTATTG ATATTGAGCA TCAATTAAAA GAGCATCAAG GTGATTTAGA ATATCTTAAA 300

TATGCnAAAG ATTATGGnTT TAGTGGTAAA ACAATAGCGC ATCGCCTTAA TATGACGG 358

(2) INFORMATION FOR SEQ ID NO: 2962:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2962:

TTTGGGCATC ATTAGGAAAA TTCTTTGAGC AACTTTAGTG TCTACTGGGT AATACAATTT 60

TATCACCATG TTTTTCTAAT AAATCTTTTG CGAATCGATT TTATCTTCTT CTAATAATGA 120

AATACCAATT TCTTTACCTT GCGCTTTTAA GAAAGTATAA GCCATACCTC CGCCGATGAT 180

AATTTTATCA GCTATGTTAA CTAAGTTTTT GATGACATTA ATTTTGTCAG ATACTTTTGn 240

GnCACCTAAA ATAGCAACAA CTGGTTTATG TGGATCGTTA ACTACGCCGC CAATAAACTT 300

AATTTCTTTA TCCATTAAGA ATCCAGCTGC AGTTTCTAAA TGTGTAGAAA TACCAACATT 360

ATTn 364

(2) INFORMATION FOR SEQ ID NO: 2963:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2963:

GTTGATTTCT TGAAAGATAA TAAAAAATTC AAAGAAATGG GATCTAGGAT TCCTAAAGGT 60

GTCTTACTTG TTGGACCTCC AGGTACTGTT AGAAACATTA CTTGCTAGAG CGGTTGCAGG 120

TGAAGCTGGC GCACCATTCT TCTCTATTAG TGGTTCAGAC TTTGTAGAGA TGTTTGTTGG 180

TGTTGGTGCG AGCCGTGTTC GTGACTTATT CGATAATGCT AAGAAAAACG CGCCTTGTAT 240

TCATGATGAA CGTGGAACAA ACCCTAAACC AnTATTAGTT GAAnGGATGG TTTnCGGTGG 360

AAAATGAAGG TG 372

(2) INFORMATION FOR SEQ ID NO: 2964:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2964:

TTAGCAGAAC GCCCACAAAA CCTATCTCTT GCTGTAAAAG AATTTGTGAA nCTGCTGGCT 60

TAAAACGTGT TGGCATAATT GCAGCTTTAG GAGCTACAGT TATGTTAGGT TTAAGTACAA 120

TTAAAAAATT ATGCCGTAAA TAGAGCAAGA CATAAACAAT AATTTAGGAG TCTGGAACAA 180

TAATCAATGT TCTAGGCTCC TAAATGTTAT ATTGGCAGTT CTGAAACATT TATAAATCTT 240

TGATTATGAA CTCACAACAG TGCTCTATGC TTTTATAGAT TTTAATAAAT TAGCCATTTC 300

AATTGCACTT ACTGCTGCTT CACACCCTTT ATTGCCAGCT TTCGnACCTG CnCCTTCCAC 360

AGCTGGGCAA TACTGCCAGC CG 382

(2) INFORMATION FOR SEQ ID NO: 2965:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2965:

GGGAATCATA CAATCATTAC CAATAAACAT GTTACTTATC ACATGAAAGT CGGTGATGAA 60

ATCAAAGCAC ATCCTAATGG TTTTTATAAT AACGGTGGTG GACTTTATAA AGTTACTAAG 120

ATTGTAGATT ATCCTGGTAA AGAAGATATT GCGGTCGTAC AAGTTGAAGA AAAATCAACG 180

CAACCAAAAG GTAGAAAATT CAAAGATTTC ACTAGCAAAT TTAATATAGC ATCAGAAGCT 240

AAAGAAAATG AACCTATATC AGTCATTGGT TATCCAAATC CTAATGGAAA TAAACTACAA 300

ATGTATGAAT CAACTGGTAA AGTACTATCA GTGAATGGAA ATATAGTGAC ATCTGATGCG 360

GTTGTCCAAC CTGGCAGCTC TGGTTCACCT ATATTAAATA 400

(2) INFORMATION FOR SEQ ID NO: 2966:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2966:

TGGGGATTCA CAGGCTAATA CATTTGACTT TATTAGCTGG TGGCGGTAAC GGCGCTGAAC 60

TTTAAATGCG ATTCAAAGTG CTGCAATTAT AAGTGCATTC CCATTCTCCT TTGTCGTCAT 120

ACTCATGATG GTAAGTTTCT ACAAGGATGC GAACCAGGAA CGTAAATTCC TAGGTTTAAC 180

ATTGACTCCG AATAAACATC GCTTACAAGA ATATATCAAG AGTCAACAAG AAGTTATGAA 240

TCTGACATTC TTGAAAAGCG TCAGTCACGT GAAATATAGA GAAAAAAGAT AACTAATAAA 300

GTTTAGTTAA GTATTTTAAT AACAAGTAGT ATGTCATTCT AGTAGCTAGA ACGGTnATAC 360

TACTTGTnTG TTTTTGTGGA AATTGAGTAT TTCAAAGGTT 400

(2) INFORMATION FOR SEQ ID NO: 2967:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2967:

ACGAGGAATT AGTGAAGTAC AATATTATCG GTGGTTTTGA TTTAGGTGTT GTTTCAGACG 60

ACTTTAAAAA TCACATGTTA ATAGCTGTAA CTGAATTAAG AACAAAAGAT GAAATCGATA 120

CATTTGTAGA AAAGGCTGGT GAGTTAAATG ACTAGTAAAT CAAGTCCATT AATTTTTGAA 180

AGATCTCGTG AAGGCAGATA TGCATATTCA TTACCAAAAA GTGATATTAA AACAAATTCT 240

GTTGAGTCAT TGTTAGATGA TAAATTTATT CGTAAAAACA AAGCGGAGTT TCCTGnAGTT 300

GCTGGAACTA GACTTnGTAC GTCATTAATC CTGGACCTTT CCAAATAAAA AATTCCGGnG 360

GTAGACACCG GGTTTAACCC ATGGGGT 387

(2) INFORMATION FOR SEQ ID NO: 2968:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AACAAGTGCA AGTGAGTCAA CATCAGAAAG TGCGTCAACA TCACTCAGTG ACTCAACAAG 60

TACAAGTAAC TCAGGATCAG CAAGTACGTC AACATCGcTC AgTAACTCAG CAAGCGCAAG 120

TGAATCCGAT TTGTCGTCAA CATCTTTAAG TGATTCAACA TCTGCGTCAA TGCAAAGCAG 180

TGAATCCGAT TCACAAAGCA CATCAGCATC ATTAAGTGAT TCGCTAAGTA CATCAACTTC 240

AAACCGCATG TCGACCATTG CAAGTTTATC TACATCGGTA AGTACATCAG AGTCTGGCTC 300

AACATCAGAA AGTACAAGTG AATCCGATTC AACATCAACA TCATTAAGCG ATTCACAAAG 360

CACATCAAGA AGTACAAGTG CATCAGGATC AGCAAGTACA TCAACATCAA CAAGTGACTC 420

TCGTAGTACA TCAGCTTCAA CTAGTACTTC GATGCGTACA AGTACTAGTG ATTCACAAAG 480

TATGTCGCTT TCGACAAGTA CATCAACAAG TATGAGTGAT TCAACGTCAT TATCTGATAG 540

TGTTAGTGAT TCAACATCAG ACTCAACAAG TGCGAGTACA TCTGGTTCGA TGAGTGTGTC 600

TATATCGTTA AGTGATTCGA CAAGTACATC AACATCGGCT AGTGAAGTAA TGAGCGCAAg 660

CATATCTGAT TCACAAAGTA TGTCAGAATC TGTAAATGAT TCAGAAAGTG TAAGTGAATC 720

TAATTCTGAA AGTGACTCTA AATCGATGAG TGGCTCAACA AGTGTCAGTG ATTCTGGCTC 780

ATTGAGCGTC TCAACGTCAT TAAGAA 806

(2) INFORMATION FOR SEQ ID NO: 2969:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2969:

ACCATCTACT CCGTTAATAG TTACACTGTT ATCATTGGTG TTTGGACTTT CAGCCCTTGC 60

ATCTAAAAAT ATAAGCTGAT TAAAATCTGT TATTACTTCT TCCTTGTAAC CATCTATGAT 120

TTTTACAAAA GATTGCATTA ATTAGTCAAA CCTCCCATAT AATTATTTGC ATTTGCTCTA 180

TGCCCACTTT GTTTTGACAA TATTTTTTCT AAACCTCTAA TTGCATCATT AGAACCTAAG 240

GATTATCCTG AGAAGAAACA GTTTGAATCA ACGCATCTGT TAATTnATTn CCTTTATCAC 300

TTAACATAAC AATTTGGTTC AACAATTTnC AACTGTAGAA GTATCATTAT T 351

(2) INFORMATION FOR SEQ ID NO: 2970:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2970:

AGTGCTTGAT GAATTTTGAC CACAAATTCA AATGTATCAG GCGTTTCTTT TATCCATTTC 60

AATATATTTC TTTCCGGTTG TATCGCATAG TATGTCGCAT CTAATTCGAC AACCGGAAAA 120

TGTCCAGCAT ATGTTTTAAG TTTATCGGTT TGGCGTTCTA AATCTTCATA TAATGAATAG 180

TGATCACCCC AACCTGTTAA TCCGATGTTT ATCATATATA TCACCAATGT CATCATACCA 240

TATAACTTTT ATCATAATCA TTTCAGCGAA CTTTAGTTTG ATGTTTTTGC TTGATTAAAA 300

TCTTTTCGGC GAnCCTCAGC TTGATGTTTT TCGTTGATTA AATGGTAAAT AGnnACGCA 359

(2) INFORMATION FOR SEQ ID NO: 2971:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2971:

CAGACGGTCA AGAATCTTAT ACTTATCAAA ATTTATACTG TGAAGCGAGT CTATTGGCTA 60

AAAGACTCAA GGCTTATCAA CAATCTCGTG TTGGGCTATA CATAGATAAT TCGATTCAAT 120

CGATCATTTT AATACATGCA TGTTGGTTGG CAAATATTGA AATTGCGATG ATTAATACAA 180

GGTTGACACC TAATGAGATG ACGAATCAGA TGAAGTCAAT CGATGTACAA TTGATTTTTT 240

GTACCTTGCC ACTGGAATTA CAGGGTTTCA AATTGTATCG CTGGGTGATA TTGAATTCGC 300

TGGAGGGATA TTACAnCGAn CAGTTGTTGG GCAACACAAT GGGTATCCAT TTGAACCATC 360

GGATGnAACT TTGTGCCGAA GGTCGCCTCC ACATnTAATG 400

(2) INFORMATION FOR SEQ ID NO: 2972:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2972:

TCAACCGCTT TACAGCCAAC CGGCGACGCT GACATGGATC GCCTGGCCCA TGCCCACGCC 60

TTGGCGCCAT CATTATTAAT TGCTGCAGTT ACGGTATCTT TAATTGCGTT AAATAAACCT 120

AAATCACCGA AATGTTATTC GCTTAACGTT TTGTTGTTGT TATTTTAAAA TAAATTTGAT 240

GCAATTAGTT TGTTTATCCG CACAACATCT TATAATGTAC TTAACTGTAT TTTAAAGAGA 300

AAAGAAATAC AGTTAGGCAT TCAAAACTGT ATTTAACACA ATTAAGTTGC CTGAATTCGT 360

ATTTAAGTCT TATTGAACCT TTTTnAGATA An 392

(2) INFORMATION FOR SEQ ID NO: 2973:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2973:

ATTGCAATGA TAGCAATCGG AATCGCACCT GCTAAAATAA ACGTTGTGCC ATCCGTCGCA 60

TTTGTACCAC GAATCACAAT GTCACCAAGC GTAGGTGCTC CTATAAATGA TCCAACGGCA 120

ACAACACCTA TCGCAACAAC CAAGGCAATA CGAATGCCAC CGATAATAAC CGAAACAGAT 180

AACGGTAATT CAATCATTCG TAGCACTTGA TTGCGTGTCA TTCCCATACC TTTGCCAGCA 240

TCCTTAATAT TCGCATCAAC ACTAGCTATA CCAGTATAAG TGTTTTTATA ATTGGAAGTA 300

ACGCATATAA AAACACTGTT AAACTACTGT TCTGAnCTAG CCTGACTACA TTAAATAGTn 360

ACATTGCATG ACTGGACTGn TGGATATATT GCATGGATnC 400

(2) INFORMATION FOR SEQ ID NO: 2974:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2974:

GTATTCTTTA GGTAATGCAA CTTTTAATCC TTTAATATCT TTACCAATTT CAGATGTAAA 60

GTCTACATCA TCAACTGGTG CACTTGTAGA GTCATTAACA TCTGCACCAG AAATAGCTTC 120

TAATACGATT GCATTATCTT TTACATTTCG AGTCAATGGA CCAATTTGGT CTAATGAAGA 180

TGCAAAAGCA ACTAATCCAA ATCGAGATAC ACGACCGTAT GTTGGTTTCA TACCGACAAC 240

GCCACAATAT GGCAGCCGGT TGTCTAATTG AACCACCTGT GTCTGGAACC TAAGCTAAAT 300

GGTACTAAGC CAGCTGCAAC TGCTGCTGCA GATTCCACCT GAnGGAACCA CCTGGGCACG 360

(2) INFORMATION FOR SEQ ID NO: 2975:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2975:

GAGATCGCGG GTTCGATTCC CGTCGAGACC GTACAAATGC CTATCCAAGA GATAGTTTTG 60

TnTTGCGTTT AATATTATAT TAATAAAAGA TATATGGACG AATGATAATC ATATTGATTT 120

ATCTGTTCGT CCATTTTCTT TAAAATGTAT GAACCTCAAG TAACTTAGTG GTTGGATATG 180

AAAGATAAAC GTnGACAATA AAATCTTTAT TAGACGTACA AACATATGCT ACTGTCAACA 240

TATTTCTTCG TTGTGATATG CCACCAGTCC TCCATAACAT CAATTGTTAA AGTAACGAAT 300

AACGAATAAT GATATTTnAT TTCTGAGCCA TGACGTGCCA CTAGAAGTTG CCCATTATCC 360

T 361

(2) INFORMATION FOR SEQ ID NO: 2976:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2976:

TGCTGCTTCT GAAGCGGAGT AATTGTGTAT ATCAAATGTC GCTTTTTGAT CAGGAACATG 60

ATGTAAAGGT GTATATGTTT CACCTGTTTG CTCATCATGT AACACGGCAT GCCTATGACT 120

GAATGTACCA CGTTCACTAT CTTGACCAGT TAAGCGAATC GGTGTACCAT CTTGTAAAAT 180

TGTCGCAAAT GCAAGTnGTT CTGCTTGTGC CCAATCAACT AAACCATCTT CTTTATTAAA 240

CGGCTCATGA CGCTTCTCAA GAACTTTGTT TAACTTTTTn CAAAATGTTA AAGCCATCCG 300

GATATGTTAA CAATGCATCA TTATTTCTTT CAAGTGATCC AAAAGTAAAG GnTTGT 356

(2) INFORMATION FOR SEQ ID NO: 2977:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2977:

CTTTAGAGCG ACACCTAGTC ACTGCAGCAA GCTATTTCTT TATTTGCTAT GCTATAnATC 60

GTTAATTACT AGACCTATTG CTGGTAGATT GATGGATGAT AAAAATGAAA ATATTATTGT 120

CTACCCAGCA TTTATCATGC TTTTCCTTTC ATTTGTATGC TTAATTTCAA GCTATCAAAG 180

CTGGTTAATA TTACTTGCTG GTGCTTGCCT AGGTTTAGGG TATGGAAATT TATCATCTGC 240

AATGCAATCT ATTGCGATAA AAGTCTCACC CCCGATTAAA TATGGTATCG CGACATCTAC 300

TTTTTACGTT GGTCTAGATG CCAGGTGTCG GCTTCGGTCC AGCATTCCTT GGGTTAnTTA 360

CGCAGnGTTT T 371

(2) INFORMATION FOR SEQ ID NO: 2978:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2978:

TTGTAATTTC ATGATTACAC CTCAATTGTT CTTGTTGTTA AAACTCAATA TTTAATTGTC 60

TGCGCTCAAT AATTTGTTGT TTAAGTTGCT CAATATGATT TGATTGGAAT TCTTCCAATA 120

ATGCTTTTGC TATTTCAAAT GCTACGACAT GTTCGCAGAC GATACTTGCT GCAGGAACAG 180

CACAACTATC AGAACGTTCA ATTGTTGCTT TAAAGTCTTC TTTAGTATTA ATGTCTACTG 240

AATTTAATGG nTTATATAAC GTTGGAATTG GnTTCATTAC ACCATTACGA TAATTGGCAT 300

CCATTGACAT ACCGCCTCTA ACCACCTAAG TGATTAGAnC ACGATAATAC CAATTCACTA 360

TATAT 365

(2) INFORMATION FOR SEQ ID NO: 2979:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2979:

TGATTATATA AATCTAACCA GCCAAGTTTC GTCTGCGGTG AGACATTGAC ATTAATTGCT 60

GCAGATAATG ATTTAACAAC ATGTGTGGCA TGTGATTCAT TAACGATGAC AATATCATGT 120

TGGCGATGGG TAACATTGTT AACATTGCTT CATTTAAAAC GATATCGAAT TGATTGTCAT 240

CAAAGGGCAA TTTAACAGCA TTCGCTTGTT GAACTTGAAT ATATGATTCA nGACCTGCTG 300

CGGAAATGTT TTCCGTGCTT TTTCTAAGCC TTCnTATTAT ATCAACGCCT GAnGTGACAC 360

CAnAGTGTGA GCCAGATAAA TAGAGGTGTG CACAGATACA 400

(2) INFORMATION FOR SEQ ID NO: 2980:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2980:

TTTCTGCTTT TGATAATCTT TCATCAATGC AAAAGCTACA TTGGACAGTC CTATAATGGA 60

AATAATGTTT ACAATTGCCA TTAAGCCCAT AAATAAGTCT GCCGTATTCC ATACTGTTTC 120

TGTTTTTACA ACTGCACCGA CAAAGACAAG TACTACAACA AGACATCTAA AGATAAATAA 180

TATTACACGG TTTGTTGATA AAAATTCAAT ATTAGATTGA CCGTAATAGT AATTACCTAC 240

AACAGATGAA AATGCAAACA GTGnAACGCT TATTGGTTAA GAAAATACCT CCAGCAGAAC 300

CTAAATGCTC CTTAAGTGCC GATTGGGTAA CTGCAACACC nTGGAGGGCG TTTATCACCA 360

AATTTnCGTC CCGAATATAG TAAA 384

(2) INFORMATION FOR SEQ ID NO: 2981:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2981:

AATTCTAACG ATATCACCAT TTTTACAACC ACGTTCTCTA AGCGCATCAT CAATACCCAT 60

CGAACGCATT TGACGAGCAA ATCGACGTAC TGCTGGATCA CTGTTAAAGT CAGTCATTTT 120

AAACATTCTT TCAATAGCAT TACCACTTAC CACATAAGCA CCATCATCAT CTCTTGGAAA 180

TTGTAAATTT ATCTTGTGAC GGTGTATGTT TATATAATAC TCGGTTAATG CCAACTGACT 240

CCTCTTCTTC AACTGTGGAG TCAACATCTT TATATTCTTC TGAATTTATC TGCTTATTGC 300

ATATGAATAA TTGnnCAATG ATTATCACGC GTTATTGTTG GAAACTGGGA TTAACTGGCA 360

(2) INFORMATION FOR SEQ ID NO: 2982:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2982:

CCTCAACCGC TTTACAGCCA ACCGGCGAGC GCTGnACATG GATCGCCTGG CCCATGCCCA 60

CGCCTTGGGC nCATCATTAT TAATTGCTGC AGTTACGGTA TCTTTAATTG CGTTAAATAA 120

ACCTTCCATT GAAAACACTC CTTAAAATTT AAATTTGAAG ATAACAAAAA CGTGCGTACT 180

TTnTGAAATC ACCGAAATGT TATTCGCTTA ACGTTTTGTT GTTGTTATTT TAAAATAAAT 240

TTGATGCAAT TAGTTTGTTT ATCCGCACAA CATCTTATAA TGTACTTAAC TGTATTTTAA 300

AGAGAAAAGA AATACAGTTA GGCATTCCAA AACTGTGATT TTAACACAAT TAAGTTGGCC 360

TGAATTCCGT ATTTGAAGTC CTAATGGAA 389

(2) INFORMATION FOR SEQ ID NO: 2983:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2983:

ATATTCCTAT GACAATGTTC AGGCAACGAT TCCAAGGATT AAGAAAAGAT CAACCGGTAT 60

ACTTATGTGA TGCCAATGGG ATTGCTAGCT ATAGAGCCGC TCGTATTTTG AAAAAGAATG 120

GATATACAGA TATCTATATG TTAAAAGGCG GCTATAAAAA ATGGACTGGA AAAATAAAGT 180

CTAAAAAATA GTTTTTGTAA ATTTAATATA CGATTTAATA AAATCTGAGT GTTAATTGAT 240

CATCAATAAC AATACTCAGA TTTTAATTTT TTAACAAAGT CTGTTACTAT ATTTCTCTAG 300

CTTCACTGAT CATTAAACCT TAGTTTCAGC ATAATTAAGG AAGGTCCGnC CCATTTCCAT 360

CGnGnTCCAT TACCGCCAC 379

(2) INFORMATION FOR SEQ ID NO: 2984:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2984:

ATGCTGAAAA TATGGTGCCG TTTATATGAA TCAATTTGAA TCCGAACATA ATCCGGATAC 60

ATATTTTCAT ACATTGGGAC CCGAATTGAC TTCAGCATTA CAGCAAATTG ATTATTTTGT 120

GGCTGGTATT GGCTCTGGCG GTACATTTAC AGGTACGCAC GTTATTTAAA GCAACATCAC 180

GTGCAATGTT ATGCCGTTGA GCCAGAAGGG TCCGTGTTAA ATGGAGGGCC AGCTCATGCA 240

CATGACACTG AAGTATCGGT TCTGAGAAAT GGCCGATATT TTTAGAGAGA CGCTTGTAGA 300

TGGGnTATTT ACGATTAAGA TCnAGATGCC TTTCCGAATG TCAAAGTTTG CTATAATGAn 360

GGTGTAGTAA GCAG 374

(2) INFORMATION FOR SEQ ID NO: 2985:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 464 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2985:

GGAGCCACCA TTGGAGCAnG TTACGGTGGA AAAGATACGG nAAGGTTnGT ATGACTGTAn 60

GTCTTGGATA GAGTAACAAA CCTAATTTGT TAACTCTAGG CCCCATATGT CGCAGTACCA 120

TCTGCATGTG TTGTTAcATT GTATGCATTT GTTTTACTTG GCTTCTTGtA TGTCGGGCGA 180

GCTCCGTATG ACACTTGACC GTTTGCATGT GTTGTTACGT TGTATGCATT TGTTTTGCTT 240

GGCTTGTTTT GTGTTGGGCG AGCGCCATAT GATACTTGGC CGTTTCCATG TGTTGTTACG 300

TTATATGCGT TTGTTTTGCT TGGCTTGTTT TGTGTCGGAC GAGCTCCGTA TGATACTTGG 360

CCGTTTGCAT GTGTTGTTAC ATTGTATGCA TTCGTTTCGC TTGGCCTCCT GTATGTCGGA 420

CGAGCTCCGT ATGATACTTG ACCATTGCAT GGGTGGTACG TnnG 464

(2) INFORMATION FOR SEQ ID NO: 2986:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2986:

AACTATTATA TTAACATACA ATGTAGGGAT GTGATGCGCG TGAAGTTTAG GGATAAAGAT 120

AATCGTCAAG TTAATTTGAC ATTTAAAAAG GATAATGAGA TAGCAGATGG CAATCATGTG 180

CTAGCTATTC CAACGTTTAA AAATCAATTG CTTTTTACCA AACATAATTT ACGGGGGATT 240

GAATTTCCTG GTGGTAAAAG GGAACGCGGG GnAAAGTAGT GCTGGAAGCA GTTACACGTG 300

AATTATATGA AGAAACAGGC GCCAAATTGA AAAATGnTTA TTACATAGCA CAATGTnCC 359

(2) INFORMATION FOR SEQ ID NO: 2987:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2987:

TAGAATTCTT CTAATGAATG AGCTTCTTTA GAATGATAAC CATAACGAAT TCCGTCAAAA 60

CGAGAAAGGT TTGACGAAGC TTCTGATGAT GCAATCACGT AATATGATGG AATACCAAAT 120

TTAGTATTTG GCAATGATAC TTCCTCAACG ACAGCACCTA AAGATTTTAA AGTTTCTACA 180

GCGTTTTGAA CTGCTTCTTT TACGTCATCA GCTACACCTT CACCTAAGTA TTCTTTAGGT 240

AATGCAACTT TTAATCCTTT AATATCTTTT ACCAATTTCA GATGTAAAGT CTACATCATC 300

AACTGGTGCA CTTGTAGAGT CATTAACATC TGCACCAGAA ATAGCTTCTT AATACGGTTG 360

CATTATCTTT TACAnTTCGG GTCATGGnCC CATTTTGGTC 400

(2) INFORMATION FOR SEQ ID NO: 2988:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2988:

ATTCATTCAT AATTATCAAT CCTTTGTGTT AAATTACTAT ATAAATAGTG TACGnATTTT 60

CGAAATTTGT GATCATAAGT TTATTCAATG CTAAACAATA AGGTTGAGAC ATAATCGTAT 120

CTCAACCTTG AAATTATTAT ACGTTGACGT CACTAGTCAT TCAGTTTTCT TAATGCTGCT 180

ACAATCTCTT TTTTAGTATC TTGTACTTCA GAAGCTTGCT TAATCACTTT TGCAGGTGTA 240

CCAGCAACAA CTGCACCAGC TGGTACATCT TGTGTCACAA TCGnGCCACT GGCAACAATA 300

nGATTATAAC CGTGGAG 377

(2) INFORMATION FOR SEQ ID NO: 2989:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2989:

CCAGGnACCT GGACACGCCG GGTCTTATCA TCAATAATAG TAGCATGACA AATCTACTAT 60

TTTTTCGCTA ATAAGTGGAT GTAATGCTAA TAATGTTGCT GTAGGGAAAC AGCCAGGATT 120

AGAAATGAGC TTCGTTCCAT TGTTATCAAA CGATTGCCAT TCTGAAATGC TGTAAATAGT 180

CATGATTCAA ATCATCTTGT GCCTGCAGCA GTTTCTTTGT AATATGCTTC ATATATTTCA 240

CGnTTCTTAA TTCTAAATGC GCCAGATAAA TCGATAACAT GAATACCTTT TTCTACTAAG 300

GGAGGGATAC ATGTTTTACT TACGGGTGCT GGTGTCGCAA AGAAAATTAC ATCAAn 356

(2) INFORMATION FOR SEQ ID NO: 2990:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2990:

TCATTTTCCA AGTGAGACTC TGCTCTTGCT TTGGCTAATT TAGCTCTTTC AACATCAATT 60

TCTCTTGCAG TTTCTGCAGT CTGAACAATG ATTGAAACTT TATCTTTTCT AACTTCAACA 120

AAGCCATCGC TTACAGCAAT ATATTCAGTT CCATCGTGGA AATTTCACTT TTACAAAGCC 180

TGTTTTTAAA GCAGCTACAG TTGGGAATAT GTCCACTCAT GACACCTATC TCACCAGCTG 240

TTGTTTGCAT AACAACGAGT TCAACATTAT CACGATTGTA AACAGAACCA TTAGGAGTGA 300

CAATATCTAG GTTTAAATGT CCATTATCCA TTCCnCCnGA ATTGGnTGA 349

(2) INFORMATION FOR SEQ ID NO: 2991:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2991:

ATGGCCACGT TCATGCCAAT AGCTGTCGTA GTCGCATTTT CACGTTCTAG TATTGCATTT 60

TTTAAATGCG ATGTGTGCTC TACATAACGG CAAATTTTAA GTTTATGAAT CAACATATCA 120

ATTGCTTCGT TTCGAGACAT GTCGTGGATC AGTAATTATC ATAGTTTGTT GATCAAAAAC 180

ATGAGAAGGT TTATTGAGAT GTGAATGTTT CGCGGTGTTA TCTACATTGT CAACCTCTGT 240

ATCATGTTGT GTAATATCTG TATCATGAAG TTGCGGTTGC GCTGGTGCAT CTACTGCTAT 300

AACTGGTGTA TTGCGTTTTA ATAATAGTAC AGTAGTnCAT TGTnGACAAG ACTnACCGAC 360

TTA 363

(2) INFORMATION FOR SEQ ID NO: 2992:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2992:

AAGTTTATTT TAAAATTCGT AATAAAAATA ATAAACTCAT CGAACGATTT AATGGTCTAG 60

GTTTCCATAT CAACTATGAG TACATTAAAT TCAAATTCGA ATCACGTAAC GTAAAAGATC 120

AAACAATCCC TGAATAAAAC ACCAAGCAAA TACCCTACAG TACATCATTA GCATGTATTG 180

TGGGTTTTTC TACTTTTTGT AAATATTGAn AATTATnAGT AGTTGTTTTT TACTATTAGG 240

GCAGAATGCT TTACAATAAC ATGCAAGTGT CAATTAAGGG GAGCACTTGC ATAAATAGTA 300

TAGGnGAGTG AGTAGTCCTG GCCATTTCCT GGAATTCCTT AATCGGCAC 349

(2) INFORMATION FOR SEQ ID NO: 2993:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2993:

TTTGTGCAAT AAGCGCTTTT TGTTCGTTTG CTTTTGTTGC TAATTCATCT TTCGCAACAT 60

CTTTAATTGT TGTATCTGCA GTAATACCTT GAATATCAGC AACTGCTTGA TCTTTAATTT 120

GCGTAACATC ATTAGTTGTT TGTGCATTTA AGATATCTTG ATACGCTTTT TCTTTAGCTT 180

TTGCTTGATT TTGAGTTGTC ACAGCTTGAT CAACATCATT TTTAGCATTG ATTTAACCGC 300

TGTGCTGGTT GCGGCTTGAA TTGAATCTTC CAGGCTTCGC TGACTACACA TACACAGTGA 360

GnGnAATATT TCGGCTGAAC GCGTGCATGT GAAnGCTCT 399

(2) INFORMATION FOR SEQ ID NO: 2994:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2994:

AATGACAGGA ATCGTCGTTG CCTTTACTAA TTGACCAGTT AATTCAAAGT TAGGTCCGGA 60

CATTTTGCCA TCTTTAGCAA TATCAGTATA TATAATGCCG CCAAGAGGTA TATCCGATAA 120

CCGTCTCACA AACTAAATAA ATTTAACTCT GTGTCCTCTT CCCATCCGTT CACTTTAATA 180

TCTTCTCCAT AGGCATCAAC AGATAAATAA ATGCGACCTG GAAATGTATG TGCCATCTCT 240

TTAAGCCAAT CAGTATCTTG AATACCTTTC GTTCCAACTA TGCAATAATT AATCCCTGCG 300

GCAAAGTAGT CCATGATTTG TGACTT 326

(2) INFORMATION FOR SEQ ID NO: 2995:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2995:

CTAATGCCGA TGAGCAAAAC ACAAGCATTA GAAATTATTA AAAAAGTTAG GTACGTATAC 60

AACATTGATT TTGATAAACC GAAGTTAGAA ATGTGGATTG ATGTATTAAG TCAAAATGGA 120

GATTATCAAC CAACTGTAAA AGCGGTAGAT GTTTATATCA ACAGTAACAA CCCGTACCCG 180

CCTAACTTAC CAGCAATCAT GCGTAAGGAA CCTAAAAAAG TATCTATCGA GCCAGTAGAT 240

AACGAAACCG CTACACACCA TGGGAAAATG CAGAATGACC CGAATTGTCA GACAAGGAAA 300

ATAGCGCTAG ATAGTTCATG AATAGTTGGC AGATTGGGGC GAACGATGAT ACGnCATTCG 360

ATTGAAGTCA TATCGTCGTA CTTAACACCG GACGTTnGAA 400

(2) INFORMATION FOR SEQ ID NO: 2996:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2996:

GAATGTAAGT GTCCCTTAAG CATAGTGCTC CCACCTTAAA TTTTGTTACA TACTTTCATG 60

GAATGTACGA GAAATTACAT CTAATTGTTG TTCACGTGTT AATTTAATGA AGTTAACAGC 120

GTAACCAGAT ACACGGATGT TAACTGTGGG ATATTCTTCT GGATGTTCCA TTGCATCTAT 180

TAATGTTTCA CGGTTAAATA CGTTAATATT TAAGTGGTGA CCACATTGCA TTGCGTAACC 240

ATCTAACATA CTAGTTAAGT ACGGTTTGAT CTCTGGnTCT TTACCTAATG ATTTGGnACG 300

ATACTGATGT ATTGAAATAC CATCCTTACA GCATCGTAAG GGGTCCTAGC CACAGAACTT 360

ATGAAGAAAT GCACCTTTTn GGCACnGGCA TGCATGGGGT 400

(2) INFORMATION FOR SEQ ID NO: 2997:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2997:

ATGATATTAA CCTGTTTACA AGATGGTTGA TACTTGCGCA TGAnATTTGA ATCTTCAACA 60

CCATATTATT ATGGTACATA CGAAACTGAA AATGAATCCA TAGTTACTGA CAAAGAAAAA 120

ATCTTAGTAT TAGGCTCTGG ACCAATTCGA ATCGGCCAAG GTGTAGAATT TGACTATGCG 180

ACAGTTCACG CCGTTTGGGC AATTCAAAAA GCAGGGTACG AGGCGATAAT TGTGAATAAC 240

AATCCAGAnA CAGTTTCAAC AGATTCTCAA TTTCTGACAA ATTATACTTT GAACCTTTAA 300

CTGAnGAGGA TGTGATGAAT ATCATTAATT TTGGA 335

(2) INFORMATION FOR SEQ ID NO: 2998:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2998:

GCAGTAACTA ACTTTTGTAC AAAAGGATCA TTTTTATCAA CATAATGTGG TGGTTGGACT 120

TTACCTAATT TCACTTCAAA GtATTGTTGA ATCTCATTTG CAAAACGATC CATAGCTTTT 180

TCAAATTCAA ATCCTTCTGG GTAGCGTAAt TGATACCGAA AAGACCTGCG TTTTCATTAT 240

CATATGTAAT AACACCAATG TTAGTTGTCA CGTCACCCAT GgACATCTGT ATGGgAATTT 300

CATTCCCAnC TTTTTCACCA AAATCnGGAA TTGAAATAAG TGAGCGATTA CGAAATGGCG 360

ACAAACGCCT GTGGCATTGA TnGAGCAAGA TTnAAGG 397

(2) INFORMATION FOR SEQ ID NO: 2999:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2999:

AAAGCTGTGT TGGTAAAGAG TTTTGTCGAT TTGGTACGCA ATACACGACA CGACTTGGCA 60

TTCGTTTAGA AAAAACATTT GAATACATCG ATACACCTCA TAAATTCAAA ATGGGTGTAT 120

CAGGCTGCCC AAGAAGTTGT GTTGAATCAG GTGTTAAAGA TTTTGGTATT ATCTCAGTTG 180

AAAATGGGAT TCCAAATCTA TATCGGTGGT AATGGTGGTA CAGAAGTTGA AAAAGCTGAA 240

TTTTTAACAA CTGTAGAAAC AGAAGATGAA GTAATCAAAT TATGTGGTGC TTTGATGCAA 300

TATTGAnCGC GAAACAGGTA TATATGCnGG AAAGAACCAG CGCCCAGGTT AAGAAGACCT 360

GGATTTGAAA ATGTnAAAAG AAGTCCTTAC CTGGGCCCCG 400

(2) INFORMATION FOR SEQ ID NO: 3000:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3000:

AACGGTAGTA TTACAGAAAG CTCTACTTAT GGTGATAATG ATACACCAGC GCCACCAACT 60

GACGAATTAG GTGGTAGTTG GACACTATGG AAAAATTTAG CGCGACAAAG TCCTGAATTT 120

GGTAATCCTG ATAAGTTTTG CCAAAATATT CCTAAAAAAA GTTGGTTTGT TTCAGCAACT 180

TCTACAACAA ACAATAAAGA GATTATCGAT ACAATAGAAA GTATTTGTAA ACGTGACCCA 240

AGTTTTACAA TCAATCGTCA GCmACAGTTT aAAGACCAaC CTGrAAATGA AaTATCTACA 360

TGGATTTATG CCTTATATyC AGATGTAAaC GGCGATTATA TTAAAAAGCC AATTACAGAA 420

TGTAGTGGTA ATGAAATATG CCAAGnATGG CTGTATCnCT TnGGTGTATC AACTGACAAG 480

ATTGAAGACT TAGCAAAACA TGCGTC 506

(2) INFORMATION FOR SEQ ID NO: 3001:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3001:

ATTGATGGCA TCGAAAAACT TTAATAAGAC AACAAGTTGA TGAGATATAT GTATATAGGT 60

TTGGCATGGA TTTCGATTGC AGTTAATTAG AATAGCTCAA TGCTATAAAT GTAAGTAGTT 120

GATATGAAGA AACTAATGAA CTAAATGCAA GTATTGTCTA AAACAATCAT TTTATTGAAA 180

TTTAGTAGAG CTGAAATTAA TATAACGTCG TTAATTGAAT AACGCTTATG TTATAAGAGC 240

ACTCATACCA nACCATAATC ATCTATAGnT ATAACAATTC ACGTATAAGG GGCTGTGTTT 300

GGCATAGCCC TTAGGTATAC ACCTAATTCC CATTAAAATA GTAGGGGnTT AAA 353

(2) INFORMATION FOR SEQ ID NO: 3002:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3002:

CAACAAAATG TCTATATGGT AAGTGGTAAA ACGAAAAATG ATGAAGACTA TTCATCAACT 60

ATTTTATATA ACAACGAAAA AGAATTACAA AAAATTACTG ATGCTGCTAA AAAGCAAAAC 120

GGTGTAAAAT TAACGATTAA AGAAGAAGAA AAACAAAGTG TCTTTGTGAG TATACTTTCA 180

ACATTAATTC CAGTTGTAGT CATAGCGTTA TTATTTCTTC TCTTCCTAAG CCAAGCACAA 240

GGTGGCGGTA GTGGCGGTCG TATGATGAAC TTTGGTAAAT CTAAAGCAAA AATGTACGGT 300

GATnAATAAA CGTCGTGTTC GTTTCTCTGA TGTAGCCAGG GGCCAGATGn AGGAAAACCA 360

AGGnTTAATT GGAAATTGTT GGTTTCTTGG AAAGGTAATG 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3003:

ATAACATCGG CACAGCAGCT AAAATAACCA TACCCAAAAT GAnTGTATCT TTAAACGTGC 60

ACCGTAAAGn CTTCCGACTA GCCATGTATA AGCTTTGGCA GCAGATAATT GCTTCGTTGT 120

AATGAGTAAT CCTTGGACAA GCGCAATAAA CAACGTTTGC ATCGAAATAC CGATGATTAT 180

GAGTGTTGTC GGGCGTATTT GTCCTTTCGT TTGAAACACT AATAGTATCA TCATTGCAAC 240

TGCGCCACCT AATACTGCAA ATAGTGGAGT AAATGTATTG TTAAAGGCTG AAAATGCAAT 300

AAAGACAACA GCACTTAAGC TAGCACCACC TGTGATACCG CTAATATCAG GTGAGGCCAA 360

TGGnnTTTTT TTATACATTT TGGCAACATT TAACCACTTC 400

(2) INFORMATION FOR SEQ ID NO: 3004:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3004:

CTAATAACAA ATGCGATGAT GATTAATACT AATTTACCTG CTGCTAATAC AGAATCTCCA 60

AGGAATGAGA AGAATGGTTG ACGTTCAACT TCATTGTTTT TAAGACTGTA GATAATATCT 120

TCTTTCTCTT CAACACTTAC TGGATTCAAC AAGCATGACA CAATAATCGC GTTAACGGAT 180

ATTTAGTGGA ATTGCCGTTA GTACCAGTTC TCCTGGTACC ATTTGTACAT ACGCACCTAC 240

AATAGCTCCC GATACAGAGC TCCATTGACA TCATTGCGAT TGTTAATACA CGCATTTCAT 300

TnCAGACGTT TTAGTTGCTC ACTTGGATAC GGGCTAAnGC TTnCGTGAAT TGCC 354

(2) INFORMATION FOR SEQ ID NO: 3005:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGTCAGCTTA TTGAACAAGG GACACGTGAA TCAGTCTTGC ATCATCCAGA ACATGTTTAT 60

ACGAGATTTA TTATCAACGA AGAAGAAGAT TAATGATCAT TTTAAACATG TGATGAGGGG 120

TGATGTACAT GATTAAAATT AAAGATGTTG AAAAGTCATA TCAAAGCGCA CATGTTTTTA 180

AGCGTCGTCG AACACCTATC GTGAAAGGTG TGTCATTTGA GTGTCCAATC GGTGCGACGA 240

TTGCGATTAT CGGAGAAAGT GGTACGGnTA AATCGACGTT TGAGTCCTAT GATATTAGGT 300

ATTGAGGAAC CGGATAAAGG TTGTGTACCC TTAAATGATC CACCGATGCn TAAGAGGAAG 360

TGAGCCGCCA CCnATTGG 378

(2) INFORMATION FOR SEQ ID NO: 3006:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1785 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3006:

ACnTTAGTTG GCCAAGCCTT TATCCGGAAT TATTGGGCCT TAAAGCCCCC TTAGGCGGTT 60

TTTTAAGTCT GATGTGAAAg CCCCgGCTCA ACCGTGGAGG GTCATTGGAA ACTGGAAAAC 120

TTGAGTGCAG AAGAGGAAAG TGGAATTCCA TGTGTAGCGG TGAAATGCGC AGAGATATGG 180

AGGAACACCA GTGGCGAAGG CGACTTTCTG GTCTGTAACT GACGCTGATG TGCGAAAGCG 240

TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG AGTGCTAAGT 300

GTTAGGGGGT TTCCGCCCCT TAGTGCTGCC AnTAACGCAT TAAGCACTCC GCCTGGGGAG 360

TACGACCGCA AGGTTGAAAC TCAAAGGAAT TGACGGGGaC CCGCACAAGC GGTGGAGCAT 420

GTGGTTTAAT TCGAAGCAAC GCGAAGAACC TTACCAAATC TTGACATCCT TTGACAACTC 480

TAGAGATAGA GCCCTTncTT CGGGGGACAA AGTGACAGGT GGTGCATGGT TGTCGTCAGC 540

TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAAG CTTAGTTGCC 600

ATCATTAAGT TGGGCACTCT AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG 660

ACGTCAAATC ATCATGCCCC TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA 720

AAGGGCAGCG AAACCGCGAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT 780

AGTCTGCAAC TCGACTACAT GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG 840

GTGAATACGT TCCCGGGTCT TGTACACACC GCCCGTCACA CCACGAGAGT TTGTAACACC 900

CGAAGCCGGT GGAGTAACCT TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG 960

TATATTCGGA ACATCTTCTT CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT 1080

GAATGTTTAT TTAACATTCA AAAAAATGGG CCTATAGCTC AGCTGGTTAG AGCGCACGCC 1140

TGATAAGCGT GAGGTCGGTG GTTCGAGTCC ACTTAGGCCC ACCATTATTT GTACATTGAA 1200

AACTAGATAA GTAAGTAAAA TATAGATTTT ACCAAGCAAA ACCGAGTGAA TAAAGAGTTT 1260

TAAATAAGCT TGAATTCATA AGAAATAATC GCTAGTGTTC GAAAGAACAC TCACAAGATT 1320

AATAACGCGT TTAAATCTTT TTATAAAAGA AAACGTTTAG CAGACAATGA GTTAAATTAT 1380

TTTAAAGCAG AGTTTACTTA TGTAAATGAG CATTTAAAAT AATGAAAACG AAGCCGTATG 1440

TGAGCGTTTG ACTTATAAGn ATGnnnGATA TGTTGAATAT CCATATCTAA AGCTAGATCT 1500

AAACTTTGTT CAAAATCTTC AATCGTCTGT TTCGGTAAAT GATACATTAA ATCTAAACTG 1560

ATTGATTTAA TACCTGCGTT TTTAGCATTT AACACCGAAG TGTAAATATC TTCAGTATTG 1620

TGCGTTCTAC CTAAAACAGA CAATAACTCC GGCTTGAATG TTTGAACGCC CATTGAAATC 1680

CTTTTTACTC CATATTTCTC TAATAGTTGG ACTTTCTCTT TAGTTAACTC ATCAGGATTT 1740

GCTTCAAATG TATACTCGCC TGTGATTGTA AACGTATCAC GTATT 1785

(2) INFORMATION FOR SEQ ID NO: 3007:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3007:

TGCAAAAAAC ACAATAACGA TAAATGTTCC CATTGATCCT ACAGCATCGC GAACATTTTA 60

CCTAAGTCTT TTGTATTTTT AATTTCTTTG CTTAAAATCC CATAAACTAA TCCAGGTACT 120

AAAAATACGA CAAGAATAAT TAATCCGACA CCGTTAATTA ATGGCGATCG TCTAGTAAGC 180

TGCCTGTTTT AGCATTTCTT AAAAAGCTAT GTCAGGAATG GCTGTAATAA TTAATAAAAT 240

AATTGnGCTA TGAACTGATA TTTGCCATTT TAAAAnATGT GCTCTTTGTC AGAATATGTG 300

AGATGTnCTC ATGGCATCAT GCATTAAACT GCATCATATT TTCCTAATCT AGGATAATGA 360

(2) INFORMATION FOR SEQ ID NO: 3008:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3008:

TTGCCTTCAA ACACATACTT GTAGTCGGAT GATCACCTGT TCCAAAAGnC ATACCTGGGT 60

CGAGCTCAAT GCAAAGCTCT TCATCCGCTT CTTTAGCATA TGTTTCCCAA CTAGGAACTA 120

TTGTGAACTT CTTCGACGCT CGGGAATGGA TGGAAATAGT TTTTCCATTC ATTTTCCCAA 180

TCCGTCTCTG CAATAATTTG CTCACTGAAT TGAACGTTAT GTTGATCAAG TTCATCTAAA 240

TTTAATAACT CATCTTTGAA TTTGCTGTCG CAACTGTATC ATCATAAGTG CATTTCAGTA 300

AAATAGGCTT nGCAAnCTTA CTCCCTTATC TGGGATAAAG CCTCGGTTTT 350

(2) INFORMATION FOR SEQ ID NO: 3009:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3009:

TCTTATATCA CCAGGAATTA ACACTGCCTT TTGACCACTT TCTTCAATCA CTTGGCGTAC 60

TTCTTGTGCA TCTTGTTCTT CACTCGGAAG ATAGTTAATC GCTACATCTG CACCTTCTTT 120

AGCATACGCA ATTGCTGCTG CACGCCCTAT TGCTGAGTCA CCACCTGTGA CTAAtATTTT 180

ATAGCCTTGT AAGCGTTGAT GACCTTGGTA AGACGTTTCG CCACAATCGG GTGCTGGCGT 240

CATTTCAGAT TGTAAACCCG GTACCTCTTG TTCTTGTTTT TCaTAATCCG TTGTTTTAAA 300

TTTTGTTCnA GGaTCTkGAG CkGCCAtTTT TtGACAyCtC CGTATnCGCT TAATGGGTAT 360

CATTTACCCC AATCTTCCTA AGG 383

(2) INFORMATION FOR SEQ ID NO: 3010:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 388 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3010:

TAATTCAACG GGAATTTTCC CTTTGAAGTT AACATAACGG TAGGCTGCTT TAACAGCTTC 60

ATCATCGGGC GCTTCGACAT CTTCTAATTC ATATGCAATG CCCAATGTTT TCCACTTATG 120

AACACCTAAC TGATGATATG GCAGAATTTC AAACTTTTCG ACGTTATCAA GAGAATTAAT 180

TGTCGAATCC ATACCAGGTG GTTTCATATC TGACAGTTTG CGCGCGAAGT TAAAGGATGT 300

GTGTATTAGG GCTTTCCCGG TCCATCCAAA TAnGGTTGGT CCATTAATCC ATAAGGTTTT 360

AnAATCnAAA TAATAATCCA GTCCGGTA 388

(2) INFORMATION FOR SEQ ID NO: 3011:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3011:

ACTGCTGTAA CGTCAGTTGA TCTTTTCATT CTTGGTTTAA TTTCTGAGAC GTTACTTGGT 60

TGnGCnAnGC CACCAATTGC CATACCGACA GATTGGAAGA ACAATGCATC AGTTCCACCA 120

ACACCAAAGA TGTCACCAAG TACAACGAAA CCTACATATC CAACTGTAGA TACAATTAAA 180

ATACCCATTG CTTTTTTAAA TTCAGGATTA TCTGATTGAC GTnCATTTTT AGCTTTAAGT 240

GAAGTAAGTG CTACACCAGT AACTAATAAT ATCATGGCGA TTAAACCAAA GATAATTTGA 300

GTCATTGAAG ACCATTCACC TAAAAAGATA ACGCTGGAAT AATGGTGTAC CCAACTAATT 360

GGCATACCTG GTAGGAAACT GGGCATAGGT ATTTGGATAC 400

(2) INFORMATION FOR SEQ ID NO: 3012:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3012:

TTATCGGATT CGTTAATACT GGCGGTTTAC GCAATAGTTT AGATGTAGAT GATAACAATG 60

TGCCTATTAA ATTTAAAGAA GAGTTCGAAC CTAGAAAGTT TGTTTTCACT AACGGCGAAA 120

TTAAATACAA TAGCAATTTC GAAAAAGAAG ACGTACCGAA TGCATCAAAC CAACAAAGTG 180

CGTCAGATTT AAGTGATGAG GAACTTCGCG GAATGGTTGC GAGTATGCAA ATGCAGGTGG 240

CACAGTAAAC GTATTAACAA TGGGATTAGC TCAACCAAAC GCTATGTTAA CACCACAGTT 300

GACTGACTGG AAACTACCAA ACCAGTACTG AGGGGnCGTT AATAATGAGT GTTTCCACTT 360

AAGCATAAAC TTTTGTTGGT CTTAAACGGC ATTAGTGTCG 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3013:

GGCTGTAATG AAAATCCAAA AGCCAAGCTT ATTTAATTCG CCTTCATGTG TGCGTGAATC 60

AATAGTGTTT GTATCATGAC TCATGACTTA CAGCCTCCCT TTCTTTAATA CGCGCTTCTC 120

TTAATCTAGC TTCAGTTTCT GCAACTTCAG CAGCAGGGAT ATGATATCCG TGATCGATTT 180

GGAAACTGCG ATAAATCATA GTACCAAAAA TACCGAATAA ACAAATTAAT GCTGGAATTA 240

CAGTTTCGAA AATTAAGAAG AAACCGCCGA TAGTCATAAA GATACCAATC CAGAATCCAA 300

CAGGAGTAAT GGTTTGGCAT ATGGATGGCC TTGGnAATAA TGGGTTGnCC TAAGTAATGG 360

CCGACCAAGG TCCTTTCCAn ATCCACCAA 389

(2) INFORMATION FOR SEQ ID NO: 3014:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3014:

AATCGCTTCG GTTAACTGTT CTAACCATTC GTAATAAACA TGTGTATGAT CAAGCTGAGC 60

TTTAATTTTT TGTGCCTCTT GTGTTTCAGC TTCAGTTAAA TCACTGCTTT CAAGTAATGG 120

ATTGATAATA GCTTGAGCAT CTTTTACTGC TTCGACATTG ATGTCAATTT CACGCTGGAA 180

TTTTTTAGTG AAAAAGTTTC GGAAAAAGAT GAAAAAGTCT TTCTCGGCGA TAAAATGTGT 240

TTGCGGCTCC TCTCGTAAAT TGTGGTTAAC AATATCAAAT TCCTGCAATT CCTAACGCAG 300

CACTCATACT nGTTGCnCAT TGCAATGATG ACGCATTCAC AGGGCAACTG CTCAACACAT 360

GGGCATAAAG TTCCACACTC ATAGGCAACA ATCATGGCGG 400

(2) INFORMATION FOR SEQ ID NO: 3015:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3015:

nCCTATCTCT GGTCGAGAGT CTTTGAGCTG AAAAATGTGA CACACAAAAT TGCAATGGnA 60

TCAACAAATG TTTCCCATTG TGGATGGTCT TGACTAAGTA TTTGGTGTTC AACTTGGTGA 120

TTTGCCATGA CTAATACCAT GTCATTTGTA CTTGTATCGC CATCAACAGT AATCATATTA 180

AATGTATGGT CAGTCGAAGA TTTTAATAAT TGATGAAGTG TATTCGATTC AATCGATGCA 240

TCGGTTGTTA TAAAAGCAAG CATGGTAGCC ATATTTGGGT GAATCATACC TGAACCTTTG 300

GTGCTACCAC CAATTGTAAC GGTTTACCAT CGATTTTAGT GATACAGCGA TATGTTTTGT 360

ACAGGTATCA GTGTTAAAA 379

(2) INFORMATION FOR SEQ ID NO: 3016:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3016:

CATATAAATT GCTAACGTGC CACCATTCAC TAAGGAATTG ACATCCACTT CATTTTCTTC 60

TGAATCTTTA AAGTGACCTG TAGAAAATGT CACACTTTTA GCAACTGTAC GCATTGTCAA 120

ACCTGTCTGC ATAGTAGCAA CTGCTGCGCT CGCTGATGTC ACCCCTGGTA CAATTTCAAA 180

CGCAATATGA TGTTCATTTA GTATGTCGAC TTCTTCTTGC ACACGACCAA ATATCGCTGG 240

ATCGCCAACT TTAAGTCTAA CAACCTTGTT ATATCGACGC GTGCTTCCAC GATACAGTCA 300

TTATTTTTCT GGCGGAAAAT GTTTGGAAAC GGCTTTTACC AACAnGGTAA TTCAGAGGCA 360

ATCGCAATGn AAATTACGGn TCACnAACGG TCATTGGATG 400

(2) INFORMATION FOR SEQ ID NO: 3017:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3017:

CCTTTTTCTC TTCTTTCATA TCTGCAAACG TGCATCAATT TTAGGATCTA AATCTCCAAA 60

TGCTTCTGCA ACTGGTTCAG AGCGTTCATA ATACATACGA ACTTTTGGAT ATAACGCTTT 120

TCATTTAACT GTTCATCAGT ATATTTATCA TATGCTTTTG TTGCTTGTTT TAATTCTGCT 240

TTAACACCAT CATCTTTTTT CGATGTCTTT GAATCATCCT TCTTACTATC GTCGTTCCCC 300

ACATGCAGCA 310

(2) INFORMATION FOR SEQ ID NO: 3018:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3018:

TCGCTTTGTA AATTCTGGAA CAAAGnCAGT CATGACAACA ATTCGTGTTG CACGTGCATA 60

TACTAAAAGA AATAAAATTA TAAAATTTGC TGGATCTTAT CATGGCCATT CTGATTTAGT 120

ATTGGTTGCA GCAGGTAGCG GCCCATCTCA GCTCGGTTCT CCAGACTCAG CTGGTGTTCC 180

AGAAAGCGTC GCACGTGGAA GTCATTACTG TACCTTTCAA TGATATTAAC GCCTATAAAG 240

AAGCAATTGG AATTTTGGGG TGATGAAATT GCCGCAGTAT TAGTAGAACC AATTGTTGGT 300

GAACTTTGGG AATGGnnAAT GCCTCAACCT GGGATTTTTA GGAAGAGGGT 350

(2) INFORMATION FOR SEQ ID NO: 3019:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3019:

ATATCATGTG CCAGTGAAAG CGGCACTGGn CGGATATGGC GCACATATGG ACATTATGAA 60

AGAGTACCAA TTAATCATTT TAGCGCCACA AGTTGCGTCT AACTATGAAG ATATTAAGCA 120

AGATACAGAT AGATTAGGTA TTAAATTAGC GArGACTCAA GGTGCTGAAT ATATCAAATT 180

GACACGrGAT GGCCAAGCAG CCCTTGATTT CGTTCAACAA CAATTTGAAA ATTAAGAATA 240

GGAGTTTTTC ATATGACTAA AACATTACCT GAAGGATTTT ATTTTTGGTG GAGCAACAGC 300

AGCATATCAA GCAGGAAGGT GCGACCAAAT TACGGGATGG GTTAAAGGTC GCGTGCATTG 360

GGGATACGGT ATTTTAGGAA GGAAAACTTA TTTGGTACCA 400

(2) INFORMATION FOR SEQ ID NO: 3020:

(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3020:

ACGTTCGTCT TACGTTTAAC GCCATACGGT GTATTAGCAA TTATGGnCCA ACACATTATC 60

GACAAGTGAC TTTGGCGCCA TTTGGACTTT AGGAAAAATT CTTAATCGCA TCGTACGCTG 120

CATTAATTAC GATGTATATC ATTCACTTAA TTATTTTAAG CCTGTTAGGT ATTAGCCCAA 180

TTCGCTATGT TAAAAAGACT TTGGAAGTAT TAATCTTTGC ATTCACATCA CGCTCAAGCG 240

CGGGTGCCTT ACCAATGAAT GTACCAACAC CAACCAGACG TCTAGGCGTG CCAGAAGGTA 300

ATGnCAATTT CGCTGCGACA TTTGGAATGG CGATTGGACC AAATGGGTGG GCAAGnAATT 360

A 361

(2) INFORMATION FOR SEQ ID NO: 3021:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3021:

CAATGACCAT GACCAGTTGA TTTGGAACAA TGATTGACAT TGGAGCTATG CATCAAGTTT 60

GTCTTTAAGA CTACTAAACC CACGAACCAT GTTAACCCCG TGGTGCACCA TCACCAATTG 120

nCTCGATCTA ATTCAGTTAA TTCAGATTCA TGTTTTTTAA ACGTTTCTTC TAAATTTAAT 180

AAACGTGnCT TTCATATCAT TCACTTTCAT TTGTGnCCAC CTCATAAATG TATATTATCA 240

TATTCACTCT TATTAAAGTA TGACTGTTGT TGGTGCTAAA AATGCTCCAA ATATTCGGTT 300

TATTAGGCAC GATAGTTATA GAAAAACCTG ACAGTCTAAA GATGTCATAT AATCAC 356

(2) INFORMATION FOR SEQ ID NO: 3022:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3022:

GTGTTTGGTC CAATATCCAT ACCTTCTTGG nTCTGCTGGA ATTGAATCAG ATGGTACTAC 120

AGTGATTTTG GCATCATTAG nAAAATTCTT TAGTCAACTT TAGTGTCTAC TGGTAATACA 180

ATTTTATCAC CATGTTTTTC TAATAAATCT TTTGCGAGTC GGATTTTATC TTCTTCTAAT 240

AATGAAATAC CAATTTCTTT ACCTTGCGCT TTTAAGAAAG TATAAGCCAT ACCTCCGCCG 300

ATGATAATTT TATCAGCTAT GTTAACTAAT AA 332

(2) INFORMATION FOR SEQ ID NO: 3023:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3023:

AAAGGTATTC CACAAGAATT AGCTTTGCAA AAATGCCAAA GCAAACAGAA GATGGnACAA 60

TTTAAAGTGn CCTACAATCA TGAATGAGGA GGACGCGTAA GATGAGCATT CGCTACGAAT 120

CGGTTGAGAA TTTATTAACT TTAATAAAAG ACAAAAAAAT CAAACCATCT GATGTTGTTA 180

AAGATATATA TGATGCAATT GAAGAGACTG ATCCAACAAT TAAGTCTTTC TAGCGCTGGA 240

TAAAGAnAAT GCAATCAAAA AAGCGCAAGA ATTGGATGAA TTACAGGCAA AAGATCAAAT 300

GGATGGCCAA T 311

(2) INFORMATION FOR SEQ ID NO: 3024:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3024:

ATTAGACATT ACAAGGTGCA GTACGTGCAA CATATTAGAC ATATTGAATT AAGTGGTCAT 60

GnAAGGTATT GACAGTTAAA AAAGTTGAAC AATTAGAAGA AATCGAGGGC TTAATATTAC 120

CTGGTGGCGA GTCTACAACG TTACGTCGAT TAATGAATTT ATATGGATTT AAAGAGGCTT 180

TACAAAATTC AACTTTACCT ATGTTTGGTA CATGCGCnGA TTAATAGTTC TAGCGCAAGA 240

TATAGTTGGT GAAGAAGGAT ACCTTAACAA GTTGAATATT ACTGTACAAC GAAACTCATT 300

CGGTAGACAA GTTGACAGC 319

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3025:

GGTGCCAAGC AATAAATATG ACTATGCTCA AACTGAATTA ATGGTGGGTG TGTCGCCATC 60

GTAATTGGAT CGTCTGAAGG CGCATATAAA TGATAGTGCT CTTCGAATAA AGGTAGCATA 120

TGTAATTGTT TGTGTTTACG TATTTCTGGT GGTAAGTTCC GTGAAACCCA ATGTCTATAT 180

TCCCATTTAA TACGCTATTT ATAAnTGTGT CATGTTCTAA TAAGCTCGGT ATGACATGTG 240

TATCATTTTG TAAAATGAAC GTTTGGATAA GnGGGAGTAA CATGTGGGAT ACGTCACTCT 300

CATCAAGCCA TGTAGATACn 320

(2) INFORMATION FOR SEQ ID NO: 3026:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 328 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3026:

TCTCAACAAA TGCATCCAGT ACTTAAATTG GCATTATAGT AATTTAAGnA CAATATATCA 60

ATATTTCTCC TTATCCAGCA ACAGCAAATT TATTGGTAAG GTGTACGATT GAACCTTTAG 120

TCAATGAAGC AGGTACATTT GGATTGGCCA GGTGGATTTA CTTCAACTGA GCGCTTTGTG 180

AGAATGGGCA TTTATGAAAG CAAACATTGC TCAAAACAAT GATAAAGAAA TGGATTTAAT 240

GAATGCATTT TATTTATTAG ATGCGGTAAA TATACCGATT GGAATTGTAC GTCCGCATGA 300

TGCTGACAAT CACTATACGA TGTATCCA 328

(2) INFORMATION FOR SEQ ID NO: 3027:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3027:

ATTGAAAATA TGTGTTCTnT GTAAAATTTT AATCGTTCGC CACGATGCTG TTGATAAAAA 120

TTCAAAAACT GGAGTTGATC TTCTAGTTCA ACATAATCAT CGTAATTAGA CATGTAACCT 180

TTGATTAAGA TTTCAAGTAC ATGATCTTCG ATAGTATTGn TTTTAACTTG TTGTTGAGCC 240

GCTATATCTT CCATCGTGGA ATTGTTCAAG CAATTTTGTA TAAGTAATAT AAGTTCGATT 300

TAATGAATGT AGGTTTCATT AT 322

(2) INFORMATION FOR SEQ ID NO: 3028:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3028:

CAAGAATCTT ATACTTATCA AAATTTATAC TGTGAAGCGA GTCTATTGGC TAAAAGACTC 60

AAGGCTTATC AACAATCTCG TGTTGGGCTA TACATAGATA ATTCGATTCA ATCGATCATT 120

TTAATACATG CATGTTGGTT GGCAAATATT GAAATTGCGA TGATTAATAC AAGGnTGACA 180

CCTAATGAGA TGACGAATCA GATGAAGTCA ATCGATGTAC AATTGATTTT CTGTACCTTG 240

CCACTGGAAT TACGAGGGTT TCAAATTGTA TCGCTGGATG ATATTGAATT CGCCCnCCGG 300

GCnTATTACA ACG 313

(2) INFORMATION FOR SEQ ID NO: 3029:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3029:

CTTCCAAAGA AAAGACCACA GTTTTTGACG CATCAATATG GTGCAATTTT AGAGACACTG 60

TAGTTGCAGA AGATGGTTCA GTTGGACTTT GAAGACAATC GTTATACAGA AACACGCGTG 120

CCGCTTATCC AATTAATCAC ATTGACAATA TTGTAGTACC ATCTAAAGCA GCACATCCAA 180

ATACAATTAT TTTCTTAACT GCGGATGCAT TTGGTGTTAT TCCACCGATT TCAAAGTTAA 240

ATAAGACCAG CAATGTATCA TTTCTTGAGT GGTTCACTTC TAAATAGCTG GnCAGAGCGT 300

GGTGTGACAG ACCTGACCAT CATCTCAACA TGTTCGnGCA CCGTCTTCCG TACATCnACT 360

(2) INFORMATION FOR SEQ ID NO: 3030:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3030:

TGATGGATTG GCTAGCAGGT GTTTACATTA ACTCATTAAA TGTTATTCAC TACATGCACG 60

ATAAATACAG CTATGAACGT ATTGAAATGG CATTACATGA TACAGAAATT GTACGTACAA 120

TGGCAACAGG TATCGCTGGT TTATCAGTAG CAGCTGACTC ATTATCTGCA ATTAAATATG 180

CACAAGTTAA ACCAATTCGT AACGAnGAAG GTCTTGTAGT AGACTTTGAn ATCGAGGCGA 240

CTTCCCTAAA TACGGTAACA ATGACGACCG TGTAGATGAT ATTGCAGTTG ATTTAGTAGA 300

CGCTTCATGA CTAATTACGT GGTCATTAAA CATATCGTGA TTCAGACCTT CCATGGGnGT 360

ATTACCATTA CTTCAACGTG GTnTCGGGTA GAAACTGGGT 400

(2) INFORMATION FOR SEQ ID NO: 3031:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3031:

nGCGTTTAAT CACATCTTTT TGATAATGTT CCCTTACCAT TTCTTCATGT GCATCTGCAT 60

AGTCTTTTCC AAATGGCAAA CTAAACTGAT ATGCAACTTT TAAATAGGCA TCTATATGCG 120

ACTCGTCAAC GATGGCAATT TCAACGTCnA GTTACGCGGA CAAATTGGCA AGCGCATCAC 180

TTTCTATGGC ATACAATTCC ATAATACCTA GTTCAAAATT CATATCTTTA AAACATAGCC 240

ATCCAATGGA TTATCAAGTT GTTCATTTTC CGGGAAAACT nAAACGCATA AATGATTTGG 300

AACCTTGATT TGTATGTGA 319

(2) INFORMATION FOR SEQ ID NO: 3032:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3032:

AAGAAGTGGC AATTATGATT GATGCTCTAG CTGACAAAGG GAAAAAAGCA TTAGAAGCAT 60

TATCTAAAAA GTCACAAGAA GAAATTGATC ATATTGTTCA TCAAATGAGC TTAGCAGCTG 120

TTGATCAACA TATGGTGCTA GCAAAATTAG CACATGAAGA AACTGGAAGA GGTATATACG 180

AAGATAAAGC GATTAAAAAT TTATACGCTT CTGAATATAT ATGGAATTCA ATAAAAGACA 240

ATAAGACAGT AGGGATTATT GGTGAAGATA AAGAAAAAGG ATTAACGTAT GTAGCGGAAC 300

CAATTGGTGT TATTTGTGGT GTTACCGCCC AACCACCAAA TCCCTACGTC CGACCACCTA 360

TTTTTAAAGC CGATGGATTT GCCATTTAAG ACnGGGAATC 400

(2) INFORMATION FOR SEQ ID NO: 3033:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3033:

TAGCGGTAAT CGAAATTGGG GACTAAATTT CGCAAAAGCG GGTCGCACGA TATCAGAAGA 60

GTATAATGTC CCTTTATTAA TGAAGTTTGA GTTACATGGA AAAAACAAAG ACGTTATTGA 120

ATTTAAGAAC AAGGTGGGTA ATTTTAATGA AAACCATGGA AGAGAAAAAG TACAATCATA 180

TTGAATTAAA TAATGAGGTC ACTAAACGAG AGAAGATGGA TTCTTTAGTT TAGAAAAnGA 240

CCnGAGCTTT AGTAGCTTAT TTAGAGGAGT AAAnGACAAA ACATCTTCTT CGACACTGAA 300

TCG 303

(2) INFORMATION FOR SEQ ID NO: 3034:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3034:

CTnCGCTATT TTGTAGGACA TCTTCTAAAG TGCTAGGnGA AGAGATTATA GAATAGGCAC 60

TATCAATACC GAAATCGTAA ACATGTTGAT AATTTTCGCC TAGACTGCCA CAAATCGCGA 120

TGACAGGAAT ATGATATTGT TTTGCAGCTA ACGCAACGCC TGACGGGTGT TTTACCAAAG 180

TGATGAAAAT CTGTAATGTC AAAGACGGAC ATCAATGACT TTTGTTGAAA GTTGTCTCAC 300

AAAACGnTAA TGAATGCTGC GGCCCATGAC CGGCCAGCTG 340

(2) INFORMATION FOR SEQ ID NO: 3035:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3035:

AAAGAACATG GTGTAGCAAT AGTCTCTGGA GGTGGAAGCG GACATGAACC TGCGCATGCC 60

GGTTTTGTTG CAGAAGGTAT GCTAGATGCA GCGGTTTGTG GCGAGTATTT ACATCACCTA 120

CACCTGATAA AATATTAGAA GCTATTAAAG CAGTAGATAC TGGTGATGGT GTATTACTAG 180

TTGTAAAAAA CTATGCAGGT GACGTGATGA ATTTCGAAAT GGCACAAGAG CTTCCAGAAA 240

TGGAAGGTAT AAATGTTCAA ACTGTTATTG TTCGTGnCGn CATTGCTGTG ACAAACGnGT 300

ACA 303

(2) INFORMATION FOR SEQ ID NO: 3036:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3036:

GGGGAAAGTA AATTAACAGC TGTGTAGAAT AATTAAGGTT TTAATTTATA TAGAACAACT 60

TATTGTAAAC TTTTCATTTC TTAAAGTTTA CAATGGTGCT ATAATAATGG TCATGAAATA 120

CGAAAGGAAG GAAAAAATGA CnACAAAACA GTTAGTATAT ACAGCTTTAA TGACAGCGAT 180

TATCGCTAGT TTAnGATTGG TACCGGTAAT TCCACTACCA TTGnCTTCAG TACCAATTGT 240

ACTTCAAAAC AGTGGTATTT CTTAGCAGGG GCGATTTTAG GACGTAAATA TGGCACATTA 300

AGTGTTATCG TCTTT 315

(2) INFORMATION FOR SEQ ID NO: 3037:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3037:

GCACCAATTG ACGAAGGAAT ACCGAATCCC ATTGTTCCTA AACCACCGCT TGTAACCCAT 60

TGTCCGTGAT TTTTAAATGG ATAAAATTGA GCTGCCCACA TTTGATGTTG TCCCACGTCT 120

GTAGTAACAA TTGCTTCACC ATTTGTAATT TTGCCGATAT ATTCGATTGT TTGTTGTGGC 180

TTACAAAATA CTTGATCTTC TTCACCAAGT TTAAATGGGT GTTTCTGCTT ATTATTTTGA 240

CAATGTTTAA CCCAGTCACT GTGTTCTATA GTCTCAACAT TTTTATCATT TAAACCnTCC 300

AAAAAACCTT TACAnGCCnG CAAAAAAACC 330

(2) INFORMATION FOR SEQ ID NO: 3038:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3038:

GTGAGTCCAC ATAATAACTT TGACGTCCTG TTAATGTTCT AAAAGGTACT AGACGTTCTA 60

TATTCGTTGT AAATGGTGAA TATCGTCGAC CTTGTTTATT TGAACCTGGG AATACTGCTG 120

TCGGTATTAC TTCTCGTGGT TGTGAAGTTA TATTTAAAAA CGAAATTTTC TCAGCAGCGC 180

TGTCGCTAGA AATATCTTTT AACGGCATTC CAGTTTGTTC TTCGAGATCT TCATATGGAT 240

TTTTGTGnAT AATTnACCAT TCGTAGCAGA TGGAAATACT TGAGTATnGG CATCAGCGAC 300

ATTGACGTGC TGTATCAATA CGTGGACGAT TCGC 334

(2) INFORMATION FOR SEQ ID NO: 3039:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3039:

GGTCTGATCG TGGTGAATGA AAAAGGTTCT TCTCTGTAAT GAATTATCTC TTACCGATGC 60

AAGATATTAT GAGCATGCAT TGCTCAGCAA ACGTTGGTGA AAAAGGCGAT GTTGCATTAT 120

TCTTTGGTCT ATCTGGCACT GGTAAAACAA CCTTTATCGG CTGACCCACA CCGTAAACTA 180

ATGCAAAAGC AATTAATCTT TCCAAAGAAA AAGAnCCACA GnTTTTTGGA CGCATTCAAA 300

TATGGTGCAn TTTTAGAGAA CACTGTA 327

(2) INFORMATION FOR SEQ ID NO: 3040:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3040:

GTGATATTCA CGAnCGTTAT TTTCAATATT TGATAAGTAG AAAnTATGAC GATCTTCATG 60

AACAGCATCT TGTTCTTCGT CAAATTCAAC GTCATCAAAA CGTTTGAAGA ATGTTTCATA 120

TGCATCAACA GATACTTCAG TACGGTTATT TAATAATGCT TTATGTGCAG CTTGGATCTA 180

AATGATCTTT GTAGCCTTCA ACTnAATGTC GCACTATAAA ATTCACCAAC TGAACCTGAG 240

CCATAACTGA ATAAACCGAT TGTTTCCACC AGCTTGTGAA TCTCGATTTT CAAGTGAATG 300

ATATT 305

(2) INFORMATION FOR SEQ ID NO: 3041:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3041:

GTTGTGTACC TTAAATGATC AACCGATGCA TAAGAAGAAA GTGAGACGTC ATCAAATTGG 60

TGCTGTATTT CAAGATTATA CGTCATCATT ACATCCATTT CAGACTGTTA GAGAAATCTT 120

ATTTGAAGTG ATGTGTCAAT GTGATGGACA ACCTAAAGAA GTTATGGGAA GTCCAAGCAA 180

TTACATTGTT GGAAGAAGTC GGTCTATCTA AGGCATACAT GGATAAATAT CCTAATATGT 240

TATCAGGTGG AGAGGCGCAA CGTGnTGCAT nTGCGCGTGC AATATGTATT GAACCCnGAA 300

ATATATTTTG TTTGGAT 317

(2) INFORMATION FOR SEQ ID NO: 3042:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3042:

AATCTTCGAA AAATAATGCA ATGCAGATTC CGAAAAAAAC AATATGATAG AAACACCTCA 60

ATTAAATACA ACGGCTAATG ATACATCTGA TATTAGTGCA AACACAAACA GTGCGAATGT 120

AGATAGCACA ACAAAACCAA TGTCTACACA AACGAGCAAT ACCACTACAA CAGAGCCAGC 180

TTCAACAAAT GAAACACCTC AACCGACGGC nATTAAAAAT CAAGCAACTG CTGCAAAAAT 240

GCAAGTTCAA ACTGTTCCTC AAGAAGCnAT TCTCAAGTAG GTTATTAAAA CACGGATGGT 300

GCTAATAGCT TnGCAACAAC GTGGGCTTTA AAATTCTCCA ACTTTAGTTT T 351

(2) INFORMATION FOR SEQ ID NO: 3043:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3043:

ACGnCCTTAC TGGnTACTTG GTTGATAAGT GTTAATCCAA ATGACGTCCT GCTACGTACA 60

GCTTTACGAA TATTTAATGC ACGTGTGATA TTTTGAGAAA ATACACCGCC TGGCTAAACC 120

ATACTCAGAA TCATTAGCTA TATCAATTGC TTCTTGATCG TCCTTCACTT TAATCACTGT 180

TAACACTGGT CCAAATATTT CTTCTTGTGC TAATTTGTGA TGATTGTCTG GCACnCAATT 240

AATGTCGGCT CAAAGAAGAA CCCTTTATCT AATCCATTTT CAGTTAAGCG ATGACCGCCT 300

GCTAAAATTT GTGCATCCG 319

(2) INFORMATION FOR SEQ ID NO: 3044:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3044:

GTCATATAAT CTAACATTTG TGTTATCTGT TAATTAACTG GnTTTTACCT TAATTTGTTA 60

CATTGnTCTG TATTAAATCT TTTTGTAACC ATTGGTTACT TTTTCAGGTG GAATTTCAAC 120

ACCCATGTCA CCACGTGnCA ACCATTAAAC CATCAGACAC TTCAAGAATT TCCGCAATAT 180

AAATTCACGA ATTTCTAAAA CATCACTAGG TACGACGTAC GAAACTTGCT GCAATGAAGT 300

CAACATTTTC TTTAATACCG AAACGGATAT CTTCAGCATC TT 342

(2) INFORMATION FOR SEQ ID NO: 3045:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3045:

TAATATCATG TTGTGCTTTT AGTGCTTCGG CAATTTGTTT TGTACTTACT GACCCAAACA 60

ATTTACCACC TTCACCAGTT TTTGCTGATA CTTCAACTTC AATGTTTGAT AACGTTTCTT 120

TTAATGCTTT ACATCTTCAA TTTCTTGTTG GCGTTCTTGT TTTGCACGTT TTTTCTGTAA 180

CTCTAATTGT TTAAGGTTAC CTGGTGTTGC TTCTACAGCA TAATTCTTTT TCAATAAGAA 240

GTTATTTGGC ATAACCTACT GGTACTTCTT TAACTTCACC TTTTTTACCT TTACCTTTAC 300

CTTTAACAnC TGTGTAAAAA TTACTTTCAT GCAGnTCACT CCTACTTAAA TGTTCCGTAA 360

TGCCTGTTGT AATGTGCCAA CGCCnCTCGA CGTGACACCT 400

(2) INFORMATION FOR SEQ ID NO: 3046:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3046:

AATCACTGTT TCATTACTTG TTCCAAATCT GnATTCAAAC TATTGTTCAA AGATTCTAAT 60

TCCGCTTTAT TTTTATCTTT AATCGCTTTT GTCATCGCAG CATCTTTAGn CATCGACTTn 120

CTGTTGCAAT AGTTTAATTT TAGAACCCGC ATCTTTACTA GCCAATTTCT CTTCATAAGC 180

AATTAATGAC TTCGTTAATT GCGAAAGTGT ATCTTTTTGA TTATCATTCG CTTTTGCATC 240

TTCAAGCTTT CTCACATCTG CATTTGACAG CATTACTTGC ACTATTATCT TCAAGCGATA 300

ATTTCT 306

(2) INFORMATION FOR SEQ ID NO: 3047:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3047:

ATGGATCATA TTAGCACGTA AAAGAAAATT CTGTTCATTA TGAAGAAGTG CCAGAnGTTG 60

AATTTAAACG CACATATGTA TGTGAAGATA TGTCTAAATG TATTTGTTTA TACAACGCAC 120

CTGATGAAGA AGCGGTAnTC GCGCGCGCAA AGCAGTTGAT ACACCGATTG ATGGCATCGA 180

AAAACTTTAA TAAGACAACA AGTTGATGAG ATATATGTAT ATAGGTTTGG CATGGATTTC 240

GATTGCAnTT ATTAGAATAG CTCAATGCTA TAAATGTAAG TAGTTGATAT TGAGGAACTA 300

ATGAAC 306

(2) INFORMATION FOR SEQ ID NO: 3048:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3048:

GACAGGCTAC GAGATATTTT AAACAAATTT ACATCAAATC CAGTATTAGG TGTTATTGCA 60

GGTATCGTTG TAACTATTTT AATACAAAGT AGTTCAGGTA CGACATTATC ACAATCGGAC 120

TGGTAACnCT GGATTTATGA CATTGAAACA AGCCATTGGA GTGATAATGG GTGCTAATAT 180

CGGAACAnCG GTAACTGCAT TTATTATCGG TATAGATTTA GGCGAATATG CAATGCCAAT 240

TTTAGCATTA GGTGCATTCT TGAATCTTTT TCTTTAAACG CTCTAAA 287

(2) INFORMATION FOR SEQ ID NO: 3049:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3049:

CATATAAATA GCGnTACATC GCGCCATTCT TGATCTGnAC ATATCTTTCT TAGGTCCAAC 60

CGTGAATGAT TACGTCCATG ATAACGTACA AACGCAATTT CATTTGTGAT TCGATTGACT 120

AAAGGTACAC TGCCATCTTT CACTTGTGGT TCATCAACTA CTGCATGAAT GATTTGATGT 180

AATTCTACAC ACATTGGAAA GCTTGTAATG CTGTCTTACA TACAAATATA TTGATATTTG 300

TGCATGCAGT CAACCAGGCG GAAATGACCA TACCATGCTA ATTTTCTGGT AnGAAGGCCT 360

ACATATCTAA A 371

(2) INFORMATION FOR SEQ ID NO: 3050:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3050:

CGCCAAATAA AGATAATACA CGTATTGGTG AAGATATAAC TGTAACTGCA CATATCTTAA 60

TTGATGGCGA AACAACGCCG ATTACGAAAA CAGCAACATA TAAAGTAGTA AGAACTGTAC 120

CGAAACATGT CTTTGAAACA GCCAGAGGTG TTTTATACCC AGGTGTTTCA GATATGTATG 180

ATGCGAAACA nTATGTTAGG CCAGTAAATA ATTCTTGTCG ACAnATGCGC AACATTGAAT 240

TTCCAATTTG TTGGAnCATA TGGGCTAACA AGGTGTTTAG GCATATCTAC TCGTCTTATT 300

GGGTGCATAT GTAATGGCAA GCA 323

(2) INFORMATION FOR SEQ ID NO: 3051:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3051:

CCGnACCAAT CGGTTTACAG TTCATTGGTA AACCATTCGC ATGAAAAAAC GTTATATCGT 60

GTCGCTTATC AATATGAAAC ACAATACAAT TTACATGACG TTTATGAAAA ATTATAAGGA 120

GTGGAAATCA TGCATTTTGA AACAGTTATA GACTTGnGTT CACGTAGAGT TAAAAACGGA 180

CTCAAAAATG TTTCTCCATC ACCAGCGCAT TTnGAGCAGA ACCTAACTCA AATACGAATG 240

GTATCGCTTA GCATATCCAG TGCTTACCAG TTGTTAATAA GCGTGCGTAG ACGGGCATGC 300

GTGCTGCAAT GCCTAAATAG GAACG 325

(2) INFORMATION FOR SEQ ID NO: 3052:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3052:

CTTTTAATCG CTTGAAAACT ATAGGTAAGA CAATACAAGT AGCTACAAAG CCATATATTA 60

CTGTTAATTG ACCTATGAAA AAATATCCGC TAACGGGTGC CGTCAATCCT GCGATAGCAA 120

TACCAATAAA AAGTACAGTC CACGAAGGAT AAACATTTTC AAGTGAAAAA TCTTTTAAAT 180

ATTTTATTGA AAAAATAATC ATATGCGTCA TAATTCCCAC AAGGCATAAA ATCCAAATAG 240

GCGTATTAAG CTATTGTAAA GTTTGTTACT AAAAAATGTT TTAAATAGTG TnCTAAAAAG 300

CCGGCATGAA AATGTGTGAC CTGATGAACT GAGGCTGTTA TTGTCTTCAC TTATTAAATT 360

TGTCTAGTCT AAAGGTGATC CAATCAGAAG CAAGTCCGCA 400

(2) INFORMATION FOR SEQ ID NO: 3053:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3053:

AATGAGATGC GAAGGATGAT CAGAGAAAAA GTCTCTCAAT CAGGTGTGAA AGTCAGATGG 60

TTATCACAAC TTTGGCGTAC GTTTTCGATA TAATGCACTA GGTGATTTAA ATACGAGCAA 120

TATTGTTTCT TCAAAAGAAA GTTTCGGTAT TACTGAAGTG TGAAATCTGT CTCTATGCAT 180

GCCGGATCGA CATTAGCATT ACTAATCCAG AGAAAGCAAA AGGTATTGTG TATACACCAG 240

AACATTGCCA GCGAAAAGTA AATGGTCACA GCTGTAGAnC AAGGTATTTA TAATGGGGGC 300

GGTAAAGCAG AAGGCCCCTA TGTAGCATTT CnTAAAGnTG GGAAAAGGTA AAGCAGCATT 360

ATCGGTG 367

(2) INFORMATION FOR SEQ ID NO: 3054:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3054:

TnATTTATCT nAGCTCATGA CATGATGGCT GTTCACATTG CAAGGCGTTG ATGATnAAAT 120

AAGGAAAGGC ATTAGGAAAA AGCCACAGGG AAAACATTTC AGCAGCAGGT TCTTGGAATC 180

ATATATTCAA GTTCAACAAG CGAATGCTGT TAAATTGCCC TTTGGATGAC AATCAATTCG 240

ATATCGTTTT AAATGAAGCA ATGTTAACAA TGTTACCCAT CGCCATAAAG GAAAAAGCAT 300

TACGCGAGTA CTACCGAGTC TAAAGCCTGG GGGTATCTGT TAACACATGA TATTGTCATC 360

GTTAATGAAT CACATGCCAC AC 382

(2) INFORMATION FOR SEQ ID NO: 3055:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3055:

CTTAAGATTA GGTGTGCTTA ATTAGTACTG GCTGGGAACG ATAAAGGCAT ATTGCAAAAA 60

ATAGAACATC CATATCCATT AAATGTATTT ACGCTAAATA TTGnCGACTT ATATTTTTAG 120

ACATAGAGAA GAGACAAGAC AATTTTTAAC GATGCAACGA CAGTTAGGCT GAGGCAGTTA 180

AAACAAATAT TTGATACACA TGTTGnCAGA TAAAAGTCAG TGTTCCCATC AAATGCnAAT 240

TTTGTACTAC TAAAAGCTCA GCAGCGCAAC AATTAGGACA ATACGTATAT GAACAAGGGA 300

TTTAAACCTC GCTTTT 316

(2) INFORMATION FOR SEQ ID NO: 3056:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3056:

GTTCACCATC CGTTTATTTC AATGAAAAAA TCGACAAAAA TGGTCGTGAA AACTATGATG 60

CAACAATTAT TCCAAACCGT GGTGCATGGT TAGAATATGA AACAGATGCT AAAGATGTTG 120

TATACGTACG TATTGATAGA ACACGTAAAC TACCATTAAC AGTATTGTTA CGTGCATTAG 180

GGTTCTCAAG CGACCAAGAA ATTGTTGACC TTTAAGTGAC AATGAATATT ACGTATACTT 240

AGAGAAAGAC nGCACTGAAA ACACTGACCA GCGTATTAGA ATCATGACGT TACGTCCAGT 300

CTTAGCAGCG TGGGnCGTAT 380

(2) INFORMATION FOR SEQ ID NO: 3057:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3057:

TATGTGATGG ACTTAAAAAA ACGAACTCAA TTAATACAAT GGGCTCAAGA AAAAGAAGAA 60

CGATTTATTA TAGAAGATGA TTATGATTCC GAGTTTAGAT ATTTCGGCAA ACCCATTCCA 120

GCAATTCAAG GTCTATATTC AAGAGGAGAA AAAGTGATTT ATATCAGTAC ATTTTGCAAA 180

GTCTATTTTT CCTAGCTGTT CGAGTTGGCA TATATGGTGT TACCCTATTC TATnATGGAA 240

AAAATATCAT TTCTnCAAAA TCCACCATTG GAAGGGCAAC ACTGGTAACC TGTTTCATAT 300

GGCAAAACCT TATTGGCAAC GTTTnAT 327

(2) INFORMATION FOR SEQ ID NO: 3058:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3058:

CGAAAAAGGA GAATGAAACA TGAGGTAATA CAACATTACA TGCAACAACA ATTTATGCGT 60

GTAAGACATA ATGGAAAGCA GCTATGGCTG GAGATGGGCA AGTAACGCTT GGTTCAACAA 120

GTCATCATGA AACAAACGGC AAGAAAAGTG CGACGTTTAT ATGAAGTAAA TGTTAGCTGG 180

TTTCGCAGTA TGTAGCAGAT GCGTTTACTT ATTTGAAAAA TTCGAAACAA nATTACAACA 240

GTTTAGTGGT AACTTAGAAA GAGCnGCTGT TGAATTGGCA CAAG 284

(2) INFORMATION FOR SEQ ID NO: 3059:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AAAGAAGCGG ATGAAGAGCT TTGCATTGAG CTCGACCCAG GTATGGCTTT TGGAACAGGT 60

GATCATCCGA CTACAAGTAT GTGTTTGAAG GCAATAGAAA CATATGTATT GCCACAGCAT 120

TCAGTAATTG ATGTTGGTAC TGGCTCAGGT ATATTAAGTA TTGCAAGTCA TCTAATCGGT 180

GTAAAACGTA TTAAAGCGTT GGATATTGAT GnAATGGCAG TGAGTGTAGC TAGAAGAnAA 240

CTTCAGAAGA nATCATTGTG AACGTTGAAT TGGAAGCTGT TCCAGGTTAA CATATTGGAA 300

AG 302

(2) INFORMATION FOR SEQ ID NO: 3060:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3060:

TTTTTAAnGA CACATTGnGC TGTGTTTAAT GCATGAAAGG AACCACTGAC ATGCATnAAA 60

TCTTTGAATG GTTCTTTATC AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTTAAATCAA 120

TATAATTCAA AAAGGGTCGA GGATATGAAA TCACATCTTC GACCCTTTAT TTACTATTTT 180

AATTCAGCCA CACGCAAACG GTTATTTGCT CTCTCTAAAG CTCTTTCGGC TCTATGGAAT 240

ATCAGTATTG TCGTCAATCA TTTTCCAAGT GAGACTCTGC TCTTGCTTTG GCTAATTTAG 300

CTCTTTCAAC ATCAATTTCT CTTGCAGTTC 330

(2) INFORMATION FOR SEQ ID NO: 3061:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3061:

CGATCAATCA ATATAATTCA CGGCGCAAAA CGTTTATTTA GCATGTTCTT GCAGACTCTG 60

AAACTGGCAT TAAACCTTCC ATTAAGATTT TTACCATTCT AGGCATTAAT ACCATTACTG 120

CAGCCATTGA CATTCCTAAA TTAATGATGT CTCCAGGTTT GTAACCTGCT AAcACACCAA 180

TACCTAAmCC TAAAATTAAG CCGACAAATA TAGACTCTCC AAATGCGCCA AAACGTTTTT 240

GAATTGnTTC AGGATCAGCA TCTAACTnAT TCAGACCGGG TACTTTTTGT AACAATTTAA 300

(2) INFORMATION FOR SEQ ID NO: 3062:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3062:

TATAAAATCA ATGATTTTAA CAAATAAAAA CGTACCGCAA ATACTGCAAA TAACAGCAAA 60

TACTAGTTTT AATAAAATAT GACCGGTTGG AAAGAACAAT AAAGCAATTA AAATACCTAG 120

TTTAGCCCAT TCCATCGTTC CAGCTGTAGT CGGACTAACA AACTTATTTT GCATCATTTG 180

TTGGCATTAT CAAGCCTGCT GAAAGCCAAC GAACTTCCAG CAATTAAAAT ACTCATCGTC 240

CTTGGTATTC GGGCTTGGAG AATAAAATGA TTCCGCTGGT GACTCAGTTG AAATGTAGTG 300

AAATCTTTGA ATTGGATAGT TnCACTGCAC ACCTGATGGn AnCAACGGAA 350

(2) INFORMATION FOR SEQ ID NO: 3063:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3063:

TTAGTGATTT TAACGTGTAT CGGTAATTTT AAATAAATGT TTAATGCTTT TGAAAATACA 60

GTTCTAACCG AAGACGTCGG GTACACTGAA TCACCGGAAA CGCCAAGGTC TTTTATTAAA 120

CCTTGTTCAC TATATTGCAT ATACTGTGGA TGCTGTCGCA ACACATTGAT TTGATAAGGA 180

TGTGTTGGTA ATAAAATAAA ATCTTTGGGT ATCTCTGATA TATCTATGTC TGCTAATTGG 240

ATACnACACT TTCTCAACCT GGATCCTTCC TTTTACCTnC CACCATAGCC GCGTGGAnCA 300

GGAAACCATC CTGGGATGCA CCAGCCAAAA TAAATGCCAA TT 342

(2) INFORMATION FOR SEQ ID NO: 3064:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GTCCAGCTCC AGAACCAAAC TTAACAGTAT TATGGTCAGT ACGTTTACCT GACAACTTCA 60

AAACATACTG TGCAAAAATG AGTATTAAAA CAAGTTCTAT CCAATATGAA AATGATGACA 120

TTATGCGTGA AAGCTATGGC GATGACTATG GTATCGCnTG TTGTGTATCA GCGATGACAA 180

TTGGTAAACA AATGCAATTC TTCGGTGCAC GTGCGAACTT AGCnAAAACC TTACTTTACG 240

CTATCCATGG TGGTAAGATT GAAAATCTGG TGCACAAGTG GGCCCAACCT CCGAGGGATT 300

nACCAGCGGA GTAATT 316

(2) INFORMATION FOR SEQ ID NO: 3065:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3065:

TGATTGCGTG GATCAGCAAC TTCAAAGATT AACAAATAAT ATTACTTGGG CAGATAACCG 60

CGCTGCAAAA TATGCAACAG TAATAAATGA AGTGCATGAT GGGCAATGCG ATTTACCAGC 120

GnACAAGCAC AnCGGTTTCA TCCTATGTCG CCATTAGCGA AGATTTTTGG ATGAAACATG 180

ATGGCCAGAT GTATTTCCAC GTACTGCTAA GTTTGCAGAT ATTAAAACAT ACATTTCTAT 240

CATTATTGAT ACATATATCA TTGATTATTC CATGGCTTCC GCnACAGGGA TGTTAATTAG 300

AACATAGATT GGAGTGAGGC AT 322

(2) INFORMATION FOR SEQ ID NO: 3066:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3066:

TATAAAGAAT CCTGCCTTAC CTAAGAACAC TTGTCTTGTC GTTAAGACTG ACTCTAGACT 60

CTTATGTTTA TTATCAACCG TTAATAAACT TACCATCAAG AGTGCACCTA CCCATACTGA 120

CAGTGCAGTA TAGAATGGTG TCATACCTGA ACCATAATCC TTAACTGGGA AAACATCAAC 180

AGTCTTCTTA TTAATAGATT GCAATAATAC CCGCTGCTTT TTCAAATCAT TCTAnTGGTC 240

GATTAATTGT CGACGCATCA TCTTGTCAAT TCTTGAAATT TATTCGCTTT TCAACTTTCA 300

CACGCTGACA TAC 373

(2) INFORMATION FOR SEQ ID NO: 3067:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3067:

TTCAGAGTTC GGAACATAAG GCGCTACAAT GTTGTGTTGC CAGTAGTTGA CTGAATATGC 60

GTTTGTAACA AGCTTTTTTC GATTCTAGTC AACAGTAATT AAATTTATGA TATGGGCAAT 120

ACTTTGTAAT ACTAATATTA AATGGCGACT TTATTTCACT ATGTTATAAG AGTGCCATTT 180

GTTGATAAAG GnATACTAAA GGGTATCGTT TGGAATTTTA GTAACTAGAT ATGTTCGGGT 240

ATAGACCGnA TTGTGGATAC GTAAATTTAA TGCnATGAAT TTTAAAATGA AAACATGACA 300

TTAAATGAAT C 311

(2) INFORMATION FOR SEQ ID NO: 3068:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3068:

TATGATTATC TAGTAAGTAA ATTGCTGACG CGCCGAATAC CGCAAAGAAT ATAAAGCAAA 60

CTAACGCCGG GACAAAAAGT ACACCTAGGA ATAAATTCTT TAATCGTACG TCCTTTTGAC 120

ACACGTGCAA TAAnATACCT ACAAATGGGT GCCCAGGnTA TCCACCATGG CCCAGTAAAA 180

GATTGTCCAA TTTTGTAACC ATTGGGAATT TTTGACCACC TGTCGGAATG CGTAAACTCA 240

TACTTAAAGA AATTTGCATT ATAATTACCT AGACC 275

(2) INFORMATION FOR SEQ ID NO: 3069:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AAATGGGTTC TGTGACATTA ACGTCTACAA AAGATGGTTC AGAAGAAACA CACGAGGCTG 60

ATGGTGTATT CATCTATATT GGTATGAAAC CATTAACAGC GCCATTTAAA GACTTAGGTA 120

TTACAAATGA TGTTGGTTAT ATTGTAACAA AAGATGATAT GACAACATCA GTACCAGGTA 180

TTTTTGCAGC AGGAGATGTT CGCGACAAAG GTTTACGCCA AATTGTCACT GCTACTGGCG 240

ATGGTAGTAT TGCAGCnCAA GTGCAGGGAA TATATTGACA TTAACGATCA GCCTAAnTCC 300

GAGCnGATTA GATGTGAGCG G 321

(2) INFORMATION FOR SEQ ID NO: 3070:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3070:

GTTTGACCTG CATATTTGAC AGTCATAACC TTTGTATCAC CATTATATTA ATATCAAAAT 60

CTTGGAACGT GTTATTTGAG nTGACATTTA ACTTCGCAGC ATTATCAGCT GTTGAACTTG 120

ATGTATACGT TGCGCAACCC ATAACTATCT GTGTTACAAT GCACCAAACG CACCTCCACC 180

AGCTACATTA GATGGGCAGC TTCGCCTTGC AGCTGATTGG TTTAGATGAT TGTGATACGA 240

TCCAATTTGA AGCCAAATnG TACTTAAGCA CAATCCTACT GCGGACCGTT TAACCCTGTT 300

TCACCTATAC ACTGnTGAAA GGCAAACCGT ACCACTCACC ATTTCCATGC CTTCCATATT 360

TGGTTACCAA ATTTACTTTT CCCnGAAAAA TGAAACTCTT 400

(2) INFORMATION FOR SEQ ID NO: 3071:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3071:

TGGCCATTTG TCATTGCATT TTTACCGTGG GTGTTGATTA TTATTCCTTA CTTACTATTT 60

AAATCGGATA CACTAAATAT TATTCATACG GGTGATAATA TTGCACGAGG TCTAGGTGTA 120

AGGTTAAnCA GAGAACGTTT AATATTATTC TTTATCGCAG TGATGTTATC ATCTGCTGCT 180

GTAGCATAGC AGGTTCAATT TCGTTTATCG GATTAATGGG TCCGCATATT GCCAnACGTA 240

(2) INFORMATION FOR SEQ ID NO: 3072:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3072:

GACTCCCTGC AGGTCGACGT CTAGAGGATC CCCCCACAGC AATTCACTTA TACATGTAAC 60

AGTGTGAAAT AATAACGTCA CAACGGCATA ATACACATTG CAACGTCCCA ACAACATATC 120

ATAGAATCGT AACGGCATGA CATCAACACC AAACCTGGGC TATAACACCA TAACAGCGCA 180

ACGCCACATC ATAGGCACTA CATCAAGTCG CATCGTAGCA CCAGCACATC AAAGTAACAT 240

GGGCATCAAC ATCAAACCGG TCTATAACAC CATAACACCG GCAATGCCAC ATTCATAGGC 300

ACTACATCAA GTCGGCATC 319

(2) INFORMATION FOR SEQ ID NO: 3073:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3073:

ATATACGCTT ATCAGCTGGA GCTCAATAGA TGGAGGATGA TTATGGGGCT ACCGGTTCTG 60

TCTATAGCAC TGGTCTATCA GCTATGTGGA TTACAATCGG TTTAACATTA GGTGCTTATA 120

TAAATTACTT TGTTGTTGCT CCTAGACTTC GTGTTTATAC CGAATTAGCT GGAGATGCAA 180

TTACATTACC AGATTTCTTT AAAAATCGTT TAAACGATAA AAATAATGTG TTAAAGATTA 240

TTTCTGGATT GATTATCGTA GTATTCTTTA CATTATATAC nn 282

(2) INFORMATION FOR SEQ ID NO: 3074:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3074:

AATCGAnAAA TCATGGATGT ACTTGAATCA AATGCAAACA GCGAAGTGTn TTGAATTGCA 120

TGGTAGCGTT ATAGACGAGC CAGTAGAAAT TCAATCAATT AAAGTATATG TTCCTAACGA 180

TGATGAAGGT CGTACGACAA CTGTAATTGG TAATGCTTTC CCTGACTCAG AAGTTAAATG 240

CATTACACCA GCAGATATCA TkGCTTCAAT GAGTTACTTC TTTAACTTAT TAAGCGGtAT 300

TGGGtATACA GATGATATTG GACCATTaGG TAACCGTCGT TTACGTTcTG tAGGkGGaAT 360

TACTACmAAA CCaATTCCGT ATCgGTTTAT CCAAGA 396

(2) INFORMATION FOR SEQ ID NO: 3075:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3075:

ACCTACATTT GCAGTTGTCG GTGTATAACC GGCTGGTGTT GAAAACTCTA CACTATAAGT 60

TCCATTGCTT AAACCAGTGA ACTGATATTT ACCATTTTCA TCTGTTGTCG TACGATCTAA 120

TTCTTTACCG TTACTATCTT TAAGAATGAC ATAAACACCT TTAATCCCTT TTTCATTGGC 180

ATCTTGTTTA CCATCTTTAT TTGTATCTCC CATACATAGT CACCTAGATT ATATTCnTTT 240

GGGCGCCATA GCAGTTGATG AGCATTCACA TTGAAAAACT ATTGACCACT ATATTAGTTT 300

GCAGTGCTAA GnATAACATT TCCATACGTG ACATACTGAT AGACTGTGAG TGATGTATGC 360

GCTGnTGCTC ATAACG 376

(2) INFORMATION FOR SEQ ID NO: 3076:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3076:

TTACATCACC AATTAGACGT TATCCTGATT TAACAGTTCA TCGTTTAATC CGTAAGTATT 60

TAATTGAGAA ATCAATGGAT AACAAAGAAG TGAAGCGTTG GGAAGACAAA TTGCCTGAGT 120

TAGCTGAACA TACTTCTAAA CGTGAACGTC GTGCTATTGA GGCAGAACGT GATACTGATG 180

AATTGAAAAA AGCAGAATAT ATGATTCAAC ATATTGGTGA TGAATTTGAA GGTAATGTCA 240

AAnGCnGnGA TATACGTTTG AGGCGCAATG C 331

(2) INFORMATION FOR SEQ ID NO: 3077:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3077:

AATCATATGC ATCGATTTCC AGCAACAGCA ACCATTCATC CTATGTCCCA TTAGCAAATT 60

TTTTGGATGA AACATGAATG GCAAGATGTA TTTCAACGTA CTGCTAATTT GCAGATATTA 120

AAACATACnT TTCTATCATT ATTGATACAT ATATCATGAT TATTCATGGC TTCCGCAACA 180

GGATGTTTAT TTAGAAACAT TAGATTGGGA TGTTGAGGCA TAGAACTGCT GGGTATTTCC 240

AAGGAAATGT TGCCGGAATT ATTCCAACAA CTATTGATGT AAGTATGAAA GAACGTATGC 300

AACATAATGG GCTAATAAAG TACACCGTnT GTTAATGGTG CnATG 345

(2) INFORMATION FOR SEQ ID NO: 3078:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3078:

GATTATCAAG CGATTGATCA AGTATCATCA TTGTTGAAAG AAAAATATGG CATTGCACAT 60

TCAACGTTGC AAATTGAAAA CTTGCAATTG AATCCATTAG ATGAGCCATA CTTCGACAAA 120

TTAACATAAA TAAAACATTG TAGCGCCTAA AACATTAATC TATGTCATAG GCGCACGTTT 180

CGTTTTATAC TTATGTTGCA TCATTTAAAT GATTTTCGTC AATTTCTTTG ATGCTATCTA 240

CATCTAACAC GAGGTTAACT TGCGTTGATT TTGATAAAGT GATCATAGCT TTTAGTACTT 300

GAGGATTTTT ATTGTTGCTG TTACGAATGT GGTCATGTTT AATGCGGGAC AGTAATTTAA 360

GTTGTTTTTT TACAATTGAG AGTGTGATAT TTCGATTCGG 400

(2) INFORMATION FOR SEQ ID NO: 3079:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3079:

AAACGTTTAA TATACACTTT TACACGTCGC CTTCATTGAA GCGAATTGCC ATAACCTTCA 60

CATTATATAT AGTTCTTTCC ATATAAATGT CCAAATTTTT AGAACAACGC AATArATAAC 120

CATCCACCTA ACTTATCAAA AATTTAAGTG GATGGTTTTT CATTTTCATT TATATTTATA 180

TTAGTGTTAA TCCAATCATA GATTTATCTA TATGCACTGC TCTATACaTT TCCTCaTTTA 240

ATTTGCyTTA CTTTCATTTA TATCATTATC AGAACACTTG GCGTGTCATC GnTATTATTT 300

CGCATCTTTG AnACGTTTA 319

(2) INFORMATION FOR SEQ ID NO: 3080:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3080:

TCAAATGCAT CTAGGnCACA TTATTCTATT TGGGCATTCT TAGTGCTGTT CTTATTTGCG 60

GCTTTAACGT CATCTATTTC TTTATTAGAA TTAAATGTTT CTAACTTCAC GAAGAATGAC 120

AATACAAAAC GTAAAAAAGT CGCAGTGATC GGTAGTATTT TAGTATTTAT CATTAGTATT 180

CCAGCAACCT TATCnTTTGG TATCCTAAAA GATGTAAGAT CGGTGCGGGA ACGATTTTTG 240

ATAATAAGGA TTCCACCGTT CGAATGTAAT GAAGCCATAA GCGGG 285

(2) INFORMATION FOR SEQ ID NO: 3081:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3081:

ATCATAGCGT TTCTCCTAAA AATTACGATT AATCAAAGTA TGCCATTATT TAACTTTAGT 60

TTCTTCAGAA TTATTTGCCC CATTATCATG TTTTTCTTCT TTATTAACAG CATTTTTATC 120

ATTTTTAACA AGATACAATT TACCAATTAA TGGGCGGTGT GCGTGCTGGT ATGGGTTATA 180

CTGGTTCACA CGATTTAAGA GAATTACGCG AAGAAGCACA ATTTACACGT ATGGGTCCTG 240

CATTCTAATT AAGATAAAGG AGAACGACAA ATATGGGAAA TGGCAAAGGA CCAAGAGTTA 360

ATCCTTGTCT TAGGACTTTG GTAGGCCATT ACACCCATTA 400

(2) INFORMATION FOR SEQ ID NO: 3082:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3082:

TGAATTTGCT CCAAATAAAA ATACAATTGC CATTAAAATC ACCAGATATT ACAAGTGGCA 60

ACATGTTAGA AACACCGTTC ATTAAGTGTT TATAGAATGC TTTACCTGGG CTTATTTCTT 120

GACTGTCATT TGAGTTACCT GGCAACAAAA GGTTTACGAC TTGTATCTAA TGAATACCAT 180

CTGCTACTGG TnCTTCTACG ACATTTTTAC CATCGAnGCG GTCCGTCTCA ACATGTACAT 240

CAGCAGCA 248

(2) INFORMATION FOR SEQ ID NO: 3083:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3083:

TACTAAAGGT TTAAATCAAA AATGGCTAGG TATCGTATTT GCGATTTTAA TTACAATTAC 60

ATTTGCATTT GTATTTAACA CAGTGCAATC TAATACAATT GCGGAGTCGT TAAATACGCA 120

ATATAATATT AGTCCAGTAA TCACAGGTAT TATTTTAGCA ATCGTAACAG CTATTATTAT 180

ATTTGGTGGT GTACGTAGTA TTGCTACGTA TCCTCGTTAA TGTACCGATA TGGCTATCAT 240

TACATGGTAT GGTTTAGTAA TAATGCTATT AATTTAGACC AATTGTCCnA TGATAGGACG 300

ATATAAAAGG CATTGGnACG ACAAGnACTG GTGCGCTGAG GGCTCGGTCT CCAGGACAAC 360

GGGGTATC 368

(2) INFORMATION FOR SEQ ID NO: 3084:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3084:

TTGGACTTTA TAAAGTTACT AAGTTGTAGA TTATCCTGGT AAAGAAGATA TTGCGGTTGT 60

ACAAGTTGAA GAAAAATCAA CACAACCAAA AGGTAGAAAA TTCAAAGATT TCACTAGTAA 120

ATTTAATATA GCATCAGAAG CTAAAGAAAA TGAACCTATA TCAGTCATTG GTTATCCAAA 180

TCCTAATGGA ATAACTACAA ATGTATGAAT CAACTGGTAA AGTATTATCA GTGAATGGGA 240

TATAGTGnAT CGGATn 256

(2) INFORMATION FOR SEQ ID NO: 3085:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3085:

ATATGCATAT GCTTCTTTAG GTGAACGAAT ATCTGGTTCA GATACGATTT CAATTAGCGG 60

TGTACCTTGA CGGTTCAAGT CAACTAATGA ATACTCCACC TTTATGTGTT GACTTACCAG 120

CATCTTCTTC CATGTGAAGA CGAGTAATAC CGATTCGnTT TGTTTCACCG TCGACTTCGA 180

TATCGATATA TCCCATTTCA CCAATTGGGT TGATCAATTG AGAATTTGAT AGCTTTGGGA 240

TATCGGGATA GAATAGTCTA CGGTCAACTA GATCnGGTGC GAnTCCATAT TTAGTGCCAT 300

GCAGCACGCA T 311

(2) INFORMATION FOR SEQ ID NO: 3086:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3086:

ATGTAAATGA TCATCCTTCA TAATAACAAC GATTACTGAT CTTGATCATG ATTTTGAACA 60

ATAACAACTG CTTTATTAAT ACCTTGTATA CGCTCGAGnC ATGCCAACCT CTGACAACTC 120

AATCCTAAAC CCTCGAATCT TAACTTGTTT GTCCTTTCGA TATAAATAAT CTATGTTGCC 180

ATCGGGTAAC AAACGAACGA TATCACCACT TCCTATACAT CAGCTGATTT ATATTTGAAT 240

(2) INFORMATION FOR SEQ ID NO: 3087:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3087:

GTAAAGATTT CAATTCATCA TCTTTAAATA AACTTAATGG TAATTnGTTA TACCnAATAA 60

AGCCTTCTGG ACACTTCCTT TAGACCGACG ACCGTCTTAG CTAATGTCGA TTTCCCTGAC 120

CCTGATTCAC CGACAATGCC TAATGTTTCG CCTTTTCTAA TAGCCAAGTT AATATCATAA 180

CTGCTCGGTA TGGGCTGCCC CTCGGTGATG TGTAATCCAC GCTCCACGCG ATCGATTTTA 240

ATAAAATATC ATGGTT 256

(2) INFORMATION FOR SEQ ID NO: 3088:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3088:

AAGGTTATTT GAATGATCAA GGTATCCACA AAAGAGGTGC TGAAATAGAT CGACTCGTTA 60

AAGGATGTAC AGGTGTTAAA CGTACAACTG GACAGCATCC AGGGGGTATT ATTGTAGTAC 120

CTGATTACAT GGATATTTAT GATTTTACGC CGATACAATA TCCTGCCGAT GATCAAAATT 180

CAGCATGGAT GACGACACAT TTGATTTCCC TTCCTnTCAT GATATGTATT AAAACCTGAT 240

AAACnTGGAC ACGTGATCCC ACCATGATCG ATGCCTCCAG ATTATCAGGA ATGATCCAAA 300

ACCATACCTG AGATGTAAGA GTATCAGTAT TAGACnC 337

(2) INFORMATION FOR SEQ ID NO: 3089:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3089:

AAACATTACT TTACGCTATC AATGGTGGTA AAGATGAAAA TCTGGTGCAC AAGTTGGTCC 120

AAACTTCGAA GGTATTAACA GCGAAGTATT AGAATATGCC GAnATTCAAG AATTTGATCA 180

AATGATGGAT TGGCCTAGCA GGTGTTTACA TTAACTCATT AAATGTATnA CTACATGCAC 240

GATAATACAG CTATGACGAT TGAATGGATT ACATGTACAG AATTGTCCGn CCATGGCACA 300

GGA 303

(2) INFORMATION FOR SEQ ID NO: 3090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3090:

CTTTCGTTAA AGGGGCATAT TCATATAATG GATGGTCATT AATAATAATT CCTGCCGCAT 60

GTGTAGATGT ATGTCTTGGT AAACCTTCTA ACTTTTTACA AATACTGAAC CAGCGTTCAT 120

GTCGATGGTT TCGATGTACA AACTCTTTAA AATCGTCAAT TTGATATGCT TCATCAAGTG 180

TAATTCCTAA TkTATGTGGG ATTAAACTTG GAAATTTCAT TtAATGTAAC TTCATCAAAC 240

CCCATAATTC TTCCAACATC TCTAGCAACT GCTCTTGCAA GCAGATGACC GAAAGTCACA 300

ATTCCAGATA CATGTAGCTC GCCATATTTT TCTTGGACGT ACTGAATGGA CCCTTTCTCG 360

GnGTGTATCT GCAAGGTCAA TTTTCATTnT CAGGCATGGT 400

(2) INFORMATION FOR SEQ ID NO: 3091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3091:

TTGTTTTTTC ACGTTCAATn ATTATCTTCA ACTTGTGACT ACAGATTTTA AAATGGAATT 60

TACAAGTATC TTCTTCAATA TTTTGCATCA TGATATCAAA TAATTCATGA CCTTCATTTT 120

GATAGTCACG TAATGGATTT TGTTGTGCAT AAGAACGTAA GTGAATACCT TGACGTAATT 180

GGATCCATGT GTCGATATGG ATCAGTCCAA TGGCTATCAA TAGAACGAGG TAAAATCATA 240

CGCTCAAACC CCATCCATTG GnTCCTCTAA GATACCTTTT GACCTTGGAT AGCnGCTCAA 300

(2) INFORMATION FOR SEQ ID NO: 3092:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3092:

CGACACCTCA ATAATCATAT CGTAATGTTC AACTTTTCCT GATTTAAATG TAATTTCATT 60

TCCATTGATA GCATTAATTT CCTCATTTAA ACGGTATGGA ATCTCCCGCT TATCTAATTC 120

ATCAAGTATA GGTTGATTCA GTCGGCATCC ATAATTTATT TATCTTATCA GATCGATGAA 180

TAAAGTAGGG TGTAAACCAC GTTCCATAAA GATTTCAAGG AACTCCAATG GAACATAACC 240

TGCACCTACC ACCAATACTT TATCCACTTG GATTGGCTTG GAGGAATGGT CGGATAGGCA 300

TCCAGGGCCT CCAAAATTCC nAGGGGAAAn GGTAATATCC ACCTTCCAAG GCCAAGGGCC 360

AATTGGCACC TGGCCACCCA GGGnCTTAAA AAGGGGTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3093:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3093:

TTATACCCGn CAAATTCATA AATATAGTnC CTTTTCAATA GATTGATATG TATGTCTAAA 60

TGTATCGATT AACTTTGCTA ATGCTGCTTC ATCTAATGGT CGGTCTGCTA ATTTTAAAAA 120

TGTATTCTTC AATAGGTATT CCCATATAAT GCGTTATTTC TTTAGATGAT GGTTCCGTTA 180

AGCCACATGC TTTAAATGCA CTTTGTGTTG CTACTTCACC ACATTTTTTC GTGTCTGCCA 240

ACGTACCATC AA 252

(2) INFORMATION FOR SEQ ID NO: 3094:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AATCTATTAA TAATGAAGAA AAAATTGTAC TAGCACGTAG ACGGTTAATA AAGTTCGATA 60

AAGATATCAG TATTCCATAT ATTCTAAAGC AAGCATATTC TAAAGAAAAA AACAGTTATA 120

TATTCTTGTT AGAATCACAA GATTCTATAT TCTTTTCACA AACACCTGnn CAATTAATAA 180

AGGTCAATAA TAAAATCTAT CGACTAAAGC TGTGCAGGTC AATTAAACGG TCACAAGTGA 240

GGCCGAGGTA CAAAAAATGT TGAGCATTTT AAAGTATAAA CTTATCGACA CGnTTGTGTG 300

CAGTTTTCAT GTTT 314

(2) INFORMATION FOR SEQ ID NO: 3095:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3095:

GGTGAGGCGG CATTGAGAAA AAATGCTGAA GTAATCGAAG CTGTATCGCA GTCTTGTTTG 60

ACAACAGGAT TTTGTTTATG GTGCCAATTA GCTTTTTCAA CGTATTTAGA AAATGCCACG 120

CAGCCACATT TAAATAATGA CTTACAACAG CAATTGTTAT CTGGAGAAAT ATTAGGTGCT 180

ACCGGATTGT CTAATCCCGA TGAAGTCATT TAATGGATTT AGAAnAAGTT GGACCCTTTG 240

AAACACCACC TTAATGTTGG ATGGGACCAA TTGGGTGGTC CAGTGGGAnC GTAATGCCCA 300

GCTGTAAAGT nATAATCCAA GGAAAGACCC AT 332

(2) INFORMATION FOR SEQ ID NO: 3096:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3096:

TTTATGCATA CGCGCACTCA TCACACTACC GACAACAACA TCATCTTTTC GAGCATATCT 60

ACTTAACAAC GTCATGACCA CACTCATAAA GAACATAAAA TCAGTAATTT GATGCTTTTC 120

TACATACTTT TGAAGTAGCT GTCTCATTTG TTGATTCATG TAAATGACAT CATGCTCCAT 180

TTGTCGGTTT AATAATTGGT CTAACATAnT CTGTCGGGTA AGCCTAAAAT AGGGTACTTC 240

ATCCTTGAAT TGAGGATACC CATATTGGTC CTAAGGTTCG GTCCATATCC ACGGATGGCG 300

ATTTAAGGTT GGATAAAGGT GCCGTTAAGG ATCCAATTCC 400

(2) INFORMATION FOR SEQ ID NO: 3097:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3097:

ACTCTGGTCC TTCTGCATAA CTGCCGTAAA TAATTCACCT TCATCACACG CTGTACCTAC 60

CAATAATCCC nCACGATATA CGTGGAATTC GAGGTGTACG GTAGAAATAC TTCACCAATG 120

ATGCACTTAC AATTTTAAAT AGATTTTTAA GACCTTGTTG GTTTTGTACA ATTAATGTGA 180

CATGACTAGG TCTTGCACGT TTATATGCAT CTTCATTACT GAGTTTTTTG GTTGATTTnC 240

GTTATGATTT AATACGGCTA ATTCT 265

(2) INFORMATION FOR SEQ ID NO: 3098:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3098:

CTAATGTATC AGTTTGGCAT GAATTCTTTT GCATCTTTCA ATAATTGTTG TGATCTTTTT 60

TAGTCACATC ATCAATTTTC TTATCTTCGT ATAATGCTTT TTCAATCTTA TGATATCCTG 120

ACCATTCTTT TTCCTTTTTC TCTTCTTTCA TATCTGCAAG CGGGCATCCA ATTTTAGGAT 180

CCTAAATCTC CCAAATGCTT CTGAACTGGT CAGAGCGTCA TAATACATAC GACTTTTGGA 240

TATACGCTTT TnCTTGGGCA TACATTATTT CAATCGTTTA CAAATTTTTC TGACCTTTTA 300

AAATCATTnA CTGTCAnCAG A 321

(2) INFORMATION FOR SEQ ID NO: 3099:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATCCGCAATC TGAGAAACAT CATCTTCGAG TTGTTGGAGG GTTCCAATTT TCAAGTCATA 60

AATCAGATGA TGAATGGCGA GAGTTTGGAC TAAATCATTT TGTATTACCT GAAGTTTTAA 120

TTTCAACTGA TAATAATGGG ACATTTTTAA CTTATACAGT TAAAAGGGAA AGTTTTACTG 180

TTGAGGCATT GAACGATTTA ATGGATTGTT CAACAATATA TCGGACATAG AGTGGACGAC 240

CAATGGGGGA ATACCAGAAT GAGATATTAT AAAACA 276

(2) INFORMATION FOR SEQ ID NO: 3100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3100:

GTCATTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAC nTAAAACGTT 60

GTTAATAACT TGCCGGGCTT CACACTAATC AATGGTGGCA AAGTAGGGGT GTTTAGTCAT 120

GCAAnGTTAA GAACGAGCAT GTTTGATTCA GGAGATAATA AGAACTATCA AGCACAAGGA 180

AATGTAATTG CATTAGGTCG TATACATGGA ACTGATACGA ATGACCATGG CGATTTT 237

(2) INFORMATION FOR SEQ ID NO: 3101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3101:

nCGATATAAC AAGGTTGTTA GACTTAAAGG TGGCGATCCA GCGATATTTG GTCGTGTGCA 60

AGAAGAAGTC GACATACTAA ATGAACATCA TATTGCGTTT GAAATTGTAC CAGGGGTGAC 120

ATCAGCGAGC GCnAGTTTGG CTACTATGCA GACAGGTTTG ACAATGCGTA CAGTTGCTAA 180

AAGTGTGGAC ATTTTCTACA GGTCACTTTT AAAGATTCAG AAGAAAATGA AGTGGGATGG 240

TCCATTCCTT AAGT 254

(2) INFORMATION FOR SEQ ID NO: 3102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3102:

CAATCACTCA TGTAGTAATT GATACCTAAG AAGTCGTTTA AATCTTTGGC TGCATCTAAA 60

ATGGCATAAT CTTCATnTGT AATGTTTAAT TTACCGCCAn TAACAGATAA GATATGTTGC 120

ACACCTTCCA TCGTTTCACG AGTAATACTT ACCTAAATAT GTTGCATCTA AGATGAATTT 180

ATTATGGATG GATATCTTCT AAATTCTGCT GCACGGGACA TCTTCAGGAT TTGGATGGTT 240

(2) INFORMATION FOR SEQ ID NO: 3103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 328 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3103:

GTTGTAAACT TCAATTGTTC AAATAAATAA CACATATCAT TGGAGGTGAA TTGATATGCC 60

AGATTCAATC ACAATTATAG ATGAAAACAA AGTGGTTGAT GTTGTATTAA TTGCAGGTAG 120

AATTTTACTT GAATCAGGTG CTGAnACATA TCGAGTTGAA GATACAATGA ACCGTATCGC 180

ACATAGTTAT GGTCTTCATA ATACATATAG TTTTGTCAGT TCAACTGCAA TTATTTTTTC 240

ATTAAACGAT CGAACAAGTA CAAGATTAAT TCGTTACAAG AGCGTACAAC AGATTTAGGG 300

AAnGTGCGAA TAAGCGGGGn AATTCTTC 328

(2) INFORMATION FOR SEQ ID NO: 3104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3104:

TTTTGCTTTG TGCGCTAATA ATCTAATGTT CGTGGAACCG nAACCAGAGA TATTACAAAT 60

ACATCATCGA CTAATCGCAG GTGTCGTTGA TTCTCCAACA ACATGTGCCT GTTTGCCGAG 120

CTGATTTAAG GCGGCATTGC AAAACTATTC GCCACGAATC CTGAACGTCC TTTGCCAGCT 180

ACAAATATAT GTTCAGCATG TAGTATTTTG GATGCAAAGT TGAAAACTCA TCCGCTTCAA 240

CATGTGACAA AGTCACTTTA ATCnA 265

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3105:

ACTAGTAGAG TATCTAATGG TGATTTAATC ATTATTACTG CTGGTGTACC AACTGGTGAA 60

ACTGGAACTA CTAATATGAT GAAAATCCAC CTAnTTGGTG ACGAAATTGC TAATGGTCAA 120

nGTATTGGAC GTGGATCAGT TGTTGGTACT ACATTATTGC TGAAACTGTT AAAGATTTAG 180

AAGGTAAAGA TTTATCTGAC AAATTGATCG TTACTAACTC AATCGATGAA ACGTTTGTGA 240

CCT 243

(2) INFORMATION FOR SEQ ID NO: 3106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3106:

CTATTGCGTT TGGGTAAATC TAAAGCAGGC GTAnATTATC AAAGTTTGGG ATATGCAACC 60

AGCACACTTA TTCTTTATGA TTGCAGCGCC AGAAGTGGnG CCCAAACACA TCTAGATGCT 120

TTACTAAGTT GTCTGGTATT TTAATGGATG AAAATGTACG TGAGAAATTA TTACATGCTT 180

CATCACCTGG AAGAAGTACT AGCGATCATA GATGAGGCTG GATGATGAAG TGGA 234

(2) INFORMATION FOR SEQ ID NO: 3107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3107:

TTTTGAAGCG GCATAATCAT GAAGAATAGG ACTAGGATTA TAACCTTGTA CAGATGATGT 60

CGTTGTAATT GACGCACCCG GTTTTAAATA TTCCAATGAC TTTTTGAACT GTCCAAAATA 120

GCGGnTAGAn ATTCGTTTCA AATGTTTCTG TAAATGCCTC AGTTGTAAAT CCATGAATAT 180

(2) INFORMATION FOR SEQ ID NO: 3108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3108:

CTTTAAGTTA CGTTCGGCTT TGATTAAAGT AAAACGTGGT ACTGTTTCCT ATGACAAGAG 60

TCTAATTGGA TACAATGTAA ACAAAATGGT GnATTTGTAT TATAGATAAT AAACATTCGn 120

TATACATTCA ACATATCGAT GACCACTTGG ATTAAGCAAC GTAATATCAT TCGTACTGCT 180

CAAGAAATGA CAAACGAAAT ACGAGAAAAT TTTGAGTCAT ACACGTCATT TAGAATGAAT 240

AGTATTATGC AAGTACT 257

(2) INFORMATION FOR SEQ ID NO: 3109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3109:

CTTAAAGCCA AGTCGATCTG CTAATTTTGC AAGTGTCACT GAATCTTGCA ATGCCTTTTG 60

TGCATCCTTA CCTTCATCTA TTAAGGCATA GTCTAATACG CTTAATTTAA CCAATCCGTC 120

ATCTCCAAAC TTATCCTGTC ATGTCAAACC GACATAACAT TTGTAGCGTT CTTAATACCA 180

TTCCCTCTGC ATATACCCAC GTATATGATA ACGTnTTTCA nTTAACT 227

(2) INFORMATION FOR SEQ ID NO: 3110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3110:

TTTCTTCATC GTTTGTGAGA AAGAGGTATT TTTAATTGGG AAAnCAGGTA AAAAGGATGG 60

AAGTACATAA AAAGAGCAAT GCTTGGGCAT TATTCCnCTT GTTATTATTT GTGGCGTTGT 120

GATAACGTAA TTGTGCGTTA TTAATGAATC GAAAAGAATC ATTGCTAAAA AGTGAGTCTC 240

CGAAAGGCGG CCTTCAACTG TTAAGAGTGA TTTATTGCAG GCTTCAATCG CGAAATGGTG 300

CnAAGCGCGT ATTAGCACTA GCCGAA 326

(2) INFORMATION FOR SEQ ID NO: 3111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3111:

CTACGGCGCC TTGCATCTTT CCCAACAATT AACCCCAACT CTATTAGCAC AGATTTATCA 60

ATTGATTCAT AAGCTTCATC AAAGGGTGAA CTAACATGCA TTAACGCTTC TTTAATATCA 120

ATTAAGTCGG CATGTTCAAC ACCAATTTTC CCTTTTTTAT TTTTAGCTTT TTCTCTATCA 180

ATATACGCAT GTTTAACACC TTTGACATGT TCAGTAAATT GTGACTTCCT nAATTTTTTA 240

TCCTCCCTTG GTGnnGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG 300

(2) INFORMATION FOR SEQ ID NO: 3112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3112:

TTATTGTTAA CACAAGGnTT CGAACAAGGT TGGTTTAGTA CATTTTCAAT CATTTGTCTG 60

AGCATTTTTA TCATCACTAC GTTGATATTC ATCATCATCG AACGTCGACA TGAAGTACCT 120

TTTATTGATT TCTCAGTATT ACGCAACCGT CCGTTCATTG GTGCATTTTT AAATAACTTT 180

GTTTTAAATA GCGGTCTAGC GTAACAGGGT CTTTCATATA TGCTCAACAC ACCTGGTTTA 240

TCGCGCGCAA TCGGACTGTT ACATGCCAAT GCCATGGGCG TTCGAGATCG TTAGTGAAAG 300

CACATAGTTC GGGCAATGAG CCACATGGTC GTGTCCGTCA CGCACACATA TAGCAGCT 358

(2) INFORMATION FOR SEQ ID NO: 3113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3113:

TCGGTCTTGA AAACCGACAG GGGACTTAAC GGCTCGCGGG GGTTCGAATC CCTCTTCCTC 60

CGCCATCAAT ATTTATATTA AATTCTATAT ATAATGAAGG TAAGTGCTCA AATTTTGAGT 120

ATTTACCTTT TTTATTTGTC TTTGAATGGC TCGTAATTTT TGATAATAGA AATGATAAGG 180

CATTGAGATT GGAAGGGCAT TTGGCTTGTG CAAnATACAT AGCnAAATGT CGTTGTTGTT 240

TTGTGATAGA T 251

(2) INFORMATION FOR SEQ ID NO: 3114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3114:

TTTAAGTGAA TTnCTTTGGG TTACAGAAwT TTCAACAACT TTAAAGCACG TATAATGATG 60

ATTTTCAGCT TGTACAAAGG AGAAAAAAAG AAGACAACCA AGCCCAATAA TGGACTGGCC 120

GCCTAATAAT AAAAACTCTA AAAGTTGTAT TTTAAAAATA GTTCTTTAAA TTATATACCC 180

ACCACATTTG GTGGAGaACC GTTAAACAAT GCATAGTTGC TTAACTTCCA ATATTGAACT 240

CATCATTACA ATTTGACATA GAGTCTATTA AAGCGTGTGC CATTTGAGTC CACTTTTATT 300

TGTATTGTAT AGAGAGAAAT AAAAAGAAAC CTTGTTTTAC AAGGTTTCTA ATACGTTATG 360

TTATGTAAAT AACAGTTAAT TATACCGGTG GTCGGGGTCG AACCGACACT CCACAAGTGG 420

AACGgGATTT TGAGTCCCGC GCGTCTGCCA ATTCCGCCAC ACCGGCTTAA TGGTAAACAA 480

AAAACTTCCC TTTGGAAGCA ATTATGGAGC GGAAGATAGG ATTTACACCT ATACCTCGTT 540

CCGGGAAGGA ACGTGtTCTA AAAGTTGAAC TACTCCCGCA AATATTAAAT TATGGAGCGG 600

AAGATAGGAT TTACACCTAT ACCTCATTCC AGGAAGGAAT GTATTCTAAG AGTTGAAATA 660

CTCCCGCATT ATTATTAAAT TATGGAGCGG AAGATAGGAT TTGCACCTAT ACCTCGTTCC 720

GGGAAGGAAC GTGTTCTAAA AGTTGAACTA CTCCCGCATA AACCTGGAGG CGGCAACCGG 780

ATTTGAACCG GTGATAAAGG TTTTGCAGAC CTCTGCCTTA CCACTTGGCT ATGCCGCCAA 840

TAACTGGGCT AGCTGGATTC GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG 900

CTTGGCTATA GCCCATTAAT AATAAGGGCG GCTGAAGGGG ATCGAACCCT CGAATGTCGG 960

CGAACCCACA CCAAAGGTTT TGGAGACCTC TATTCTACCG TTGAACTATG CCCCTATTAA 1080

AAATAATAAA TGGAGGGGGG CAGATTCGAA CTGCCGAACC CGAAgGAGCG GATTTACAGT 1140

CCGCCGCGTT TAGCCACTTC GCTACCCCTC CATAAATGGT GCCGGCCAGA GGACTTGAAC 1200

CCCCAACCTA CTGATTACAA GTCAGTTGCT CTACCAATTG AGCTAGGCCG GCTAAGAAAT 1260

GGTTCAGGAC AGAGTCGAAC TGCCGACACA TGGAGCTTCA ATCCATTGCT CTACCAACTG 1320

AGCTACTGAA CCATAATAAA AATGTAATGA TGGCGGTCTC GACGGGAATC GAACCCGCGA 1380

TCTCCTGCGT GACAGGCAGG CGTGTTAACC GCTACACTAC GAGACCTATA AAATATTGCG 1440

GGAGGCGGAT TTGAACCACC GACCTTCGGG TTATGAGCCC GACGAGCTAC CGAACTGCTC 1500

CATCCCGCGA TAATAAAAAA TAATGGCGGA GGAAGAGGGA TTCGAACCCC CGCGGCCCGT 1560

TAAGGCCCTG TCGGTTTTCA AGACCGATCC CTTCAGCCGG ACTTGGGTAT TCCTCCATTA 1620

TTATAGGTAA ATCGCTATTA ATTATAAAAT TAAATGGCGG TCTCGACGGG AATCGAACCC 1680

GCGATCTCCT GCGTGACAGG CAGGCGTGTT AACCGCTACA CTACGAGACC ATTAGTAAAA 1740

CGGAGGAAGA GGGATTCGAA CCCCCGCGAG CCGTTAAGCC CCTGTCGGTT TTCAAGACCG 1800

ATCCCTTCAG CCGGACTTGG GTATTCCTCC AAAATTATAT GGaCtTGCAG GACTCGAACC 1860

TGCGACCGAA CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA 1920

ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG 1980

AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAA TAATATGGTG 2040

GAGACTAGCG GGATCGAACC GCTGACCTCC TGCGTGCAAA GCAGGCGCTC TCCCAGCTGA 2100

GCTAAGCCCC CATAATAATT ACAGTATATC GGGAAGACAG GATTCGAACC TGCGACCCCT 2160

TGGTCCCAAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA 2220

TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 2280

GGCGCATATG TTTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAcGgTGATC 2340

ACTCACCGCA GGATTTTAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA 2400

AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TGTATTCTAC 2460

CGCTGAACTA CTTCTGCATA TGCGGGTGAA GGGAGTCGAA CCCCCACgCC GTAAGGCGCT 2520

aGATCCTAAG TCTAGTGCGT CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG 2580

GATTCGAACC TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGA GCTAATGGCT 2640

CTTCCATGGT GCCGGCCAGA GGACTTGAAC CCCCAACCTA CTGATTACAA GTCAGTTGCT 2700

CTACCAATTG AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCGA 2760

AAACTGCCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT CGACTACCAT CGACGCTAAG 2880

GAGCTTAACT TCTGTGTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA 2940

CATATGAATG TAATTTATAC ATTCAAAACT AGATAGTAAG TAAAAGtGnA TTTTgctCGC 3000

AAAACATTTA TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC aCATGTCACC 3060

ATGCTTCCAC CTCGAACCTA TTAACCTCAT CATCTTTGAG GGATCTTATA ACCGAAGTTG 3120

GGAAATCTCA TCTTGAGGGG GGCTTCATGC TTnAgGATtT TCAGCACTTA TCCCGTCCAC 3180

ACATAGCTAC CCAGCTTATG CnTTGGCACG ACAAcTGGTA CACCAGAGGT ATGTCCATCC 3240

CGGTCCTCTC GTACTAAGGA CAGCTCCTCT CAAATTTCCT ACGCCCACGA CGGATAGGGA 3300

cCGAACTTcT aCGACGTTCT GAACCCAGnC sTGTACCGCT TTaATGGGCG AACAGCCCAA 3360

CCCTTGGGAC CGACTACAGC CCCAGGATGC GATGAGCCGA CATCGAGGTG CCAAACCTCC 3420

CCGTCGATGT GAACTCTTGG GGGAGATAAG CCTGTTATCC CCGGGGTAGC TTTTATCCGT 3480

TGAGCGATGG CCCTTCCATG CGGAACCACC GGATCACTAA GTCCGTCTTT CGACCCTGCT 3540

CGACTTGTAG GTCTCGCAGT CAAGCTCCCT TATGCCTTTA CACTCTATGA ATGATTTCCA 3600

ACCATTCTGA GGGAACCTTT GAGCGCCTCC GTTACCTTTT AGGAGGCGAC CGCCCCAGTC 3660

AAACTGCCCG CCTGACACTG TCTCCCaCCA CGATAAGTGG TGCGGGTTAG AAAGCCAACA 3720

CAGCTAGGGT AGTATCCCAC CAGCGCCTCC ACGTAAGcTA GCGCTCACGT TTCAAAGGCT 3780

CCTACCTATC CTGTACAAGC TGTGCCGAAT TTCAATATCA GGCTACAGTA AAGCTCCACG 3840

GGGTCTTTCC GTCCTGTCGC GGGTAACCTG CATCTTCACA GGTACTATGA TTTCACCGAG 3900

TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGCCTTTCGT GCGGGTCGGA ACTTACCCGA 3960

CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCGA 4020

TTCGTAGCTT CGCAGAAnct ArCcACTCCT CTTAACCTTC CAGCACCGGG CAGGCGTCAg 4080

cCCtATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT TTGATAAACA GTCGCTTGGG 4140

CCTATTCACT GCGGCTCTTC TGGGCGTTAA CCCTAAAGAG CACCCCTTCT CCCGAAGTTA 4200

CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG CTCACCTTAG AATTCTCATC 4260

TTGACTACCT GTGTCGGTTT GCGGTACGGG CACCTATTTT CTATCTAGAG GCTTTTCTCG 4320

GCAGTGTGAA ATCAACGACT CGAAGACACA ATGTCTTCTC CCCATCACAG CTCAGCCTTA 4380

ACGAGTACCG GATTTGCCTA ATACTCAGCC TTACTGCTTA GACGTGCAAT CCAATCGCAC 4440

GCTTCGCCTA TCCTACTGCG TCCCCCCATC GATTAAAACG ATTATAGGTG GTACAGGAAT 4500

ATCAACCTGT TATCCATCGC CTACGCCTGT CGGCCTCAGC TTAGGACCCG ACTAACCCAG 4560

TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGCTCCA CATGTCCTTA CGATCATGCT 4680

TCAACGCCCT TAGAACGCTC TCCTACCATT GTCCAAAGGA cAATcCACAG CTTCGGTAAT 4740

ATGTTTAGCC CCGGTACATT TTCGGCGCAg TGTCACTCGA CTAGTGAGCT ATTACGCACT 4800

CTTTAAATGA TGGCTGCTTC TAAGCCAACA TCCTAGTTGT CTGGGCAACG CCACATCCTT 4860

TTCCACTTAA CATATATTTT GGGACCTTAG CTGGTGGTCT GGGCTGTTTC CCTTTCGAAC 4920

ACGGACCTTA TCACCCATGT TCTGACTCCC AAGTTAAATT AATTGGCATT CGGAGTTTGT 4980

CTGAATTCGG TAACCCGAGA GGGGCCCCTC GTCCAAACAG TGCTCTACCT CCAATAATCA 5040

TCACTTGAGG CTAGCCCTAA AGCTATTTCG GAGAGAACCA GCTATyTCCA GGTTCGATTG 5100

GAATTTCTCC GCTACCCTCA GTTCATCCGC TCACTTTTCA ACGTAAGTCG GTTCGGTCCT 5160

CCATTCAGTG TTACCTGAAC TTCAACCTGA CCAAGGGTAG ATCACCTGGT TTCGGGTCTA 5220

CGACCAAATA CTAAACGCCC TATTCAGACT CGCTTTCGCT ACGGCTCCAC ATTTACTGCT 5280

TAACCTTGCA TCAAATCGTA ACTCGCCGGT TCATTCTACA AAAGGCACGC CATCACCCAT 5340

TAACGGGCTC TGACTACTTG TAAGCACACG GTTTCAGGTT CTATTTCACT CCCCTTCCGG 5400

GGTGCTTTTC ACCTTTCCCT CACGGTACTG GTTCACTATC GGTCACTAGA GAGTATTTAG 5460

CCTTAGGAGA TGGTCCTCCC AGATTCCGAC GGAATTTCAC GTGCTCCGTC GTACTCAGGA 5520

TCCACTCAAG AGAGACAACA TTTTCGACTA CAGGATTATT ACCTTCTTTG ATTCATCTTT 5580

CCAGATGATT CGTCTAATGT CGTCCTTTGT AACTCCGTAT AGAGTGTCCT ACAACCCCAA 5640

CAAGCAAGCT TGTTGGTTTG GGCTCTTCCC GTTTCGCTCG CCGCTACTAA GGGAATCGAA 5700

TTTTCTTTCT CTTCCTCCGG GTACTAAGAT GTTTCAGTTC TCCGGGTGTG CCTTCTGATA 5760

TGCTATGTAT TCACATATCG ATAACATGAC ATAACTCATG CTGGGTTTCC CCATTCGGAA 5820

ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT 5880

CATCGGCTTC TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACTTAAT CTATGTTTCC 5940

ATCCTACAGG AAACGCGTTA TTAATCTTGT gaGTGTTCTT TCGAACACTA GCGATTATTT 6000

CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA 6060

TATTTTACTT ACTTATCTAG TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA 6120

AGCAATATCA CTTTAACCAA AAAATATTTG AATGTTAAAT AAACATTCAA AACTGAATAC 6180

AATATGTCAC ATTATTCCGC ATCTTCTGAA GAAGATGTTC CGAATATATC CTTAGAAAGG 6240

AGGTGATCCA GCCGCACCTT CCGATACGGC TACCTTGTTA CGACTTCACC CCAATCATTT 6300

GTCCCACCTT CGACGGCTAG CTCCTAAAAG GTTACTCCAC CGGCTTCGGG TGTTACAAAC 6360

ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC AATCCGAACT 6480

GAGAACAACT TTATGGGaTT TGCTTGaCCT CGCgGGTTCG cTkGCCTTTG TAATGTCCAA 6540

TGTAGCACGT GTGTAGCCAA ATCCATAAGG GGCATTATGA TTTGACGCAT C 6591

(2) INFORMATION FOR SEQ ID NO: 3115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3115:

GGTGCCAAGC AATAAATATG ACTATGCTCA AACTGAATTA ATGGTGGGTG TGTCGCCATC 60

GTAATTGGAT CGTCTGAAGG CGCATATAAA TGATAGTGCT CTTCGAATAA AGGTAGCATA 120

TGTAATTGTT TGTGTTTACG TATTTCTGGT GTAAGTTCCG TGAAACCAAT GTCTATATTC 180

CCATTAATAC GCTATTATAA TGTGTCAGGT CCAATAAGCC CCGGATGACA TGTGTATCCA 240

TTTGGAAATG GAACCGTTGG GAAAGTGGGA ATAACATGGG GGAACGTCAn TCCCCnCCAA 300

GCCCATnGAG GTACCTTTAA TTTTA 325

(2) INFORMATION FOR SEQ ID NO: 3116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3116:

CCGnTTGAGT TCGGTGGCGA CATGATTGAT TTTGTAAGTA AGTATGATGC AACATGGGCT 60

GnTTTACCTA CTAAATTTGA GGCGGGTACT CCATTAATTG CTCAAGCATT GGGCTTGTCA 120

GAAGCTATTC GCTATTTAGA ACGCATAGGT TTTGATGCAA TTCATAAATA TGAACAAGAA 180

TTAACGATAT ATGCTTATGA GCAAATGTCT G 211

(2) INFORMATION FOR SEQ ID NO: 3117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3117:

AACGTnTTTT GAAATGATTG CGGCGATGTT GGCGACAGTT AAAGTAGGTG GCATCTTATA 60

TACCTATCGA TATTGATTTT CCGAATAAAC GACAAGGTGC AATTTTGGAG GATGCTAAAG 120

TAACTGCAGT CATGTCTTAC GGCGTTGnAA TTGAAACGAC ATTACCAGTC ATTCAATTGG 180

AAAATGCTAA AGGCTTTGTT GAATCAAAGG 210

(2) INFORMATION FOR SEQ ID NO: 3118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3118:

TTAATTGATC CTAGCTTGGT TTGCCTCTGT CACTTTATCA TTGATATTTT GGACAGTTGG 60

GTTGCCATTC AACACTTGAT TAATTTCAGT TAACTTTTGA CGCGCTGCTT GTAATTTTTG 120

GGTGTACGCA TTTAACGAAC GGnCGTCATA CCTGTTGTAT CCGTTGGTTG ATTAATGCTT 180

GTTCTAAATT GCGTTTCCAA GTTTnAAGCG GCGCTTATCT GGTGT 225

(2) INFORMATION FOR SEQ ID NO: 3119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3119:

CCAACATGAT GCTAGTTTGA TTAAGTTTCT TCTAAACAGA CTTCAAACGG CATGGTTTAG 60

CATATCCTAT TAAGGTTGAA TCGCGTTAAC AGCACATAGG AAATGCTGTT AGGCGATGCA 120

GAGTGCGATT AGGCAGCTAC TGGAAAATTA TTGTTTGATT TGCCAGTTAT TATAAACTGT 180

GTGTGTTGAT GnCGAnCACA ACCCCTCCGA ACACGCTTAA TG 222

(2) INFORMATION FOR SEQ ID NO: 3120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3120:

CGGCGATTAT ATTAAAAAGC CAATTACAGA ATGTAGTGGT AATGAAATAT GCCAAGAATG 60

GCTGTATCAC TTAGGTGTAT CAACTGACAA AATTGAAGAC TTAGCAAAAC ATGCATCTAA 120

tACGATTCCT GTTTATATGC CATATATCAC ATCTTATTTC ATGGACGCGT GCTATCGGCG 180

nACAGACCTT TTAGTCGTGC CCGGCATGCA ATCTnCAGGA ACTTAGGCAT TTATTGGTGA 240

ACTTTG 246

(2) INFORMATION FOR SEQ ID NO: 3121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3121:

CAAATACCTT CTCAACnTTG TACTTTTTGC CTAATTGAGC TGCACGAATT GCTGCAACGT 60

ATCCACCAGG ACCTGCTCCG ATTACTATAG aTCTGTTTCA ATTGGGAAAT CTCCAACTAC 120

CATGTTTTAC CCCTCCATTA ATAATAATTC TGGATTATTT AATAAACGTT TAATGTGATT 180

CATTGCATTT TGGCCAGTTG CACCATCAAT TTGTCTGTGG TCAAAGCTTA ATGAkrtGCt 240

AATACTGGTG CTGCAACAAT TTCTCCATCT TTAACGATAG GTTTTTGAGC AATACGGCCA 300

ATTCCTAAGA TTGCTACTTC TGGGGTGATT GATAACTGGA GTGAACCATT GTCCACCAGC 360

TGAACCGATA TTACTGATTG TGCATnnGCA CCTTnCATT 399

(2) INFORMATION FOR SEQ ID NO: 3122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3122:

CAGACAAACC TTGAATTATT CTACCTATAA TTAAAAATGC TGGCAAAGGT GTAATGATGA 60

TGAGTAATGA ACCTACAACA TTTAATATCA ATCCTACATA AGTAATTTTG ACGCGACCAA 120

ATTTATCAGC AACATCACCA GCACCTACGT AAACCAACCA GCCAATAAGG CAGATAAGCT 180

AACAGCGTAT TATCGTTCCC ACGTCACTAC TATATGTGGA TGTATGGGAC ACAGTTTACC 240

G 301

(2) INFORMATION FOR SEQ ID NO: 3123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3123:

GGAGCAAATT TATCATCTGC AACTAGACAC AACATCACTG TTATTAGTAC CGGGTTATAT 60

AGTAGCAGTC ATTGTTGGTG CACTAAGTGG TAAAATCGGC GAATATCTGA ATTCAAAACC 120

AGCGATTATC ACAGCAATTA TTTAATAGCA CTGAGCTTGA TTTACCTGCA TTGCAGTAGG 180

TAATCACATT CAATCTCGTC ATTCTATGAT ATCTTGCAGT AGCTTGCTTA ATGATGCACT 240

TACTACGAGC ATAAACATGT CTATATGCAG GTGCATGTTA TATTATATAT GGCGACGAGA 300

TCGTnGGCCn ACGTTAACTA ATTCnGCATG TCTAGCCTCG AATTATATAG TAGGAGCGTA 360

GTACGCCAAC TGCCACGA 378

(2) INFORMATION FOR SEQ ID NO: 3124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3124:

TATTGCAAGA AATGAACTGC TGATTTTTAT AGTTTTAGTG GTCATAAAAT GCTTGGACCA 60

ACAGGTATTG GCGTATTATT TGGTAAACGT GAGTTACTAC AAAAAATGGA ACCGATTGAG 120

TTCGGTGGCG ACATGATTGA TTTTGTAAGT AAGTATGATG CAACATGGGn CTGATTTACC 180

TACTAAATTT GCAGGTCGGG TTACTCCCAT TGAATTGGCT CCAAGCCAAT TGGGGCTTGG 240

CnAGGAAGCC T 251

(2) INFORMATION FOR SEQ ID NO: 3125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3125:

CGGTTAAGTA ATACAGGATG TTCTCTAATT ACTTCTTCCA ATACGTCCCA AACTTCATCA 60

TCCATACGTT CGATTTTACT CTTCGCATTT TTAATGTTAG TTGCAATTTC ACGTTGAACT 120

AATTCTTTCA TTACGAATGG TTTAAATAGT TCAAGTGCCA TTTCTTTTGG TAAACCACAT 180

TGGTACCATT TCCAnGCTTG GACCCnACGG CAATTACCTG AACGGTCCCG GAA 233

(2) INFORMATION FOR SEQ ID NO: 3126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3126:

AATAGATTCC CGGGATTCAA AAGCATGGAT GTTGTACCTT GTTGTnCTCC ATTGGCAATG 60

TACTACCTGA TGTCAAGATG AATTATCCAT CACTTTGTTG ACGTGCTTTA TTTTACAGCA 120

TCAATTTGAT CCAATCGAAA TACCAGATAA CTTAGACTGT GTCCCAGTAA AATAACGATC 180

AATCACATCA TGAGACAAGC CAATCGCTTC AAATATTTGT GCCCCTTGAT AACTTTGCAC 240

TGTCGAAATT CCCATCTTAG CCATTACTTT AATGACACCT TCTGACAATA CATCCGTATA 300

TGTCtTAACA TTATCGACAA CGGTGCCTTG TAACCCTTCT GTCAATGTCA GTTGTTCAAC 360

TGTACGTTGC GCTAGGTATG GCACAATTGa TTCGCGCCAT ATGCGAGTAA ACA 413

(2) INFORMATION FOR SEQ ID NO: 3127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3127:

GTCGTAAATA CTGAACAAAA ATCACGGCAT ACTGTGCAAA TTTnTGAAGA AGCTCAAAAA 60

CTATTACAAG CACATCATGC GATTGTAGAA GGATATATCG AATCAGCTTT AGAGCGTGCG 120

TAnATCATCT TCTACATACA TAGGTAATTT TATGGCGATT CCTCATGGAG CATCCTGTAA 180

AAAGTTTTAC AATCACATGT GCTTATTTT 209

(2) INFORMATION FOR SEQ ID NO: 3128:

(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3128:

TAAATTAATG GAGTTTGGTA CACGTCGTCG CAAGAAATTG ATGCAGTGGG GCGCTAGAGC 60

TGCTTACATC GGGGGCTTTG ATTCTACAAG TAATGTTAGG GCGGGGAAAT TATTTGGTAT 120

ACCTGTGTCT GGTACACATG CACATGCATT TGTCCAAACT TATGGAGACC AATATGTTTG 180

CCTTCnAAAA ATATGCTGAA AGnC 204

(2) INFORMATION FOR SEQ ID NO: 3129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3129:

GAAATACCAT TAATATAATA GTCGGTAAAT TAAGAAACGT GGTGCGCGAT TCACAACAGA 60

AATCTTAACT TATCGAAGTA TCCTGTTTTC TCTGCAACAC CAATACCAAT CATCACTGCT 120

AGTACTAAGC CTAATGCGGG AACTCTGAGA AATTTTTAAT CGTATTCTTC TTATCATCGT 180

AAATCCATCT GGCTATTATA TTTTAATATA AnGGTTTGAG CTACCGGATG CTAACGnAC 239

(2) INFORMATION FOR SEQ ID NO: 3130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3130:

ATCACAATAA ACATTTTAAA ATTCTTGTTA TCATAATCAT TAAAAGGTAT TAACCTTAAT 60

AATATATTCT CTnGTCTCAA CCTTAATCGT ATACTTCAGA CGTCTGTTTG TAGACAATAA 120

AGTCATTCAC GTCTTCATAT GTCATCAnAT GTTTATCATG ATATGATGAT ATATAATCGG 180

TATATACTGT AGATATTACA CATAAGAGAG GATATAATAT GAAAAGGTCA TTAAGATGTG 240

CTGAGAGCTG TGTATCAGT 259

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3131:

TGTGCCTGCC ATTTTGCAAT ATCTTCATCT TCACGTGGTA ATGCACAAAA ATGTTTACCA 60

TGTGCATTCA CAACTTCAAA AATATGTTGA CATGTGATGT TACTTGATCA TCACGCGTTG 120

CCATGGTATG CAAGTGCTGC GATAAATCTG CGGCACCTTC GACTATCATG CTAACCTTCG 180

CTTGTnnATA TCGCAATGGC ATACCCCTTC AACATCTTCT ATCATGG 227

(2) INFORMATION FOR SEQ ID NO: 3132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3132:

ATCGCAGTGA TGTnATCATC TGCTGCTGTA GCnTAGCAGG TTCAATTTCA TTTATCGGAT 60

TAATGGGTCC GCATATTGCC AAACGTATCG TTGGACCACG TCACCAGTTG TATTAACCAA 120

TTGCCATTTT AGTAGGGGCA TGTATACTTG TAATAGCTGA TACAATTGGC CAAAATTGTA 180

TTACAACCAG GTGGGGTTCC AGC 203

(2) INFORMATION FOR SEQ ID NO: 3133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3133:

AGCATTTAGT TTAGCGGCAG TAGCTGCAGA TGCACCGGTA GCTGGCACAG ATATTACGAA 60

TCAnTTGACG AATGTCACAG TTGGTATTGA CTCTGGTACG ACTGTGTATC CGGACCAAGC 120

AGGTTATGTC AAACTGAATT ATGGTTTTCn AGTGCTAATT CTGCTGTTAA GGTGACACAT 180

TCAAAATACT GTACCTAAGG A 201

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3134:

CATTTGTAAC TGTTATTGTT TATAACTTCT GTGTGAAGCG CAATATTACA ATTAAAATGC 60

CGAAAGAGGT ACCGnCGAAT ATTTCACAAG TATTTAGGAC TTAATTCCAT TTTCAGCGGT 120

AATCATCATT CTTTATGCAT TAGGATTTnG TCAATCGCAA CCAGCTTTAA ATCAAAATGT 180

AGCGGAGGTA TTTTAAAATT ATTCGGT 207

(2) INFORMATION FOR SEQ ID NO: 3135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3135:

AACACCTTTA GGTCGTGCAG GTCAACCTGT TGAGTTATGT GGTACTTATG TGCTATTAGC 60

GTCAGAAGGA ATCAAGTTAT ACAACCGGAC AAGTnTTCGG TGTTAGCGGT GGAGTGCAAn 120

TAGGTTAGGT TTGTATGAGC TTTTAATTGA GCACCATAAT GTTAATTTAG TTACTTCAAT 180

CCATTAAATT AAATGAATTG GTG 203

(2) INFORMATION FOR SEQ ID NO: 3136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3136:

CACATCCAAT GCAnTCTACT AAATCAGACA CACCACAATC TCCAACCATA AnACAAGCAC 60

AAACAGATAT GACTCCTAAA TATGAGGTTT AAGAGCGTAT TATACAAAAC CGAGTTTTGA 120

ATTTGAAAGC AGTTTGGATT TATGCTCAAA CCATGGACGA CGGTTAGGTT TATGATGTTA 180

TTCCAATAGG TTCACTATAA ATAGCTTAGT T 211

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3137:

ATTGGGAAAT GTTCCCCCAC CACCTACAAT TTGTGAATAC AAACAATACG TATTGCAATG 60

GACTTTACCT GGGCTTACCA AGTGAATGTA TACGTCACGT ATGATACGAT TGTAGTTGnA 120

AAATAATGCG AACAGAAAAT CGTTATAAGT ACAAATAATA CAGGTGACTC AACTCCTGCT 180

TTTAGATTAA CAAATCTCCA ACCGATACAA TGAGTGCTTG CAACATACCA AGCATTATAA 240

AGAATCCTGC CTTACCTAAG 260

(2) INFORMATION FOR SEQ ID NO: 3138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3138:

CATAAGCAAT TAATGACTTC GTTAATTGCG AAAGTGTATC TTTTTGATTA TCATTCGCTT 60

TTGCATCTTC AAGCTTTCTC ACATCTGATT TGACAGCATT ACTTTCACTA TTATCTTCAA 120

GCGATAATTT CTTAACTGCA CTTACCACTT GCTCAATTGC TTCTGCnTAT TGTCATTCGA 180

TATCGGAGTA GTAGGAAGTG CnGAATTCGG CA 212

(2) INFORMATION FOR SEQ ID NO: 3139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3139:

TATTGGTTTT TATGCGAATA TGGATAATAA AAGGTCTCAC GACATCATTG ATAAATCGCT 60

TGAnATGTTG CGACGCTTAG ATCACAGGGG CGGGGTCGGC GCAGATGGCA TCACTGGTGA 120

TGGCGCAGGT ATTATGACTG AAATACCTTT TGCATTTTTC AAACAACATG TAACGGAGGA 180

GCACCTGTTA GAAAAGAAGG GAAATTACCT CGTGAAGTCA TTCGTTATGA GTATGACCTA 300

GAATATGGTA CAAATGTTTT AACAATGGCA CAAAGATGCA ATTGAAACCA GGTnCAACGT 360

GTGTTAnTAC AGG 373

(2) INFORMATION FOR SEQ ID NO: 3140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3140:

AGCCTTATAA TAAAGTGCCT TTCATAGCAA TAAGTTGTGT CCATTGACCT ATTACATTTT 60

TCGTTTTGTA CATTAAATAT AAGAAATACG GTGCACCAAT AATTGCTACG ACAATACCTG 120

CTGGAACCCC CACCTGGTTG TAATACCATT TTGGCCATTT GTATCAGCTA TAACCAAGTA 180

ACCnTGCCCC AACTAAAATG GCATTGGGTA AAACCACnTG 220

(2) INFORMATION FOR SEQ ID NO: 3141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3141:

GAGGAGCAGC ACAACCAAAT ACACAACCAG CTGGACAAGG TGATCAAGCT GATCCGAATA 60

ACGCTGCACA ACACAACCTG GAAATCAAGC AACACCGGCA AACCAAGCAG GTCAAGGnAA 120

TAACCAAGCA ACACCTAATA ATAATGCAAC ACCGGCAAAT CAAACACAGC CAGCGAT 177

(2) INFORMATION FOR SEQ ID NO: 3142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3142:

CTTTTTTAGC ATTTGGTTTA ACAACCnGGT GTTGCAGTAT CCCCACTTAA GGTCTGTATA 60

ATTTCATTTT TATGTTCCTC GATAACTTGT ATTGCTGCTT GTTTTCCTCC ATCTGTCAAT 180

CCATCATTTG ATTGAGAGAA nCAG 204

(2) INFORMATION FOR SEQ ID NO: 3143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3143:

GTGATGCCAT ATAAATTGGC AATAATGGCA CAAGTACTGT CAGTCCAGCA ATCGCTATAA 60

ACTGACTGAG CCATAAAATG CGAAAGTTAC TGCGCCATAT AGACTGATTA ATCATATGTC 120

ACCATTGGAT TTGGTACGGT AGTTAAACCT GAAGGCATAC TACCCTCCAC CCACTTATTC 180

AACGTTGGAT nATAGGCAAT GGGTAATTAA AAATTTTGTT TTTGAAATGG GCCCACGGGC 240

TTGTTTTAAT CAAAATTAAA AAATTGTGGT nCTTGGACC 279

(2) INFORMATION FOR SEQ ID NO: 3144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 514 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3144:

TGACTTAATC AAAGCATTTG ATCAAAACAC CAGAATACCA TTATTCTTTA ATATGTTGTA 60

CAGTAAACTC TnTATTATTT GTTGCTGTTG GATCCATTGT TCGTCTTTCA ACAAAAACnT 120

GACCCAGAAT GAAGTCCGAT AGAGTCAACA AAGCtATAGT ATTTGTAACC ATCTTTTAGT 180

TGATaAATGC CACGCGCATC TGTTATTGCG TCATTTTTAG GTAcAAATTG AATTTkGAGA 240

TTTCTCaCaT TATCAGGTAC TTTAAATAAA CGCAAAGTTG GACCGnCTTC AACAGTCTTT 300

TCAGCAATCG TATCATTAGT ATCAGCATTT TTGATAATAA CATTTGTTGC GCCTTGACCG 360

TTTTTAGTAG TCATTGTATT AAATCAAGGT TAATTCAGAA TTCGGATTTA CTGTTAATGC 420

TTTCTCGATA CCATTAAAAT CGCCATGGTC ATTCGTATCA GTTCCAGTAT ACGGCCTAAT 480

GCAATACATT TGCCTGTGCn TGATAGTnCT TATT 514

(2) INFORMATION FOR SEQ ID NO: 3145:

(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3145:

ATTCAGACTT TGCATGTGGA ATGGCCACGT TCATGCCAAT AGCTGTCGTA CTCCCATTTC 60

ACGTTCTAGT ATTGCATTTT TTAAATGCGA TGTGTGCTCT ACATAACGGC AAATTTTAAG 120

TTTTATGAAT CAACATATCC AATGGCTTCG GTTTCGAGAC ATGTCCGTGG ATTCAGTAAT 180

TAACCATAGT TTGGTTGGAT CCAAAACCAT GAGnAGGGTT TAATGGAGGA TGTnGAATGG 240

TTCnCCGGTG GTTAATCCTA CATGGTCCAC CCTCCTGGTA ACCATGGTGG TGGTAATAAC 300

CC 302

(2) INFORMATION FOR SEQ ID NO: 3146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3146:

CAGGAATAGG ATCATTTGCA TCCATAGCTT CACTTATTTT TTCAGAAGCT AGCGTACAAT 60

CATTTAAATC TACGCCACCT TCTTTATCAA TAGAGATTCT AAGAAAATGA TCTCTACCCT 120

CTTTGACCAT ATTCAACGTC TACAAGTTCC AAAATTCAAG GTCTTCCCAT AATTGGGTTT 180

AACCAATCCA CTTTCTACCT GGTTTCCGGT AAATTTTTAC CTCCATACCA GGGnCCTCCC 240

CCTTTTTTGG GCCAAAATAG GAAAAAnGAG GCGGGGGAAA TCCTCCCCCC AATTCCnTTC 300

CTGGCCCTGG AGGTTTCCAC CTAAATTTTT TT 332

(2) INFORMATION FOR SEQ ID NO: 3147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3147:

GAGAGTGGTT AACAAGCAAA TAGAAATAAT TAAAAATGCA GATGCAGATG CATCGGCGAA 60

CnCCAACAAA TGCAGAAGTT GCTGAATTCC AAATGTAACG ATACCTGCCC ATGAGCGATG 180

TGCTCAGAAT GATCAGAGCT AATG 204

(2) INFORMATION FOR SEQ ID NO: 3148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3148:

CAACCGGGAC AGGTGGGGTT ATTGGACGTT ATTTTTGGCC TTTGGATTTT AAGATATTGG 60

TCGAAAAGAG ATTACATAAA ATTGTGGCCA AATGCGGATT GCATATTATT GTAACGCCGn 120

CTATTGCATT GTTGATTGTT AGGnCTATTA ACTATCTGGA TCTGTATGCC ATTAGCCAGG 180

TTTTGTTTCA GACAGTTTAG TTTCAGTAGT TAACGGA 217

(2) INFORMATION FOR SEQ ID NO: 3149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3149:

CTATTATTAT ATTCCGCGGT GTACGTATAT GTGCTACGTT ATCTTCGTTA ATTGTACCGA 60

TTATGGCTAT CATTTACATT GGTATGGTTT TAGTAATATT GCTATTTAAT TTAGATCAAA 120

TTGTTCCTAT GATAGGTCAC GATTATTAAn AGTGCATTTG GTCATCGAAC AAGT 174

(2) INFORMATION FOR SEQ ID NO: 3150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3150:

GGGACCGAAT TGACTTCAGC ATTACCAGCA AATTGATTAA TnTTGTGGGC TGGTATTGGC 60

TCTGGCGGTA CCATTTACAG GTACCGCACG TTATTAAAGC AACATCACGG GCAATGTTAT 120

A 181

(2) INFORMATION FOR SEQ ID NO: 3151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3151:

GTTTTAATTG AGCGACATAC TCTTCTGTTA GCTCTGCTAC TTTTTAAAAT AGAGCGATTG 60

ACATCAAACA TAACTGCTAA ACGCTCAACG TCTGCCTTCG TAATGGCTTT TGTAGAAATT 120

CTAACTAAAT AATTTCGAAT GCTATCATTG GTTGTnTCAA CAGCTTGATG CT 172

(2) INFORMATION FOR SEQ ID NO: 3152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3152:

ATGGACGTTG AGACATTTAT AAGCGATATA GATTTCGCAT GTTGCATTTA TTAAACCTAA 60

TAATGGTAAA CGACAAGTGT GACTGTTACT GGACTTTAAT GAAGGTAGTA ATCAGAATGG 120

AAATCAACCA AAAGTAGGTA TTTGAATnTT GGGAATAATG AGACATAGCG AGAGTGTATA 180

TGCAATACGA CAGTACTnTA AATTAAGAG 209

(2) INFORMATION FOR SEQ ID NO: 3153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3153:

TTCTCACAAA GCGCTCAGTT GAAGTAAATC CACCTGGACA ATCCAAATGT ACCTGCTTCA 60

TTGCCTAAAG GTTCAATCGT TAnACCTTCC AATAAATTTG CTGTTGCTGG ATAAGGAGAA 120

ATTATTGGTA TATTGTCTTA AATTACTATG ATGCCAATTT AAGGTCTGGA TGAT 174

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3154:

GGATCACATC GTTCATTTAC ACAATCTATT AATATTCAAT GGCACAATAT AGTGTTTATG 60

GCATTACGGA TATGATTTAG TAGCnCACCA TTATTAACCG ATCTCTATCT GTTAAAAGGA 120

ACTTAAGAGC AATGTTTGCG CATCATCATT TTATGTTGCG TCTTTGCACG AGTTTTGCGA 180

AACTTTACAA TATTTGTTGC GGATGATTAT TTAACTTTTG GAGAATGTTG ATGGCACAGT 240

CCACTATAnC AATCAGTATC GCAATGG 267

(2) INFORMATION FOR SEQ ID NO: 3155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 490 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3155:

AATTAAAAAT CAAGCAACTG CTGCAAAAAT GCAAGATCAA ACTGTTCCTC AAGAAGCAAA 60

TTCTCAAGTA GATAATAAAA CAACGAATGA TGCTAATAGC ATAGCAACAA ACAGTGAGCT 120

TAAAAATTCT CAAACATTAG ATTTACCACA ATCATCACCA CAAACGATTT CCAATGCGCA 180

AGGAACTAGT AAACCAAGTG TTAGAACGAG AGCTGTACGT GTTtAGCTGT TGCTGAACCG 240

GTAGTAAATG CTGCTGATGC TAAAGGTACA AATGTAAATG ATAAAGTTAC GGCAAGTAAT 300

TTCAAGTTAG AAAAGACTAC ATTTGACCCT AATCAAAGTG GTAACACATT TATGGCGGCA 360

AATTTTACAG TGACAGATAA gTGAAAyCAG GGgATTATTT TmCacGAgTT ACCAGATatT 420

TAcTGGTAAT GGAGACGTGG GATTATTCTA ATTCAnATAA TACGATGCCA ATTGCAGACA 480

TTAAAAGTAC 490

(2) INFORMATION FOR SEQ ID NO: 3156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3156:

CCTTCAGTAC CTTGTAATAG TTAnTTAAAT GTTCCGATCA TCGTGTAGTG TGATTCATCA 60

TACCGGCCTT TTCAATTGAA TACGATCTAA ACCGTTTCGT CAGGTGCTAG TAAGTTACCT 120

TCGCCACCTA AATAAGAAGT TCACTCGTTA CGATTTTTTC AGATAGCATC ATTGGTGGAT 180

TCGTAACTTG TGCAACAGCT GTTTAAGTAT TAATAGTGAT TCGGTCGTCT TCACATGCAT 240

TGGCGCACAA TCCnTGCACC GT 262

(2) INFORMATION FOR SEQ ID NO: 3157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3157:

ATGGTAAAAA TTGCACTATC TGCTCGGGAA ACGATTTTGC ATAACCTATT GTTAATTTTT 60

TACCTGTTGA TTTAGCTGTA TCTGnCCATT TTTTGAGCTT CTGCTGTCGT TTTAGCCATT 120

GGGTTTTCAC ACATCACATG TTTACCAGCA TGCAACCCTG GCTACAGTAA 170

(2) INFORMATION FOR SEQ ID NO: 3158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3158:

CCAGGCAGAG GAGCAGCACA CCAATACACA ACCAGCTGGA CAAGTGATCA GCTGATCCGA 60

ATAACGTGCA CAAGACAACC TGGAATCAAG CAACACCGGC AACCAAGCAG GTCAAGGAAT 120

ACCAAGCAAC ACTAATATAA TGCACACCGG CAAATCAACA CAGCAGCGAA TGTCCAGCAG 180

CAGCGAACCA GCAGCACTGT AGCAGCAACG ACAACTCAGn CCAATGTAGC ATATGGTGAG 240

GCAGTTTATA GACATACATT GTGnCCTGCA TTCACAGTGG ATAGCAGGTC CACTGTACTG 300

TACAGTAAGT An 312

(2) INFORMATION FOR SEQ ID NO: 3159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 171 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3159:

AATCACATCA AAAACTTCAA TTGTTTACGT TGGCAACTAA CTTTATGTTA GAACGCACAC 60

AATATCTAAT GTTTAAAATC TATCGTCGCA AGATGCTTCC TGnTAATTAT CAGTGCCATT 120

TTCGATTGGG TTATACAATC TAGTAATCGC ATGATAATTT AATGCTACAA G 171

(2) INFORMATION FOR SEQ ID NO: 3160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3160:

CTTGTTCATT TAATCCATAT AGTATACGAC GATGTACTGG TTTTAAACCG TCACGAACAT 60

CTGGCAATGC ACGAGCAACG ATAACACTCA TCGCATAATC TAAAAATGAT TCACGCATTT 120

CACTGGTAAT ATTTCGTTCA TTAATCnTGA TTGAGGGAAT TCCGCCCATC CAGAnGTCCC 180

CCCTCCAAAG TTCAGTTCCA CAGGGGCTAG A 211

(2) INFORMATION FOR SEQ ID NO: 3161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3161:

GCACAGGTAG CGGTAGTGGC GGTCGTATGA TGACTTTGGT AATCTAAAGC AAAATGTACG 60

ATAATAATAA ACGTCGTTTC GTTTCTCTGA TGTAGCAGGG GCAGTGAAGA AACAAGATTA 120

TTGAATTGTT GATTTCTTGA AGATATAAAA ATTCAAGAAT GGGTCTAGGA TTCCTAAGGT 180

GTCTTCTTTT GGGCTCAGTA CGTAAACATA TTGTAGAGCG TGCAGTGAGT GGCGCACCAT 240

CTCTTTTGGG TCAGnTTTGG AGTTTTGTTT GTCGGCTGTC GGATTnTCGT ATGTAGGAAC 300

GGCTGTTCAC TTnCGTGGAT G 321

(2) INFORMATION FOR SEQ ID NO: 3162:

(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3162:

AACATTTGAG CAATATCAAG AAACATTAGA GTATATTTTA TCCCATCATG TAACTCGTAA 60

TACAGCAATT ATTGCTTTGG GTGGTGGTGC ACTGGTGATT TTGCTGGGTT TATTGCGGCG 120

ACACTTTTAC GAGGCGTGCA CTTTATACAA GTGCCAnCG 159

(2) INFORMATION FOR SEQ ID NO: 3163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3163:

GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGAC AAGTCTTACG GCATCTTCTA 60

TTTTTAAGCT TGAAATTTAA CAAATCATAA GCCGTATGAA TATTTAAATA TGCCACCATG 120

ATTGAATGGC CCCTTTCTAT TAGTTAnGTT TTGTGCG 157

(2) INFORMATION FOR SEQ ID NO: 3164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3164:

TATAAAAATA TAACGCGGAC AAAAAAGTGA GTTATTACTG ACAAAGTATn TGAGATTGTA 60

ACAGGATATA TGAAGCAATA TCAGTTGATC CAACTGTCAT AGGTATTTCA TCAGCAGGnG 120

TTGTTGATGA ACAAAAAGCG AAATTGTATA GCAGGCCAAC ATTCCGATTA TAAAGGTATA 180

ATTTTAAGGA TTATTAAAAT CATGTCTCTT ATGTCA 216

(2) INFORMATION FOR SEQ ID NO: 3165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3165:

AGAAACACTT CTATTGAATC GTCTTACTGC TGTTCTCTAT TTATAACACT TCGTATTGAA 60

TGAATTCATT ATGCCTATTT GACACATTAT TGAAGTTTTC CTAATGCCTG GATCCTTTAT 120

ACGTTACGGC TTCGTGCTAT GTTTTGGTAC ATAAAGCTTT GACATATCGA nATTC 175

(2) INFORMATION FOR SEQ ID NO: 3166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3166:

ACTGTTACAA CAAATTAAAA ATACAACAAG CGAGATATAG TTATTGTTGC TGGAnTGTAC 60

CAAGTAGTAT TCCAAGCGAT GCTATGGCAA ATTGCACAAA TTACAGCACA GACAGGTGCT 120

AAATTAGTAG TCGACGCTGA AAAAGAATTG GGCTGAAAGT 160

(2) INFORMATION FOR SEQ ID NO: 3167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3167:

TGTGGGGGAA ACCTGCACAG CAAAAACTAA AGCTTATCGA TACATCTAAA CATTGTATTA 60

TAAAATCAGT GCATCCTAGT CCACTGTCTG CATATAGAGG ATTCTTTGGA TCAAAACCGT 120

ATTCCAAAGC GAATGCCTAT TTAGCGTCAG TAGGnA 156

(2) INFORMATION FOR SEQ ID NO: 3168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3168:

GTGGCGAGAA ATACCGCAAG CATAAAGATA TCTTTGATCC AACTTACCAA CAGATCAACG 120

GAAAAGTACC AGGTAACCAG GAATCAAGAT CCAGACACAG GAAAAGTGAT CGAG 174

(2) INFORMATION FOR SEQ ID NO: 3169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3169:

TCAAACGGGG TCAATTTCAA ATGGAAAAAT TATACCGCAT CTTCTCCTGA TAACTACGTG 60

ACCTTATCTT CTTTATATTT GCAGACCACG AACATTCAAA CTGCATGCTT GCTCGATTGG 120

CAATGTCATA TAACTAGTAA CATGATCATC nCATCAAATT TAGTATGTCA AATGTCCCAA 180

TCAnTAATTT GATCGGTGTT GCTCAATTGA TTA 213

(2) INFORMATION FOR SEQ ID NO: 3170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3170:

AAAGCACCTT TTCCTAATGA AAGTTGTGCT ACTGGTATCT GTGTTTGATT TACAAAATCT 60

TCTAATTCTT GATGGAGGTG AAAACTGTTA ATTTCATGTC CAGTAATGAT GATAGGCTGC 120

TTCGCTTGAT GCAGTTTAGT TGCTAATAAC TCTATATATG TTGATGCATC CGTATATTTA 180

GTTGCCGTCA CTTCAAATGG TGTCGGTATC TCAATTTCAG AGATTGCGAC ATCGATTGGT 240

AAATGTAAAt GAACTGGGCG TCTTTCGGCG ATTGCTGTAT TAATTAAACG TGGTATTTCG 300

GTTGTTGCAT TTTCAGGTGT GATATAACCT GTGCACGnTT ATATGTGCAA ACATTTTTCG 360

ATAGTCGTCA AATGTACCnn 380

(2) INFORMATION FOR SEQ ID NO: 3171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3171:

TAGAAgGTAA GAAGGATCCT ATCGGTGCAA TGGGATATGA TGCGCCAATT GCAGTGTTGA 60

ACGAGCGACC AGAATCACTA TTTAATTACT TTAAACAGCT GTTTGCACAA GTTACGAATC 120

CACCAATTGA TGCGTATCGT GAAAAAATCG TAACGwGTGA ACTTTCTTAT TTAGGTGGCG 180

AAGGTAACTT ACTAGCACCT GACGAAACGG TTTTAGATCG TATTCAATTG AAAAGGCCGG 240

TATTGAATGA ATCACACTTA GCAGCGATTG ATCAGGAACA TTTTTAAATT AACTTATTTA 300

TCAACGGTAT ATGAAGGGGG ATTTGGGAAG ATGCGTTAGA AGCATTAGGC CGAGAAGCAG 360

TGGAATGCTG TTAAGCAAGG GCGCTCCAAA TTCCTAGTGG T 401

(2) INFORMATION FOR SEQ ID NO: 3172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3172:

ACATAATTTA AAATAATATT ACATTTGTAA TGGnCACCAA GTAACGTTTC GGTTGCTTGG 60

TGTTTTTTGG TATGAATTAC TTTCTGTTAC AAAACAATCT AAAGCGTTCT GTTATGTTTT 120

ATTAAGATTT AATTACAAAC GGAAACTAAA TGTAATAGAA TAAACT 166

(2) INFORMATION FOR SEQ ID NO: 3173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3173:

ATAATGAGAn TGTTGTACGT TATGGTGGTG GAAGTGCTGA TGGTGATTCA GCAGTAAATC 60

CGAAAGACCC AACTCCAGGG ACCGCCGGTT GACCCAGAAC CAAGTCCAGA CCCAGAACCA 120

GAACCAACGA CCAGATACCA GAACCAAGTA CCAGACCCAG 160

(2) INFORMATION FOR SEQ ID NO: 3174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3174:

CTTTATATAA AGAAGGAATT ACTAAACATA CAGTTAGATT ACTTCATGCA ATCGAATTAG 60

AACGTTTGAA TTTAAGCCGT AGATTAGGTT TTGAATTATC AACAGCnAAA GAATCACGTA 120

TTGAACGGGG GTTATTTAGA ACGTGATAAA GAAGGATG 158

(2) INFORMATION FOR SEQ ID NO: 3175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3175:

TATTTGAAGA TGGCTGTGTA CAAAAATCGG TGTTACGTGA TCATGATACT GTCAGAATTT 60

ATAAACCATG GCTAACAGCA CATCAGCTTT CATTGCCCnA GTATGTCGTC AGAGAAGATA 120

CACCTAATCG CTAATTAATG AGGTTTGGAA ACAT 154

(2) INFORMATION FOR SEQ ID NO: 3176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3176:

AGAAGGTATT TTAGCTCAAT CTCCAGGTCT AAAGGTTGTT ATTCCTTCAG CCCATACGnT 60

GCGAAAGGTT TATTAATTTC TTCTATTAGA AGTAATGACC CAGTCGTATA CTTAGAGCAT 120

ATGAAATTGT ATCGTTCATT CCGTGAAGAA GTACCTGAAG AAGAATATAC AATTGACATT 180

GGTAAGGCTA ATGTGAAAAA AGAAGGTAAT GACATTTCAA TCATCACATA CGGTGCAATG 240

GTTCAAGAAT CAATGAAAGC TGCAGAAGAA CTTGAAAAAG ATGGTTATTC TGTTGAAGTA 300

ATTGACTTAC GTACTGTTCA ACCAATCGAT GTTGACACAA TTGTAGCTTC AGTTGAAAAA 360

CTGGTCGTGC AGTTGTAGTC AAGAAGCACA CGTCAAGCTG GTGTTGGTGC ACAGTTGTAG 420

CTGAATTAGT GACGTGCATC CCTTCATTAG AAnnCCTATG GAAGAGTGCA CA 472

(2) INFORMATION FOR SEQ ID NO: 3177:

(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3177:

TGAAAGCTGG CGAATACAGT GATTGTCATG ATGCGGATCT AnTTGTCATC TGTGCTGGTG 60

CTGCACAAAA ACCTGAGAGA AACACGTTTA GATTTAGTAT CTAAAAACTT GAAAATATTC 120

AAATCAATTG TTGGTGAAGT AATGGCATCA 150

(2) INFORMATION FOR SEQ ID NO: 3178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3178:

TTACTCTATC TTGATTTGAC GAAATACTAT TAnGCTAATA TCGATATTTT AAAAACGAGA 60

TGATGTTCCA AAGCAAGCCA TTTCGATGGA CTGCTAATAT TCTTCAGCCA AACGTATCAT 120

TTTACTCGCA TTTGGTGAAA AGAAACGGCT GCTATTACAC ATTTAT 166

(2) INFORMATION FOR SEQ ID NO: 3179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3179:

CTTCGACTCT AGAGGATCCC CGCGCTCAAA TTCTAGTGTT AGATGATAGT GGATTAGTTG 60

ATAGCAATGG CTTTGCAATG CCGATGTTAC TCGCAATAAG TCATGTGCAT CAATTACTTA 120

TTAAAGCAGA TTTACGTATG TCTACAAGTT TAnTTCGCTA AATCTGGTGA 170

(2) INFORMATION FOR SEQ ID NO: 3180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3180:

AGCTAAGGTT GCCnTGGGCG TTGCCCCAnT TGGTTAGTCC AGGTGGTCGC GGTGGCCATC 60

GGTGTATTCG CCAGGTCCTT CAGCCAGGGT TTTTACTATT ATATCCAGTT GTAGCATTCA 120

TGATTGGGGC GATTCGAGAT AGATTCATCA ATGAAATTAA TTTCTGGATT TTATTCGTTG 180

GTATTTATTT GGGTATACAT AAGTATGGTA CATGATAGGC AGATATACAA CATTACAACA 240

TTCATTCTAC TATGCTGGAA ATAACATGAC AGTGATGACA CTACTATCCC CGTCGCA 297

(2) INFORMATION FOR SEQ ID NO: 3181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3181:

CACTAGGTAC CCCAAAACGC CAGAGGAACT TGGTTAAATC GCACTTACTT GGTGGCTCCA 60

ATCAACTGGT ACTTCATAAC GTTTGGCATC TTCGCCACTT CACCACTATT ACTCTTTCCA 120

CCTAATTGGT TCATGGCTTG TGCTAACGTT TCATGTGCTT CCGCTGAAAT CGATCCATAA 180

CTCATCGCCC CTGTATTAAA GCGTTTGACA ATGTCACTTA CCGGTTCAAC TTGGTCGATG 240

TCAATCGgTG TACATGCTTT AAATTCAAGT AAATGTCTAA TGTGaTCTGT TCTATTTTTG 300

TTnCACCGnT TnCAGAGTAT GCTTTAAATT GCGCCATAGT CCATTTTCT 349

(2) INFORMATION FOR SEQ ID NO: 3182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3182:

TACCAACACG TACACCTTCT AAAATAACTG CATTTGCACC GTnTTAATAC ATCATCCTCG 60

TTTATAACCG GTGTAAGCAC TAGGGGGTTC AATCACACCT GCTAATACTG CGCCAGCCCT 120

ACATGTACAT TTTTACCAGT TGTAGCACG 149

(2) INFORMATION FOR SEQ ID NO: 3183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3183:

GCGGTGCCGG TGTTGCAATT GGCGCAGTGG TGTTGGTAGC ATGTGGTCTT TCAATCAATG 60

TTCAATACAC CAGGAGATCC GGAAAAGATG CGTATGAATT TTATGGTAAG TGCACCAGGC 120

ATTACCACAC CACGCAAnAA CATGCAT 147

(2) INFORMATION FOR SEQ ID NO: 3184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3184:

CAGCGATATG TTGGCGTTGA AAATCTGCAA TTTGTTCATA ATTCTCTGTT AAAGAACGAC 60

TTAAATTGAT AAAAATGGAT ACGATCTCTT GGTAAACAGT GACATTTTCT CAATCGGCGT 120

ATGATGTTTG TGGCACCGAC CATCGAGAAC ATGAAAATCT CATGTCCCAC GCTAGTCGnC 180

(2) INFORMATION FOR SEQ ID NO: 3185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3185:

GGTAAATACG TATTAATCAG ATTAAGATCT GGTGAAGTTC GTATGATCTT ATCTACTTGG 60

CCGTGCTACA ATCGGGnCAA GTTGGTAACC TACAACACGG GTTAGTTAAC GTTGGTAAAG 120

CCGGCACGTT CAAGATGGGA AAGGTATCCG 150

(2) INFORMATION FOR SEQ ID NO: 3186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GAATTTnAGG TGAATCAGAA GATTAACGCT GTTGCGTCCT AAGCTAACAG ATACTGGTTC 60

GTCAGTTGTC GTTGAAAAAG CGAATGAACA ATTTAATAAA ACCGTAACTC GAGCATTATT 120

AGAGGAAGCT AACCAAAGCA GGTTTA 146

(2) INFORMATION FOR SEQ ID NO: 3187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3187:

AAATTGGCGA GTATGTTGTT ATTGGGTCAG TACTCTGAAA TTAACAATAG nTACGATTGA 60

AAATGGTGTC ATGTATTCAA CAGTCTGTTG TTAATGTATG CTAGTCGTGG TGCGAATACT 120

AAGGTCGGAC CGTTTGCGCA ATTGAGACCA GGCGCGCAAT TAGGG 165

(2) INFORMATION FOR SEQ ID NO: 3188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3188:

CAGTTTAGTG GAGACGAATC TAAACGAAAC AAAGCGATTG GACGTGCATC AGTTGTACCA 60

ACATTCTTTG GTGTAAACGn AACCAATTTT ATTTGGTGCC ACCACTAGTT ATTGGAATCC 120

TGTGTTCTTT ATTCCATTTG TATTAGCACC AATTGTTAAC GTATGG 166

(2) INFORMATION FOR SEQ ID NO: 3189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3189:

AACCCTTTAT CTAATCCATT TTCAGTTAAG CGATGACCGC CTGCTAAAAT TTGTGCATCT 60

GATTCTTTTG CTGCATCAAT ATATGATTGA ATTTTATCTA ATTGATCCTT ACCAGTTTGA 120

(2) INFORMATION FOR SEQ ID NO: 3190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3190:

TCCCCCAAAG GGTTTAAGGG GTTAACCCGG GTTTGGGAAA AATTTTTTAA CCCCCCTTAA 60

AnTTCCCGGG AAAAAGGAAA CCCGGGTTTT TAAAAAAAAC CCGGGGTTCC CAAAAATTTT 120

TTGGGAAAGG GAAAGGAAAA AAGGGTTAAA AAATTTTTGG GAAAAACCCG GGCCCAnAAA 180

AAAGGGTTTT TTTCCCCTTA AAAAAAATTT AA 212

(2) INFORMATION FOR SEQ ID NO: 3191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3191:

CTTCACTGAC TTTAGCAATT TCATCACCTT TTGCCCCTAC AACGATAGCT AATGATTTAT 60

ATTGTAAACT CAnATGACCT TGTTGAATAC CTTCTGACAC AAGCGCGCGA CATGCTGCAA 120

AGTTTTGCGC TAAACCAACG GCAGCAAC 148

(2) INFORMATION FOR SEQ ID NO: 3192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3192:

CTGCTAATCC GAAATCTTTT TGGAGTTTTA TTAAACCAGC TGCTTCTAAT AGTTTAAGTG 60

CACGTGCTTG GTTTGACACA TCATTTGGAA TGACAACTTT AGCnCCATCT TTAACCTTTT 120

TGACATCTTT AATTTTATCT GCAGAAATAA ATCCATCACG GATGGCTCTT AAATATATGT 180

TACGTGATAA TTTCTCGAnA AATGGCTTCC CT 212

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3193:

TCGTGCAGTG GTCTTCTGTT AATTGGTGAA TTTGGATACT GGTTATATTC AGCTGCACCG 60

CAAGCAACTT CTATTGATGG CCnAACTGCC TTTTTACCTC AAGCAATGGG TATGGTAGTT 120

GTTGCAGTCA TTTATGGCTT T 141

(2) INFORMATION FOR SEQ ID NO: 3194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3194:

AATAACGTTC TGAAAAACGA AGATGTTTTA AATGCCTATA TCCGCGGTCG TGGCGGAATG 60

GCAGACGCGC TAGGTTGAGG GCCTAGTGGG AGAAATCCCG TGGAGGTTCA AGTCCTCTCG 120

GCCGCATCAA AATTCTTAAT TTAAATAAGC GGGTGTAGTT TAATGGCAAA ACCTCAGCCT 180

TCCAAGCTGA TGTTGTGGGT TCGATTCCCA TCACCCGCTC CATAGATAAT TTTAATGAAC 240

ATTGAAAACT GAATGACAAT ATGTCAACGT TAATTCCAAA AACGTAACTA TAAGTTACAA 300

ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTATGGAGA GTTTGATCCT 360

GGCTCAGGAT GAACGCTGGC GGCGTGCCTA ATACATGCAA GTCGAGCGAA CGGACGAGAA 420

GCTTGCTTCT CTGaTGTTAG CGGCGGACGG GTGAGTAACA CGTGGaTAAC CTACCTATAA 480

GACTGGGATA ACTTCGGGAA ACCGGAGCTA ATACCGGATA ATATTTTGAA CCGCATGGTT 540

CAAAAGTGAA AGACGGTCTT GCTGTCACTT ATAGATGGAT CCGCGCTGCA TTAGCTAGTT 600

GGTAAGGTAA CGGCTTACCA AGGCAACGAT GCATAGCCGA CCTGAGAGGG TGATCGGCCA 660

CACTGGAACT GAGACACGGT CCAGACTCCT ACGGGAGGCA GCAGTAGGGA ATCTTCCGCA 720

ATGGGCGAAA GCCTGACGGA GCAACGCCGC GTGAGTGATG AAGGTCTTCG GATCGTAAAA 780

CTCTGTTATT AGGGAAGAAC ATATGTGTAA GTAACTGTGC ACATCTTGAC GGTACCTAAT 840

CAGAAAGCCA CGGCTAAtAC GTGCCAGCAG CCGCGGTAAT ACGTAGGTGG CAAGCGTTAT 900

CGGCTCAACC GTGGAGGGTC ATTGGAAACT GGAAAACTTG AGTGCAGAAG AGGAAAGTGG 1020

AATTCCATGT GTAGCGGTGA AATGCGCAGA GATATGGAGG AACACCAGTG GCGAAGGCGA 1080

CTTTCTGGTC TGTAACTGAC GCTGATGTGC GAAAGCGTGG GGATCAAACA GGATTAGATA 1140

CCCTGGTAGT CCACGCCGTA AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCTTAG 1200

TGCTgGCAtA ACGCATTAAG CACTCCGCCT GGGGAGTACG ACCGCAAGGT TGAAACTCAA 1260

AGGAATTGAC GGGGACCCGC ACAAGCGGTG 1290

(2) INFORMATION FOR SEQ ID NO: 3195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3195:

TGGTACAGAG TTATCGCTGG TGGTCCTGTT CGTGCCGTAC TTGAATTATC AGGTATCACT 60

GATATCTTAA GTAAATCATT AGGATCAAAC ACACCAATCA ACATGGTTCG TGCTAACAAT 120

CGATGGTTTA CnAAACCTTA 140

(2) INFORMATION FOR SEQ ID NO: 3196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3196:

CTATTGGATC AGGAGGCAAC TACGCTTAAG CGCAGACTGC CCATTGAAAC GCCATGCATC 60

GCATTTGTCG CCTGAAGAAA TGGCATATGA GAGCTTGAAA GTAGCGGCTG ATATTTGTGT 120

CTTTACCAAC GnTAATATTG TTGTC 145

(2) INFORMATION FOR SEQ ID NO: 3197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TGTCGAGTTG GAATTGGACG ATTGAATATC CCATCTCCAT CACTATCAAA GTATGGGAAT 60

TGAATTGTTT CTAATTCGTA TCCACCTTCT GTCATTGATA ATGTAGGGTT AATTTTAGAA 120

CCATCTkCTG TTTCTAGTTT TAAGTTCCAC TTCTTACCTT CTTCCCAACG TTGACCCATT 180

GTGCCATTAG GTACTACTAA ACTATCGCTG ATTGCATCAT GAATAACTGG CTTCCATTCn 240

CCTTGCTCTG TTGTTTGACC TAAGTCACTC GCGCTnAAAA ATCGACCCGC TTTATATCCA 300

TnTTCAGCTG 310

(2) INFORMATION FOR SEQ ID NO: 3198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3198:

TGCTTTATTA ATGCATTGGC TAATAATCCA CTTGTACCAC CACCGGCACA AAGTACTAAG 60

AGGTTTGTTC TGTGATATTT GAAGCTTTAG TGCATCGTCT GATACACCAC TTGCCGCTAA 120

AATTGAATCA GCTTTTnTCG 140

(2) INFORMATION FOR SEQ ID NO: 3199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3199:

TGGTGATTTC AAATCATGAG ACTGGGACAA AATGATGTTT TCATAAAAAT TATTTCGTTG 60

TTCCACTCTC ATGATTTTTT TGATGAACAT AATTACATGA TTGATTGCAT CATTTGTTAA 120

AACCAGTGAT TGCAACCTGC CATTCACAnG GAAAATTACC TAATAAGTGG CGTATTTACC 180

AGTC 184

(2) INFORMATION FOR SEQ ID NO: 3200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3200:

TTGAGAAGCG TTTAGGAAGT AACGTTTAAC GACGACAGTC GTTCAATGCG ATCAAAATGT 60

TTTAACACAT GAATCGCTCT CGTACTATTC GTGTGTGACA CATGTTCTTC CAGCATTTGC 120

TTAATGAATG CTTTTTCTTC TTGGTnTTTA ATCTTTGTAA ACG 163

(2) INFORMATION FOR SEQ ID NO: 3201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3201:

GTTATGTTTG AGACTATAAT GAATAAATAT TTAGAAATAT GACTCCGATT GTTCGATGCT 60

TAATTCAGTT AGAAGCATCA TAAGAATGCA TGATTACTGG TGTAAAGATA CGTAATGTnT 120

TGTATTGACT GGATGTCTTT GGATAGAGT 149

(2) INFORMATION FOR SEQ ID NO: 3202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3202:

CAAGTGACTG AGATTACTGA AGTAAACCCG TTACCGCCAC ACTATATTTG TCCGAACTGT 60

AAAACGAGTG AATTTTTCAA TGATGGTTCA GTAGGATCAG ATTGATTTAC CTGATAAACG 120

TGTGAAnTTG TGGAGGCCAC TATTAAAGAA GACAGAATCC GTTGAACATT TAGATAAGGG 180

AAAGTCCGAT TC 192

(2) INFORMATION FOR SEQ ID NO: 3203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3203:

CGCCATCTAA CGTTTTTTGT ATTCGTTGTT GCTGAGCTAG TTGTAAGTGC CnCATTAAGC 120

ATCTTATAGC GTGATAGCCA TGCGCCAACG TACAAATCTG CTCCGTATTG TACGCACCAC 180

TAAGCAGTAC ACACCAGTAA CATTTGATAG CGTTATAGCG CAATATACAG TACA 234

(2) INFORMATION FOR SEQ ID NO: 3204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3204:

AACGCCATAA GCTACATGTA TGCTTCTTGC ATGGTTATCA TCCTCTCTTA ATGACTATCT 60

TTTAATTACG nAATGGCTTA CCAGTTTTTA ACATATGTGC AATTCTTTCA TATGATTTTT 120

AGATTTAGTA GCATAAGCAA TTTCTCCACG TTGATGTACG TGATGTAATG ATTCTGGG 178

(2) INFORMATION FOR SEQ ID NO: 3205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3205:

TATTAATCAC GTTGTTGTGC GTTCGTGTTT TCGCAGTATT GATTTGTTGT TGCGCATTAT 60

GCATTGCATT ATTGTACTGC GTAATTGTAC CTGGCTTTTT ACCTTCAGTG CTTACTGGnT 120

CATCTAAATG ATTTTTAGCT GTGATTA 147

(2) INFORMATION FOR SEQ ID NO: 3206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3206:

CAGCTGTACT AGTTGAGCGT ATTATCCAAA ACATTTTACG TGATGGCATT GATGTCGATC 60

GACTTTCAGT CGTAACGTTT ACAAACTTAA GCGCACGTCA nATGAAGCAT CGTGTAGACC 120

(2) INFORMATION FOR SEQ ID NO: 3207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3207:

TAGGGACTTT GAAGCGGAGA GTCTAATGCA TATGGGCAGC ATTATGATCA GCAACTGCTG 60

AGAAAAATCC AGTTCTAGCT TGGGATTTAA ATGTGGAGTG GnTTAATGAA TGCATTAAGA 120

AGCTGCAAGA ACTTATAAGT GTGCA 145

(2) INFORMATION FOR SEQ ID NO: 3208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3208:

AAACGGTTTT AGATCGTATT CAATTGAAAA GGACCGGTAT TGAATGnAAT CACACTTAGC 60

AGCGATTGAT CAGaACATTT TAAATTAACT TATTTATCAA CGGTATATGA AGGGGATTTG 120

GAAGATGCGT T 131

(2) INFORMATION FOR SEQ ID NO: 3209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3209:

ATAAATTTAT CTATAATCTG TTGCTTGTTT TnCTGTTCTA CAAGTATTTT CACATTAGGT 60

CCCGCATCCA TTGTAAAATA ACACGGATAC CCCGCTTCTC GGCATTCGTG AACAGCGCCA 120

TGACATCATA ACTTTCTGCA CAGTAGGAAC GGGGGTG 157

(2) INFORMATION FOR SEQ ID NO: 3210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3210:

AACGTAATAG ATATGGTACT TACTACATGG GAGAGAGTGC TAGATTCACA AACGGCAATC 60

AACCAATCAC AGTAAGAGAA GTGGGGCCAT TCTTATCTnG TCCAGTGGGT TATCAGTTCC 120

AACCTGGTGG GTATTGTGAT TAT 143

(2) INFORMATION FOR SEQ ID NO: 3211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3211:

ATGCATACTG TATGTGTTCC AGCATATACA ATTTTGnCCA TCTTTAATGA CAACTGTACC 60

ATTTTTCACA ACATTTAATT CATCTAATTC CTTACCCTTC AAAGTTTATC TGTTGATCTC 120

GGTAAAATTA ATTCTGC 137

(2) INFORMATION FOR SEQ ID NO: 3212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3212:

ATTCACGCTT TAAAGGACGT AAATACACGA CTAGGCTGTT TACCTTTAGA TCTAAATCAG 60

AACAATTTTT TTACCATGGT GTTCCCCTTG AATTAGGAAT TTTATATAAA AATAAGCGGG 120

AAGCGTTGTG CCCCGCTTAC TCATAAGCTT TAATTAATGC TAAATAGTCT GACACTAGCG 180

ATTTGATAAA ACTATACTAA AATTATTTAG AAGTCACTAA GATGCTAATG ACGACnAnT 239

(2) INFORMATION FOR SEQ ID NO: 3213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3213:

CATCCTCAGA GTAGGAATAG CCATACCATC GAATAATTCA CGTACTGTTT CGAATTGAGG 60

TTCAAATTCT TGAGTTGTAT AGAGCTCGAA AATnTTTGCC CATTAGCATA ATCAGACTTT 120

TCAAAAGTCT TGATATTTGA TACCCACGCT 150

(2) INFORMATION FOR SEQ ID NO: 3214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3214:

CTAAGCATTG GTTTAAACTA ATGTTCAGAG CTTTnTGTGG TTTGTAAAnA CAAGTATATT 60

nCGAGAACAC GTTTTTGTAT AGAGTCTCAA TTATAAAAGT TAGAATAGTT GACAACAGTG 120

TTACGATATT ATTAAACAAC TGTcTATCAT TAACGAAAGC AATTAACAAG AGTACtTGTT 180

GTGAAATCAT CGTTTAATAG TCAAAGATGA TCATCGTAGG gTAGACAACA TATCaTTGAC 240

TtAAGGAAGG GGAATGACCG ATGGGATTAA AAGATCAAGC TGTTACCTGG AGAAGGTATT 300

TTCATCAATT TCCAGAACTA TCCGATAAAG AATTTAAGAC TACACAAAAA ATTAAAGATA 360

TTTTAACAGA ACATCATATT AGAATATTAG ACTTACCAC 399

(2) INFORMATION FOR SEQ ID NO: 3215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3215:

CAGGTGAAAG CACAAGAGGA TTTGCTGTTT ATTTCTCTCC TGAAATTAAG AAATTCATTG 60

CAGATAATTT AGATAAATAA TTAAAACTTA GACATTCACC CAATCCTGAC AAAATATACT 120

ATAACTAACA TTTATTAATA TATATTGCAT TATTTAATAT GCATCAAAGC CAATCAACGr 180

TTGATTTTCA CCAACTCAAT TGTTGATTGG TTTTATTTAT GTATGAATGA ACAACTTTTT 240

GACATCATTA AGAATATAAA TGCGTTTGAA AGCATTTGAA AGCnACAACA TTTCTATAAA 300

ATTTTTCAAT AACAATTGCG CCACTAAAAC TCAAAATTTC CACCACCAAC ATCCAAATTA 360

(2) INFORMATION FOR SEQ ID NO: 3216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3216:

AGTTGCATCA ACTGAATCCA ACGCTACGCA ATACGAATTA TTCCAATCTG GCATGCGTGT 60

TGGTAGAGAA ATTTTAGCGA CATCTCGAGC ACGGTTTACC TTGCCTTTnT TGGTGGCCAA 120

CTTGCTTTAT GCTATGGGTT TTTCAAACTT AAA 153

(2) INFORMATION FOR SEQ ID NO: 3217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3217:

CTTTGCATAT TCTGGTTTGT AGTATTCATG GTCCGTCAAT TGTAGACCCA TCAATTGCAG 60

CCATTACATA TGCGGAATAT CGAAGCGAAC TTCAAGTTGC TTCAAGCTGG TAGAACACGC 120

AnATAAAATT ATTACATC 138

(2) INFORMATION FOR SEQ ID NO: 3218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3218:

CACTCCAAAC CAAGGATTTA CGTGCTTTAT ATnGAGGTAA AGCACATCAT GTkGTTaATT 60

TTATGCmTTT TaTTGCmCmA GraTTAaGAG AAATTTTAGC nTCTTTAGGT TTGAAACGTG 120

TAGAAGACTT AGTTGGAAGA ACTGATTTAT TACAACGATC aTCAACATTA AAAGCGAATA 180

GCAAAGCGGC TAGTATTGAT GTTGAAAAAC TGTTATGTCC TTTCGATGGG CCAAACACAA 240

AAGAAATTCA ACAAAATCAT AATCTTGAGC ATGGATTTGA TTTAACAAAT TTATATGAAG 300

AACAACGTGA TGTAGGGGTT ATTACAGGTA GTGAGATTTC GAAACAATAT GGAGAAGCAG 420

GACTTCCTGA AAATACAATT AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTTGCAGC 480

ATATGCA 487

(2) INFORMATION FOR SEQ ID NO: 3219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3219:

ACCAACTCGG AATCATGCAA TGAACACCAT GGTTGAAATA AGTGAATTGC ATAAGTATCC 60

TGGCCTGGCA ATGCTGGTAT AACCTAAAAC CTTGTTGCAC GnAATGTATT CGCTACAATT 120

AATGTACCTG CAAAACCGTT TAATAAGAAG TTCGAAATCG TTGCACCTGT ATATGG 176

(2) INFORMATION FOR SEQ ID NO: 3220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3220:

CTGATTTAGG TAATCTTTGC GCAATTGTTT TTTTACAGTT TCGGCAAATG GGTGCCCnGG 60

CAAATAAATA TTGGCTATGC TCAAACCTGA ATTAATGGTG GGTGTGTCCG CCATCGTAAT 120

TGGGnCCGCC TGAAGGGCCG CATATAAATG ATAGTGCTCT TCCGAATAAA AGGTAGGCCA 180

TATGTAATTG TTTTGTGGTT ACG 203

(2) INFORMATION FOR SEQ ID NO: 3221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3221:

AGCTAAATCT TGCCAATATG GTATCAACTT TTCATTCCAC TGATAATCAT AAATTTCAGA 60

GCAATGCCAG AAATGTATTA ACAACTGGCA CGTCTAATAG ATTGCTAACG GATTGTTTAC 180

GTACGTTCAT CGGCTTCTTT CGCTTCTATC GGATCTGGAG AATTGGGATG TTATGACCAC 240

TGAACCACTT ATTTGTAAGC TCTGTCGTGA TTGACTTCAT AATGCTTGCG CTTGnCCTCA 300

TTTCTAACAA CTCATCCTAC TTACnAAATT ACCCCnGGGG TACACCTGGT CCACTTCATC 360

A 361

(2) INFORMATION FOR SEQ ID NO: 3222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3222:

GGGGCTCCGn GGAGGCAAGG GTAGAAAATG ATGTAAACGC TGCATTACTA GGCGAATTGA 60

AATTACATCA ATATCAAGCA GAACGGATCT TTTGTATGAC GCTTGGTACA GGCATTGGGG 120

GTGCGTACAA GAATTAATCA AGGTTCATGT TG 152

(2) INFORMATION FOR SEQ ID NO: 3223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3223:

TTTGTTAAAT ATAGGCCCTG CAATGAGTGT ACTGGAATGG CAATAATCAT ACCATACAGT 60

AATACATCTC CAACATTTGC CTTnAATTCT TTTCCCATGA CTACCGGTCC TGGGATGTGG 120

TGG 123

(2) INFORMATION FOR SEQ ID NO: 3224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3224:

TGGTTGGTAA CCGTAAATTA ATGCCTGACA ATGATATTAG CTnCCTAAGC ATATTTCTGA 120

TGATTTAACA CATTATGAAA CGAGA 145

(2) INFORMATION FOR SEQ ID NO: 3225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3225:

GGTATTGTCT AGTCAATTAC TAACACCATT TAATTGTGGn AAGCAAAAGC TAAAGGTTAT 60

CGTGCGCTAT TGCAGGCATT GATGCTTCCA ACAAAGTCGA GTATTCAGTT GCATCAAAAG 120

TTTGCTTTT 129

(2) INFORMATION FOR SEQ ID NO: 3226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3226:

GACACTACCG TTCCCACGTA GCATCAATCG TCTCAGTCGC ATCGTAGTCA TCTGTATGTG 60

TTCCAGCATA TACAATTTTG CCATCTTTAA TGACAACGTA CCATTTTCAC AACATTTATT 120

CATCTAnTCC TACCCTCAAA GTTATCGTTG ATCTCGTAAA TAGTCGGCAA 170

(2) INFORMATION FOR SEQ ID NO: 3227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3227:

TTACTGCTTT ACGTTTATCA TTTTCTAATT CAnAAATTCG TCATTCAGTT TCAACTTTAT 60

CGACAGCTGG ACTTTGCGCA GATAAATGTG CTGCTGTAAT ATCTAACACA TCGATTGCTC 120

TTATCTGGCA ATAATCGTTG 140

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3228:

GCGCCTATAA TTGCGCTACT TGATTTAATT GAGTAGATAA ATCTAATCCG AATAAATCCG 60

TGACTTGCTT GATAAATAGC AACAATGCTn CAACTAAACC AGTTAGTACT GCTTTGTTTT 120

(2) INFORMATION FOR SEQ ID NO: 3229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3229:

GGCTATACAC CGACTACAGT AACATCTGGT AGCGACATTG AAAAAGACTC TAATGGTTTA 60

ACAACAACAG GTGTTATTAA TGGTGCTGAT AACATGTACA TTAGATAGTG GnTTCTACA 119

(2) INFORMATION FOR SEQ ID NO: 3230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3230:

TGGGAATAGC AACCAACAAT GCGACAACAA AGCCCGCTAC AAATCTCCAT nAACTAATTG 60

CTAAATGTTG GAAAAATTTC TCCAGTCAAC AATGAAAGGC CATATGACTT TTTCCTACAA 120

GAGCAGGG 128

(2) INFORMATION FOR SEQ ID NO: 3231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AATGCAGCTA TTACTTTTCA CAGATTCCAT ATCGTTCAAC ATTTAAATAG AGAACTTAAT 60

AAGTATCGTG TACAAGTTAT GAATGAnTAC CGTAATAAAA AAGGACCTGA TTATACAATT 120

TTC 123

(2) INFORMATION FOR SEQ ID NO: 3232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3232:

GCCTCAAAGA ACATGCTGAA CAGTCATCGC aTTCATATAG TTTGAAGTCT CGTTTAAAAC 60

CATATCTATC ATTACGGTAT GCATATCTTT TAAAACCTAT TCTTTTGTTA TTAGGACATA 120

TAAATTCATC ATTAAGTTCG TCATATTTCC AATTTTGAGT GTCGAAAATG TCACTTTTAA 180

ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGGCGTT TTATTAAAAT 240

CATCTATAAT GGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT ACAAATAACC 300

GAAGtATTTT GAATCATTGT TAAAAATGGA ATTAAAGTTC TAGTATCTGT CGGGTTTTGA 360

AATAGGTCAT AGGATAAAAC AAATTGAGAA TTTGTCGCTA TTTGTAAATT GTATCCTGGC 420

TTAAGTTGGC CATTTTTCAT ATGGTCTTCC TTCATTCTCA TAAAAGTTGC ATCATGATCA 480

GTTTTAGAAA ArCTATTTCT ATCTTTAAGA ATCGATTTTT GTTCTTCATA TTTATTTTTT 540

CTTTCGGAAT AATCATCAAA TTTmTTTTTG AACTTCTTAA TCTTAGTTCT TTTTTaCGGG 600

TCTGTTTTCT AATTTGAGTA CTATCTTCGT TCTCAATAGA ATGATTTAAA yCTTCGATTT 660

CTTTATCTAA ATGACTACCA ATTAAATCTA TTTCTTCTAT TGTTAAATCG CTATCTCCAT 720

CTTCTTTTAT CTCTGGTATT ATTTTTTCTT CAACTAAGTC ACGATATAAT GTTTTTGAAT 780

TTTCGTTCAA TTTCGATTCG TGATTTTGAA TACTTTTCTT CCACACAAAT GTATACCTAT 840

TGGCATTAGC TTCTACTTTT GTACCATCAA TAAGATTTTG CTTTAAACAT TGACTATGAA 900

ACTGGATAAA TAAAGATTCA ATTAACGCAT CAGTATTAGG ATTCACTCTA ATACGATTAA 960

TAGTTTTATA AGAAGGTGTT TGATTTTGAG CTAACCACAT CATTCGAATA CTGTCATGAA 1020

GTAATTTCTC TATTCTACGA CCAGAAAATA CAGATTGAGT ATATGCATAT AAGGTGATTT 1080

TTAACATCAT TTTTGGATGA TAGGATGTTG CGCCACGATG ATGTCTGAAT TTATCGAATT 1140

CGCTATCAGG TATCGTTTCA ACAATTTCAT TAACATATCG CGAAATATCA ATTTGAGGAA 1200

GGCACTTCAT TAATTTAGTT TAGTGGTATT TATTAAATTA TACGAAGGGA CCCAACACAG 1320

AAAATTCAAA TTATTGAATT AAACATTTAT GTGCAAGTTT GGCAAAGTGT CTTATTTTTT 1380

AAAAGTATGT AAAAGTAAAA TTACATGTTA ATACGTAGTA TTAATGGCGA GACTCCTGAG 1440

GGAGCAGTGC CAGTCGAAGc CGAGGCTGAG ACGGCACCCT AGGAAAGCGA rCCATTCAAT 1500

ACGAaGTATT GTATAAATAG AGAACAGCAG TAAGATATTT tCTAATTGAA AATTATCTTA 1560

CTGCTGTTTT TTTAGGGATT TATGTCCCAG CCTGTTTTTT GTGATTTTTA ATAATTTGAA 1620

TATGGrAAAT GTATTAwTCt CTCATTTGTA TAGATT 1656

(2) INFORMATION FOR SEQ ID NO: 3233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3233:

TTGCTCATAA ATCTTTTCTT GGCGCTCTGA ACACTATCTT CTATTCTGTC GGAATTTTTC 60

AAACATAGTC TTATCATTTn CTTCTAATCG CGTTAAACGC CAATCTTGTT CATGTCGTTT 120

GGTAAATCCA 130

(2) INFORMATION FOR SEQ ID NO: 3234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3234:

GCCACGATAA AGAAGTAAGA ACAACACATG GTGTTACTGG TACAGGCTCA TGTTCTTGGG 60

AAAGTTATTT GTGnAAAATG GTGTGAATTA CCTGGGGAAA AATCAACAAA CTGACTATCC 120

AA 122

(2) INFORMATION FOR SEQ ID NO: 3235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3235:

AACCAGGATA TGAAATCTGT GACTTATTGC GTTAGATCGT TTTGTAACTG CTACTATTGA 60

AGAAGCAGAC CAATATAAAG GTACCATTCA TTGCAAAAGC ATTACATGCA TGAACCCAGT 120

TGACATTTAG TTAGAGATGG AAGATAGTAT TGTGCATTTG CAGnTTCCAC ATG 173

(2) INFORMATION FOR SEQ ID NO: 3236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3236:

GCGGTGTGCA TTTGAAAATG TTATCAAGAA TATTGAGTTA ATTCGCAACG ACATTATACC 60

AGCGATTAnA AAGCATTTAT CAAAATACGA GGGGCGTCAT CATGAATATT GTATTATTGT 120

CA 122

(2) INFORMATION FOR SEQ ID NO: 3237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3237:

TTTTTTGCCC AAAATTTTTG GGTTTTTTTT GGGTTAAAGG AAAAAAAATT TTTAAAGGGG 60

GGGGGGGGTC CCCCAAAAAT TTTTTTCCCT TCCCTTTGGT TTGGTTTTTT GGGGGGGGGG 120

CCCCCCCCCT TTGGAAAACC CCTTAAAAAA ATTTAAnGGT TAAATTGGAA AAAAAAATTT 180

AA 182

(2) INFORMATION FOR SEQ ID NO: 3238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3238:

GATGAnGTTC GACAACGTAT TGTGGCAGAT GTTGCAGTTG ACTTTGAAGA A 111

(2) INFORMATION FOR SEQ ID NO: 3239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3239:

AGTTGATCGT ATTTTCCAGA AGAGACAGAA TTAATTGATT ATCGTGTTAG TTCTGTCACT 60

GAAGGTACTG ATGCCCAAGC AGnAGTACAT GTAAGTTTAT TGATTGAGGT AAGACTGTCA 120

(2) INFORMATION FOR SEQ ID NO: 3240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3240:

TACACATCTn TCTACGATTG TAGTTTATCG ATAGGTTTCG CATCATGAAA CGTGATAAAC 60

AACCAACATG ATGCTAGTTT GATTAAGTTT CTTCTAAACA GACTTCAAAC GGCAGTGTTT 120

AGCATAT 127

(2) INFORMATION FOR SEQ ID NO: 3241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3241:

GACTAAAATA CATGTTGGAA TACTTGGTCC CATGGGAAAA TATTGGACTG GGTAACCCAA 60

TCACGGCTTC TGAAGTAGTT CTTTnTCTTC TATTAAAATA GCGACGGAAT CACACCTTCT 120

GCGG 124

(2) INFORMATION FOR SEQ ID NO: 3242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3242:

TACGTGTATA CACCGTTATC TTTATGGCTT TGAATTTCCA TAATAAATAC ATACGGnTTT 60

TGTGCAGAGC TCAGCACATA ATCATCTTTA ACTATAGTTT CTGGGAATCA CTTCATAGTT 120

TT 122

(2) INFORMATION FOR SEQ ID NO: 3243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3243:

AACCTTTTCT GCAACCATAC GCCATAGgTA TGtTTTCTTT TTACAATTAA AGaGCCAACC 60

GTTGTTATAG TCTAACAATG GTTGGCTCCT CTTATTTTAT GTGCTAAAAA TTTATAGGCA 120

ATTTTATTAC AACAATGTAC ATTTAAGGTG ACCTTCATGC CAAAATCGCA TCACTCATTT 180

AATGGAAGCA GCACGTCTTC ATACAAAGTC ACGATCCTAA T 221

(2) INFORMATION FOR SEQ ID NO: 3244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3244:

TTGCATTTTG ATTGTCTGGT GACCTTGGCA ATGACAATTC CCGCTTGCAA TCGGTATCTT 60

CAATATTATA ATCAGGTCTT GCCTTAGATT TTCGCTAAGT ACCGGTGATT CTCTACCATC 120

ATACTCACCT CATGnGCTAT TTTTCTAGAG TGCTTCTTTT CACACTTTAT CTTATAAAAG 180

GCTAGCTACT ATTACCGATT TATCATTATT AGTGGTTTTT ACCn 224

(2) INFORMATION FOR SEQ ID NO: 3245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3245:

GAAAGAGATT AGTGACAAGT TGGTTGTACT ATTACGTTAA AATTTGGAGA TTATGTGTGG 60

TGTTCAAGTA TGCGTTCAnT AATTGATATT GGCGCACCGT ATAACCATGT CAAAGTA 117

(2) INFORMATION FOR SEQ ID NO: 3246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3246:

CTACAGGCTT TCGTACCACA GGATCAAAAC TACGCACTGT GCCTTGTACA TACGCATGAT 60

CAGCAATGAC ATTCCAAGTA TTACCACATG ATATTTGnCC AATTGTTACT ACCGTTC 117

(2) INFORMATION FOR SEQ ID NO: 3247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3247:

TACACAnCTT TCTACGTGTG TAGTTTATCG ATAGGTTTCG CATCATGAAA AGTGATAAAC 60

AGCCAACATG ATGCTAGTTT GATTAAGTTT CTTCTAAACA GACTTCAAAC GGCATGT 117

(2) INFORMATION FOR SEQ ID NO: 3248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3248:

CCCGTCCTTT GGTGGAACCG TTTTGTAGAA TTAAATAATA TTACAGAGCC GCTAGCAGTA 60

ACGATCCAAA CGAATTTACC ACCATCACGT GGATTAGGAT CGAGTGCACT GTCGCGGTTG 120

CnTTTGGTCC TGCCA 135

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3249:

AAAAGCCAAC CCATGnAATG TTGGATTGGC TTTTTACATG CCATCTGAAT CTCTAATTTT 60

AAAAAAATAT GGAATATAAA TAAGACAGTA AAAATTAAAT TTCAGT 106

(2) INFORMATION FOR SEQ ID NO: 3250:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3250:

AACGCTGAAG CAGATAAAAA ACGTCGTGAT AGAAGTAGAC TTAAGAAACG AGTCTGACAn 60

TCTAGTATTC CAAGTTGAAA AAACTTTTAA CTGTATTTAG GCGAAAATAT CGGTGAAGAA 120

GA 122

(2) INFORMATION FOR SEQ ID NO: 3251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3251:

GAACGTTGAG ATGTCACAAA CTGGTGAAAG TGCACGTTCA ATGCCAATGA CTGATAAAAC 60

CAAATTCATC AATCACAATT ACTCCGAAAG CnGGTACAGG TCACTCAGTA AGTAGTAATC 120

CCAGTACATT AA 132

(2) INFORMATION FOR SEQ ID NO: 3252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3252:

GGAAAATCTT CAAATTCTGC AAATTGCCAA TTTACCTAAT AACCAAACAT CTAAGGCATG 60

TGTAATGCTG CTACnTCCGC TTCGTCATCA GCTACAATGA CAAATACAGG TGCCA 115

(2) INFORMATION FOR SEQ ID NO: 3253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3253:

TTTCGTCAAA TTATGGGAAT AAAATAATCA TATTTAAGAT AGTAAATATT GAATAAGTTG 60

CTTTGAAATT TATAAAATGA AAGTATAGTG TCATGGGnAG TATAATAGTC AGATATATAT 120

GTAACGGCAC TATATTGAAA 140

(2) INFORMATION FOR SEQ ID NO: 3254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3254:

AAATCTCCTA CTTTTTCTAC CCATAAATAA TTGGCTAACT TTTTCATCTT ATCTTCATCC 60

TTTCTCTTCT ATTTAAAATG CTACAAATAA ATTTCCGCGA GTAATTTTAA TGTTTTACAA 120

CGCTGTTCAA TACCTGGAAT AAGCGGTGCT ACTAACACCT CATCAACTTC ArACGTAGCA 180

ATGAAATCAT CTAATTGTGC TTTAACCTwT TCTTGTGTAC CTGcAATGAT GCGTGCTTGg 240

ATGTGCTTGA ATCATCTCTT TGTCTCGATC ATTAAGCTTA TACTTTTGTG CTGTGTCTAC 300

TGAAGGAAAA TCTTCAAATT CTGCAAATGT AATTTACCnA ATAACCAAAC ATCTAAGGCA 360

GTTGTAAGCG GCnACTTCCG CTTCGTTATC AGCnACAAG 399

(2) INFORMATION FOR SEQ ID NO: 3255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3255:

ACCATTCGTC AAAATATTCC AACACGCATT TAGGTGTGCA AGGTATCGGT ACCTAACAAC 60

GAAGCTATCG TCTCACTAnC CTTAAAAGAT TTTAGAACAA CAGCTGCACT CATCAT 116

(2) INFORMATION FOR SEQ ID NO: 3256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3256:

AAAGACCTAA GGTTATGTAA TTGGCCTAAA TTTATTAATC GTTTAAnTTC AGTTAGTAAA 60

AAGTCTGTGA GTAAGGGTGT ATGGAAACTG GTTAAATATT ATAGAG 106

(2) INFORMATION FOR SEQ ID NO: 3257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3257:

AACGTCCATC GTAATACCTT TTGTGTCTAA TGTAACTTGT ACATCGTCTA ATAATAAGTT 60

GACGATATCT TGACAATGCA TCTTTATCTA GATGTAAGAn TTCAACGGAT GCCG 114

(2) INFORMATION FOR SEQ ID NO: 3258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3258:

TTAAAGCAGT TAATCCACAG GGAAAGTGGT TAATACAGTT GGGCTCTGGT GGATAGTACA 60

GTTGCAGGCA TGGTGGGCTG GGAATTGCTT CAGGGTTTAA CGAnTGGGAA AAGCCTT 117

(2) INFORMATION FOR SEQ ID NO: 3259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs

(C) STRANDEDNESS: doubl
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3259:

GGACCGCCAT ATCGTTGGCA ATCATCGCAC CTATAATCAT CGCAAGTATA ATAATATTAG 60

CACCTTGCAT ACTTTTTAAC CAGGTTGTTA ATGCCTCAAA AATATTAGAA ATTGGTGCCC 120

GnTT 124

(2) INFORMATION FOR SEQ ID NO: 3260:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3260:

TACCAATGTA TATCCATATA CTTTTATCAT AATCATTTCA GCCGACTTTA GTTTGATGTT 60

TTTGCTTGAT TAAAATCTTT CGGCGATCTT CAGCTTGATG TTTTCGTTTG ATTAAATTGG 120

TACAATAnAT 130

(2) INFORMATION FOR SEQ ID NO: 3261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3261:

GGCCTTTTTG GGCCGGGGTT GGAAATTGGG GTTGCCTTAA TTTTTTAATT AAATTTTGGA 60

ATTAAAAAAG GAAAAAnTCC AAAGGTTAAT TTTAAAAAAA GCCCAAGGTT TTAAAAATTC 120

CCCCAACCAA AAAGGGGGGG AAAAAAGGTT GGGGGTTTTA AAAATTAnCC AAGGTTTTTG 180

GGGCCCTCCC TTGGGGGTTG GGAATTAAAG GTTAACCAAG GTTTTTGGCC AAGGGGCCCA 240

ATTGGGGGTT GGGGCCCTGG GGGAAAAATT TTGCCCTTTC CCAAGGGGTT TTTTAAAACC 300

CGGATTTTTG GAAAAAAAAA AGCCCATTTT CCCCCCAACC CnAAAGCCCA GTTCCCGCCC 360

ATTTTCCCGG GGTAACCCTG CCCCCACCGG GGCCATTTTT 400

(2) INFORMATION FOR SEQ ID NO: 3262:

(A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3262:

TGGTTCAATG GAAACGTGTA CCGCAAATnC CGTTAAATGT TGTTGGATGT TGAGAGACGT 60

GGCTGAACTG GCACATTTGG GCAATGACCA ATGGAACAAG CTAATGGGCA AGCGATTATT 120

GCGACGGCTG ATGG 134

(2) INFORMATION FOR SEQ ID NO: 3263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3263:

TTTTTTTCTG TTGGTACTTG TTTTGTGGTT GGCGATTGTG GTGTGTCTGA nTTAGTAGAT 60

TGCATTGGTT GTGGCGTGTT TGCTTGATGG AGGTGTTGTC ACTTT 105

(2) INFORMATION FOR SEQ ID NO: 3264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3264:

GTTCCATCAT TCCCACCnAT ATCCAACATG TGGGCTACTG CAATGCTTTA GGCGTCAATG 60

CCTCATCATC ATCACAGCGC CAGTAAATGC GTATAATTAA ATTAATT 107

(2) INFORMATION FOR SEQ ID NO: 3265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3265:

GTCGTAACAA TGGTTCGTTA CCAAAGCATA nTTCGCCTTC TTGGCATCG 109

(2) INFORMATION FOR SEQ ID NO: 3266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3266:

TTACCTTTAA AATAAnGTTC TCCACTAGTT GGGCTAAACA AATTACATAT TTTGCTTTTG 60

GAAATGTACT TTTTACCACT ACCTGATGGA CCTATAATGG GCAA 104

(2) INFORMATION FOR SEQ ID NO: 3267:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3267:

TAAGCCATCA GAAACAAATG CATATAACGn AACAACACAT GCAAATGGTT CAAGTATCAT 60

ACGGTGCTCG TCCGACATAC AAGAAGCCAA GCGAGAACGA ATGCATACAA TGTAACA 117

(2) INFORMATION FOR SEQ ID NO: 3268:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3268:

GCTGCACAAG CACAACCTGG AATCAGCAAC ACCGGCAAAC CAnCAGGTCA AGGAATAACC 60

AAGCAGCACC TCATAATAAT GCAACACCGG CAATCAAACA C 101

(2) INFORMATION FOR SEQ ID NO: 3269:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3269:

CATACCCTAT TTTAGATATT ACCTTATTAC AAAATATTTT TACATTAATG TCAGCTGCAG 60

GTTAGTATTG TTTTCCAAAA TTTACCGGTC ATCTTTGCCA ATTGGGTGTC GCCAATCGGG 120

ATTTATCCTA GGAAGCCGAT TAAAAGGGTA CTGCCAGGGT TTTAGCCTGC nGCTGCCTCG 180

GGGTTTTCTT TAAATTAATG nAACCGC 207

(2) INFORMATION FOR SEQ ID NO: 3270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3270:

ATATTCGCAC CACCATAAAC ATAGATGGTG TTTTGTCCTT CTGCATTCAC AGTGATAAAA 60

GGGCTTGGnC CCGTTTTTGC TTCAGCTGTT TTGAATAATA TATGATG 107

(2) INFORMATION FOR SEQ ID NO: 3271:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3271:

TTGGTTACAC TTCTGCTAGT TTTAGTAACG ATGGTCCAAG ATTGTATGAG CCTATTCATG 60

GATCAGCACC AGATATTGCA GGTAAAAACG TTGCCAATCC ATTTGGGATG GTTCTnATGC 120

TT 122

(2) INFORMATION FOR SEQ ID NO: 3272:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3272:

GAAGGATGAT GATTCGGAGC AnCTTCTTGC AGAAGAnGCG GnAATAACGT GACATATTGT 60

TGCGAGCGCT TGACAATCTA TTCTTTTTAA AGAAAGCGGT TGTTAGACAA TGCATTAAGA 180

GAAATTAAAG CGGmGTTTAC TTTTGTAAAT GAGCATTTGA TTTTtTGAAA ATAAAGCAGT 240

ATGCAGGCGC TTGACTAAAA AGAAATTGTA CATTGACAAC TAGATAAGTA AAGTGAAAAT 300

ATAGATTTTA CCCAAGCAAA ACCGAGTGAA TAAAGAGTTT TAAATAAGCT TGGATTCATA 360

(2) INFORMATION FOR SEQ ID NO: 3273:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3273:

TCAATTTTAA CTGCAAATAA TAAAGCTGCA TGATTTACTT TGTACATTAT TGTAATTTCA 60

GTAATACGAG GCAATGTCAG TnGCAGTGTT TAATAAATTT TGTTCGCTAT TT 112

(2) INFORMATION FOR SEQ ID NO: 3274:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3274:

TACATTTATG CAATCAACGT TACATTCAAT CGTTGGAGAA AATTGGCTTT ATTGACTTAC 60

TAAAATCTAA AAAATCATAT GAAAGAATTG CACATATGTT AAAAACtGGT AAGCCATTAC 120

GTAATTAAAA GATAGTCATT AAGAGAGGAT GATAACCATG CAAGAAAGCA TACATTGTAG 180

CTTATGGGCG TTCAGCGCAG CGAAAGCAAA GCAAGGCGCA TTATTCCACG AAAAGACCTG 240

nTGATGTCGC AGCCAAAGTA ATTACAAGGC GTATTTGAAA ACGTATTGAC GGGAnAAATT 300

CCAATAAGGA TTATGGATTG nAAGATGGTC CATTTG 336

(2) INFORMATION FOR SEQ ID NO: 3275:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC TGTTTTCGAA ACTAATTTTA 60

CCGGCGATAT CTGGCATCTT TTATTTCGGC ATTTTTTCAA ATCATGGTTA TTCCAGTTTG 120

GCGGCTTAAA AATTCnTT 138

(2) INFORMATION FOR SEQ ID NO: 3276:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3276:

CATTATACGA GnATAAGTAA AATTGATGAT GTGACTAAAA AAGATGCACA ACAATTATTG 60

AAGATGCAAA AGAATTGCAT GCCAAGCTGA TACATTAGAT A 101

(2) INFORMATION FOR SEQ ID NO: 3277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3277:

TGGTTATTCG TTCCTGATCG TTGTTGGTAT CTCACTATTC AAnATTTATC GTGTGGCATT 60

ACTTTAGTTA CACCAGGTAC ATTTGAACCT GGCACTTGTT GCGAGTATTT CCGGTCTCGT 120

CATT 124

(2) INFORMATION FOR SEQ ID NO: 3278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3278:

GACTTTTTGA CCAGTTGTAG CACGACCACC GAGAGTAGCA TTGCATATGC AATCATTGTA 60

CCTTCGCCAA CGACTGnGCC AATATTAATT GTTGCGCCCA TCATAACGAC 110

(2) INFORMATION FOR SEQ ID NO: 3279:

(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3279:

TTGGTATATA GAGGGCAACC GCACCTGATA AAATGTGnCA CAGTTTTTAC AAGAGGTTAA 60

GGAATGAGTT TGGAGGCATA CGAGCATCAA GATACCATTC GATGTTAGTA ATT 113

(2) INFORMATION FOR SEQ ID NO: 3280:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3280:

TTACCGTCAC CGTAATCAGT CCATACTTTA TCAGCTATAC CGGCTTTAAC AGCATAAATG 60

TTCGTTCCTG TAGGCATACC AAAGnCGATA CCATAGTGAC G 101

(2) INFORMATION FOR SEQ ID NO: 3281:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3281:

ACTATGTTTG AnAAATTCGA CAGAATCAGA AGCACAGTCT GAGAACGCAA GAAAAAATTT 60

ATGACAAGTT AGATAGAAAT TTCGACGAAC TAAGGGCGTG ACCAAGAAGA AGATGA 116

(2) INFORMATION FOR SEQ ID NO: 3282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3282:

ACTTGGTTAG ATAATATAGC GTCGATTGTA TCACGAGTGT CTGTTCCAGT CATTATAAAA 60

CGTCGTTCTG ATGCTTTTCC TGAATCAT 148

(2) INFORMATION FOR SEQ ID NO: 3283:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3283:

AAATGACGAT AGAGTCAGGT ATTAACTCAT TTTnCAATAG TATCAGGAAG ACTACCAAGC 60

TTATGTTGAA GGGCATCTTT TGGCGTTACC GGGTTGGGCA 100

(2) INFORMATION FOR SEQ ID NO: 3284:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3284:

TTAAGAAACC GAGCAGCGCA TAAnCCTGCA GTACCTTATC GCTTCTAGAT AATCCGATTG 60

CGACACCATT GCAAGATGAC CGGTAATTTT GGAACATATA C 101

(2) INFORMATION FOR SEQ ID NO: 3285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3285:

TAAAATATTT CGCATCCCTA CACGCTAAAA TAATACATTA CACTTAAAAC GGCTGTTTTA 60

AAGCATCCTC CCATAAACAT CATCTAGTTG ATAATAGGGG GGGGGn 106

(2) INFORMATION FOR SEQ ID NO: 3286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3286:

TTTAACAATA CCTCAGAACA TACTATGGAA ATTGCTGCAA AGTTAATTGG GCATGCATAT 60

TGATCATAAT GCGCTTTTAA ATAAAATGGT GGAGA 95

(2) INFORMATION FOR SEQ ID NO: 3287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3287:

TCGAAATAAT ATCTACGCAC ACTGATAACA TAAAAATGCC TGGTAGAATA CTAATGAAAT 60

AAGTGCATAC ATGACCACAT GAATGCTAAT AACATGCnAG AACCCATTTT TTGAATATTT 120

CACCACTCGA ATCATCAATA C 141

(2) INFORMATION FOR SEQ ID NO: 3288:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3288:

TAGCTGGACC AGAACACGGT TCGACGTTGC AGGAAGTCTT GAACAGTCGC TGAACGCCAA 60

GGCGATACTT GGGTTATCCA TGGTGAAAGn AATGGATTGG TGGTGCA 107

(2) INFORMATION FOR SEQ ID NO: 3289:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3289:

GCTTTGCAAT GCCGATGTTA CTCGCAATAA TCATGTCGCA TCAATTACTT ATGGAAAGCA 60

GATTTACGTA TGTCTACAAG TTTAGGCGC 89

(2) INFORMATION FOR SEQ ID NO: 3290:

(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3290:

TGTTACGCCA ACAACAAATC CTACGTCGAC AACTATTTTT AAGCGATGAT TGCAATTAGA 60

CAGAAATCCA ATCATTTTTG CATTCCATCC AGTGCACAGA ATnTCGAG 108

(2) INFORMATION FOR SEQ ID NO: 3291:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3291:

GATCAAGnCC TGAGAATTTA ATTTAATTTA TTTTTATATT GGAGATGGTT AAAATGCTAA 60

AACTCAACAT GAGTAACCAA AATATTGCCC TTAAAAATGC TGATCATTG 109

(2) INFORMATION FOR SEQ ID NO: 3292:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3292:

TTGATAATTT TGATATAGAA AGTTATTTAA AATTCGAATA AAAATAATAA CTCATCGACG 60

TTTAATGGCT AGGTTCCAAT CAACTATGnG ACATAAATTC AAATTCGATC ACGTAACGAA 120

A 121

(2) INFORMATION FOR SEQ ID NO: 3293:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3293:

GCGCGTAATA CCTGCAGTAC CTCTATCGCT TCTAGATAAT GCGGTTG 107

(2) INFORMATION FOR SEQ ID NO: 3294:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3294:

AAAATGTTAA ACCAAAAAGT TTGGTGAGTT ATAATATGGA ATATTAAATC TGTAGAAGAT 60

AAAGCGAATA TAAAGTGATT AACTTTGGTA ATAAAGAATT AACAGCGAAA n 111

(2) INFORMATION FOR SEQ ID NO: 3295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3295:

CCCCGACTAA ATCGAACGCT TTAATGTAAT GATTTGTCCG AATCCCCATC CTGCACCTGA 60

TAATAAGGCG AATAGCAAGT TGGTTCCCGT nGGGAAGCCA CTTGA 105

(2) INFORMATION FOR SEQ ID NO: 3296:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3296:

ATTTATTCAA AACCCGCCAC ATGGGGCAAC GGTTGCCATG GCATGATAGT CCAGATACAT 60

GGAAAGGAAT ACAGTCCGGT TAACACTCCA TTAAAAACCT GCGGGTTGGT TAAACCATTT 120

AACCTAAATG GGTTCCAAGG GTTAACGCGG TTTAAATGTT TGGAAAGGTT TnCCCAGTTT 180

CCAAAAAGTT TTTnATTCCC C 201

(2) INFORMATION FOR SEQ ID NO: 3297:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 415 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3297:

TTTAGACTTT CATCAGTGTT GAATATTTCT CCTTTAACGG TTATAGGTAA TATTTCCTGA 60

GAAATATTTC CATTCTTTAC ATTTTCCGCT GTCAATTGAT GACTTCGATA AGCAAATTCA 120

TCTTGTAATT CTCTTGAAAC ATCATACATC TkGGCCACAT TTTCAGCACC TkGAATCATT 180

GATGGGTCGC TCATTTCAGG TGCAAATGAT GCACGCTCAT AAAACTCAGG TAATGCTGTT 240

TCGTACACAG AATGCGGTCG TTTGATTTTC CAAGGTGCTC GACTTGTACT TTCAACACCA 300

CCTGCAATAT ATACCTTGCC AGCtCCGGCT TGGATCATGC GACATGCATA TTGaACACTT 360

TCAAGTCCAG ACCCACATTG cCGATCGrTT GTGaCGCCAG TATTGAAGCT TAAGC 415

(2) INFORMATION FOR SEQ ID NO: 3298:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3298:

TTAATTGCAG CAGAGCGACT AGCTGATTCA GAGGTGTTAG TTTGTACGGT AATAGGATTC 60

CCATTTAGGT GCATCGACCA ACTGCCCGAC GAAAAGCCAT TTTGAAAACC AGAAnGATGC 120

CGATTCAAAA ATGGGTGCCA AGATTGAAAA TTTGGACCAA TGGG 164

(2) INFORMATION FOR SEQ ID NO: 3299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3299:

GTAGATGCCA TTTTCACGTT TCTTAGTTAT TGGCATTTTT TAAATGCGAT GTGTGGCTTC 60

TACATAACGG GAAATTTTAA GTTTTATGAA TCnACATATC AATTGC 106

(2) INFORMATION FOR SEQ ID NO: 3300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3300:

AAAAGGTGTT ATGAGATTAG TAAATCAnTA GACAAGCAGG TAAATTAAGT GATGTCGCGT 60

CATTTAAGGA AGCGATTCAC AATCGAGAAC ACAAAGTACA AC 102

(2) INFORMATION FOR SEQ ID NO: 3301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3301:

TTAAAAGTTT GGAGATTATC GTGTCGTCTT CAAGTATGCG TTCATTAATT GATATTGGCG 60

CACCGTATAA CCATGTCAAA GTACCATTTG nAATCAGTCA TTGGCGCATT GGCTGCCCTA 120

GCGTTCA 127

(2) INFORMATION FOR SEQ ID NO: 3302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3302:

CCAGCTAGAC GATTGCTAAG GTATTGGATG TTTGAAACGT CCATGGACCC AATTGATTAA 60

TTGGnTGTAA CTCGGTCAAT GGGTATATCC TAAATGCACT GGCCTGCTGG TGTTCTTCTG 120

GGCGTTGCTT CGGAAAT 137

(2) INFORMATION FOR SEQ ID NO: 3303:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3303:

ATATAAATTA ACGACGCGTT AATGCAGGCT GATGTGATTT TTATTGGTTT CCCAATTTTC 120

AAGCTTCCAT CCCTGGTGCT TTGAAAAATG TGTTTGATCT ACTTCCAGTC AATGCGTTTC 180

GTGACAAGGT AATAGGACTT GTAGCGACAG CAGGTTCTAG TAAACATTAT TTAATTCCTG 240

AAATGCATTT AAAACCAATA TTGAGTTACA TGAAAGCACA TACGATGCAA ACGTATtATT 300

TATTGAAGAG AAAGATTTTT CAAATCAACA AATTGTCAAT GATGATGTTG TATTTCGGTT 360

AAAAGCGTTG GCACAATCCA CAATGCGAAC TGCCAAAGT 399

(2) INFORMATION FOR SEQ ID NO: 3304:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3304:

CACCATTATT TACAGGACCT nCGATGACGT GTGGTCCTGT GTTAAGACAT AACATAATAT 60

TCTACCTTTG TAATCAGTAC GGGTTTATCT ATCACAGTAC GG 102

(2) INFORMATION FOR SEQ ID NO: 3305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3305:

TCAGCGTTAT CAATGAnTGA CTCTAATGCC TTTTTACCCA TTTTTGTAAA TGGAACATGG 60

AAGCATAGAG ATGCGrAGTC AGCTAGCGAC TTACCTTGAC GTTTTGCGTA TTCATTCCAG 120

CTTTGTTGGr ATGAGCGGAT ATAAGCATCT TTAGATAATG CACCATCAAC TAATGGATAT 180

TTATGTCCAG TTGGACGCCA GA 202

(2) INFORMATION FOR SEQ ID NO: 3306:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AAGATAGGGA TTTACACCTA TACCTCGTTC CGGGGAAGGG TCGGTGTTCT GAAAAGTTGG 60

AACTACTCCC GnCAAATATT AAATTATGGG AGCGGGAAGG ATCAGGGATT TGACACCTAT 120

GACCTCCATT CCCAGGGAAG GGAATGTGAT T 151

(2) INFORMATION FOR SEQ ID NO: 3307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3307:

AATTTCGTTA CCTGCGCCTT CTTTTTGCGG TTTTTAAATA AGCGAAAATT TCAGGCGGTA 60

AGACATAACG TCCCAGAATA GCTAGGG 87

(2) INFORMATION FOR SEQ ID NO: 3308:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3308:

ATGATGGCAA AGTCACCAAA CTGATTGTGC ACACCAATCC ATCCATCTGC GCTGTAAATA 60

ATGGTTCGCA ATAATTTTAA AATACCTTCC GCTACATTTG ATTTAAAGCT GGTTGCGCAn 120

TGGACTAGA 129

(2) INFORMATION FOR SEQ ID NO: 3309:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3309:

GTTCCTTTTA TCGTAGTTGG TGGGACTCCT TATCGGCATC GCGGCTGGAC TCTAGGCGGT 60

GGAnACGGAC ATTCAAAAGG GATTTAGTTC ATCCCAGATG GATTTCATTT TGGGGAATTC 120

CATTTGGA 128

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3310:

GTACGATTCA GCATAAAGTA CACCACATTT GTCACTACGA CATCTGTAGC TGGTATTGAT 60

CATGCAATCA TGAATAACGC TAA 83

(2) INFORMATION FOR SEQ ID NO: 3311:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3311:

CTGAGGATAA AGCGTCTCCA AGATAAGTCT AAAGATCATC ATAATGGGCA AAAAAGGTGG 60

CAGCGATTCG GTGGCTGGGA ACAAG 85

(2) INFORMATION FOR SEQ ID NO: 3312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3312:

ATTTTATGTC TAAATGCTGG ACCAACAGTA TTGGCTATTA TTTGGTAACG TGATTACTAC 60

AAAAAATGGA CCGTTGAGTT CGTGGCACAT GATTGATTTT GTAAGTAAGT ATGATGCACA 120

TGGGCTnTT 129

(2) INFORMATION FOR SEQ ID NO: 3313:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCACCTAAAA TTAATCAAGG GACTTAACAT TGGCGAGTCA AGGTATTGAT CAAGCTAATG 60

GCACAGTTAA ATGATGCCAA AG 82

(2) INFORMATION FOR SEQ ID NO: 3314:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3314:

ATGTTATGGA AGAATATTGA GTTAATTGGC AACGACATTA TACCGGCGAT TAAAAAGCCT 60

TTATCAAAAT AGTGAGGGGC GTCATCA 87

(2) INFORMATION FOR SEQ ID NO: 3315:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3315:

TGAACCCGTC GTTGCCCATT TGCCGGTTCC CGAAAGCCGG CGCCnACGGT TCTCCCTGCC 60

TAAATAGGGG ATGGAATATT AAACCATCTG CACCTGGTTT AACACGCTTT GCAATTTGAG 120

TTAAGACATC ATAAGG 136

(2) INFORMATION FOR SEQ ID NO: 3316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3316:

CATTGGCTGT GTCCATTTTT AATCGTTGCG AGTACGTnTA TTAGCAACTT GGAACTGCCA 60

TTGTTAATTT CAGCTGTCTG TTACATTTCA ACCATAGTCT TTCACAAT 108

(2) INFORMATION FOR SEQ ID NO: 3317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3317:

ATCTGAAGCT GGGTTTACTA GAGAAGGTAT GTACGTGACA TGAATTACTA ATGGATTTAT 60

TCATCGAGTT ACATCTATAG TTTATTAAAT CAGATACGCC AAAATGCnAA TTAGCTTACA 120

AAGATGATGC ATTAAATGCA CG 142

(2) INFORMATION FOR SEQ ID NO: 3318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3318:

AACATTATGT TAATCAACCT AATGAACGtC TTTATAAATT ACGCTAAACA ATATACAGAT 60

ATGCCGTTTC TTATCATGCT GGATGAAGAT GAAAATGGAT ATAAAGCGGG TCGATTTTTA 120

AGAGCGAGTG ACTTAGGTCA AACAACAGAG CAAGGCGAAT GGAAGCCAGT TATTCATGAT 180

GCAATCAGCG ATAGTTTAGT AGTACCTAAT GGCACAATGG GTCAACGTTG GGAAGAAGGT 240

AAGAAGTGGA ACTTAAAACT AGAAACAGAA GATGGTTnTA AAATTAnCCC TACATTATCA 300

ATGACAGAAG GTGGATACGA ATTAGAAACA ATTCAATTCC CATACTTTGA TAGTGATGGA 360

GATGGGATAT CATCGTCCAA TCCnAC 386

(2) INFORMATION FOR SEQ ID NO: 3319:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3319:

ACAATGAATG ACATGATTCG AGGTGGACGA CCCCTCCTAT TTTGCATAAA TGCTTTTTGA 60

ATCGCCGGTC ATAATGTTCG TTGnCCAATT AACTCAATAT TCTTCATGAC ATTTTCAAAT 120

GGC 123

(2) INFORMATION FOR SEQ ID NO: 3320:

(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3320:

GGCGAACTGT CAATTGCCGG TATACAACGT ATTTTAAGAG CTGCAGAACA TnCGGGTGTT 60

AAACGTGTGG TCAATGACTG CCAACTTTGG TGCAGTTGGT TTTA 104

(2) INFORMATION FOR SEQ ID NO: 3321:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3321:

GCGCCGGTTT TAACAGGTAA TTTAAAACCA AATACTGATA GTAATGCATT AATAGTCAGC 60

AAAATACAAG TATT 74

(2) INFORMATION FOR SEQ ID NO: 3322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3322:

TCACTCAGGG GGAGATGTCA ATGGGTCAAC ATTATTTGAC AAGGTGTGGA CAGACATGTG 60

TTATACGGGA AATTGGGCGA CCGCACT 87

(2) INFORMATION FOR SEQ ID NO: 3323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3323:

TGCCAAATGT TCCCATAATT TCATTACGAn TCTTAAGTAG GTGGCTATCA TTACGATGCG 60

AATGCGGTCG GAAAGATAAA TAGCTTCATC AATGTCATGC GTCACTAAAA TAATAGTTGA 180

TTGCGTTTTA TGTTTTAGTT GCACTAGTTG ATCCTGAAGT TTATAACGTG TAAATGCATC 240

TAATGCACCT AATGGCTCAT CCATCAATAT AACGTTAGGC TTATGCACAT GCGCTCGACA 300

TAGTGCCAAA CGTTGTTTCA TACCCCCGGA cAGTTGCTCG GGAAAATGCT TTCCCCTGTC 360

TTCTAAATCA ACTAATTTAA GCTGTGCGTT AATCTCTTCA 400

(2) INFORMATION FOR SEQ ID NO: 3324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3324:

GAAACCATCG ATTGTAGCAC GAACCATGTT GGATTGGTGT GTTTGnATCC TAATGTATTT 60

ACTTAAGATA TCAGTGATAC CTGTCTAATT GCAAGTACGG TCAGGA 106

(2) INFORMATION FOR SEQ ID NO: 3325:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3325:

TCTGAAnTCG CTGTCTGAAT CTGGAATCAC TGTCTGAAAT CCGAAATCGC TAATCTGAAA 60

TCCTGAAATC CGCTAATCTG AAACCTGGAA GTCGCTGGTC TGGAAGCCCT GAA 113

(2) INFORMATION FOR SEQ ID NO: 3326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3326:

TGTCACGTAC TTGCTGTTCA ACAAATACGT CTTACTGGAC GTGCACCTCA TTCTTCATCA 60

TAGCCTTCTT CATTAACC 78

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3327:

AATTGAAAAT TATCTTACTG CGGTTTTTAG GGGTTTATGT CCCAGCCTCT TACTCnAATT 60

ATATTCACTA TCCATTAGAC CAAATGGGCC ATTTCCAATA ATCCCGCGGT GGTTTCCGA 119

(2) INFORMATION FOR SEQ ID NO: 3328:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3328:

GTGTTAAAAC GTCACGACGT TTGTTTAAAA TGATGCGTCA TAATGTCTAC ACTTTGCTTG 60

CGATCATTCA T 71

(2) INFORMATION FOR SEQ ID NO: 3329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3329:

CTGACGAACC TTGCATCATT TAACTGTCCA TTAGCTTGAT CAATACCTTG ACTCGCAATG 60

TTAAGTCCTT 70

(2) INFORMATION FOR SEQ ID NO: 3330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3330:

CCAATCTCG 69

(2) INFORMATION FOR SEQ ID NO: 3331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3331:

GGACACTAAC ATTAATATGG ACTGGTAATG TTGCTGTTAA TAAACTCATA CCAAATCCTG 60

GGCATCTCTT 70

(2) INFORMATION FOR SEQ ID NO: 3332:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3332:

CCTTGGGCAC CTTCAATTTG CATATTACGA CGTTTTGCAG CTTGGTTCAA TTGGCAATAA 60

CTACACCTAG TGCAGTTGGA TC 82

(2) INFORMATION FOR SEQ ID NO: 3333:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3333:

ATAAAATAAT TAGAACTCTA ACATTGGTTT AACTAATGTT TAGACTTTTT GTGGTTTGTA 60

AAAACAAGTA TATTGA 76

(2) INFORMATION FOR SEQ ID NO: 3334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3334:

TGGTAAGTTG AATAAAGTAT TGAAATCGTT GCCAATATCT TTATACCGTT GGTTCCTGGC 60

ATTTATTGGG AGGC 74

(2) INFORMATION FOR SEQ ID NO: 3335:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3335:

AGATAGTTAT GCGCAGTTAA AAACGGTGAA ATGTATTTGC AATAATATGC ATATAGGCAC 60

CATACGAGTA AGGG 74

(2) INFORMATION FOR SEQ ID NO: 3336:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3336:

TTGAATCATT GTTAAAAATG GAATTAAAGT TGCTAGTATC TGTCGGGTTT TGAAATAGGT 60

CATAGGAGAA AACAGG 76

(2) INFORMATION FOR SEQ ID NO: 3337:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3337:

CCAAAGAGGC GTTATTAAGC TATTGATAAA AGTTATGTTA CTAAAAAATG TATTTAAATA 60

AGTAGTACCT AA 72

(2) INFORMATION FOR SEQ ID NO: 3338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3338:

ATAAGTCGTT CTACCGTATA GCCGTCATTA TTAATCACAA ATAATACCGG TTTAATATGC 60

TGTCTGGTCA TAGTT 75

(2) INFORMATION FOR SEQ ID NO: 3339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3339:

TTCATCAAAG TATTCCAATG GGAGAAAAAG CACAATAACA TTATCACTGG ATGCTAAATC 60

TAAAGGAACC TC 72

(2) INFORMATION FOR SEQ ID NO: 3340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3340:

GTAAAAATAT TTTAATGAAT GTCTTCACTG GAGAACCATT GACAACCTGG TACAAGTGGG 60

ATTATTGGCG TTATTTT 77

(2) INFORMATION FOR SEQ ID NO: 3341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3341:

AACCAAGGAT GGATTGCTAT TTTAATCCTT GGTTGCTCTT TATTTTATTT AAATTGTAGA 60

ACCTAGA 67

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3342:

CTGGCAAAAG CACGTTTTAC AAGCATCAAT CCATTAATTA ATAATTCCAT TAAATGTAGA 60

TTCACAGGGA TATG 74

(2) INFORMATION FOR SEQ ID NO: 3343:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 415 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3343:

GTTTGATCAT TAGAGAGATA TAGATATGCC GTAGAAAATA ATATGTCATT TGCGGATATC 60

ATGGTTAAAG AAGAAATGGA ATTAAGCGGT AAATCACGTG ATGAAGTGCG AGCGaAATGA 120

AACAAAATTT AGATGTCATG CGAGACGCAT AATCAAAGGG ACGACAGGTG ATGGGGTTGA 180

AAGTGTAcGG TCTACACTGG TCATGATGCT GCTAAACTAC GTGATTATAA TGAAACACAT 240

CATGCTTTGT CTGGGATATG AAATGATTGA CGCACAAGGG TGCCATTGCA ACAAATGAAG 300

TCAATGCTGC CGATGGGTAT TATTTGTGCA CGCCAACAGC TGGTTCCTCG GGTACCATTC 360

CCGGTGGCAC TTTTAAATTA GAAAAAACAC TGGATnGAAC CAGAAGAGCC AATGn 415

(2) INFORMATION FOR SEQ ID NO: 3344:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3344:

TCCTATACCA CCACCGTCAA CAGCTCCTGC CATCGATCGT ACTTTCAATA AGTCCAATAA 60

TCGCAGTGGT AATTTCTAAT ACTA 84

(2) INFORMATION FOR SEQ ID NO: 3345:

(A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3345:

CGGGAGGTGT TAAnTCTTCA CAAAATGCCG TACTATTCTT TGATGnAATC CATCAAATTA 60

TCGGTTCAGG TGCCACAGGA AGTGATTCAG GTAGCnAAGG GTTATCTGAT ATTTTGAAAC 120

CTGCATTAAG TCGTGGTGAG ATTTCTATTA TTGGTGCaAC AACACAAGAT GAATATCGAA 180

ACAATATTCT TAAAGATGCT GCATTAACGC GCAGATTTAA TGAAGTGCTT GTTAATGAAC 240

CAAGCGCTAA AGATACTGTT GAAATTTTAA AAGGTATTCG CGAAAAATTC GAAGAACACC 300

ATCAAGTAAA ATTACCAGAT GACGTATTAA AAGCATGTGT TGACTTATCA ATTCAATATA 360

TTCCACAACG ATTATTACCA GATAAAGCAA TCGATGTGTT AGATATTACA GCAGCACATT 420

TATCnGCGCA AAGnCCAGCT GTCGATAAAG TTGAAACTGG AGAACGAATT TCTG 474

(2) INFORMATION FOR SEQ ID NO: 3346:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3346:

AAAATTAATA ACTCCTTGGT TATTGATATG CCTAAAGAAG AAGGTACAAT ACAACTAACA 60

TTAG 64

(2) INFORMATION FOR SEQ ID NO: 3347:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3347:

AGGAATAACT TGATATTGAT GATAAAATCG TCAAACGGCA CTAATATTTA AAAAACAAAT 60

GTTTTAAGTT GTTGATTTAA AATATTAAT 89

(2) INFORMATION FOR SEQ ID NO: 3348:

(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3348:

ATAACTTGTA CTGCTTCCCA TTAATCACTG TGTCTCTTCA CCAGGAGCTG GCATTTCTTT 60

AAAGAACAnT TCTGATAAAG GTACAATTTC ACCGGGCATA ACTTCAT 107

(2) INFORMATION FOR SEQ ID NO: 3349:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3349:

CAACGCATCC TGCACTTTTA CCTATTCCTG AATCACCGGT AATTAGTACA CCAACACCGT 60

AAACATCTAC TAAA 74

(2) INFORMATION FOR SEQ ID NO: 3350:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3350:

AGATGCACCT ACTTCTAACT GTCGCCAACA TCGCCGCAAT CATTTCAAAA CTACGTTCTG 60

TA 62

(2) INFORMATION FOR SEQ ID NO: 3351:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3351:

GCTGCAAACA ACAAACTATT TTTGATTAAA TTGTGGATAT GATGGTAACC AACCAAGTCT 60

(2) INFORMATION FOR SEQ ID NO: 3352:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3352:

ATTGAACGCA AGATTTCGAT ATAGAACATC TAGCGACGTC GATTCGCAAG GTTGAACCAT 60

CTACATTAGG TGAGGAA 77

(2) INFORMATION FOR SEQ ID NO: 3353:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3353:

TAATCAACAC GAGGAGATGC TATTTAATGT CATCTGACAC AAACAGTTTA GCACATACA 59

(2) INFORMATION FOR SEQ ID NO: 3354:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3354:

TTATGTAACC GACGAATGCT GCGATAGTGC TACGCCATCA CCGCCAGCTA ATCCGATTG 59

(2) INFORMATION FOR SEQ ID NO: 3355:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3355:

TAACTATACC TTTAGGGTTA CTACCACGCT TAGGTAGGTC ATAACCTTTA ACCACATCT 59

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3356:

AATAACGCTA AACCTAAAAT GCTAAATAAT CCGCCGAACA ACATGCCGTT GTTTGTTGA 59

(2) INFORMATION FOR SEQ ID NO: 3357:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3357:

CCAGAACCAC CCACGCCCTT TGAATATGGG AACTCAAAAC GATCTACTGG CTGATGTAAT 60

TACCCCTGTT TTGATTG 77

(2) INFORMATION FOR SEQ ID NO: 3358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3358:

AAGTTAGGTC TAGGGAACAT CGATAAATTA CCAGTAGTAA ATGCAGTTGA ACAACCAGA 59

(2) INFORMATION FOR SEQ ID NO: 3359:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3359:

CATGACCTTT AAATTGCATA TCTTCTGCAT CAGGTGCATC GCTTTTAACA ATAACGTCA 59

(2) INFORMATION FOR SEQ ID NO: 3360:

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3360:

ACGCGACAAC ACCGCCCTCA ACTAAAGTAG AAGCACCGCA ACAAACAGCA AATGCGACA 59

(2) INFORMATION FOR SEQ ID NO: 3361:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3361:

GATTTGATCG AATTGAACGA ACATTTGCTT CTCAAACGAT TGCATCTATT AAAGAAGTAT 60
GTCTAG 66

(2) INFORMATION FOR SEQ ID NO: 3362:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3362:

GGTTGCACAT CTTTTACTAC AAATTTCGCT GGTAAAGATG TTGCAAAAGT ATGTCCGT 58

(2) INFORMATION FOR SEQ ID NO: 3363:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3363:

CCTTGAAACG GCAACATTTT TGGGTCCTTC TCCATCATTT TATTTAAAAG CGCATTAT 58

(2) INFORMATION FOR SEQ ID NO: 3364:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3364:

TTGAGAATTT AGGAGGTTAA TGCGTTGATT AAAAGTGGCA AGCACGTGC ACATACGA 58

(2) INFORMATION FOR SEQ ID NO: 3365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3365:

GTTTTTTTAT TTTGGATAAA AGGAGCAAAC AAATGGATAT TAACTGGAAA TTGAGATT 58

(2) INFORMATION FOR SEQ ID NO: 3366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3366:

ATTCATCGGT AATGACATTA TTTTTACTTT GTAATTTCAG TAACAGTTGA TCATCATG 58

(2) INFORMATION FOR SEQ ID NO: 3367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3367:

TAAATTAACA GCCGGATGAA ATGAAAGGTG CTACATGCAC AATCAGTAAT ATCGGTTC 58

(2) INFORMATION FOR SEQ ID NO: 3368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3368:

TACCTACTGG TGAGATTGGC GAACTTGCAA TTAAGGCTAA AAATGTCACG CCAGGATA 58

(2) INFORMATION FOR SEQ ID NO: 3369:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3369:

TTAAACGGAG AAGGCTTTAC TTTACATGTT GAGGAAGGTC AAGAAGTTAA ACAAGGTG 58

(2) INFORMATION FOR SEQ ID NO: 3370:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3370:

CTGCTAAACT ACGTGATTAT AATGAAACAC ATCATGTCTT TGTCTGGTAT ATGTAAATGA 60

TTGACGGC 68

(2) INFORMATION FOR SEQ ID NO: 3371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3371:

ATTACCAACA GCGAAAATAT TGAAAAGCTG TAAAAAAGCT GGTGCAsmCm TACTTGGATT 60

GAGAATTTAG GAGGTTAATG CGTTGATTAA AAGTGGCAAA GCACGTGCAC ATACGAATAT 120

TGCACTTATA AAATATTGGG GTAAAAAAGA TGAAGCACTA ATCATTCCAA TGAATAATAG 180

CATATCTGTT ACATTAGAAA AATTTTACAC TGAAACGAAA kCACTTTTAA CGACCAGTTA 240

ACACAGGATC AATTTTGGTT GAATGGTGAA AAGGTTAGTG GCAAAGAATT AGAGAAAATT 300

TCAAAATATA TGGATATTGT CAGAAaTAGA GCTGGCATCG ATTGGTATGC AGAAATTGAA 360

(2) INFORMATION FOR SEQ ID NO: 3372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3372:

ATTTCAACAA CTTTAAAGCA CGTATAATGA TGATTTTCAG ACTTGTACAA AGGAGAAA 58

(2) INFORMATION FOR SEQ ID NO: 3373:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3373:

AAACCGAGCA GCGCAGTAAA CCTGCAGTAC CTTTATCGCT TCTAGATAAT CCGATTG 57

(2) INFORMATION FOR SEQ ID NO: 3374:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3374:

AGTACGAATA TTACCTTTAT TTAATGGGTG AGCTAAGTTA CTTTTCATTT CTTCGTG 57

(2) INFORMATION FOR SEQ ID NO: 3375:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3375:

GGTGAAGTAT AACTTTGTAA TGGCAGCGCA CTTAATGACT GCCAATAATT GTGACCAACA 60

ACTAACAGAC 70

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3376:

TTCCAAACTT CATTAGGTGA TAGCTTTAAT TTCAAGGCTG GCAATCGCCA TAACAAG 57

(2) INFORMATION FOR SEQ ID NO: 3377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3377:

TCCTTCAAAG TCAATGGATT TGATCCTCAG AGGACTCAGT GTATCCTCCA AGTGACCTGG 60
CTCGCATCCA 70

(2) INFORMATION FOR SEQ ID NO: 3378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3378:

ATGAATCATT AAGCCTTTCG GTGCATATGC TGCAAGACTT TGACCAGCAT GACCAT 56

(2) INFORMATION FOR SEQ ID NO: 3379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3379:

CCAACGACTG CGCCAATATT AATTGTTGCG CCCATCATAA CGACAGCACC ATCTTC 56

(2) INFORMATION FOR SEQ ID NO: 3380:

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3380:

ACAAAAGCAT CAAGCTGTTG AAACAATCAA TGATAGCATT CGAGATTATT TAGTTAG 57

(2) INFORMATION FOR SEQ ID NO: 3381:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3381:

CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA AATAACCGAA GTATTT 56

(2) INFORMATION FOR SEQ ID NO: 3382:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3382:

GAACACACAG GCAACCCAAA GCAGTGACGG CGAAAnTTGG ATTGATCTTG CAGCATTGAA 60

GAAGATCGCG ATGACTATAC AATCAATATC GAGTAGAAGA CCGAT 105

(2) INFORMATION FOR SEQ ID NO: 3383:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3383:

nGTATGTGAA AACTATTTGG CGATATTTTA GTGATGAGCC TCAGTGATCC TGGTTCCTGG 60

TTATCACCTC TGCTAGTTTA GTACCGATGG TCCAAGATTG ATGAGC 106

(2) INFORMATION FOR SEQ ID NO: 3384:

(A) LENGTH: 57 base pairs
(B) TYPE: nucl ic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3384:

TTCTTCGTCA AGATCAATCT CTTCAAGTAC AATCTTTAAT ACCTTCTGCA CCCATTT 57

(2) INFORMATION FOR SEQ ID NO: 3385:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3385:

CGGGCATCTT AAAGCCGATG TTTATCCTGT AATCCTCCAA AAGGAAACAT GTACCTCAAT 60

TAGAG 65

(2) INFORMATION FOR SEQ ID NO: 3386:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3386:

CATTTTTAAT TATTTCTATT TGCTTTTTAA CCACTTCTCT GACTGCTTCC GAATCATTTT 60

TCTTAACTGC A 71

(2) INFORMATION FOR SEQ ID NO: 3387:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3387:

TTAGAAAATG ATAAACGTAA AGCAGTAAGT GCTGAAGAAT ATAAAAAAGC TGACG 55

(2) INFORMATION FOR SEQ ID NO: 3388:

(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3388:

TCTTCGACAA CTTTAATAAT ATTAGCCAAC GCAGTGTCCC CGCCAACTTT TGTTGC 56

(2) INFORMATION FOR SEQ ID NO: 3389:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3389:

ATTTATTAAC GATTAATGAC GCTGGCATGC CAATTCCAGA TGATCATCGT CGTATC 56

(2) INFORMATION FOR SEQ ID NO: 3390:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3390:

AAATGCTATG TACCCACTTT AGATGAAATT TTAGTAACGT TATGGCCCGA AATGCCAACT 60

ATTATATTGA 70

(2) INFORMATION FOR SEQ ID NO: 3391:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3391:

CAAACGCAAT AGCTGGTGAC TTAACTGCGG GCACTTGGCA TGTGGATGGC AATACTTCG 59

(2) INFORMATION FOR SEQ ID NO: 3392:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3392:

GCATCTACTG GGAAACGATT ACAAATTGGT GATTTATTAC AAAAGCCAAC TGTAT 55

(2) INFORMATION FOR SEQ ID NO: 3393:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3393:

TTTATAAATA TCCCAGTCTG AACGCGATTC CCATAACGGA TCAATGGCAG GATTG 55

(2) INFORMATION FOR SEQ ID NO: 3394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3394:

TGCTTACGCT CAGTGACATA ATCTAATGTG GCACGTAAAG CGCCACCATA CCACC 55

(2) INFORMATION FOR SEQ ID NO: 3395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3395:

AGTCACCATT TGTTGGTACA GGTTATGGAA CACGTTGCAG CACGTGATTC TGGTGCGG 58

(2) INFORMATION FOR SEQ ID NO: 3396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3396:

CAAATGCATT TAAAACCAAT ATTGAGTTAC ATGAAAGCAC ATACGATGCA AACGT 55

(2) INFORMATION FOR SEQ ID NO: 3397:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3397:

TGTTGATGAG TCGTGTTTTA TCTCAAGATG TGTTACTCAA AAAGTTATAG AAGA 54

(2) INFORMATION FOR SEQ ID NO: 3398:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3398:

CTTCGTCAAG ATCAATCTCT TCAAGTAAAT CTTTAATACC TTCTGCACCC ATTT 54

(2) INFORMATION FOR SEQ ID NO: 3399:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3399:

AATGAAAAGC TAGCTGTAGT TGCAAGAAAA ACTGGCTTAG CGATGGCAGT TGGAT 55

(2) INFORMATION FOR SEQ ID NO: 3400:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3400:

(2) INFORMATION FOR SEQ ID NO: 3401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3401:

TAAAAATCGC GCACTTAAAC CGCTTATGAC AATCATTATT ACCGCAATAT GCTTG 55

(2) INFORMATION FOR SEQ ID NO: 3402:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3402:

GGCACCTCCT TGGATTATTT TTCTTCTACT GTTACTAAGT GCTTAACTTT GTTG 54

(2) INFORMATION FOR SEQ ID NO: 3403:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3403:

GATAAGTCTA ACAAGTGGCA CCCATAATCG ATTAAACTAC CGCCACCTTG CAACGTTT 58

(2) INFORMATION FOR SEQ ID NO: 3404:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3404:

TCGTTTTCGT CCCCAAATTC TGCCAACTTA TTCATGAACT TATCTAGCGC TATTGTTCTT 60

TGTCT 65

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3405:

AAATTTCAGC ACCAATTGTT ATTGGACGAC ACCATTTAGA TGCTGGTTCA GTTGC 55

(2) INFORMATION FOR SEQ ID NO: 3406:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3406:

TCGATTTCAG CGGAACACAT GTAACGTTAG CACAAGCCAT GAACCAATTA GGTGGC 56

(2) INFORMATION FOR SEQ ID NO: 3407:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3407:

AATTGCTAAT GGTCAAGTAT GGACGTGATC ATTGTTGGTA CTACTTATTG CTGAAACTGT 60

TAAAGATTAG AAGG 74

(2) INFORMATION FOR SEQ ID NO: 3408:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3408:

TGATTTCACA CTTGATAACG GATACTTCGA AGAGATACAT CAGCAGCGTT CAGCTCAGAT 60

AGTGCTCA 68

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3409:

TATGATTAGA AAAAGGGGAA TTTTTATGGA GTATAAGAGT TACTATGATT CGCC 54

(2) INFORMATION FOR SEQ ID NO: 3410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3410:

TATCTTTCAT CATTGAAGAA GATCGCGATG ACTATACAAT CAATATCGAG TATA 54

(2) INFORMATION FOR SEQ ID NO: 3411:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3411:

TTGAAGTGCA CGAATCGAAT TATTGTAAGC AGTAATACTT GCCGGCTTCT TAC 53

(2) INFORMATION FOR SEQ ID NO: 3412:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3412:

TAGCCGATGG AACCCCATAA CGGTTGCCCT ATAAAAGTAT TGTTTTTGTA TAGTGCTAAA 60

TCA 63

(2) INFORMATION FOR SEQ ID NO: 3413:

(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3413:

ACTACCATTG CTTGTTCCGG TTTCACAACT GGTTCAGTAT CATTTACAAC TGC 53

(2) INFORMATION FOR SEQ ID NO: 3414:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3414:

ATGCTGTTGT AAACGGTAAT ACAACATACC TGCCCAACCC GGTAACGCCA AAAAATGTCC 60

TT 62

(2) INFORMATION FOR SEQ ID NO: 3415:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3415:

ACTTAGATCA ATCACATGAT GCCTCACGGA ATCCATTATT TGAAGGTCAT GTTAG 55

(2) INFORMATION FOR SEQ ID NO: 3416:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3416:

TTAGTTCCAG CAATACCTGC TACAGTTGCT GCAGATGCTT CTTTCACCCA TGG 53

(2) INFORMATION FOR SEQ ID NO: 3417:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3417:

TGATTTAGGT GCAAAAATTG TAGGTATCGC TGAGGCTTAC GGTGCATTAC ACGATCCAA 59

(2) INFORMATION FOR SEQ ID NO: 3418:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3418:

CGTGGTCACC ATCACCAATT GCTCGATCTA ATTCAGTAAT TCAGATTCAT GTT 53

(2) INFORMATION FOR SEQ ID NO: 3419:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3419:

TGGACCTACT GCAATAACTG AACGTCCTGA ATAGTCAACA CGTTTACCAG TAAGT 55

(2) INFORMATION FOR SEQ ID NO: 3420:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3420:

TGTCTCCGGT ACCGTTTGCA CCAGGAATAA AGATGAGCAC GGGTCCTTGT CCG 53

(2) INFORMATION FOR SEQ ID NO: 3421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3421:

AAATTAAGAA AATTCATTGC CAGATAATTT AGATAAATAA TTAAAACTTA GACCATTCAC 60

CCCAATCCCT GA 72

(2) INFORMATION FOR SEQ ID NO: 3422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3422:

CATATGTTAA ATGGACTCGC TAGATTTAAG TCGCAATAGT AGCGGCCGTT TCTT 54

(2) INFORMATION FOR SEQ ID NO: 3423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3423:

CACGTTTCAA ACCTAAAAGA TGCTAAAAAT TTCTCTTAAT TCTTGTGCAA TA 52

(2) INFORMATION FOR SEQ ID NO: 3424:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3424:

ATCGCCTAAC CAAGATGCAC CATCGGTGAT TTTATCGCCT GCCGCTTCAA CCAT 54

(2) INFORMATION FOR SEQ ID NO: 3425:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AATAGAAAAT GTACGTAGCG GTATGATGAG GATTTCGCAG ACTAGTTTAG GGTCAAGTG 59

(2) INFORMATION FOR SEQ ID NO: 3426:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3426:

CCAACGCCAG ATCCAGAACC AAGTCCAGAC CCAGAACCGG AACCAAGCCC AG 52

(2) INFORMATION FOR SEQ ID NO: 3427:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3427:

CCATATTAAT GGTTATGTTT ATGTGAATGC TTGCTTGCTG GACTTGTCTT TT 52

(2) INFORMATION FOR SEQ ID NO: 3428:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3428:

TAAAACAGAG ATTGATACTG CAGAAGATAA CTGTATCTCT CCATCTACTG TA 52

(2) INFORMATION FOR SEQ ID NO: 3429:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3429:

TGAAAATCCA CAAGTCGCAC GTACAGTGTT TGAAAAAGGT ATTATGGCGG CA 52

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3430:

ATAATTCTTC CAAATATATG AAAATGGATT TGTTCTTTTT TTATAAAAAT CTTATGCTTT 60

TTAACTAATT GTAAGA 76

(2) INFORMATION FOR SEQ ID NO: 3431:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3431:

CTGCGGGGGA TAACTGTATC TCTCCATCTA CTGGTAAGTC GTATTAGAAC TAAAGCGGCT 60

(2) INFORMATION FOR SEQ ID NO: 3432:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3432:

GGCTTCAGGC TCATTGATAG GTAAAAGTTG CAAAGCCTGC AAAGCGATTG GG 52

(2) INFORMATION FOR SEQ ID NO: 3433:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3433:

TCGCACGATA CGCCTCCGAA TGAAGAAGGT TTATTGTGCG ATTCTTTTAT TGTTAAATTT 60

TAAATTTTT 69

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3434:

GATCGCTATC CATTAGCTAA ATTTAAACGT TCAAACTCAG GTACATGTTA C 51

(2) INFORMATION FOR SEQ ID NO: 3435:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3435:

TATAGCTACT GCTGCAGCTG CGGCCATTGC AGATGCTGAA CCAACTTCAG C 51

(2) INFORMATION FOR SEQ ID NO: 3436:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3436:

ATTAAAGCCA ACATTAATTT ATCCACTATT AACAATAACG GCTACAGGCT TATTAATGAT 60

TTATACCTTT 70

(2) INFORMATION FOR SEQ ID NO: 3437:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3437:

TTTGTTTGTT GATTCTTCTC CACCTGTTTC AGGTAGTTCA GATTTCTTAG A 51

(2) INFORMATION FOR SEQ ID NO: 3438:

(A) LENGTH: 51 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3438:

GTGAATTCCG TAATTACATT TTAGGCTTGA TTTTCTATCG CTTCTTATCT G 51

(2) INFORMATION FOR SEQ ID NO: 3439:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3439:

TTAAGACAGG TTCCTTATGG GACTCTAACA ACGTATGGTG CTATTGCCAA A 51

(2) INFORMATION FOR SEQ ID NO: 3440:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3440:

CACTAGAAGA AACGGATTCA TCAGCTATTG GTATCGATTA CCATACTGCT GTGGA 55

(2) INFORMATION FOR SEQ ID NO: 3441:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3441:

CTTCTGGCAA TAGACCGCGA GTTACTGGGG GCAAAACCAG TGTGTAAAAC CGGAACTACT 60

ATGAGGGGCA TGAAAGT 77

(2) INFORMATION FOR SEQ ID NO: 3442:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3442:

GTTCGGTTGT GACAGTCAGT GGACGCGTTA CCAAATGGGC GGGAATTAAA GCAAA 55

(2) INFORMATION FOR SEQ ID NO: 3443:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3443:

ATGAACTTTG GGATAAAGGT GATGCCCAAA CTTTCCGTAA CTCATGATGA T 51

(2) INFORMATION FOR SEQ ID NO: 3444:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3444:

CAACGCAGCA AAGCGGAGTG GCCCTTTACC TTCACAGAAT AATGGTCTAA T 51

(2) INFORMATION FOR SEQ ID NO: 3445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3445:

ACCGAGCAGC GCACTAAACC TGCAGTACCT TTATCGCTTC TAGATAATCC 50

(2) INFORMATION FOR SEQ ID NO: 3446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3446:

CCAATGCAAC GATCCAGTTA TTGTGTTGGC GCAATTGATT AATAGTATTC 50

(2) INFORMATION FOR SEQ ID NO: 3447:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3447:

GCGCATCATA TCCCATTGCA CCGATAAGAT CCTTCTTACC TTCTACAAGT 50

(2) INFORMATION FOR SEQ ID NO: 3448:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3448:

GTTCTTACTT CTTTATCGTG GCTCCAACGT GCTCTGTACA TTTTTTCCCA TCTCTCTACT 60

(2) INFORMATION FOR SEQ ID NO: 3449:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3449:

CAACACCACC GACACCAGAA GTACCAAGCG AGCCGGAAAC ACCAACACCG 50

(2) INFORMATION FOR SEQ ID NO: 3450:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3450:

TTATCACGGT ATATGAGGGG ATTTGAGG 88

(2) INFORMATION FOR SEQ ID NO: 3451:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3451:

TGCAAAACGT TATGAAGTAC AAGTTGATGG AAGCAACAAA GTAAGTGCGn 50

(2) INFORMATION FOR SEQ ID NO: 3452:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3452:

CAGTTAAGTC ACCAGCTATT GCGTTTGGTG ATCTTAAGCA GGCGTGGATT ATCAAGTTTG 60

GGTA 64

(2) INFORMATION FOR SEQ ID NO: 3453:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3453:

TCGTAAACAA TATACTATCT CAACATTTAT TCATCCAATG GAGATAACGT ATTGCGCGGT 60

TTAACAGGTA ATTTAAACCA AATACGGTAG TAATnATTAA TAGATAGCAA ATCAAGTATA 120

AAGAATAAGT A 131

(2) INFORMATION FOR SEQ ID NO: 3454:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3454:

TTAAAAATGC AGTTATGGCC TCTAAAATCG TATTAAGCAT ATTAGCGCCC 50

(2) INFORMATION FOR SEQ ID NO: 3455:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3455:

TGCTACATGG CGTTACGGTC AAGATCGTCA ACGATTGATG GGTACAATTG A 51

(2) INFORMATION FOR SEQ ID NO: 3456:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3456:

ACAAACTGCC AACGATTGGT CGTGTGAATC ATCCAGTGGA AGAAGCGCAn 50

(2) INFORMATION FOR SEQ ID NO: 3457:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3457:

AATCACGTGA GAAGGATACA GCTATTAGTA TCGGTATCAT CGCATTGATT 50

(2) INFORMATION FOR SEQ ID NO: 3458:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3458:

(2) INFORMATION FOR SEQ ID NO: 3459:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3459:

GGGCCAACAA ATCGGAAACT GCCAATTGGA CGGTTGCCGT CATCAAACCC 50

(2) INFORMATION FOR SEQ ID NO: 3460:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3460:

TGCTTCCGCT AGAGGATCCG GTATTGCTAG TCAATTACTA CACCATTTAA ATTGTGGAAG 60

CAAAAGCT 68

(2) INFORMATION FOR SEQ ID NO: 3461:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3461:

TGGTCTTCGC AATCCACGGA TATACCTTAG TACCAGGTAA TTGACCACCT T 51

(2) INFORMATION FOR SEQ ID NO: 3462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3462:

AAGCTATTAA TGTAATTTAT CAATTGATTG TGCAACGGAC ATCATCTACA AGACCG 56

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3463:

ATACCAAATG TGAGAAACTG GAGCAGCAAn TTCAATGTGA CCCATTCTTT 50

(2) INFORMATION FOR SEQ ID NO: 3464:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3464:

TCTTTACGGC GTGGTTCTAA TCGCATCTTT TTCAATCTAA GTGCGTTTnT 50

(2) INFORMATION FOR SEQ ID NO: 3465:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3465:

AAAGAAGATT GGAACGTGTA TTGACGACTG CACCCAGGTA TGGGTGTTCG CCCGACA 57

(2) INFORMATION FOR SEQ ID NO: 3466:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3466:

ACATCCGAAA GATGACTTGT TTAAAAAAGC AGAGCATGAT TTGCTTACTA TGATTACACG 60

CGG 63

(2) INFORMATION FOR SEQ ID NO: 3467:

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3467:

TACCGATGAT TTCCGAGACA TAGACCGGCC TGTCTGGGGG TCAACTGGAA CTTGGTC 57

(2) INFORMATION FOR SEQ ID NO: 3468:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3468:

TGTTCCTAAT ATTTATGTTG TAAAAATGTA CAATCTAATT AAAGCAATAG TCTTGGGCA 59

(2) INFORMATION FOR SEQ ID NO: 3469:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3469:

TCCATGATCG TTCAACATTT AAATACACAA CTTAATAAGT ATCGTGTACA AGTTATG 57

(2) INFORMATION FOR SEQ ID NO: 3470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3470:

CCCTGTTCAG GCTATCCTCT AAAGTGACGA TATAGAATAG CGATTAATAT CGCGATAGT 59

(2) INFORMATION FOR SEQ ID NO: 3471:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3471:

TACGCCATCA nCGCCAGCTA ATCCGATTGC GACACCTAAT GCGAAATCAT 50

(2) INFORMATION FOR SEQ ID NO: 3472:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3472:

AACGTCATCA AATGGAAGTA CGTGACGTTC ACTACTCTCA CTATGGCCGT ATGT 54

(2) INFORMATION FOR SEQ ID NO: 3473:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3473:

TAATAGGCAT TCCCATTAGG TGCGTCGACA ACTGCAACGC AAGCATTTGA AACAGA 56

(2) INFORMATION FOR SEQ ID NO: 3474:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3474:

TTTTAAGAAT GTCGCGTTAT CTGCGCCCAT TGGATTGACA TACTTCATAC GTATA 55

(2) INFORMATION FOR SEQ ID NO: 3475:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GCCTTTAGGT AAAATGGGCA GAAATGCTAA TCATTTTGGC GGCGAAATGA AAAA 54

(2) INFORMATION FOR SEQ ID NO: 3476:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3476:

AAAnCATTCG CAATCGACCA TAATTTTTTA TGTAATTCAG CTTGTTGCTG 50

(2) INFORMATION FOR SEQ ID NO: 3477:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3477:

GGAnGACCAT TAATCGATAT CGGTACACAC GCTTTAGATT TAACGTTATG 50

(2) INFORMATION FOR SEQ ID NO: 3478:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3478:

TGCCTCCTTA CGCCATGATG CTTATTCAAA GTAAATTGCT TTGCCGGACT TTGCAGACTG 60

(2) INFORMATION FOR SEQ ID NO: 3479:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3479:

GGTCTTTCAG CTGCTAACGA GTTCCTGTTA CTGTTCATGT CTATCACTTT GCGTTCCCTC 60

(2) INFORMATION FOR SEQ ID NO: 3480:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3480:

CAAGTATCAT ATGGACGGCT CGCCCAACAC AAAACAAGnC CAAGCAAAAC 50

(2) INFORMATION FOR SEQ ID NO: 3481:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3481:

ATTAAACAAC ATAGCTCGGC TAATCCTTTA AAGCTTTTGA GTTTTTCTGT TGTAGAACAA 60

GA 62

(2) INFORMATION FOR SEQ ID NO: 3482:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3482:

TGTGGCTAGC TGTTTCTTTT TTAGGTGCTG TGTAGGAGAT GAACTGATCG T 51

(2) INFORMATION FOR SEQ ID NO: 3483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3483:

GCAGTTTATA AGTAGAGAGA CAGCTGATCA TGAGATAAAA ATGGGTAAAT ATTT 54

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3484:

TTATCTATCA CAGTACGAAT CCCCCAGAGT ACCGATTGTG ACAGCAACTT CTGCG 55

(2) INFORMATION FOR SEQ ID NO: 3485:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3485:

ATCTCTGGTT CGATTCCCGT CGAGACCGGC ATCATTACAT GTTTATTATG GG 52

(2) INFORMATION FOR SEQ ID NO: 3486:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3486:

TGTGTCACGA TAATAGGCGT AATATCACTC TTTGGCATGA TTGCCGGATG 50

(2) INFORMATION FOR SEQ ID NO: 3487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3487:

TATTTTTGAT CACACTCAAC GCACAAACGA ATGGCCTTTA CCTTCACAGA ATAATGGTCT 60

AATGTAA 67

(2) INFORMATION FOR SEQ ID NO: 3488:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3488:

TAGGTGGTCA ATTACCTGGT ACTAGGTATA TCCGTGGATT GCGAGGACAA 50

(2) INFORMATION FOR SEQ ID NO: 3489:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3489:

CAATTGTACT TCATAACGTT TTGCATTTCG CCACCTTCAC CACTATATTT TCCCATGGTC 60

(2) INFORMATION FOR SEQ ID NO: 3490:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3490:

CTAAACTGAT TGTTTTACGT AACGTTTCAT CGGCTTCTTT CGCTTCTATC 50

(2) INFORMATION FOR SEQ ID NO: 3491:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3491:

TCGATTTACC TTTCATCATT GAAGAAGATC GCCATGACTA TACAATCAAT AT 52

(2) INFORMATION FOR SEQ ID NO: 3492:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3492:

AACCTTTTCA CAAATATCAT ATAACTCTTC TAATGGGATA ATCTCTTCAT GT 52

(2) INFORMATION FOR SEQ ID NO: 3493:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3493:

GGTTTTAAAC CGTCACGAAC ATCTGGCAAT GCACGAGCAA CGTACATACG TATCTAAAGT 60

TACGCTT 67

(2) INFORMATION FOR SEQ ID NO: 3494:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3494:

TACGTTATGT TATGTAAATA ACAGTTAATT ATACCGGTGG TCTGGGTCGA 50

(2) INFORMATION FOR SEQ ID NO: 3495:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3495:

CGCTTGTTGT TGTACTTTGG CAGTTCGCGT TGTGGATTGT GCCAGCGCTT TTAAACCGTA 60

(2) INFORMATION FOR SEQ ID NO: 3496:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3496:

GGCACCGGCT TCTCTATTGC TTCTTTAGCA TATCTGCAGC TCTCTCAAGG GACATG 56

(2) INFORMATION FOR SEQ ID NO: 3497:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3497:

CACCTTTAGG ATACGCGTCT AACCACTGTG TCGCGTCTCT ATATATCGCT AAACACGTA 59

(2) INFORMATION FOR SEQ ID NO: 3498:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3498:

AAGTAATATC TGAATGCGTA TATTGTCTAA TTTCAAATTC TACAGACATC GACGT 55

(2) INFORMATION FOR SEQ ID NO: 3499:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3499:

AnTGTACACG TCCATCTTCA CATGACAACA ACGATATTTT GACCATCACA 50

(2) INFORMATION FOR SEQ ID NO: 3500:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3500:

(2) INFORMATION FOR SEQ ID NO: 3501:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3501:

TGTGTGCCTT TAAGTTGTTG ATGACACGCA TTCACGACAA CAGACATGAC AC 52

(2) INFORMATION FOR SEQ ID NO: 3502:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3502:

CTGGCTTCAA TGGCAACTTC TGTACCTGGT ACCAATGGGC GATGACCGAT 50

(2) INFORMATION FOR SEQ ID NO: 3503:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3503:

TGTCCGACTT GGCGGnATCG TAATTTAGCG CnTGTAATTC TAAAGGGACC 50

(2) INFORMATION FOR SEQ ID NO: 3504:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3504:

AACCTTCATA TTGCTTCTAA TAAGAAACCG AGCAGCGCAC CAAACCTGGC AGTACCTTTA 60

TCGC 64

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3505:

TATTGATGTT GAAAACTGTT ATGTCCTTTC GATGGGCCAA CACnAAnATA 50

(2) INFORMATION FOR SEQ ID NO: 3506:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3506:

GAATATGGTA TCAATGGTAT GCACTAAGGC TTTATGAAAT TCATTTAAAA T 51

(2) INFORMATION FOR SEQ ID NO: 3507:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3507:

CGGTTTTAAT CGGTAAATTA AATATGGATG AGTTTGCAAT GGTGTTCACA GAACATCTAT 60

TTAA 64

(2) INFORMATION FOR SEQ ID NO: 3508:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3508:

CAAGGCCTTG TTTTTAAAGC AGCTACAGTT GGCAATATGT CCACTCATGT 50

(2) INFORMATION FOR SEQ ID NO: 3509:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: d uble
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3509:

CAGATGCAAA TTGACATGGT CATCAACATC nGTnCATTAA AAGATGGACG 50

(2) INFORMATION FOR SEQ ID NO: 3510:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3510:

ACAAGAGGGT CACCCAGCTC GGTCGATTCC CACCGCCACA TCATGATATT TATTCATAGA 60

GTTTACGCAC TGTACATGAT TGAATGCGAT AAAG 94

(2) INFORMATION FOR SEQ ID NO: 3511:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3511:

ACTCAACAAT GGATATTCTT ACACTGAAAA ATGGGTAATG GTGCAAACAT AGTA 54

(2) INFORMATION FOR SEQ ID NO: 3512:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3512:

CCGGATGCAC ATTTGATGAC TGAAGTCCGC GATAAAGGGA CAAnAGTCAn 50

(2) INFORMATION FOR SEQ ID NO: 3513:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3513:

GCATTAAATT GAAACAATCG GATTTACAAT TTTCTCTTAA TGCTGTCGTC TACACAGC 58

(2) INFORMATION FOR SEQ ID NO: 3514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3514:

GTGTTCGTGT TCATGCAAGG TGAATGCGAG TGATCTGTTG GTATGGGCTT TATGCATGGC 60

AATCTG 66

(2) INFORMATION FOR SEQ ID NO: 3515:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3515:

ATGCCACTGA TAATGCnnCT GAACTTATTG ATGACTTCTC ATTAGACTAT 50

(2) INFORMATION FOR SEQ ID NO: 3516:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3516:

CGGCGACAAA GAGTAAACAC AGCGGAGGGA CAAAGCCCGC GACTAGCAAC 50

(2) INFORMATION FOR SEQ ID NO: 3517:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3517:

ATGCCTATGT AGCACCGAGT ACCGATACCG AACACTTAGC TACGCCAGTT C 51

(2) INFORMATION FOR SEQ ID NO: 3518:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3518:

GAGCATnAAG GTGATTTnGA TCGCTATCCG TTAGCTAAAT TTAAACGTTC 50

(2) INFORMATION FOR SEQ ID NO: 3519:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3519:

GATTGGTATT TAGCTTTAAA TTTATGGTTG GAATAGTAGG TGGCATATAT CGCTGTTAGT 60

ATCG 64

(2) INFORMATION FOR SEQ ID NO: 3520:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3520:

TCTTCAATCT CAGGGGCATC TACTAACATA TCATCCAGTC AATATTGCGT CACATTGTTA 60

ATCGGTTCCG ATC 73

(2) INFORMATION FOR SEQ ID NO: 3521:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3521:

TCAAATTGGC AATTGGTACG AATGTCGACT GTACTAACAT CATTAGCTCA TGATTGCCAG 60

GTGATTTCAT GGATG 75

(2) INFORMATION FOR SEQ ID NO: 3522:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3522:

TTCCAATGGG CTTCTGACTT TGGCGGTTTT AGTGCTTGGG TTGCCGGCGG TTTTGGA 57

(2) INFORMATION FOR SEQ ID NO: 3523:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3523:

TGGTGGAGGT TTTGTTTTTT CCGTGTCGGT TTTTGTTTTC GTCTTGGTTT CTTTTGTTTT 60

TGTGTTCTCT TT 72

(2) INFORMATION FOR SEQ ID NO: 3524:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3524:

ATATCACAAT ATACCGGTTT ATATGCTGTC TAATCATAGT TGAATAGTGA C 51

(2) INFORMATION FOR SEQ ID NO: 3525:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3525:

TAGACCGTCG TGGATAGTTT TGGGTACGGT AACCAATTTA TTTTGAAGAG ACCATCCTC 59

(2) INFORMATION FOR SEQ ID NO: 3526:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3526:

TAATAACGTT GCCCTCCCAT GTATATCCTA CCAACATGAC ATCTTGTACA 50

(2) INFORMATION FOR SEQ ID NO: 3527:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3527:

TTCCCAACGA GCAGTCGCAT GCGGTACTGC CACGGCATTT TGATGCAGGC CT 52

(2) INFORMATION FOR SEQ ID NO: 3528:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3528:

AAAGAAAnGA TnGnnnGnnn GnAnAAAnnn nnCCATnnnn nTAAAAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 3529:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CATTAGCCTC ATCCCCTTCG TTTAGACTCG CTATAGATGC ACTAAATGGC GATATATTTT 60

TC 62

(2) INFORMATION FOR SEQ ID NO: 3530:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3530:

CACTACCACA AAAATTATAG GTGTTGACCT TCAGGnGCAA GTAGTATGAT 50

(2) INFORMATION FOR SEQ ID NO: 3531:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3531:

GAATGCAAAA TCCATTTGTA AGGAnATCGA ATGGTTTAGT AnCTCGTGCA 50

(2) INFORMATION FOR SEQ ID NO: 3532:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3532:

GGTAGAnCnC TGTTTAGTAC TAGGGGCCCC TCTCGGGTTA CCAATTCAGA 50

(2) INFORMATION FOR SEQ ID NO: 3533:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3533:

(2) INFORMATION FOR SEQ ID NO: 3534:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3534:

CGTCAACGAT GTAAAGTAAA GCCTTGTCCA GTTTAATTTA CGAGTGGCGT AA 52

(2) INFORMATION FOR SEQ ID NO: 3535:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3535:

TTAATCCAGA AGTACCGGTG GATTTAGTTA TTGACCACTC AGTTCAAGTG GATAGCTATG 60

CAAATCCAGA AGCTCTTGAA CGTAATATGA AATTAGAATT TGAACGTAAC TATGAACGTT 120

ATCAGTTTTT AAATTGGGCA ACGAAAGCAT TTGATAATTA CAATGCAGTT CCTCCTGCAA 180

CTGGAATAGT TCACCAAGTT AACTTAGAAT ATTTAGCAAG TGTTGTACAT GTTCGTGATG 240

TAGATGGTGA AAAAACTGCA TTTCCAGATA CATTAGTTGG TACTGATTCA CATACAACAA 300

TGATAAATGG TATTGGCGTA CTAGGATGGG GTGTTGGTGG TATTGAAGCT GAAGCTGGAA 360

TGCTTGGACA ACCTTCTTAT TTCCCAATTC CAGAGGTTAT 400

(2) INFORMATION FOR SEQ ID NO: 3536:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3536:

CGTATAGAGT GTCCTACAAC CCCAACAAGC AAGCTTGTTG GTTTGGGCTC TTCCCGTTTC 60

GCTCGCCGCT ACTAAGGGAA TCGAATTTTC TTTCTCTTCC TCCGGGTACT AAGATGTTTC 120

AGTTCTCCGG GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC 180

GCATATCGTC GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC 300

CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGCTCA CATACGGCTT 360

CGTTTTCATT ATTTTAAATG CTCATTTACA TAAGTAAACT CTGCTTTAAA ATAATTTAAC 420

TCATTGTCTG CTAAACGTTT TCTTTTATAA AAAGATTTAA ACGCGTTATT AATCTTGTGA 480

GTGTTCTTTC GAACACTAGC GATTATTTCT TATGAATTCA AGCTTATTTA AAACTCTTTA 540

TTCACTCGGT TTTGCTTGGT AAAATCTATA TTTTACTTAC TTATCTAGTT TTCAATGTAC 600

AATTTCTTTT TAGTCAAGCG CTCGCATACT GCTTTATTTT CAAAAAATCA AATGCTCATT 660

TACAAAAGTA AACTCCGCTT TAATTTTTCT TAATGCATTG TCTAACAACC GCTTTCTTTA 720

AAAAGAATAG ATTGTCAAGC GCTCGCATAA GCAATATCAC TTTAACCAAA AAATATTTGA 780

ATGTTAAATA AACATTCAAA ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG 840

AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT 900

ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 960

TTACTCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGcGGT GTGTACAAGA 1020

CCCGGGaACG TATTCACCGT AGCATGCTGA TCTACGaTTA CTAGCGtTCC AGCTTCATGT 1080

AGTCGAGTGC AGACTACCAT CCGGACTGnG GACCAACT 1118

(2) INFORMATION FOR SEQ ID NO: 3537:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 424 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3537:

GGGGATCCCC AGCCAGAAGA TTTATTCAGT GCGATGATTC GTGAAATTGA AACGCAAGAT 60

TTCGATATCG AACACCTGGC GACGGCAATT CGTAAmGTTG AAACATCAAC ATTAGGTGAA 120

GAAAGTGAAA ATGACTTTAT CGGTCTGTTC AGCGATATGG ATTTGAGTTC AACGCGACTA 180

GGTAACAATG TCAAAGAACG TACTGCTTTA ATCTCTAAAG TCATGGTTAA TCTTGACGAC 240

TTACCATTCG TTCACAGTGA CATGGAAATT GATATGTTAG GTGATGCATA TGAATTCCTA 300

ATTGGGCGCT TTGnGCGACA CGGGTAAAAA AAGCAGGCGA GTTCTATACA CCACAACAAG 360

TATCTAAGAT ACTGGCGAnG ATTGTCACAG ACGGTAAAGA TAAATTACGT CACGTGTATG 420

ACCC 424

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: d uble
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3538:

ATCTCATATG TTAAAAGGTA AACAAGGTCG TTTCCGTCAA AACTTACTTG GTAAACGTGT 60

TGACTATTCA GGACGTTCAG TTATTGCAGT AGGTCCAAGC TTGAAAATGT ACCAATGTGG 120

TTTACCAAAA GAAATGGCAC TTGAACTATT TAAACCATTC GTAATGAAAG AATTAGTTCA 180

ACGTGAAATT GCAACTAACA TTAAAAATGC GAAGAGTAAA ATCGAACGTA TGGATGATGA 240

AGTTTGGGAC GTATTGGAAG AAGTAATTAG AGAACATCCT GTATTACTTA ACCGTGCACC 300

AACACTTCAT AGACTTGGTA TTCAAGCATT TGAACCAACT TTAGTTGAAA GGTCGTGCGA 360

TTCGTCTACA TCCACTTGTA ACAACAGCTT ATAACGCTGA 400

(2) INFORMATION FOR SEQ ID NO: 3539:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3539:

AATAAGTAAG TTATTTTGTC TGGTGACTAT AGCAAGGAGG TCACACCTGT TCCCATGCCG 60

AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC GCTAGAGTAG 120

AACGTTGCCA GGCAAATGAC AAATCGGAGA ATTAGCTCAG CTGGGAGAGC ATCTGCCTTA 180

CAAGCAGAGG GTCGGCGGTT CGAACCCGTC ATTCTCCACC ATTTATTCTT AGATATAGCC 240

GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCAGT AGGTTGGGGG TTCAAGTCCT 300

CTGGCCGGCA CCATCTTTTG AGCCATTAGC TCAGCTGGTA GAGCATCTGA CTTTTAATCA 360

GAGGGTCAGA GGTTCGAATC CTCTATGGCT CATTACGATT TAATTTTTAT ATTTAGCAAA 420

ATAATGCAGA AGTAGTTCAG CGGTAGAATA CAACCTTGCC AAGGTTGGGG TCGCGGGTTC 480

GAATCCCGTC TTCTGCTCCA TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC 540

TTAAAATCCT GCGGTGAGAG ATCACcGTAc CGGTTCGATT CCGGTCCTCG GCACCATTTT 600

AGCGCCCGTA GCTCAATTGG ATAGAGCGTT TGACTACGGA TCAAGAGGTT ATGGGTTCGA 660

GAGCACTTGG TTTGGGACCA AGGGGTCGCA GGTTCGAATC CTGTCTTCCC GATTACTTCT 780

TAAATTCCAT TTTATGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 840

GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTTATTTTT TACACGATGA ACATTGAAAA 900

CTGAATGACA ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT 960

TTAGTATTTA TGAGCTAATC AAACATCATA ATTTTTATGG AGAGTTTGAT CCTGGCTCAG 1020

GATGAACGCT GGCGGCGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT 1080

TCTCTGaTGT TAGCGGCGGA CGGGTGAGTA ACACGTGGGA TAACCTACCT ATAAGACTGG 1140

GaTAACTTCG GGaAACCGGA GCTAATACCG G 1171

(2) INFORMATION FOR SEQ ID NO: 3540:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3540:

CTCGGCAGTG TGAAATCAAC GACTCGAAGA CACAATGTCT TCTCCCCATC ACAGCTCAGC 60

CTTAACGAGT ACCGGATTTG CCTAATACTC AGCCTTACTG CTTAGACGTG CAATCCAATC 120

GCACGCTTCG CCTATCCTAC TGCGTCCCCC CATCGATTAA AACGATTATA GGTGGTACAG 180

GAATATCAAC CTGTTATCCA TCGCCTACGC CTGTCGGCCT CAGCTTAGGA CCCGACTAAC 240

CCAGAGCGGA CGAGCCTTCC TCTGGAAACC TTAGTCAATC GGTGGACGGG ATTCTCACCC 300

GTCTTTCGCT ACTCACACCG GCATTCTCAC tTCTAAGCGC TCCACATGTC CTTACGATCA 360

TGCTTCAACG CCCTTAGAAC GCTCTCCTAC CATTGTCCAA AGGCATwCrC ACAGCTTCGG 420

TaATATGTTT AGCCCCGGTA CATTTTCGGC GCAgTGTCAC TCGACTAGTG AGCTATTACG 480

CACTCTTTAA ATGATGGCTG CTTCTnAGCC AACATCCTAG GTTGGTCTGG GGCACGCnAC 540

ATCCTTTTCC ACTTAACATA TATTTTGGGG ACCTTGGCTG GTGGGTCTGG GGCTGnTTCC 600

C 601

(2) INFORMATION FOR SEQ ID NO: 3541:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3541:

GCnAGGACCT TnCCAAATTT GAAATCCTTT GACCACnTTT GGGGTAGAGC CCTTTCCCnC 60

GGGGACAAAG TGACCAGGTG GTGCATGGTT GTCGTCAGCT CGTGTCGTGA GATGTTGGGT 120

TAAGTCCCCG CAACGAGCGC AACCCTTAAG CTTAGTTGCC ATCATTAAGT TGGGCACTCT 180

AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG ACGTCAAATC ATCATGCCCC 240

TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA AAGGGCAGCG AAACCGTGAG 300

nTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC TCGACTACAT 360

GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG GTGAATACGT TCCCGGGTCT 420

TGTACACACC GCCCGTCACA CCACGAGAGT TTGTAACACC CGAAGCCGGT GGAGTAACCT 480

TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG TGAAGTCGTA ACAAGGTAGC 540

CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA ACATCTTCTT 600

CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT GAATGTTTGT TCATTCAAAT 660

TAATGGGCCT ATAGCTCAGC TGGTTAGAGC GCACGCCTGA TAAGCGTGAG GTCGGTGGTT 720

CGAGTCCACT TAGGCCCACC ATTAATTTAA TACCTATTTG GGGGCTTAGC TCAGCTGGGA 780

GAGCGCCTGC TTTGCACGCA GGAGGTCAGC GGTTCGATCC CGCTAGTCTC CACCATTATT 840

TGTACATTGA AAACTAGATA AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA 900

ATAAAGAGTT TTAAATAAGC TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAAGAACA 960

CTCACAAGAT TAATAACGCG TTTAAATCTT TTTATAAAAG AACGTAACTT CATGTTAACG 1020

TTTGACTTAT AAAAATGGTG GAAACATAGA TTAAGTTATT AAGGGCGCAC GGTGGATGCC 1080

TTGGCACTAG AAGCCGATGA AGGACGTTAC TAACGACGAT ATGCTTTGGG GAGCTGTAAG 1140

TAAGCTTTGA TCCAGAGATT TCCGAATGGG GAAACCCAGC ATGAGTTATG TCATGTTATC 1200

GATATGTGAA TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC 1260

CGGAGGAAGA GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCGAAATG G 1311

(2) INFORMATION FOR SEQ ID NO: 3542:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3542:

CGCTAGAGTA GAACGTTGCC AGGCAAATGA CAAATCGGAG AATTAGCTCA GCTGGGAGAG 120

CATCTGCCTT ACAAGCAGAG GGTCGGCGGT TCGAACCCGT CATTCTCCAC CATTTATTCT 180

TAGATATAGC CGGCCTAGCT CAATTGGTAG AGCAACTGAC TTGTAATCAG TAGGTTGGGG 240

GTTCAAGTCC TCTGGCCGGC ACCATCTTTT GAGCCATTAG CTCAGCTGGT AGAGCATCTG 300

ACTTTTAATC AGAGGGTCAG AGGTTCGAAT CCTCTATGGC TCATTACGAT TTAATTTTTA 360

TATTTAGCAA AATAATGCAG AAGTAGTTCA GCGGTAGAAT 400

(2) INFORMATION FOR SEQ ID NO: 3543:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 804 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3543:

GTGAGAGTGA CGTTATGTTA TGTAAATAAC AGTTAATTAT ACCGGTGGTC GGGGTCGAAC 60

CGCACTCCAC AAGTGGAAGA GaTTTTGAGT CCCGCGCGTC TGCCAATTCC GCCACACCGG 120

CTTAATGGTA AACAAAAAAC TTCCCTTTGG AAGCAATTAT GGAGCGGAAG ATAGGATTTA 180

CACCTATACC TCGTTCCGGG aAGGAACtGg TTcTAAAAGT TGAACTACTC CCGCAAATAT 240

TAAATTATGG AGCGGAAGAT AGGATTTACA CCTATACCTC ATTCCAGGAA GGAATGTATT 300

CTAAGAGTTG AAATACTCCC GCATTATTAT TAAATTATGG AGCGGAAGAT AGGATTTGCA 360

CCTATACCTC GTTCCGGGAA GGAckTGTTt CTAAAAGTTG AACTACTCCC GCATAAACCT 420

GGAGGCGGCA ACCGGATTTG AACCGGTGAT AAAGGTTTTG CAGACCTCTG CCTTACCACT 480

TGGCTATGCg CcAATAACTG GGCTAGCTGG ATTCGAACCA ACGAGTGACG GATmAAAGTC 540

CGTTGCCTTA CCGCTTGGCT ATAGCCCATT AATAATAAGG GCGGCTGAAG GGGATCGAAC 600

CCTCGAATGT CGGAACCACA ATCCGATGTG TTAACCACTT cACCACAGCC GCCATGGCAG 660

GGGCAGTAGG AATCGAACCC ACACCAAAGT TTTGGaGACC TCTATTCTAC CGTTGAACTA 720

TGCCCCTATT aAAAATaaTA ATkGGAGGGG GGCAGATTCG AAnTGCCGAA CCCGAAGGAG 780

CGGGATTTAC ATTCCGCCGG GTTT 804

(2) INFORMATION FOR SEQ ID NO: 3544:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3544:

ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60

GTTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG 120

TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180

GTGTTGGCTT ATTACCGAGT GGCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240

CATCGCATAA GTTTGATkAC AAACAAGCTT CCATGACAAA AGTACTGACG AATATCGCAT 300

TTGCGAAAGT CTCTACAAAT GCCTTTGAGG CACGTCGTTA TGGTTATTTA CGTGGATACA 360

GATACGATTA TTTTCAATAC AGCACAACGT GTCCGAAGTT 400

(2) INFORMATION FOR SEQ ID NO: 3545:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3545:

CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA TCATGCTTCA ACGCCCTTAG 60

AACGCTCTCC TACCATTGTC CAAAGGnATC nCACAGCTTC GGTAATATGT TTAGCCCCGG 120

TACATTTTCG GCGCAGTGTC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGATGGC 180

TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCaCA TCCTTTTCCA CTTAACATAT 240

ATTTTGGGAC CTTAGCTGGT GGTCTGGGCT GTTTCCCTTT CGAACACGGA CCTTATCACC 300

CATGTTCTGA CTCCCAAGTT AAATTAATTG GcATTCGGAG TTTGTCTGAA TTCGGTAACC 360

CGAGAGGGGC cCCTCGTCCA AAcAGTGGCT CTACCTCCAA TAATCATCAn TTGAGGCTAG 420

CCCTAAAGCT AATTCGGAGA GAACCAGTAT CTCCAGTTCG ATTGGAATTC TnCG 474

(2) INFORMATION FOR SEQ ID NO: 3546:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3546:

GCAATTCGTA AAGTTGAAAC ATCAACATTA GGTGAAGAAA GTGAAAATGA CTTTATCGGT 120

CTGTTCAGCG ATATGGATTT GAGTTCAACG CGACTAGGTA ACAATGTCAA AGAACGTACT 180

GCTTTAATCT CTAAAGTCAT GGTTAATCTT GACGACTTAC CATTCGTTCA CAGTGACATG 240

GAAATTGATA TGTTAGGTGA TGCATATGAA TTCCTAATTG GGCGCTTTGn GCGACACGGG 300

TAAAAAAAGC AGGCGAGTTC TATACACCAC AACAAGTATC TAAGATACTG GCGAGATTGT 360

CACAGACGGT AAAGATAAnT ACGTCACGTG TATGACCCAA 400

(2) INFORMATION FOR SEQ ID NO: 3547:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3547:

AACGTTTTCA CTTCGCCAAG CCATTTTTCT TTGTGTTTAC TTTTTATTTT GACGTTTTAG 60

ACATAAAAAA AAGAGACCTT GCGGTCTCAA TGCGGCTCAT CGCATCCATT TTTTGCCTGG 120

CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG ACGCTAAGAA CCTTTCTTGA 180

CTTGTGACAA TCGCTTGCTT CTTTCCTCTT CTTCGGCTCT CGCTTACTCA TTTAGCTCTA 240

CTAAACTCGT TGCGCTCTTT TCTCGTTTCG TCAGATTCAA ACGTTTTCAC TTCGCCAAGC 300

CATTTTTCTT TGTGTTTGCT TTTTATTTTG ACGTTTTAGA CATAAAAAAA AGAGACCTTG 360

CGGTCTCAAT GCGGCTCATC GCATCCAnTT TTTGCCTGGC 400

(2) INFORMATION FOR SEQ ID NO: 3548:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3548:

ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60

GTTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG 120

TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180

GTGTTGGCTT ATTACCGAGT GGCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240

TTGCAAAGTC TCTACAAATG CCTTTGAGGC ACGTCGTTAT GGTTATTTAC GTGATACAGA 360

TACGATTATT TTCAATACAG CACAACGTGT CCGAAGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 3549:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3549:

AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC GGTGTGTACA 60

AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA TTACTAGCGA TTCCAGCTTC 120

ATGTAGTCGA GTTGCAGACT ACAATCCGAA CTGAGAACAA CTTTATGGGA TTTGCTTGAC 180

CTCGCGGTTT CGCTGCCCTT TGTATTGTCC ATTGTAGCAC GTGTGTAGCC CAAATCATAA 240

GGGGCATGAT GATTTGACGT CATCCCCACC TTCCTCCGGT TTGTCACCGG CAGTCAACTT 300

AGAGTGCCCA ACTTAATGAT GGCAACTAAG CTTAAGGGTT GCGCTCGTTG CGGGACTTAA 360

CCCAACATCT CACGACACGA GCTGACGACA ACCATGCACC 400

(2) INFORMATION FOR SEQ ID NO: 3550:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3550:

CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 60

TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATAATATTT 120

TGAACCGCAT GGTTCAAAAG TGAAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 180

TGCATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG CCGACCTGAG 240

AGGGTGATCG GCCACACTGG AACTGAGACA CGGTCCAGAC TCCTACGGGA GGCAGCAGTA 300

GGGAATCTTC CGCAATGGGC GAAACCTGAC GGAGCAACGC CGCGTGAGTG ATGAAGGTCT 360

TCGGATCGTA AAACTCTGTT ATTAGGGAAG AACATATGTG 400

(2) INFORMATION FOR SEQ ID NO: 3551:

(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3551:

ACAAGGTAGC CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA 60

ACATCTTCTT CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT GAATGTTTAT 120

TTAACATTCA AATATTTTTT GGTTAAAGTG ATATTGCTTA TGCGAGCGCT TGACAATCTA 180

TTCTTTTTAA AGAAAGCGGT TGTTAGACAA TGCATTAAGA AAAATTAAAG CGGAGTTTAC 240

TTTTGTAAAT GAGCATTTGA TTTTTTGAAA ATAAAGCAGT ATGCGAGCGC TTGACTAAAA 300

AGAAATTGTA CATTGAAAAC TAGATAAGTA AGTaAAATAT AGATTTTACC AAGCAAAACC 360

GAGTGAATAA AGAGTTTTAA ATAAGCTTGA ATTCATAAGA aTAATCGCTA GTGTTCGAAA 420

GAACACTCAC AAGATTAATA ACGCGTTTAA ATCTTTTTAT AAAAGAnAAC GTTTAGCAGA 480

CAATGAGTTA AATTATTTTA AAGCAG 506

(2) INFORMATION FOR SEQ ID NO: 3552:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3552:

AAGCTGAGGC CGACAGTGGn GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT 60

CGTTTTAATC GATGGGGGGA CGCATAGGAT AGGCGACGTG TCGATTGGAT TGCACGTCTA 120

AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTGATGGGGA 180

GAAGACATTG TGTCTTCgAG GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA 240

AAATAGGTGC CCGTACCGCA AACCGACACA GGTAGTCAAG ATGAGAATTC TAAGGTGAGC 300

GAGCGAACTC TCGTTAAGGA ACTCGGCAAA ATGACCCCGT AACTTCGGGA GAAGGGGTGC 360

TCTTTAGGGT TAACGCCCAG AAGAGCCGCA GTGAATAGGC CCAAGCGACT GTTTATCAAA 420

AACACAGGTC TCTGCTAAAC CGTAAGtGAn TGTATAGGGG CTGACGCCTG CCCGGTGCTG 480

GAAGGTTAAG AGGAGTGGTT AGCTTCTGCG AAcTAcGaAT CGAAGCCCCA GTAAACGGCG 540

GCCGTAACTA TAACGGTCCT AAGGTAGCGA AATTCCTTGT CGGGTAAGTT CCGACCCGCA 600

GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 720

GATATTGAAA TTCGGCACAG CTTGTACAGG ATAGGTAGGA GCCTTTGAAA CGTGAGCGCT 780

AcTTaCgTGG aGGCGCTGGT GGGATACTAC CCTAGCTGTG TTGGCTTTCT AACCCGCACC 840

ACTTATCGTG GTGGGAGACA GTGTCAGGCG GGCAGTTTGA CTGGGGCGGT CGCCTCCTAA 900

AAGGTAACGG AGGCGCTCAA AGGTTCCCTC AGAATGGTTG GAAATCATTC ATAGAGTGTA 960

AAGGCATAAG GGAGCTTGAC TGCGAGACCT ACAAGTCGAG CAGGGTCGAA AGACGGACTT 1020

AGTGATCCGG TGGTTCCGCA TGGAAGGGCC ATCGCTCAAC GGATAAAAGC TACCCCGGGG 1080

ATAACAGGCT TATCTCCCCC AAGAGTTCAC ATCGACGGGG AGGTTTGGCA CCTCGATGTC 1140

GGCTCATCGC ATCCTGGGGC TGTAGTCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAAG 1200

CGGTACrmGg CTGGGTTCAG AACGTCGTGA GaCAGTTCGG TCCCTATCCG TCGTGGGCGT 1260

AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 1320

TACCAGTTGT CGTGCCAACG cATnAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA 1380

AAcATnCTnA AGCATGAAGC CCCCCTCAAG ATGAGATTTC CCAACTTCGG TTATAAGATC 1440

CCTCAAAGAT GATGAGGTTA ATAGGTTCGA GGTGGAAGCA TGGTGACATG TgGGAGCTGA 1500

CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACAAA tnCaCTTTTA 1560

CTTACTATCT AGTTTTGAAT GTATAAATTA CATTCATATG TCTGGTGACT ATAGCAAGGA 1620

GGTCACACCT GTTCCCATGC CGAACACAGA AGTTAAGCTC CTTAGCGTCG ATGGTAGTCG 1680

AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAGTTT TTTAATCAAA TTTTGGTTAA 1740

AAAATAAAAT GGACAAGATA AAAAAAGTTA TTGACTTAAA TGTTAATAAA ATGTATAATT 1800

AATTCTTGTC GGTAAGAAAA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 1860

TCCAAAAAAC GTAACTATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT 1920

CATAATTTTT ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA 1980

CATGCAAGTC GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG 2040

AGTAACACGT GGATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GGAGCTAATA 2100

CCGGATAATA TTTTGAACCG CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACTTATA 2160

GATGGATCCg CGCTGCATTA GCTAGTTGGt AAGGtAACGG CTTTACCCA 2209

(2) INFORMATION FOR SEQ ID NO: 3553:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 518 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3553:

CTAGATAAGT AAGTAAAATA TAGATTTTAC CAAGCAAAAC CGAGTGAATA AAGAGTTTTA 60

AATAAGCTTG AATTCATAAG AAATAATCGC TAgTGTTCGA AAGAACACTC ACAAGATTAA 120

TAACGCGTTT CCTGTAGGAT GGAAACATAG ATTAAGTTAT TAAGGGCGCA CGGTGGATGC 180

CTTGGCACTA GAAGCCGATG AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA 240

GTAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT 300

CGATATGTGA ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC 360

CCGGAGGAAG AGAAAGAAAA TTCGATTCCC TTAGTAGCGG CGAGCGAAAC GGGAAGAGCC 420

CAAACCAACA AGCTTGCTTG TTGGGGTTGT AGGaCACTCT ATACGGAGTT ACaAAGGmCG 480

ACATTrGACG AaTCATCTGG gAAAGwTGaT CCAAGGAA 518

(2) INFORMATION FOR SEQ ID NO: 3554:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3554:

AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG 60

CTAATTCTCC GATTTAAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTsGAC 120

TACCATCGAC GCTAAGGAGC TTAACTTCTG TGTTCGGCAT GGGAACAGGT GTGACCTCCT 180

TGCTATAGTC ACCAGACATA TGAATGTAAT TTATACATTC AAAACTAGAT AGTAAGTAAA 240

AGTGATTTTG CTTCGCAAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 300

AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGAT 360

CTTATAACCG AAGTTGGGAA ATCTCATCTT GAGGGGGGCT TCATGCTTAG ATGCTTTCAG 420

CACTTAtCCC GTCCACACAT AGCTACCCAG CTATGCCGTT GGCACGACAA CTGGTACACC 480

AGAGGTATGT CCATCCCGGT CCTCTCGTAC TAAGGACAGC TCCTCTCAAA TTTCCTACGC 540

CCACGACGGa TAGGGaCCGA ACTGtCTCAC GACGTTCTGA ACCCAGA 587

(2) INFORMATION FOR SEQ ID NO: 3555:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3555:

GAATCTGAAT CGCTATCTGA ATCCGAGTCA CTGTCGGAAT CTGAGTCACT GTCGGAATCT 60

GAATCGCTAT CTGAATCTGA ATCGCTGTCT GAATCTGAAT CGCTGTCTGA ATCTGAGTCG 120

CTATCTGAGT CGGAATCGCT ATCTGAGTCG GAATCACTGT CGGAATCTGA ATCGCTGTCT 180

GAGTCGGAAT CACTGTCGGA GTCAGAATCG CTGTCTGAGT CGGAATCACT GTCGGAATCT 240

GAATCGCTAT CTGAATCTGA ATCGCTATCT GAATCCGAGT CACTGTCTGa GTCAGAATCG 300

CTATCTGGAA TCTGGAGTCA CTGTCGGaAT CTGAGTCACT GGTCTGGAGT CAGAATCGCT 360

ATCTGGAATC CGAnGTCATG GTCTGAGTCG GGaATCGCT 399

(2) INFORMATION FOR SEQ ID NO: 3556:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3556:

ATTCATCTTT CCAGATGATT CGTCTAATGT CGTCCTTTGT AACTCCGTAT AGAGTGTCCT 60

ACAACCCCAA CAAGCAAGCT TGTTGGTTTG GGCTCTTCCC GTTTCGCTCG CCGCTACTAA 120

GGGAATCGAA TTTTCTTTCT CTTCCTCCGG GTACTAAGAT GTTTCAGTTC TCCGGGTGTG 180

CCTTCTGATA TGCTATGTAT TCACATATCG ATAACATGAC ATAACTCATG CTGGGTTTCC 240

CCATTCGGAA ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG 300

TAACGTCCTT CATCGGCTTC TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACTTAAT 360

CTATGTTTCC ATCCTACAGG AAACGCGTTA TTAATCTTGT 400

(2) INFORMATION FOR SEQ ID NO: 3557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 657 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3557:

ACAACTGGTA CACCAGAGGT ATGTCCATCC CGGTCCTCTC GTACTAAGGA CAGCTCCTCT 120

CAAATTTCCT ACGCCCACGA CGGATAGGGA CCGAACTGTC TCACGACGTT CTGAACCCAG 180

CTCGCGTACC GCTTTAATGG GCGAACAGCA AnCCCTTGGG ACCGACTACA GCCCCAGGAT 240

GCGATGAGCc GACATCGAGG TGCCAAACCT CCCCGTCGAT GTGAACTCTT GGGGGAGATA 300

AGCCTGTTAT CCCCGGGGTA GCTTTTATCC GTTGAGCGAT GGCCCTTCCA TGCGGAACCA 360

CCGGATCACT AAGTCCGTCT TTCGAcCCTG CTCGACTTGT AGGTCTCGCA GTCAAGCTCC 420

CTTATGCCTT TACACTCTAT GAATGATTTC CAACCATTCT GAGGGAACtT TGAGCGCCTC 480

CGTTACCTTT TAGGAGGCGA CCGCCCCAGT CAAACTGCCc GCcTGACACT GTCTACcmCC 540

ACGATAAGTG GTGCGGGTTm GmAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGCCTn 600

CCCACTAATA GCGCTCACGT TTCAAAGGCT CCTACCTATC CTGTACAAGC TGTGCCG 657

(2) INFORMATION FOR SEQ ID NO: 3558:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3558:

GAGTCCATGG GTGAAAGAAG CATCTGCAGC AACTGTAGCA GGTATTGCTG GAACTAATAA 60

TGGTATTACT GTTGCAGCAG GTACTTTCAA CCCTGCTGAT ACAATTCAAG TTGTTGCAAC 120

GCAAGGACAG CGGAGAGACA GTGAGTGATG AGCAACGTAT nnTnGATTTC ACAGTTGTCG 180

CACCACAACC GAACCAAGCG ACTACTAAGA TTTGGCAAAA TGGTCATATT GATATCACGC 240

CTAATAATCC ATCAGGACAT TTAATTAATC CAACTCAAGC AATGGATATT GCTTACACTG 300

AAAAAGTGGG TAATGGTGCA GAACATAGTA AGACAATTAA TGTTGTTCGT GGTCAAAATA 360

ATCAATGGAC AATTGCGAAT AAGCCTGACT ATGTAACGTT 400

(2) INFORMATION FOR SEQ ID NO: 3559:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3559:

CGACACAAAA CAAGCCAAGC AAAACAAACG CATATAACGT AACAACACAT GGAAACGGCC 120

AAGTATCATA TGGCGCTCGC CAACACAAAA CAAGCCAAGC AAAACAAATG CATACAACGT 180

AACAACACAT GCAAACGGTC AAGTGTCATA CGGAGCTCGC CCGACATACA AGAAGCCAAG 240

TAAAACAAAT GCATACAATG TAACAACACA TGCAGATGGT ACTGCGACAT ATGGGCCTAG 300

AGTAACAAAA TAAGTTTGTA ACTCTATCCA AAGACATACA GTCAATACAA AACATTACGT 360

ATCTTTACAA CAGTAATCAT GCATTCTATG ATGCTTCTAA 400

(2) INFORMATION FOR SEQ ID NO: 3560:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3560:

TTTAGGTTAT ACAGCATTGC AGGCAGGATA CTTATCAATT ACTTATTTAA TCATGGTGTT 60

ATTGATGATT CGAGTTGGTG AAAAATTATT ACAAAAAATG GGTTCTAAGC GACCAATGTT 120

ATTAGGTACA TTCATTGTGG TCATTGGTAT TGCACTTATT TCATTAGTAT TCTTACCAGG 180

CATATTTTAT GTTATCAGTT GTGTCGTAGG ATATTTATGT TTCGGACTAG GCTTAGGTAT 240

TTATGCAACA CCTTCTACAG ATACAGCTAT TTCGAATGCA CCGTTAGATA AAGTTGGCGT 300

TGCTTCAGGT ATTTATAAAA TGGCTTCATC ACTTGGTGGg CGCATTCGGT GTCGCAATTA 360

GTGGTGCTGT ATATGCTGGT GCAGTTGCTG CAACGAGCAT TCCATACAGG TGCGATGATT 420

GCACTTTGGG TTAACGTATT GAATGGGGAA TCCATGGCCA TTTATCGCAA TTTTAATnCG 480

CGATT 485

(2) INFORMATION FOR SEQ ID NO: 3561:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3561:

AAATTATGTG AAGTAAAAGG AGTACGTCCA TGCAAAATTT AGATAAGAAT TTTCGACaTT 60

TATCtCGTAA AGAAAAGTTA CaACAATTGG TTGATAAGCA ATGGTTATCA GAAGAACAAT 120

ATGTCATCGC GCAAGGTGCA TTACCCGTTG GATTATTACC GAATATCATT GTGGACGATA 240

AGGCATATGT TGTACCTATG ATGGTGGAAG AGCCTTCAGT TGTCGCTGCA GCTAGTTATG 300

GTGCAAAGCT AGTGAATCAG ACTGGCGGAT TTAAAACGGT ATCTTCTGAA CGTATTATGA 360

TAGGTCAAAT CGTCTTTGAT GGCGTTGACG ATACTGAAAA ATTATCAGCA GACATTAAAG 420

CTTTAGAAAA GCAAATTCAT AAAATTGCGG ATGAGGCATA TCC 463

(2) INFORMATION FOR SEQ ID NO: 3562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 643 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3562:

AATTTAAACC CAATTGTCTG GCAAAACGTT TTCCTTTATA AAAAGATTTA AACGCGTTAA 60

TTAATCTTGG TGCnGGTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT 120

TAAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA TATTTTACTT ACTTATCTAG 180

TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA CTGCTTTATT TTCAAAAAAT 240

CAAATGCTCA TTTACAAAAG TAAACTCCGC TTTAATTTTT CTTAATGCAT TGTCTAACAA 300

CCGCTTTCTT TAAAAAGAAT AGATTGTCAA GCGCTCGCAT AAGCAATATC ACTTTAACCA 360

AAAAATATTT GAATGTTAAA TAAACATTCA AAACTGAATA CAATATGTCA CGTTATTCCg 420

CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC AGCCGCACCT 480

TCCGATACGG CTACCTTGtT ACGACTTCAC CCCAATCATT TGTCCCACCT TCGACGGCTA 540

GCTCCTAAAA GGTTACTCCA CCGGCTTCGG GTGTTACAAA CTCTCGTGGT GTGACGGGCG 600

GTGTGTACAA GACCCGGGAA CGTATTCACC GTAGCATGCC TCG 643

(2) INFORMATION FOR SEQ ID NO: 3563:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3563:

GATAAATCCA AATAGTGCAC TATAAAAAAT AATATCTACT AAAGTATCTT TATGTAATCC 60

TTCCATACCA TCGTACACTC AGTGGTCCTA AGTTAAATGC CACAGGATCT ATATAGTTAA 180

ATACAATACC CATTCAACCT ACTCCTCACT CTTATGACTG TTCTTGATAA TTTCTTCATT 240

TAATCTTTCA CTAAATTCTT CGGCCGTGTT AATGCCCATG ATATTTAATC GATAGTTCAT 300

TGCAGCGACC TCAATAATTA CCGCAACATT TCTACCAGGT CTTACAGGTA TTGGTTTTTT 360

TTAGTGGnTT TCAGTATCTA AAATACTTAG CGTCTCTTCA 400

(2) INFORMATION FOR SEQ ID NO: 3564:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3564:

TCGTCAGCnC nTGTCGTGAG ACGTTGGGTT AAGTCCCGCA ACGAGCGCAA CCCTTAAGCT 60

TAGTTGCCAT CATTAAGTTG GGCACTCTAA GTTGACTGCC GGTGACAAAC CGGAGGAAGG 120

TGGGGATGAC GTCAAATCAT CATGCCCCTT ATGATTTGGG CTACACACGT GCTACAATGG 180

ACAATACAAA GGGCAGCGAA ACCGCGAnGT CAAGCAAATC CCATAAAGTT GTTCTCAGTT 240

CGGATTGTAG TCTGCAACTC GACTACATGA AGCTGGAATC GCTAGTAATC GTAGATCAGC 300

ATGCTACGGT GAATACGTTC CCGGGTCTTG TACACACCGC CCGTCACACC ACGAGAGTTT 360

GTAACACCCG AAGCCGGTGG AGTAACTTTT AGGAGCTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3565:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3565:

CAAACCATTT GTAGCTATTT GTAACTCTTA TATTGATATT GTTCCTGGAC ATGTTCACTT 60

GAGAGAGCTT GCAGATATAG CTAAAGAAGC AATTAGAGAA GCCGGTGCCA TTCCATTTGA 120

ATTCAATACA ATTGGTGTTG ATGATGGAAT AGCTATGGGA CATATCGGAA TGCGATATTC 180

TCTACCATCA CGTGAAATTA TTGCAGATGC AGCTGAAACT GTAATTAACG CTCATTGGTT 240

TGACGGCGTA TTTTACATTC CTAATTGTGA CAAGATTACA CCCGGTATGA TTTTAGCAGC 300

TGCACATGGA AAAGCATTAA CACTTTCATC AATGTTTGAA 400

(2) INFORMATION FOR SEQ ID NO: 3566:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3566:

AAATTACGTA CAtATTTAAA GCTGACGGCA CTATGACTGC AGGAACATCT GCCCCACTTT 60

CTGATGGTGC AGGATTTGTA GTTTTAATGT CTGGAGATAA AGTGAAAGAA CTCGGcGTGA 120

CACCTATTGC ACGATTCGTT GGTTTTAAGG CAGTAGGCGT TGACCCGAAA ATTATGGGTA 180

TTGGGCCTGC ATATGCGATT CCTGAAGTAT TGTCACTCAG CAATCTATCT GTTGAAGACA 240

TTGATTTGAT CGAATTGAAC GAAGCATTTG CTTCTCAAAC GATTGCATCT ATTAAAGAAG 300

TAGGTCTAGA TATATCACGT ACGAATGTGA ATGGTGGCGC TATTGCTTkA GGTCATCCAT 360

TAGGTGCTAC AGGCGCaATG TTAACCGCGC GTTTACtTAA TGAAATGGGT AGACGTCCCG 420

(2) INFORMATION FOR SEQ ID NO: 3567:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3567:

TACGGGAAGT AGCTCAGCTT GGGTAGAGCA CTTGGTTTGG GACCAAGGGG TCGCAGGTTC 60

GAATCCTGTC TTCCCGATAT ACTGTAATTA TTATGGGGGC TTAGCTCAGC TGGGAGAGCG 120

CCTGCTTTGC ACGCAGGAGG TCAGCGGTTC GATCCCGCTA GTCTCCACCA TATTATTTAC 180

AAACTATATA AGGCGGTGTA GCTCAGCTGG CTAGAGCGTA CGGTTCATAC CCGTGAGGTC 240

GGGGGTTCGA TCCCCTCCAC CGCCACTATT TATTAGTTGT AAAATTATAT TTAGGACCTT 300

TAGCTCAGTT GGTTAGAGCT AACGGCTCAT AACCGTTCGG TCGCAGGTTC GAGTCCTGCA 360

GGTCCCATAT AATTTTGGAG GAATACCCAG TCCGGCTGAA 400

(2) INFORMATION FOR SEQ ID NO: 3568:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3568:

TTAGCCAATC CCCATTCTGG ACGTACCTCA CTCCAATCAC TCGCAAACCG CTGCGCTTCT 60

TCCACTGGAT GATTCACACG ACCAATCGTT GGCAGTTTGT CCAAACGTTC GCGATTCGGT 120

GTTTCAGAAA TCATCGGCAT CGCGTCATTC AATGATTCAT ATGCATCTAA AGCAATAGAA 180

GATAATGTGT CTGGCACATA TACCCATGCC AACGTATCAG TAGACGTATG ATGTTCTGCT 240

ACCGCAAAAA CAGTTGTCTC TGGAnTATAC ACACCTGATT GTTTTAATCC TTGTCTGACA 300

TTTGGACGAT TACATATCAT CGCTAATAAC TTAGCATTnA AAACCGCTTG ATGCGCCACC 360

ACAAGCCCCA CATTTCAAGT GATGGCATGG nTGTGGGTTn 400

(2) INFORMATION FOR SEQ ID NO: 3569:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3569:

CCCCGACCTC ACGGGTATGA ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA 60

GTTTGTAAAT AATATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG 120

CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA CAGTATATCG GGAAGACAGG 180

ATTCGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT ACCAAGCTGA GCTACTTCCC 240

GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC 300

TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA 360

TCGAACCGGT ACGTGATCAC TCACCGCAGA TTTTAAGTCC 400

(2) INFORMATION FOR SEQ ID NO: 3570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3570:

GTTTTTATCC GTTGAGCGAT GGCCnTCCCA TGGGGACCTA CCGGATCACT AAGTCCGTCT 120

TTTCGACCCT GCTTCGACTT GTAGGTCTCG CAGTCAAGCT CCCTTATGCC TTTACACTCT 180

ATGAATGATT TCCAACCATT CTGAGGGAAC CTTTGAGCGC CTCCGTTACC TTTTAGGAGG 240

CGACCGCCCC AGTCAAACTG CCCGCCTGAC ACTGTCTCCC ACCACGATAA GTGGTGCGGG 300

TTAGAAAGCC AACACAGCTA GGGTAGTATC CCACCAGCGC CTCCACGTaA GyTAGCGCTC 360

ACGTTTCAAA GGCTCCTACC TATCCTGTAC AAGCTGTGCC GAATTTCAAT ATCAGGCTAC 420

AGTAAAGCTC CACGGGGTCT TTCCGTCCTG TCGCGGGTAA CCTGCATCTT CACAGGTACT 480

ATGATTTCAC CGAGTCTCTC GTTGAGACAG TGCCCAAATC GTTACGCCTT TCGTGCGGGT 540

CG 542

(2) INFORMATION FOR SEQ ID NO: 3571:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 619 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3571:

ATGCCCGACC ACATGGAGCT TCCAATCCCA TTGCTCTAAC CAATGAGCTA CTGAACCATa 60

aTaAAAATGT AAtGATGGCG GTCTCGACGG GAATCGAACC CGCGATCtCn GCGTGACAGG 120

CAGGCGTGTT AACCCCTACA CTACGAGACC TATAAAATAT TGCGGGAGGC GGATTTGAAC 180

CACCGGACTT CGGGTTATGA GCCCGACGAG CTACCGAACT GCTCCATCCC GCGATAATAA 240

AAAATAATGG CGGAGGAAGA GGGATTCGAA CCCCCGCGGC CCGTTAAGGc CCTGTCGGTT 300

TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC ATTATTATAG GTAAATCGCT 360

ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC TCCTGCGTGA 420

CAGGCAGGCG TGTTAACCGC TACACTACGA GACCATTAGT AAAACGGAGG AAGAGGGATT 480

CGAACCCCCG CGAGCCGTTA AGCCCCTGTC GGTTTTCAAG ACCGATCCCT TCAGCCGGAC 540

TTGGGTATTC CTCCAAAATT ATATGGACCT TGCAGGACTC GAACCTkCGA CCGAACGGTT 600

ATGAGCCGTT AGCTCTAAC 619

(2) INFORMATION FOR SEQ ID NO: 3572:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3572:

GGTGAAGACA TCACGTATCA AGAAGCATGG GCAGATGAAG AATATCGTGA AGACTTAAAA 60

GCAGAATTAA TTGATCAAGC GGTTACTTCA TTGAGCCACA AGATTTATTC AGTGCGATGA 120

TTCGTGAAAT TGAAACGCAA GATTTCGATA TAGAACATCT AGCGACGGCG ATTCGCAAAG 180

TTGAAACATC TACATTAGGT GAAGAAAGTG AAAATGACTT TATCGGGCTG TTCAGCGATA 240

TGGATTTGAG TTCAACGCGA CTAGGTAACA ATGTCAAAGA ACGTACTGCT TTAATCTCTA 300

AAGTCATGGT TAATCTTGAC GACTTACCAT TCGTTCACAG TGACATGGAA ATTGATATGT 360

TAGGTGATGC ATATGAATTC CTAATCGGGC GCTTTGCGGC 400

(2) INFORMATION FOR SEQ ID NO: 3573:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3573:

CAAATCGTAA CTCGCCGGTT CATTCTACAA AAGGCACGCC ATCACCCATT AACGGGCTCT 60

GACTACTTGT AAGCACACGG TTTCAGGTTC TATTTCACTC CCCTTCCGGG GTGCTTTTCA 120

CCTTTCCCTC ACGGTACTGG TTCACTATCG GTCACTAGAG AGTATTTAGC CTTAGGAGAT 180

GGTCCTCCCA GATTCCGACG GAATTTCACG TGCTCCGTCG TACTCAGGAT CCACTCAAGA 240

GAGACAACAT TTTCGACTAC AGGATTATTA CCTTCTTTGA TTCATCTTTC CAGATGATTC 300

GTCTAATGTC GTCCTTTGTA ACTCCGTATA GAGTGTCCTA CAACCCCAAC AAGCAAGCTT 360

GTTGGTTTGG GGCTCTTCCC ATTTCGCTCG CGGCTACTAA 400

(2) INFORMATION FOR SEQ ID NO: 3574:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1051 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3574:

TCCCTCAAAG ATGGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC ATGTGGCAGC 60

TTTACTTACT ATCTAGTTTT GAATGTATAA ATTACATTCA TATGTCTGGT GACTATAGCA 180

AGGAGGTCAC ACCTGTTCCC ATGCCGAACA CAGAAGTTAA GCTCCTTAGC GTCGATGGTA 240

GTCGAACTTA CGTTCCGCTA GAGTAGAACG TTGCCAGGCA TAATATTAAT CCACAGTAGC 300

TCAGTGGTAG AGCTATCGGC TGTTAACCGA TCGGTCGTAG GTTCGAGTCC TACCTGTGGA 360

GCCATGGCTC cTtGGTCAAG CGGTTAAGAC ACCGCCCTTT CACGGCGGTA ACACGGGTTC 420

GAGTCCCGTA GnAGTCATTA TTTTGGAGAA TTAGCTCAGC TGGGAGAGCA TCTGCCTTAC 480

AAGCAGAGGG TCGGCGGTTC GAACCCGTCA TTCTCCACCA TTTTGATTAT TAAATTATAT 540

GAATAAGCTG GAGGGGTAGC GAAgTGGCTA AACGCGGCGG ACTGTAAATC CGCTcCTTCG 600

GGTTCGGCAG TTCGAATCTG CCCCCCTCCA CCATCTATAT ATTGGGCTAT AGCCAAGCGG 660

TAAGGCAACG GACTTTGACT CCGTCACTCG TTGGTTCGAA TCCAGCTAGC CCAGCCATTA 720

GAGCCATTAG CTCAGTTGGT AGAGCATCTG ACTTTTAATC AGAGGGTCAG AGGTTCGAAT 780

CCTCTATGGC TCACTACTTG CACTTTCCAT TTTTGGGAAG TGCTTTTTTT TAGGTTCTcC 840

ACCAAATGTG GTGGGtATAT AATTTAAAGA ACTATTTTTA AAATACAACT TTTAGAGCTT 900

TTATTATTAG GCGGCCAGTC CATTATTGGG CTTGGTTGTC TTCTTTTTTT CTCCTTTGtA 960

CAAGCTGAAA ATCATCATTA TACGTGCtTA AAGTGTGAAA TTTCTGTAAC CAAAAGAATn 1020

CACTTGATTA ATTnnATCTA TATAATGCCT C 1051

(2) INFORMATION FOR SEQ ID NO: 3575:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 476 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3575:

GTGGAGCGCT TAGAAGTGAG AATGCAAGTG TGAgTAGCGA AAGACGGGTG AGAATCCCGT 60

CCACCGATTG ACTAAGGTTT CCAGAGGAAG GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA 120

AGCTGAGGCC GACACGTATG GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT 180

CGTTTTAATC GATGGGGGGA CGCATAGGAT AGGCGAcGTG sCGATTGGAT TGCACGTCTA 240

AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTgATGGGGA 300

GAAGACATTG TGTCTTCGAG TCGTTgATTT CACACTGCCG AGAAAAGCCT CTAGATAGAA 360

AATAgGTGCC CGTaCCGCAA AaCCGACACA GGTAGTCCAA GATGnGAATT CTAAnGTGAA 420

(2) INFORMATION FOR SEQ ID NO: 3576:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3576:

TTTGTTCCTT TTTTAATTTA TATATTTAAA ATACACATAT TCAAGAGCTC GAGATATAAG 60

TCAATGTACT AGGCACACAA TTTAATATTG ACAGTAATTA ACCGAACGAA AATGCGCCCC 120

GGGGCCCCAA CATAGAGAAT TTCGAAAAGA AATTCTACAG ACAATGCAAG TTGGCGGGGC 180

CCCAACATAG AAGCTGGCCA ATAGTTAGCT TTCAATAATG TGCAAGTTGG GGTAAGGGCC 240

CCAACACAGA AGCTGGCCAA TAGTCAGCTT TCAATAATGT GCAAGTTGGG GTAAGGGCCC 300

CAACACAGAG AATTTCGAAA AGAAATTCTA CAGACAATGC AAGTTGGCGG GGCCCCAACA 360

CAGAAGCTGG GCCAATAGTC AGCTTTTCCA ATAATGTGGC 400

(2) INFORMATION FOR SEQ ID NO: 3577:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3577:

TGCATCTTCA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60

TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120

ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAC TAACCACTCC 180

TCTTAACCTT CCAGCACCGG GCAGGCGTCA GCCCTATACA TCACCTTACG GTTTAGCAGA 240

GACCTGTGTT TTTGATAAAC AGTCGCTTGG GCCTATTCAC TGCGGCTCTT CTGGGCGTTA 300

ACCCTAAAGA GCACCCCTTC TCCCGAAGTT ACGGGGTCAT TTTGCCGAGT TCCTTAACGA 360

GAGTTCGCTC GCTCACCTTA GAATTCTCAT CTTGACTAAC 400

(2) INFORMATION FOR SEQ ID NO: 3578:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3578:

TAACTTAACA CGACTTCTTA AGTCATTTAG TTTTAATGTT TGATGTGTTT CTGCTAAACC 60

AATCTCCCAA GGAACACCGG CATGCTGAAT ACTCGTTTTG GGTGAAGCCC TGTACCACCA 120

TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCCAGA TGCAATGGTA 180

CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT CGCATTTTTC 240

AAATCATGTA TCAGTTGCGC TAAATCTTCT ATTGAATAAA TATCATGATG TGGCGGTGGT 300

GAAATCAGAC CGATACCTGG CGTTGGACCC TCTTGTCTTC GCAATCCACG GATATACCTT 360

AGTACCAGGT AATTGGACCA CCTTCACCAG GCTTTGCACC 400

(2) INFORMATION FOR SEQ ID NO: 3579:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3579:

AGCTACACCG CCTTATATAG TTTGTAAATA ATATGGTGGA GACTAGCGGG ATCGAACCGC 60

TGACCTCCTG CGTGCAAAGC AGGCGCTCTC CCAGCTGAGC TAAGCCCCCA TAATAATTAC 120

AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC AAGTGCTCTA 180

CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC CCATAACCTC 240

TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT TTTATTGAAA 300

ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA TTTTAAGTCC 360

TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3580:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3580:

ACGTAAATAA CCATAACGAC GTGCCTCAAA GGCATTTGTA GAGACTTTCG CAAATGCGAT 60

TATGCGATCA GCCATTTCTG CAAGGCCACC GCCACTCGGT AATAAGCCAA CACCTGCTTC 180

AACAAGACCG ATATATGTTT CACTTGCAGC GACAACAATA GGTGAGTAAA GTACAAGCTC 240

ACAGCCACCG CCTAAGGCAC GACCTTGAAC AGCTGTGACT ACTGGTTTCA AACTATACTT 300

CAAACGATTA AAGCTATAAT GTAATTTATC AATTGATTGT GCACGACATC ATCTACAAGA 360

CCGTCTTCCA TGCGCCTTTT TCCATTAAGA AAGGGTTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3581:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3581:

ATGTCATTGT TGGTACGGCT TTTCCAGAAG GATTACAAGG CCAAAACATT GCACGAACGA 60

TTGCATTGCG TGCGGATTAT CTGACACGGT ACCGGGTCAA ACAGTGAATC GCTACTGCTC 120

ATCAGGATTA CAAACCATGC GATTGCAGCC AATCAAATTA TGGCTGGTCA AGGAGATATA 180

CTTGTAGCTG GTGCGTTGAA TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA 240

ACAATCCAAC CTTACAATAT GATGATATAG GTGCGTCATA TCCTATGGGT TTAACTGCTG 300

AAAATGTAGC ATCCCAATTT GACGTATCAC GCGAAGATCA AGATGCTTAT GCTGTCAGAA 360

GTCATCAACG TGCCTATGAC GCACAACGTG ATGGGTCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3582:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3582:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT 60

TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAAGA GACCTTGCGG 120

TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT 180

AAGTTGGCTA CCATCGACGC TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT 240

CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC 300

ATTTTGACGT TTTAGACATA AAAAAAAGAG ACCTTGCGGT 400

(2) INFORMATION FOR SEQ ID NO: 3583:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3583:

AAGCAGGCGC TCTCCCAGCT GAGCTAAGCC CCCAAATAGG TATTAAATTA ATGGTGGGCC 60

TAAGTGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT GCGCTCTAAC CAGCTGAGCT 120

ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAAACTGA ATACAATATG TCACGTTATT 180

CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA AAGGAGGTGA TCCAGCCGCA 240

CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC ATTTGTCCCA CCTTCGACGG 300

CTAGCTCCTA AAAAGGTTAC TCCACCGGCT TCGGGTGTTA CAAACTCTCG TGGTGTGACG 360

GGCGGTGTGT ACAAGACCCG GGAACGTATT TCACCGTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3584:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3584:

ACTTATTTGG CGATATTTTA AGTGATGAAG CTTCAGTGAT TCCTGGTTCA CTTGGTTTAT 60

CACCTTCTGC TAGTTTTAGT AACGATGGTC CAAGATTGTA TGAGCCTATT CATGGATCAG 120

CACCAGATAT TGCAGGTAAA AACGTTGCCA ATCCATTTGG AATGATTCTA TCTTTAGCGA 180

TGTGTTTACG TGAAAGCTTA AATCAACCAG ATGCTGCAGA TGAATTAGAA CAACATATTT 240

ATAGCATGAT TGAACATGGG CAAACGACAG CAGATTTAGG CGGCAAATTG AATACTACTG 300

ATATTTTCGA AATTCTATCT CAAAAATTGA ATCACTAAGG GGGGAGATGT AAATGGGGTC 360

AAACATTATT TGACAAnGTG TGGGACAGAC ATGTGTTATA 400

(2) INFORMATION FOR SEQ ID NO: 3585:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3585:

ACTGATGACA ATTTTATCTG CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC 60

TGTTTTCGAA ACTAATTTTA CCGCGATATC TGCATCTTTA TTCGCATTTT TCAAATCATG 120

TATCAGTTGC GCTAAATCTT CTATTGAATA AATATCATGA TGTGGCGGTG GTGAAATCAG 180

ACCGATACCT GGCGTTGACC CTCTTGTCTT CGCAATCCAC GGATATACCT TAGTACCAGG 240

TAATTGACCA CCTTCACCAG GCTTTGCACC TTGCGCAACT TTAATTTGAA TTTCTTTGGG 300

CATGTTGTAA ATAATCACTA GTTACACCAA AACGCCCAGA AGCAACTTGT TTAATCGCAC 360

TTACTTTGGT GGCTTCCATC AACTTGTACT TCATAACGGT 400

(2) INFORMATION FOR SEQ ID NO: 3586:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3586:

TACAAGTATT ACCATTATCT CnAGAGGATT CTAGATAAGG GGCATGGATC ATTTGTCTTC 60

TTATGAATTT GAGCCAGATA AAGAATCTAT CTTAAGTGTA ATCTTGACCT CAATATGTTG 120

AGAGTTTGAT TTACGGAACA ATATTAGACG CAAAAGCAAG TGAGCATGCA ACACGTATGA 180

CTGCGATGAA AAATGCCACT GATAATGCAA CTGAACTTAT TGATGACTTA TCATTAGAAT 240

ATAACAGAGC GAGACAAGCA GAAATTACGC AACAAATTAC TGAAATTGTT GGTGGTTCCG 300

CAGCGCTTGA ATAATATTTA AnGGAGGAAA ATAGCATGGG AATTGGCCGT GTACTCAAGT 360

TATGGGTCCT GTAATTGATG TTCGATTTGA ACATAACGAG 400

(2) INFORMATION FOR SEQ ID NO: 3587:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3587:

AGGATTCGAA CCTGCGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120

CCCGTATAAT TAACGCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180

CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATGGTG CCGAGGACCG 240

GAATCGAACC GGTACGTGAT CACTCACCGC AGGATTTTAA GTCCTGTGCG TCTGCCAGTT 300

CCGCCACCCC GGCACTATAA AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC 360

CTTGGCAAGG TTGTATTCTA CCGCTGAACT ACTTCTGCAT 400

(2) INFORMATION FOR SEQ ID NO: 3588:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3588:

TACTATTGAC ATGTGTGAAC CCTATGTCCG ATTATTTCGC GACCTATTTC CTAATGCAGC 60

TATTATTTTT GACAGATTCC ATATCGTTCA ACATTTAAAT AGAGAACTTA ATAAGTATCG 120

TGTACAAGTT ATGAATGAAT ACCGTAATAA AAAAGGACCT GATTATACAA TTTTTAAGAA 180

TAACTGGAAA GTCCTATTGA TGGATACTAG TAAAACCATA TTTAGTAAAT ACAGATGGAA 240

TAAATCTTTT AAGGGCTTAT AAACGCTCAT CTGACATTGT AGAATTCATG CTTTCAAAAG 300

ACGATATACT ACGACACTCC TACGAACTTG TCCAGGGATT ACGAAAAGAC CTAAGGGTAT 360

GTAATTGGGC CTAAATTTAT TAATCGTTTA AATTCCGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3589:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3589:

AGAGCGAACG GACGAGAAGC TTGCTTCTCT GATGTTAGCn GCGGACGGGT GAGTAACACG 60

TGGATAACCT ACCTATAAGA CTGGGATAAC TTCGGGAAAC CGGAGCTAAT ACCGGATAAT 120

ATTTTGAACC GCATGGTTCA AAAGTGAAAG ACGGTCTTGC TGTCACTTAT AGATGGATCC 180

GCGCTGCATT AGCTAGTTGG TAAGGTAACG GCTTACCAAG GCAACGATGC ATAGCCGACC 240

AGTAGGGAAT CTTCCGCAAT GGGCGAAAGC TGACGGAGCA ACGnCGCGTG AGTGATGAAG 360

GTCTTCGGAT CGTAAAACTC TGTTATTAGG GAAGAACATA 400

(2) INFORMATION FOR SEQ ID NO: 3590:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 509 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3590:

GTTAgGAGAG CGTTCTAAGG GCGTTGAAGC ATGATCGTAA GGACATGTGG AGCGCTTAGA 60

AGTGAGAATG CCGGTGTGAG TAGCGAAAGA CGGGTGAGAA TCCCtCCACC GATTGACTAA 120

GGTTTCCAGA GGAAGGCTCG TCCGCTCTGG GTTAGTCGGG TCCTAAGCTG AGGCCGACAg 180

gTAaGGCGAT GGATAACAGG TTGATATTCC TGTACCACCT ATAATCGTTT TaATCGATGG 240

GGGGACGCAT AGGATAGGCG AAcGTGcGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG 300

TATTAGGCAA ATCCGGTACT CGTTaAGGCT GAGCTGTGAT GGGGAGAAGA CATTGwGTCT 360

TCGAGTCGTT GATTTCACAC TGCCGAGAAA AgCCTCTAGA TAGAAAATAG GTGCCCGTAC 420

CGCAAACCGA CACAGGTAAT CCAAGATGAG AATTCTAAGG TGAGCGAGCG AACTCTCGTT 480

AAGGAACTCG GCAAAATGAC CCCGTAACT 509

(2) INFORMATION FOR SEQ ID NO: 3591:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3591:

ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA 60

TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120

TCGAACCGCT GACCTCCTGC GTGCAAAGCA GGCGCTCTCC CAGCTGAGCT AAGCCCCCAA 180

ATAGGTATTA AATTAATGGT GGGCCTAAGT GGACTCGAAC CACCGACCTC ACGCTTATCA 240

GGCGTGCGCT CTAACCAGCT GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAAA 300

ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 360

(2) INFORMATION FOR SEQ ID NO: 3592:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3592:

TGGGnAACGC AACATCCTTT TCCAACTTAA CATATATTTT GGGACCTTaG CTGGTGGTCT 60

GGGCTGTTTC CCTTTCGAAC ACGGACCTTA TCACCCATGT TCTGACTCCC aAGTTAAATT 120

AATTGGCATT CGGAGTTTGT CTGAATTCGG TAACCCGAGA GGGGCCCCTC GTCCAAACAG 180

TGCTCTACCT CCAATAATCA TCACTTGAGG CTAGCCCTAA AGCTATTTCG GAGAGAACCA 240

GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA GTTCATCCGC TCACTTTTCA 300

ACGTAAgTCG GTTCGGTCCt CCATTcAGTG TTACCTGAAC TTCAACCTGa CCAAGGGTAG 360

ATCACCTGGT TTCcGsGTsT ACGACCAAAT AsTAAACGCC CTATTCAGAC TCGCTTTCGC 420

TAnGGCTCCA CATTACTGGn 440

(2) INFORMATION FOR SEQ ID NO: 3593:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3593:

TAAACGAACC AATTTTATTT GGTGCACCAC TAGTATTGAA TCCTGTGTTC TTTATTCCAT 60

TTGTATTAGC ACCAATTGTT AACGTATGGA TTTTCAAACT TTTCGTTGAA GTGTTAGGAA 120

TGAATAGTTT TAGTGTGAAT TTACCTTGGA CAACACCAGG TCCATTGGGC ATTATCATGG 180

GTACAGGTTT TGGTTTATGG TCATTCGTAC TAGCTATTAC TTTGATTGTT GTAGATATTA 240

TTATnTACTA CCCATTCCTA AAAGTTTATG ATAGTGAAAT TCTTGATGAA GAAGAAGGAC 300

GTAAAGAAAG TAATTCAGAT TTAAAAGAAA AAGTTGCAGC AAACCTTTGA TACGAAAAAA 360

GCTGATTCAA TTTTAGCGGC AAGTGGTGTA TCAGACGATG 400

(2) INFORMATION FOR SEQ ID NO: 3594:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 409 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3594:

AAGGGAATCG AATTTTCTTT CTCTTCCTCC GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60

TGCCTTCTGa TATGCTATGT ATTCACATAT CGATAACATG ACATAACTCA TGCTGGGTTT 120

CCCCATTCGG AAATCTCTGG ATCAAAGCTT aCTaCAGCTC CCCAAAGCAT ATCGTCGTTA 180

GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240

TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT 300

TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAAATAA TTTAACTCAT TGTCTGCTAA 360

ACGTTTTCTT TTATAAAAAG ATTTAAAcGC GTTAtTAATC CTCTCGCTC 409

(2) INFORMATION FOR SEQ ID NO: 3595:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3595:

AATATAAGCC CTGGATCATA CATGACCTGT ATTTGGGCAA TCCCTTCTGC TACATCTTCT 60

GCCCACTCAT TCAATATTTG TTTTGCAATA TCATCACCTT CTTCAGCTGC TTCAAACAAT 120

ACTGGCACAT GTGTGCTTCT CGTAAATCCT CCGGCAATCA TGCGCTTTTT CAATGCACTC 180

GTTGCAGCAC GTTGCTCAAA CGTTGTATTT TCAGTTGGAC GATACAATAA ATACCCAACT 240

TCATTTGCCT TATGAAGCTC ACCATTATCA ATATGACCTT GGATTATTCT TGTACGCACC 300

CCCAATGGCC TGGTACCAAG CGTCCATACA AAAGATCCGT TCTGGCTTGG ATATTGGATG 360

GTAATTTCCA ATTCGGCCTA GTTAATGGCA GCGGTTTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3596:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 596 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3596:

CTGCCGAACC CGAAGAGCGG ATTTACAGTC CGCCGCGTTT AGCCACTTCG CTACCCTCCA 120

GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG ACGGGTTCGA CCGCCGACCC 180

TCTGCTTGTA AGGCAGATGC TCTCCCAGCT GaGCTAATTC TCCAAAATAA TGACTCCTAC 240

GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGtGTCT TAACCGCTTG ACCAAGGAGC 300

CATGGCTCCA CaGGTAGGAC TCGAACCTAC GACCGATCGG TTAACAGCCG ATAGCTCTAC 360

CACTGAGCTA CTGTGGaTTA ATATTATGCC TGGcAACGTT CTACTCTAGC GGAACGTAAG 420

TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 480

CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA 540

AGTAAAAGTG ATTTTGCTTC GCAAAACATT TATTTTGATT AAGTCTTCGA TCGATT 596

(2) INFORMATION FOR SEQ ID NO: 3597:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3597:

TCATCTTGAG GGGGGCTTCA TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 60

TACCCAGCTA TGCCGTTGGC ACGACAACTG GTACACCAGA GGTATGTCCA TCCCGGTCCT 120

CTCGTACTAA GGACAGCTCC TCTCAAATTT CCTACGCCCA CGACGGATAG GGACCGAACT 180

GTCTCACGAC GTTCTGAACC CAGCTCGCGT ACCGCTTTAA TGGGCGAACA GCCCAACCCT 240

TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT 300

CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG 360

CGATGGCCCT TCCATGCGGA ACCACCGGAT CAATAAAGTC 400

(2) INFORMATION FOR SEQ ID NO: 3598:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3598:

AACCAACGGC AGCAACTACA TGACCTAATT CTTGTGCTGA CTCTACATTT AGTAGCTCTA 60

CACTTCAATT GTACCAATCA ATCGTTGACG ATCTTGATCG TAACGCCATG TAGCAATACC 180

ACGATACTGT CCGTCACGAC TCGCGTATGC ATGCGCACTT GCTTCTGCAC CACGCGTATC 240

ATTTCCTGTT GCTAAAACAA CAGCATGTAT GCCATTCATA ACACCTTTAT TATGTGTTGC 300

TGCACGATGA ATATCTACTT GGGCCAATAC AGAAGCACGT TCCATcGTTT GcaACCTCTT 360

CTCCAGTTCT CTCGCCCCTT GGCTAAATCT TTAACAT 397

(2) INFORMATION FOR SEQ ID NO: 3599:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3599:

AACCCTTGGG ACCGACTACA GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT 60

CCCCGTCGAT GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCGGGGTA GCTTTTATCC 120

GTTGAGCGAT GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG 180

CTCGACTTGT AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTTC 240

CAACCATTCT GAGGGAACCT TTGAGCGCCT CCGTTACCTT TTAGGAGGCG ACCGCCCCAG 300

TCAAACTGCC CGCCTGACAC TGTCTCCCAC CACGATAAGT GTGCGGGTTA GAAAGCCAAC 360

ACAGCTAGGG TAGTATCCCA CCAGCGCCTC CAACGTAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3600:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3600:

ATCTGAATCT GAGTCGTTGT CTGAGTCCGA ATCGCTATCT GAATCTGAGT CGCTATCTGA 60

GTCTGAGTCG CTATCTGAAT CTGAGTCGCT GTCTGAATCT GAATCACTGT CTGAGTCTGA 120

GTCGCTGTCT GAGTCTGAAT CGCTGTCAGA ATCTGAGTCG CTATCTGAGT CTGAATCTGA 180

ATCACTGTCT GAGTCCGAAT CGCTATCTGA ATCTGAATCG CTATCTGAGT CTGAGTCGCT 240

ATCCGAATCT GAGTCGCTAT CTGAGTCTGA GTCGCTATCC GAGTCTGAAT CGCTGTCTGA 300

GGTCTGGAAT CTGAnTCGCT AACTGAAATC TGAGTCGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3601:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3601:

ATTTAATACC TATTTGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 60

GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTATTTGTA CATTGAAAAC TAGATAAGTA 120

AGTAAAATAT AGATTTTACC AAGCAAAACC GAGTGAATAA AGAGTTTTAA ATAAGCTTGA 180

ATTCATAAGA AATAATCGCT AGTGTTCGAA AGAACATCCA CAAGATTAAT AACGCGTTTA 240

AATCTTTTTA TAAAAGAACG TAACTTCATG TTAACGTTTG ACTTATAAAA ATGGTGGAAA 300

CATAGGTTAA GTTATTAAGG GCGCACGGTG GGATGCCTTG GCACTAGAAG CCGATGAAGG 360

GnCGTTACTA ACGACGATAT GCTTTGGGGA GCTGTAAGTA 400

(2) INFORMATION FOR SEQ ID NO: 3602:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3602:

GCTGTCTGAG TCGGAATCAC TGTnGGAGTC AGAATCGCTG TCTGAGTCGG AATCACTGTC 60

GGAATCTGAA TCGCTATCTG AATCTGAATC GCTATCTGAA TCCGAGTCAC TGTCTGAGTC 120

AGAATCGnTA TCTGAATCTG AGTCACTGTC GGAATCTGAG TCACTGTCTG AGTCAGAATC 180

GCTATCTGAA TCCGAGTCAT TGTCTGAGTC GGAATCGCTC GCTGAGTCGG AATCGCTTGC 240

TGAATCTGAA TCACTCGCTG AGTCTGAATC ACTTGCTGAA TCTGAATCAC TCGCTGAATC 300

TGAACCACTA TCTGATGTAG GAATCACTAC CCGAATCTGA AnCGCTATCT GAATAAGAAT 360

CGCTGCCAGA TCTGAACCTG GGGTCAGAAT CTGAAT 396

(2) INFORMATION FOR SEQ ID NO: 3603:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 529 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3603:

TTTCTTATCT GTAATTTTAT CGTAAGATTT TTTCGCAATG AGATTTGGAT CGTnTTTGTC 60

CACTACAATA TCTAATAGTT TTACTTTAAG TCCAGCATTC ACAAAAAGTG CTGCCAGTTG 120

AGCGCCCATT GTGCCTGCGC CAAGAACGGT TACTTTATTA ATTGTCATAG TGATTCCTCC 180

AATTTAGTTG AGGATAAGAT AACCATTAAG ATAATTGGAA TAACGTTGCT ATTTTATAAA 240

ATTAATTAAG TATCTTTGAC AGTCATCTTA GCCTCTTATT TAAGGaAAAA GCTTTATGCT 300

TAAAATAAGT CTTTTTTAGT GAAATTAATG CATCTCATAT AATTATTTGC TATTTATACG 360

AAAGCmGaAT CTCCAGTCaA AGCGCGTCCA ATTACTAAGG CATTAATTTC ATGTGTACCT 420

TCGTACGTGT AAATCGCTTC TGCATCAGAG AAGAAACGTG CAATATCATA ATCGTCAGCT 480

AGTATGCCAT TACCACCTGT AATACCGCGG CCCATAGCTA CTnTCTCAC 529

(2) INFORMATION FOR SEQ ID NO: 3604:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3604:

CACAAGATAA GCATTGTAGA TGTGGATGCT TTAACTGGGC AAGCGATTGG TCGTCCTAAA 60

ACAGGTACAT ATGCGCTATC TGACCTAGTC GGTTTAGATA TTGCAGTGTC TGTAATTAAA 120

GGCATGCAAC AAGTACCTGA AGAAACACCT TATTTTCATG ATGTCAAAAT TGTAAATACG 180

TTGTTTGACA ATGGCGCACT CGGACGTAAA ACGAAACAAG GATTTTACAA AAAGGATAAA 240

GAAACTAAAG CTCGACTTGT TTACGATGTT GAAAAACAAG ATTATGTACC TGTATCGCAA 300

CCACAATTAC CAATTTTAAA TGAATTTAAT AAAGACTTAG TGCaTAACCT TGATACCATA 360

TTCCAATGCG CAAGACGAGC GGGGACTATT TTTATGGGG 399

(2) INFORMATION FOR SEQ ID NO: 3605:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3605:

ATCACTTGAG GCTAGCCCTA AAGCTATTTC GGAGAGAACC AGCTATCTCC AGGTTCGATT 60

GGAATTTCTC CGCTACCCTC AGTTCATCCG CTCACTTTTC AACGTAATCG GTTCGGTCCT 120

CCATTCAGTG TTACCTGAAC TTCAACCTGA CCAAGGGTAG ATCACCTGGT TTCGGGTCTA 180

CGACCAAATA CTAAACGCCC TATTCAGACT CGCTTTCGCT ACGGCTCCAC ATTTACTGCT 240

TAACCTTGCA TCAAATCGTA ACTCGCCGGT TCATTCTACA AAAGGCACGC CATCACCCAT 300

TAACGGGCTC TGGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTCAC TCCCCTTCCG 360

GGGTGGCTTT TCACCTTTCC CTCACGGTAA TGGGTTCACT 400

(2) INFORMATION FOR SEQ ID NO: 3606:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3606:

AAATCCTGCG GTGAGTGATC ACTAACCCGG TTCGATTCCG GTCCTCGGCA CCATTTTCAA 60

TAAAAACATA TGCGCCCGTA GCTCAATTGG ATAGAGCGTT TGACTACGGA TCAAGAGGTT 120

ATGGGTTCGA CTCCTATCGG GCGCGTTAAT TATACGGGAA GTAGCTCAGC TTGGTAGAGC 180

ACTTGGTTTG GGACCAAGGG GTCGCAGGTT CGAATCCTGT CTTCCCGATA TACTGTAATT 240

ATTATGGGGG CTTAGCTCAG CTGGGGAGAG CGCCTGCTTT GCACGCAGGA GGTCAGCGGT 300

TCGATCCCGC TAGTCTCCAC CATATTATTT ACAAACTATA TAAGGCGGTG TAGCTCAGCT 360

GGCTAGAGCG TACGGTTCAT ACCCGTGAGG TCGGGGGTTC 400

(2) INFORMATION FOR SEQ ID NO: 3607:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3607:

GGGTGTGCTT CTGATATGCT ATGTATTCAC ATATCGATAA CATGACATAA CTCATGCTGG 60

GTTTCCCATT CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 120

TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA CATGAAGTTA CGTTCTTTTA 240

TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTTCT TTCGAACACT AGCGATTATT 300

TCTTATGAAT TCAAGCTTAT TTAAAACTCT TTATTCACTC GGTTTTGCTT GGTAAAATCT 360

ATATTTTACT TACTTATCTA GTTTnCAATG TACAAATAAT 400

(2) INFORMATION FOR SEQ ID NO: 3608:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3608:

TAGTTTTCAA TGTACAAATA ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 60

TGCAAAnAGC CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA TTAATGGTGG 120

GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT AACCAGCTGA 180

GCTATAGGCC CATTAATTTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240

ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300

GCACCTTCCG ATACGGCTAC CTTGTTACGA CTTCACCCCA ATCATTTGTC CCACCTTCGA 360

CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTCGGGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3609:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3609:

AGGGCACTCT TACTGGGCGT GTTAAATTAC TAAnTTCAAT CAGCAGAAGA ACTAGGACAT 60

GGCGCTTTTA AAATTATTGA AACACATGCA TTAAAAGATG TACAAGCAGT ATTGGGTTTT 120

CATAATGACC CATCGCGTTC GGTAGGTACA TTTGCAATCA AAACAGGGGC AATTACATCA 180

GCAGTAGATC GTTTTGAGTT TCATATTAAA GGCGTGGGTG GTCATGCTGC AAACCAGAAC 240

AATGCAACGA TCCAGTTATT GTGTTGGCGC AATTGATTAA TAGTATTCAA TCCATAGTTA 300

GTAGAAATCT ATCTGCGTTT GATGAAGCGG TAGTAACAAT TGGACAAATA TCATGTGGTA 360

(2) INFORMATION FOR SEQ ID NO: 3610:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3610:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60

GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120

CCCATTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180

GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240

TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT 300

TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAAATGA ATTTAACTCA TTGTCTGCTA 360

AACGTTTTGC TTTTATAAAA AGATTTAAAC GCGTTGATTT 400

(2) INFORMATION FOR SEQ ID NO: 3611:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3611:

GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCG AACCGCCGAC 60

CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 120

GGCAACGTTC TACTCTAGCG GAAnTAAGTT GnACTACCAT CGACGCTAAG GAGCTTAACT 180

TCTGTGTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240

TAATTTATAC ATTCAAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA 300

TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC ACATGTCACC ATGCTTCCAC 360

CTCGAACCTA TTAACCTCAT CATCTTTGAG GGATCTTAAT 400

(2) INFORMATION FOR SEQ ID NO: 3612:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3612:

ACCCAGCTCG CGTACCGCTT TAATGGGCGA ACAGCAATCC CTTGGGACCG ACTACAGCCC 60

CAGGATGCGA TGAGCCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120

GAGATAAGCC TGTTATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC CTTCCATGCG 180

GAACCACCGG ATCACTAAGT CCGTCTTTCG ACCCTGCTCG ACTTGTAGGT CTCGCAGTCA 240

AGCTCCCTTA TGCCTTTACA CTCTATGAAT GATTTCCAAC CATTCTGAGG GAACCTTTGA 300

GnGCCTCCGT TACCTTTTAG GAGGCGACCG CCCCAGTCAA ACTGCCCGCC TGACACTGTC 360

TCCCACCACG ATAAGTGTnC GGGGGTTAGA AAGCCAACAC 400

(2) INFORMATION FOR SEQ ID NO: 3613:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3613:

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCaA 60

GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 120

CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 180

TTTAAAATAA TTTAACTCAT TGTCTGCTAA ACGTTTTCTT TTATAAAAAG ATTTAAACGC 240

GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 300

TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATTTT ACTTACTTAT 360

CTAGTTTTCA ATGTACAAAT AATGGTGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC 420

TTATCAGGCG TGCGCTCTAA CCAGCTGAGC TATAGGcCCA TTTTTTTGaA TGTTAAATAA 480

ACATTCA 487

(2) INFORMATION FOR SEQ ID NO: 3614:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG 60

AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG 120

CTAAGCCCCC ATAATAATTA CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT 180

GGTCCCAAAC CAAGTGnTCT ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT 240

AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC TCTATnCAAT TGAGCTACGG 300

GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA TCGAACCGGT ACGGTGATCA 360

CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GCnAGTTCCG 400

(2) INFORMATION FOR SEQ ID NO: 3615:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3615:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC 60

AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTTCTTTG TGTTTACTTT TTATTTTGAC 120

GTTTTAGACA TAAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCTACTCTA 180

GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT 240

TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 300

TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT 360

TTACTTTTTA TTTTGACGTT TAGGCATAAA AAAAAGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 3616:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3616:

TnGTGTCTTT CGAACACTAG CGATTATTTC TTATGAATTC AAGCTTATTT AAAACTCTTT 60

ATTCACTCGG TTTTGCTTGG kAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA 120

CAATTTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC TTTAACCAAA AAATATTTGA 180

AAGATGTTCC GAATATATCC TTAGAAAGGA GGnGATCCAG CCGCACCTTC CGATACGGCT 300

ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 360

TTACTCCACC GGCTTCGGGT GTTACAAACT CTCGTnGGTG TGACGGGCGG TGTGTACAAG 420

(2) INFORMATION FOR SEQ ID NO: 3617:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3617:

CACTAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 60

GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAT TTCTTTTTAG 120

TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT TAAATAAACA 180

TTCAAAACTG AATACAATAT GTCACATTAT TCCGCATCTT CTGAAGAAGA TGTTCCGAAT 240

ATATCCTTAG AAAGGAGGTG ATCCAGCCGC ACCTTCCGAT ACGGCTACCT TGTTACGACT 300

TCAnCCCAAT CATTTGTCCC ACCTTCGACG GCTAGCTCCT AAAAGGTTAC TCCACCGGCT 360

TCGGGTGTTA CAAACTCTCG TGGTGTGACG GGCGGTGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3618:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3618:

GATATACGCT ATGGCTGGAG CAGTGTGGCC AAATGGCGGA AGACAAACGT TTAATGCGAT 60

ATACTTAGCG CAAAATATTG GTGTGGCTGT CGGTGCTGCA ATGGGCGGCT TTGTCGCAGA 120

ATTTAGCTTT AACTATATCT TTTTAGCCAA TCTTATTATG TATGTTGTGT TTGCGCTTGT 180

CCGGTTAACn AATTTAATAT TGAAATTAAT GCGAAAGTTA AATATCCAAC TCATTTAGAT 240

ATTACTGGTA AAAAGAATAA AGCAAGATTT ATTTCATTAG TACTAATTTG TGCAATGTTT 300

GCAATTTGTT GGGTTGCATA TATTCAATGG GGAGTCTACA ATCGCTTCAT TTTACACAAT 360

CTATTAATAT TTCAATGGGC ACAATATAGT GTTTTATGGG 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3619:

TCGCACGCCT TCGCCTATCC TACTGCGTCC CCCCATCGAT TAAAACGATT ATAGGTGGTA 60

CAGGnAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCG GCCTCAGCTT AGGACCCGAC 120

TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC 180

ACCCGTCTTT CGCTACTCAC ACCGGCATTC TCACTTCTAA GCGCTCCACA TGTCCTTACG 240

ATCATGCTTC AACGCCCTTA GAACGCTCTC CTACCATTGT CCAAAGGAAA TCCACAGCTT 300

CGGTAATATG TTTAGCCCCG GTACATTTTC GGCGCAGTGT CACTCGACTA GTGAGCTATT 360

ACGCACTCTT TAAATGATGG CTGCTTCTAA GCCAACATCC 400

(2) INFORMATION FOR SEQ ID NO: 3620:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3620:

TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA 60

CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTTGA 120

GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA CTTATCCCGT CCACACATAG CTACCCAGCT 180

ATGCCGTTGG CACGACAACT GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA 240

AGGACAGCTC CTCTCAAATT TCCTACGCCC ACGACGGATA GGGACCGAAC TGTCTCACGA 300

CGTTCTGAAC CCAGCTCGCG TACCGCTTTA ATGGGCGAAC AGCCCAACCC TTGGGACCGA 360

CTACAGnCCC AAGGATGCGA TGAGCCGACA TCGAGGTGCC 400

(2) INFORMATION FOR SEQ ID NO: 3621:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3621:

CCACACCCGc AAATGGTGag CCATAGcAGG ATTCGgaACC TCTGcACCCT CTGATTAAAA 60

GTCAGcATGC TCTACCAACT GaGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 120

ACCCCCAACC TACTGATTAC AAGTCAGTTG CTCTACCAAT TGAGCTAGGC CGGCAATATG 180

TAAGAATAAA TGGTGGAGAA TGACGGGTTC GAACCGCCGA CCCTCTGCTT GTAAGGCAGA 240

TGCTCTCCCA GCTGAGCTAA TTCTCCGATT TAAAACTGCC TGGCAACGTT CTACTCTAGC 300

GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA 360

ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTAATTTA TACATTCAAA 420

ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGT 475

(2) INFORMATION FOR SEQ ID NO: 3622:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3622:

TGGACGAAAC TTTATATCGA TCAATTTCTA TCGAGTTGGA CAATGCCGAA GCGTGACAAA 60

AGTTTTTACC ATGCATGGTT GCATTTAGCG CAACATGACC ATAGTTTTAC TAAAGCACAG 120

CGCnCAAGTG ATTAAAGGCT TACCCAATGA TCCTGAAATG ACGATAGAGT CAGTATTAAC 180

TCATTTTTCA ATAGATCAGG AAGACTACCA AGCTTATGTT GAAGGACATC TTTTGGCGTT 240

ACCGGGTTGG GCAGGTATGT TGTATTACCG TTCACAACAG CATCACTTTG AACAACATTT 300

GTTAACGGAT TATTTGGCAA TTCGGTTAGT TGTCGAACAA TTGCTAGTTG GTGGATGAGT 360

TTTAAGTCAG TCGCTAAAGA TTGTGGAAAG TAAGATCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3623:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3623:

TAGATGCTTT CAsACTTATC CCGTCCACAC ATAGCTACCC AGCTATGCCG TTGGACGACA 60

ATTTCCTACG CCCACGACGG ATAGGGACCG AACTGTCTCA CGACGTTCTG AACCCAGCTC 180

GCGTACCGCT TTAATGGGCG AACAGCCAAC CCTTGGGACC GACTACAGCC CCAGGATGCG 240

ATGACCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG GAGATAAGCC 300

TGTTATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC TTCCATGCGG GAACACCGGA 360

TCACTAAGTC CGTCTTTCGA CCCTGCTCGA CTTTGTAGGn 400

(2) INFORMATION FOR SEQ ID NO: 3624:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3624:

GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCG AACCGCCGAC 60

CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 120

GGCAACGTTC TACTCTAGCG GAAnTAAGTn GnACTACCAT CGACGCTAAG GAGCTTAACT 180

TCTGTGTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240

TAATTTATAC ATTCAAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAACATTTAT 300

TTTGATTAAG TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC 360

TCGAACCTAT TAACCTCATC ATCTTTGAGG GGATCTTATA 400

(2) INFORMATION FOR SEQ ID NO: 3625:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3625:

TTAAAGAACG CTAATAACTG ATCGTAACCA CTATATATAT TGTTGTGACC TCTAACAGCA 60

TAATGTCTAA ATGTTTGTGG GATATATTGA AGCAATCCTT TTGCTGGATT GCCCTGTAAA 120

ACGTTGATGT CTCTAAGCGA ACTAGATTGA GTTATACCTG CATTTCCTCC TGATTCGTGT 180

TGAATCAAGC TAATGATATT TCCTACGTCA GCCGAAGTAA CATTAACACC CATTCGTTTT 240

GCTGCACGAC GTATATCGCC TGCCCAAGCA GATGCAGCCT TATTAACACC TGAACCACTT 300

CCTGGATGCG ACCCTTGCAT CAnTTGGGAA ATGTAnGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3626:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3626:

GATTGTGGTT CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCCTTATT ATTAATGGGC 60

TATAGCCAAG CGGTAAGGCA ACGGACTTTG ACTCCGTCAC TCGTTGGTTC GAATCCAGCT 120

AGCCCAGTTA TTGGCGGCAT AGCAAGTGGT AAGGCAGAGG TCTGCAAAAC CTTTATCACC 180

GGTTCAAATC CGGTTGCCGC CTCCAGGTTT ATGCGGGAGT AGTTCAACTT TTAGAACACG 240

TTCCTTCCCG GAAGAGGTAT AGGTGCAAAT CCTATCTTCC GCTCCATAAT TTAATAATAA 300

TGCGGGAGTA TTTCAACTCT TAGAATACAT TCCTTCCTGG AATgAGGTAT AGGTGTAAAT 360

CCTATCTTCC GCTCCATAAT TTAATATTTG cGGGAGTAGT TCAACTTTTA GAAACAGCTC 420

CTTCCCGGAA CCGAGGTATA GGTGTAAATC CTATCTTCCG C 461

(2) INFORMATION FOR SEQ ID NO: 3627:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3627:

TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTTGCCTG GCAACGTTCT ACTCTAGCGG 60

AACGTAAGTT GGCTnAnATC GACGCTAAGA ACCTTTCTTG ACTTGTGACA ATCGCTTGCT 120

TCTTTCCTCT TCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGCGCTCTT 180

TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT TTGTGTTTGC 240

TTTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA TGCGGCTCAT 300

CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC GACTACCATC 360

GACGCTAAGG GAGCTTAACT TCTGTGTnCG GGCATGGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3628:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3628:

ATGCTTTCAG CACTTATCCC GTCCACACAT AGCTACCCAC CTATGCCGTT GGCACGACAA 60

CTGGGTACAC CAGAGGTATG TCCATCCCGG TCCTCTCGTA CTAAGGACAG CTCCTCTCAA 120

ATTTCCTACG ACCCACGACG GATAGGGACC GAACTGTCTC ACGACGTTCT GAACCCAGCT 180

CGCGTACCGC TTTAATGGGC GAACAGCCCA ACCCTTGGGA CCGACTACAG CCCCAGGATG 240

CGATGAGCCG ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAACTCTTG GGGGAGATAA 300

GCCTGTTATC CCCGGGGTAG CTTTTATCCG nTGAGCGATG GGCCTTCCAT GCGGnACCAC 360

CGGnTTACTA AGTCCGTCTT TCGAnCCTGC TCGACTTGTA 400

(2) INFORMATION FOR SEQ ID NO: 3629:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3629:

TTTATAAATA TCCCAGTCTG AACGCGATTC CCATAACGGA TCAATGGCAG GATTGAAAGG 60

ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGT TTTTCATACC AAGTCGCTGC 120

CGGCAAAACA ATGTCAGAAT ATAACGGTGT TGCCGTCATT CTGAAGTCTA AAGAGACCAC 180

TAAATCTAAC TTACCTGTTG TTTCTTCACG CCACGTAATT TCTTCTGGCT TTTCATCTTC 240

ATTTGGTGTA GCTAATAACC CTGATTTTGT GCCAAGTAAA TGCTTCATAA AGTATTCTTG 300

ACCTTTTGCA GAACTTGAAA TTAAGTTTGA ACGCCATATA AATAATGATT TTGGATGATT 360

CTnTTTCAAA TCAGGATCTT CTATTGCAAA TGGGGTTTGT 400

(2) INFORMATION FOR SEQ ID NO: 3630:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 589 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTTAAGTTGT nGATTTAAAA TATTAATAAA GTGTAAATTT GACTATTGAn ATTCkrACAa 60

ATACATATTA AAATAATATT TGTTGAATTA ATTGAGTTAG GAAATTTATT TTTTAGAAAT 120

AAAATAATTA AAAATAATTC TTGACTTACA AAAACTTACG AGTTATAATT AAATCTTGTA 180

AGTGACAAAC GAACATTGAA AACTGAATGA CAATATGTCA ACGTTAATTC CAAAAACGTA 240

ACTATAAGTT ACAAACATTA TTTAGTATTT ATGAGCTAAT CAAACATCAT AATTTTTATG 300

GAGAGTTTGA TCCTGGCTCA GGATGAACGC TGGCGGCGTG CCTAATACAT GCAAGTCGAG 360

CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 420

TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATrATATTT 480

TGAACCGCAT GGTTCAAAAG TGAAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 540

TGCATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATA 589

(2) INFORMATION FOR SEQ ID NO: 3631:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3631:

CCAACTGAGC TAATGGCTCT TCCATGGTGC CGGCCAGAGG ACTTGAACCC CCAACCTACT 60

GATTACAAGT CAGTTGCTCT ACCAATTGAG CTAGGCCGGC AATATGTAAG AATAAATGGT 120

GGAGAATGAC GGGTTCGAAC CGCCGACCCT CTGCTTGTAA GGCAGATGCT CTCCCAGCTG 180

AGCTAATTCT CCGATTTAAA ACTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTCG 240

ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCGGC ATGGGAACAG GTGTGACCTC 300

CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT TCAAAACTAG ATAGTAAGTA 360

AAAGTGATTT GCTTCGCAAA ACATTTATTT TGATTAAGTC 400

(2) INFORMATION FOR SEQ ID NO: 3632:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3632:

TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 120

AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACACTA GCGATTATTT CTTATGAATT 180

CAAGCTTATT TAAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA TATnTTACTT 240

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCGCTGACC 300

TCCTGGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAn GCCCCCAnAT AGGTATTAAA 360

TTAATGGGGG GGCCTAAGTG GACTCGAACC ACCGACCTCA 400

(2) INFORMATION FOR SEQ ID NO: 3633:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3633:

ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT TTAGTATTTA 60

TGAGCTAATC AAACATCATA ATTTTTATGG AGAGTTTGAT CCTGGCTCAG GATGAACGCT 120

GGCGGCGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT TCTCTGATGT 180

TAGCGGCGGA CGGGTGAGTA ACACGTGGAT AACCTACCTA TAAGACTGGG ATAACTTCGG 240

GAAACCGGAG CTAATACCGG ATAATATTTT GAACCGCATG GTTCAAAAGT GAAAGACGGT 300

CTTGCTGTCA CTTATAGATG GATCCGCGCT GCATTAGCTA GTTGGTAAGG TAACGGCTTA 360

CCAAGGCnAC GATGCATAGC CGACCTGAGA nGGTGATCGG 400

(2) INFORMATION FOR SEQ ID NO: 3634:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3634:

TGAGCTAGGC CGGCAATATG TAAGAATAAA TGGTGGAGAA TGACGGGTTC GAACCGCCGA 60

CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCGATT TAAAACTGCC 120

TGGCAACGTT CTACTCTAGC GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA 180

CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 240

TATTTTGATT AAGTCTTCGA TCGATTAGTA TTCGTCAGCT CCACATGTCA CCATGCTTCC 360

ACCTCGAACC TATTAACCTC ATCATCTTTG AGGGATCTTA 400

(2) INFORMATION FOR SEQ ID NO: 3635:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3635:

TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT TTAGCTCTAC 60

TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 120

ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA GAGACCTTGC 180

GGTCTCAAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 240

CGTAAGTTGG GCTACCATCG ACGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT 300

CTTTCCTCTT CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCGCTCTTT 360

TCTCGTTTCG TCAGATTCAA ACGTTTTCAC TTCGCCAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3636:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3636:

TACTTATCTA GTTTTCAATG TACAATTTCT TTnTAGTCAA GCGCTCGCAT ACTGATTTTC 60

AAAAAATCAA ATGCTCATTT ACAAAAGTAA ACTCCGCTTT ATTTTTCTTA ATGCATTGTC 120

TAACAACCGC TTTCTTTAAA AAGAATAGAT TGTCAAGCGC TCGCATAAGC AATATCACTT 180

TAACCAAAAA ATATTTGAAT GTTAAATAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240

ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300

GCACCTTnCG ATACGGCTAC CTTGTTACGA CTTCACCCCA nTCATTTGTn CCACCTTCGA 360

CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTCGGGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3637:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3637:

AGCGCTCGCA TAAGCAATAT CACTTTAACC AAAAAATATT TGGAATGTTA AATAAACATT 60

CAAAACTGnA ATACAATATG TCACATTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA 120

TATCCTTAGA AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT 180

CACCCCAATC ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT 240

CGGGTGTTAC AAACTCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC 300

ACCGTAGCAT GCTGATCTAC GATTACTAGC GATTCCAGCT TCATGTAGTC GAGTTGCAGA 360

CTACAATCCG AACTGAGAAC CACTTATGGG ATTGCCTnAC 400

(2) INFORMATION FOR SEQ ID NO: 3638:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3638:

TTCTCCGATT TAAAACTGCC TGGCAACGTT CTACTCTAGC GGAAGTAAGT CGAnCTACCA 60

TCGACGCTAA GGAGCTTAAC TTCTGTGTTC GGCATGGGAA CAGGTGTGAC CTCCTTGCTA 120

TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAAC TAGATAGTAA GTAAAAGTGA 180

TTTTGCTTCG CAAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 240

CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 300

AACCGAAGTT GGGGAAATCT CATCTTGAGG GGGGCTTCAT GCTTAGATGC TTTCAGCACT 360

TATCCCGTCC ACACATAGCT ACCCAGCTAT GCCGTTGGCA 400

(2) INFORMATION FOR SEQ ID NO: 3639:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 551 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATGTCTCTAA CGCCTTTAAT AGTATTGAAC ACAATTGGGA AAAAAGCAGC GATAAAAATA 60

ATCGCAATCG CTGGCAAACT ACCAATACCA AACCATAGAA CAACAAATGG TGCCCATGCT 120

ATCGGAGATA TCGGCCTAAT CAATTGAAAT AGCGGTTCGA TAGCGTTGTA TAGCCAACGA 180

TTCCTTCCAA GCAAGAAGCC CAATGGAATA GCAACCAACA ATGCGACAAC AAAGCCCGCT 240

ACAAATCTCC ATAAACTAAT TGCTAAATGT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 300

CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 360

ATAaTGACCA TTTCCCAAaT GCCTAAGAAA aTAATAAATG TGATAATAGG TAATATAAAT 420

TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCAACAA 480

AGTCATCCAT ATGCAGGTGG ATTAAACAAA TGATGTTGTT TTACCAnGTC GTAATTTCCT 540

GATAGCCGGA T 551

(2) INFORMATION FOR SEQ ID NO: 3640:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3640:

CACTAAACTA AATTAATGAA GTGCCTTATG TATAAAAATT ATAACTTGAT CCAACTTACA 60

CTACCAATAG AAACTTCTGT TAGAATTCCT CAAATTGATA TTTCGCGATA TGTTAATGAA 120

ATTGTTGAAA CGATACCTGA TAGCGAATTC GATAAATTCA GACATCATCG TGGCGCAACA 180

TCCTATCATC CAAAAATGAT GTTAAAAATC ACCTTATATG CATATACTCA ATCTGTATTT 240

TCTGGTCGTA GAATAGAGAA ATTACTTCAT GACAGTATTC GAATGATGTG GTTAGCTCAA 300

AATCAAACAC CTTCTTATAA AACTATTAAT CGTATTAGAG TGAATCCTAA TACTGATGCG 360

TTAATTGAAT CTTTATTTAT CCAGTTTCAT AGTCAATGTT 400

(2) INFORMATION FOR SEQ ID NO: 3641:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3641:

GATTGTCCTT TGGcAATGGT AGGAGAGCGT TCTAAGGGCG TTGAAGCATG ATCGTAAGGA 120

CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CGAAAGACGG GTGAGAATCC 180

CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC 240

CTAAGCTGAG GCCGACAGnG TAgGCGATGG ATAACAGGTT GATATTCCTG TACCACCTAT 300

AATCGTTTTA ATCGATGGGG GGrCGCATAG GATAGGCGAA CGTTGCGATT GGATTGCACG 360

TCTAAGCAGT AAGGCTGGAG TATTAGGCAA ATCCGGTA 398

(2) INFORMATION FOR SEQ ID NO: 3642:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3642:

TAATGTCTAC ACTTTGCTTG CGATCATTCA TTTTAAAGCC AGACTTTTTA TAATCTTGTA 60

CAAATGCTTG CGCTACATCC TTGTGTTGAT CAAGCAATTC CCCTCTCAGT ACTAGCACAC 120

AGCAATACGC ATCAGGtATA ACGTCATCAC CATGTTTCAA AGTCTTACCT TTGCCTAACT 180

TTTCACCCAG TGCACCGAAT GGTTCGGCTA CAGAATACCC TGTaATTCTG TGTTCACTCA 240

ATGCGGCTGG CATTTCTGCT GGCGACATTT CATGATAGCT AAAATGCCCC GGTTTAATCT 300

TTAATTGTTT ACGTAATTCC TCAAGTAAAA GATAATGTGt TGAATAACgA TGTGGtATAC 360

CAAAATGGkA ATCATCGCCA TTAtTATTAA ATTCaTTTAA GTGCATACCT TTTTGTCCCA 420

TAATGACATT GCCTTCATG 439

(2) INFORMATION FOR SEQ ID NO: 3643:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3643:

ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA 60

TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120

TCGAACCGTG ACCTCCTGCG TGCAAAGCAG GCGCTCTCCC AGCTGAGCTA AGCCCCCAAA 180

GCGTGCGCTC TAACCAGCTG AGCTATAGGC CCATTAATTT GAATGAACAA ACATTCAAAA 300

CTGAATACAA TATGTCACGT TATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT 360

TAGAAAGGAG GTGATCCAGC CGCACCTTnC GATACGGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3644:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3644:

GCGAAACTGT ACGGAGCAAC GCCGCGTGAG TGATGAAGGT CTTCGGATCG TAAAACTCTG 60

TTATTAGGGA AGAACATATG TGTAAGTAAC TGTGCACATC TTGACGGTAC CTAATCAGAA 120

AGCCACGGCT AACaCGTGCC AGCAGCCGCG GTAATACGTA GGTGGCAAGC GTTATCCGGA 180

ATTATTGGGC GTAAAGCGCG CGTAGGnGTT TTTTAAGTCT GATGTGAAAG CCCACGGnTC 240

AACCGTGGAG GGTCATTGGA AACTGGAAAA CTTGAGTGCA GAAGAGGAAA GTGGAATTCC 300

ATGTGTAGCG GTGAAATGCG CAGAGATATG GAGGAACACC AGTGGCGAAG GCGACTTTCT 360

GGTCTGTAAC TGACGCTGAT GTGCGAAACG TGGGGATCA 399

(2) INFORMATION FOR SEQ ID NO: 3645:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3645:

TATTATACTT TACATTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATC 60

TTTCTTTGTG TTTGCTTTTA TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT 120

CAATGCGGCT CATCGCATCC ACTTTTTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 180

TnCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 240

CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAAATnAT ACATTCAAAA CTAGATAGTA 300

AGTAAAAGTG GATTTTGCTT CGCAAAACAT TTATTTTGGA TTAAGTCTTC GATCGGATTA 360

GTATTCGTCA GCTCCACATG TCACCATGGC TTCCACCTCG 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 758 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3646:

AGATAAGTAA GTAAAATATA GATTTTACCA AGCAAAACCG AGTGAATAAA GAGTTTTAAA 60

TAAGCTTGAA TTCATAAATA ATCGCTAGTG TTCGAAAGAC ACGAnCAAGA TTAATAACGC 120

GTTTAAATCT TTTTATAAAA GAACGTAACT TCATGTTAAC GTTTGACTTA TAAAAATGGT 180

GGAAACATAG ATTAAGTTAT TAAGGGCGCA CGGTGGATGC CTTGGCACTA GAAGCCrATG 240

AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA GTAAGCTTTG ATCCAGAGAT 300

TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT CGATATGTGA ATACATAGCA 360

TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA GAAAGAAAAT 420

TCGATTCCCT TAGTAGCGGC GAGCAnAACG GGAAGAGCCC AAACCAACAA GCTTGCTtGg 480

GGGTnTGTaG GACACTCTAT ACGGATTACA AAGGACGACA TTAGACGAAT CATCTGGaAA 540

GATGAATCAA AGAAGGTAAT AATCCTGTAG TCGAAAATGT TGTCTCTCTT GAGTGGATCC 600

TGaGTACGAC GGAGCACGTG AAATTCCGTC GGAATCTGGG GAGGaCCATC TCCTAAGGCT 660

AAATACTCTC TAGTGACCGA TAGTGGAACC aGTaCCGTGA GGGAAAGGTg AAAAGCACCC 720

gGAAgGnAGT TGAAATaGAA ctGGAAACCG TGTGCTTA 758

(2) INFORMATION FOR SEQ ID NO: 3647:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3647:

ACAAACTCCG AATGCCAATT AATTTAACTT GGGAGTCAGA ACATGGGTGA TAAGGTCCGT 60

GTTCGAAAGG GAAACAGCCC AGACCACCAG CTAAGGTCCC AAAATATATG TTAAGTGGAA 120

AAGGATGTGG CGTTGCCCAG ACAACTAGGA TGTTGGCTTA GAAGCAGCCA TCATTTAAAG 180

AGTGCGTAAT AGCTCACTAG TCGAGTGACA CTGCGCCGAA AATGTACCGG GGCTAAACAT 240

ATTACCGAAG CTGTGGATTG TCCTTTGGnA TGGGTAAGGA GAGCGTTCTA AGGGCGTTGA 300

AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAAGGTT 400

(2) INFORMATION FOR SEQ ID NO: 3648:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3648:

GTCATTGGAA ACTGGAAAAC TTGAGTGCAG AAGAGGAAAG TGGAATTCCA TGTGTAGCGG 60

TGAAATGCGC AGAGATATGG AGGAACACCA GTGGnCGAAG GCGACTTTCT GGTCTGTAAC 120

TGACGCTGAT GTGCGAAACG TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC 180

GTAAACGATG AGTGCTAAGT GTTAGGGGGT TTCCGCCCCT TAGTGCTGCA GCTAACGCAT 240

TAAGCACTCC GCCTGGGGAG TACGACCGCA AnGTTGAAAC TCAAAGGAAT TGACGGGGAC 300

CCGCACAAGC GgTGGaGCAT GTGGTTTAAT TCGAAGCAAC GCGAAGAACC TTACCAAATC 360

TTGACATCCT TTGACAACTC TAGAGATAGA GCcTTCCCCT TCGGGGGACA AAGTGACAAG 420

TGGTGCATGG TGTCGTCAAC TCCTGTCGTT GAGATGTTGG GGTAAnTCCC CGCAAnGAGC 480

GCACCCTTAA GCCTTAGTTT nCATCATTAA GTTGGGCACT C 521

(2) INFORMATION FOR SEQ ID NO: 3649:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3649:

CCAAAGTTCA TCTTTTACGA ATGAGAAATA GGTGTTGCAT ATTCAATGGT CTCATCTTGT 60

TTATAAAAGC CACCATCTAA ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC 120

ATACGTGTTT TAACACGTTC GTATCCCATT GCATCCCATA ATTGGAATGG ACCAAGTTTC 180

CAGTTGAACC CCCAGACAAG CGCACGGTCT ATGTCTCGGA AATCATCGGT AGCTTTAGGT 240

ACATTGATAG CAGAGTAATA GAAATTATTA CGTAATGTCT CCCATAAAAA TAGTCCCGCT 300

TCGTCTTGcG CATTGAATAT GGTATCAAkG TTATGCACTA aGTCTTTATT AAATTCATTT 360

AAAATTGGTA ATTGTGGTTG CGATACAGGT ACATAATCTT 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3650:

GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTCGAA CCCCCGCGGn CCGTTAAGGC 60

CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC ATTATTATAG 120

GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC 180

TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACACTACGA GACCATTAGT AAAACGGAGG 240

AAGAGGGATT CGAACCCCCG CGAGCCGTTA AGCCCCTGTC GGTTTTCAAG ACCGATCCCT 300

TCAGCCGGAC TTGGGTATTC CTCCAAAATT ATATGGACCT TGCAGGACTC GAACCTGCGA 360

CCGAACGGTT ATGGAGCCGT TAGCTCTAAn CAACTTGAGC 400

(2) INFORMATION FOR SEQ ID NO: 3651:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3651:

TGGCGCTGTG CTTTAGTAAA ACTATGGTCA TGTTGCGCTA AATGCAACCA TGCATGGTAA 60

AAACTTTGCT CACGCTTCGG CATTGTCCAA CTCGATAGAA ATTGATCGAT ATAAAGTTTC 120

GTCCATTTAA TCATTTGACG ATTCACTTGT TCGCTAAGTG GCTCACCTTG TTCATCTATT 180

ATTGCATCAC TCATCGGACG TACATCATAG TGATGATATG ATTCAGCCAT ATCACGTTTT 240

GATTTTTCTA ATAGTAGATC AGCAACAACA TCAACATTTG AATGATTCAT ATATGATGGC 300

AGGTACGTCT TTTAATGTTT TAATGTTATC AATATAAAGA TGATGTAGTG TTGCGGGATA 360

TGTAGTGAnG TTCAAGTAAC ATATCAGTAA CAAGTTGATT 400

(2) INFORMATION FOR SEQ ID NO: 3652:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3652:

CATTGTCCAA AGGACAATCC ACAGCTTCGG TAATATGTTT AGCCCCGGTA CATTTTCGGC 60

GCAGTGTCAC TCGACTAGTG AGCTATTACG CACTCTTTAA ATGATGGCTG CTTCTAAGCC 120

AACATCCTAG TTGTCTGGGC AACGCCACAT CCTTTTCCAC TTAACATATA TTTTGGGACC 180

TTAGCTGGTG GTCTGGGCTG TTTCCCTTTC GAACACGGAC CTTATCACCC ATGTTCTGAC 240

TCCCAAGTTA AATTAATTGG CATTCGGAGT TTGTCTGAAT TCGGTAACCC GAGAGGGGCC 300

CCTCGTCCAA ACAGTGCTCT ACCTCCAATA ATCATCACTT GAGGGCTAGC CCTAAAGCTA 360

ATTTCGGAGA GAACCAGCTA TCTCCAGGTT CGATGGAATT 400

(2) INFORMATION FOR SEQ ID NO: 3653:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3653:

GGTTCGGTCC TCCATTCAGT GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG 60

TTTCGGGTCT ACGACCAAAT ACTAAACGCC CTATTCAGAC TCGCTTTCGC TACGGCTCCA 120

CATTTACTGC TTAACCTTGC ATCAAATCGT AACTCGnCGG TTCATTCTAC AAAAGGCACG 180

CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTCAC 240

TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 300

AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 360

CGTACTCAAG nATCCACTCA AGAGAGACAA CATTTTCGAC 400

(2) INFORMATION FOR SEQ ID NO: 3654:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3654:

AAAGGTCCTA AATATAATTT TACAACTAAT AAATAGTGGC GGTGGAGGGG ATCGAACCCC 60

CGACCTCACG GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC TTATATAGTT 120

GCGCTCTCCC AGCTGAGCTA AGCCCCCATA ATAATTACAG TATATCGGGA AGACAGGATT 240

CGAACCTGCG ACCCCTTGGT CCCAAACCAA GTGCTCTACC AAGCTGAGCT ACTTCCCGTA 300

TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGnTCT 360

ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3655:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3655:

TATTGAAGCC TGAGTCAACA CGTACGCAAA TCGATCAAAT CATCGATGAA GCGAAACATA 60

CAATTTTAAA TCTGTATGTG TGAATCCAAC ACATGTTAAA TATGCAGCAG AGCnnCTAGC 120

TGATTCAGAG GTGCTCGTTT GTACGGTAAT AGGATTCCCA TTAGGTGCGT CGACAACTGC 180

AACGAAAGCA TTTGAAACAG AAGATGCAAT TCAAAATGGT GCAGATGAAA TTGACATGGT 240

CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 300

AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGGAT TATTGAGACG GTATTGTTGG 360

GACCATGACG AAATTGTAAA AGCGAGTGGA ATTAACCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3656:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 530 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3656:

GATGAGTCGC TGnCTGATCT GAACGCTGTC TGAGnCCGAA CGCTACTGAA CTGAGTCGCT 60

GTCTGAGTCT GAATCGCTAT CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTGTCTGA 120

GTCTGAGTCG CTGTCTGAGT CTGAATCGCT ATCTGAATCT GAGTCGCTGT CTGAGTCTGA 180

GTCGCTATCT GAGTCTGAGT CGCTGTCTGA ATCTGAGTCG CTGTCTGAAT CTGAATCGCT 240

GTCTGAGTCT GAATCGCTAT CTGAGTCTGA ATCGCTATCT GAGTCTGAAT CACTGTCTGA 300

GTCCGAGTCA CTGTCTGAAT CTGACTCACT ATCTGATTCT GAGTCGCTAT CTGATTCTGA 360

ATCTGAACCT GAGTCGCTGT CTGAGCCTGA AGTCACTGGT CTGAATCCGA ATCCGGATCC 480

GGGTCTGGGG CTTGGGTTCC GGTTCTGGGT CTGGGACTTG GGTTCTGGGA 530

(2) INFORMATION FOR SEQ ID NO: 3657:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3657:

GTTTTAACTA CGCAAGACAT CGAAGAAGCT GACGGTGTCA TAATTGCAGC TGATAAACAA 60

GTTGATCTGT CCCGATTTGT TGGTAAACGG TTGATTAATG AAAATGTTCG CGAAGGGATT 120

CATAATCCGA GAGGTCTAAT TCAACGTATC ATTAATCAAG ATGCGCCTAT TTATCAATCT 180

GAAACAAATT ATCATTCGAA AGATCGCGGT AAGTCTAAAA ATGGTATTCA AATGGTGTAT 240

CAACATTTAA TGAACGGTGT ATCGTTTATG GTTCCTTTTA TCGTAGTTGG TGGACTCCTT 300

ATCGCCATCG CGCTGGACTC TAGGCGGTGA ACGACATCAA AAGGATTAGT CATCCCAGAT 360

GGATTCATTT TGGGAAATCC ATTGGAAAAC ATTGGGTAGT 400

(2) INFORMATION FOR SEQ ID NO: 3658:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 668 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3658:

GAAGAAGTTT ATGAAACGGT TATGAATAAG CCATACACTA GATATCCAGT GTACGAGGGA 60

GATATTGATA ACATTATTGG GGTGTTTCAT TCTAAATATC TGTTGGCTTG GAGTAATAAA 120

AAAGAAAATC AAATTACAAA CTATTCAGCT AAGCCATTAT TTGTGAATGA ACACAATAAA 180

GCTGAATGGG TATTACGTAA GATGACTATT TCTAGAAAAC ATTTAGCAAT TGTGTTGGAC 240

GAATTTGGTG GTACTGAAGC GATAGTGTCA CATGAAGACT TAATTGAAGA ATTATTAGGT 300

ATGGaAATTG AAGATGAGAT GGaTAAAAAG GAAAAAGAAA AACTTTCTCA ACAGCAAATT 360

CmATTTCAAC AACGGAAAAA TCGCmACGTA TCTATATAAG GnGCGAACAG CTATGTGGTA 420

ATAAGAATCG ACTTACTCAA ATGTTAAGTA TTGAATATCC AATTATACAA GCAGGTATGG 480

TAGGCGCGGT TACTTTAATA CGCAGCAATT GGAAGATGAA ATAGATTATG GTACGCCAAT 600

TAACGTCAAA TTCTTTTGGC GTAAATGTCT TTGGTACCAA GTCAACAATC ATATACCAGT 660

AGTCAAAT 668

(2) INFORMATION FOR SEQ ID NO: 3659:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3659:

AAAAGAATGG TAAGTTGAAT AAAGTATTGA AATCAATTGC CAATATCTTT ATACCGTTGA 60

TTCCTGnATT TATTGGAGCT GGATTAATTG GTGGTATTGC AGCAGTACTG AGTAACTTAA 120

TGGTGGCAGG CTATATTTCA GGTGCTTGGA TTACGCAACT TATAACAGTA TTTAATGTCA 180

TTAAAGACGG TATGTTAGCA TACTTAGCTA TTTTCACTGG TATTAATGCG GCTAAAGAAT 240

TTGGTGCGAC ACCAGGACTT GGTGGCGTGA TTGGTGGTAC AACGTTATTA ACGGGTATTG 300

CTGGTAAAAA TATTTTAATG AATGTCTTCA CTGGAGAACC ATTGCAACCT GGACAAnGTG 360

GGATTATTGG CGTTATTTTG CCGTTTGGAA TTTAAGTAAT 400

(2) INFORMATION FOR SEQ ID NO: 3660:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3660:

CTGAGCTAAT GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GAACCCCCAA CCTACTGATT 60

ACAAGTCAGT TGCTCTACCA ATTGAGCTAG GCCGGCAATA TGTAAGAATA AATGGTGGAG 120

AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 180

AATTCTCCGA TTTAAAACTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTCGGACT 240

ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT 300

GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AAACTAGATA GTAAGTAAAA 360

GTGATTTTGn TTTCGCAAAA CATTTATTTT GGATTAAGTC 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3661:

TGATGTTTGA TTAGCTCATA AATACTAAAT AATGTTTGTA ACTTATAGTT ACGTTTTTTG 60

GAATTAACGT TGACATATTG TCATTCAGTT TTCAATGTTC ATTTTTCTTA CCGACAAGAA 120

TTAATTATAC ATTTTATTAA CATTTAAGTC AATAACTTTT TTTATCTTGT CCATTTTATT 180

TTTTAACCAA AATTTGATTA AAAAACTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 240

TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 300

CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA 360

AGTAAAAGTG ATTTTGCnTC GCAAACATTT ATTTTGATTA 400

(2) INFORMATION FOR SEQ ID NO: 3662:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 742 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3662:

CGCTCAACGT CTGCCTTCGT AATGGCTTTT GTAGAAATTC TAACTAAATA ATTTCGAATG 60

CTATCATTGA TTGTTTCAAC AGCTTGATGC TTTTGTTCAA GCTTTTTGAT CAATTTTTTA 120

TCGTCTTTTG TAATTTCGCG AATGTCTTCA AACATTGATA AGACAATCTG ACCCACATTT 180

TGTAATTCTT TTTGAGTTTC TTGTAATGCA ACACCAGGTG CGTGATAAAC AAGATCTTTG 240

TTTAAGTGCT GAGGTTTATA GTCATCAGCA ATATCTTTAC CTGGGACAAG CTTTGTAACA 300

ATCCATGCTA AACCTGCTAC AAATGGTAAT TGAATCAAAG TATTTGTTAT GTTGAAGATA 360

CCATGTGATA CTGCAATCGT CATCGCTGGT TTTAAGTGCC ATAAATCTTG TAACAAACTA 420

ATCAAATGAA TCACAACTGG CAAGAAAATT GTGAAGATAA TTACCCCGAT TAAGTTAAAG 480

ATGACGTGTA CAAGCGCCGC ACGTTTTGCA GCGATTGAGC CGGCTAAACT AGCTAAGATA 540

GCTGTAATCG TGGTACCAAT GTTATCGCCT AGtAACACAG GGaTkGCTGC GTTTAAGCTA 600

ATTAAATCTT GTTGATAAAA TTCTTGTAAA ATACCAATCG TCGCACTTGA ACTTTGAACT 660

AGCATTAAAT TGGCTTnAAA TC 742

(2) INFORMATION FOR SEQ ID NO: 3663:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3663:

ATGAATTCAA GCTTATTTAA AACTCTTTAT TCACTCGGTT TTGCTTGGTA AAATCTATAT 60

TTTACTTACT TATCTAGTTT TCAATGTACA ATTTCTTTTT AGTCAAGCGC TCGCATACTG 120

CTTTATTTTC AAAAAATCAA ATGCTCATTT ACAAAAGTAA ACTCCGCTTT AATTTTTCTT 180

AATGCATTGT CTAACAACCG CTTTCTTTAA AAAGAATAGA TTGTCAAGCG CTCGCATAAG 240

CAATATCACT TTAACCAAAA AATATTTGAA TGTTAAATAA ACATTCAnAA CTGAATACAA 300

TATGTCACGT nATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT TAGAAAGGAG 360

GTGATCCAGC CGCACCTTCC GATACGGGCT ACCTnGTnAC 400

(2) INFORMATION FOR SEQ ID NO: 3664:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 636 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3664:

AACTAATAGT TCACTTTTAC TTTTTTCTTT TTCATTATTA TCCATTATTT TTTCACCGCC 60

AAAACGAATT TCATGATGTT AATTTAAATG TTCTATGACA AAATTAAGCA ACGATGTTtT 120

ATATTTATTT CCAACTATGT CTAGATTAAA TTTCTAAAAA TAkACATCAT TTAAAAGGAG 180

CTTGGGACAT AAATCAATGT CCTAGGGTCT ATAATATTAT AkTGCTAGTA GTTGACTGAA 240

TGAAAATGCG CTTGCAACAA GCTTTTTTCA ACTCTAGTCA GGGGCCCCAA CACAGAGAAT 300

TTCGAAAAGA AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAACA CAGAGAATTT 360

CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGTGGG CCCCAACACA GAGAATTTCG 420

AAAAGAAATt CTACAGGCAA TGCGAGTTGG GGTGTGGGCC CCAACATAGA GAAATGGaTT 480

CCCAaTTTCT ACAGACAATG CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC 540

TACAATAATG nGCAAGTTGG CGGGGnCCCC AACACA 636

(2) INFORMATION FOR SEQ ID NO: 3665:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 404 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3665:

TATCATTTCC TGTTGCTAAA ACAACAGCAT GTATGCCATT CATAACACCT TTATTATGTG 60

TTGCTGCACG ATGAATATCT ACTTGGGCCA ATACAGAAGC ACGTTCCATT CGTTTGGCAA 120

CCTCTTCTCC AGTTCTCTCG CCCCTTGCTA AATCTTTAAC ATCAATTTCG CCTTGAACTT 180

TAACAACGGA CGCTGTTGCA TGATTGGATA AAATACTCAT TAAAATGTCG CTTTGGGAAA 240

tTCATTTTTT AAAAATGCAG TTATGGCCTC TAAAATCGTA TTAAGCATAT TAGCGCCCAT 300

AGCATCTTTC GTATCAACAA ATACTTTTAA AGATAGTAAC TGtTGcTCAG GrAATGTakC 360

mAtCGCTATA CGtTGGTAAC CACCACCACG CGCTTTAATA GGAA 404

(2) INFORMATION FOR SEQ ID NO: 3666:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3666:

GTGGTTCCAG TAGCAATTAT TGAACGATAT TAGGCTATCT AGTCGGCATA TTTGTAAAAC 60

AAGATCCAAT TAAATATCAA CAGGAATAAC GAATAATATA AAAGAGGTTG GGACATAAAT 120

CCCTAAAAAA ACAGCAGTAA GATAATTTTC AATTAGAAAA TATCTTACTG CTGTTCTCTA 180

TTTATACAAT ACTTCGTATT GAATGGCTTC GCTTTCCTAG GGTGCCGTCT CAGCCTCGGT 240

CTTCGACTGG CACTGCTCCC TCAGGAGTCT CGCCATTAAT ACTACGTATT AACGTGTAAT 300

TTTACTTTGA AATACTTTAA AAAAATAAGA CACTTTGCCC AACTTGCACA TAAATGTAAA 360

ATTCAATAAA ATAAATTTCT GTGTTGGATC CCTnCGTATA 400

(2) INFORMATION FOR SEQ ID NO: 3667:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3667:

CCAACAAATC TGTCTGTCGC ATCGCCTTTG TCGTTCCAAA TAAATATGTA CAAACGAATC 60

CACCAGCATA CGCnCCAAGT AATCCTGCAA TATAACCTAA ATACATATTA TCTGAGATTA 120

ATGGTAATAG TGACACACCA CTTGGGCCTA TTGCTTTGGC ACCAATATGT CCAATTCCAC 180

CTATTACAGC GCCACCAATA CCACCACCAA TACAAGCAGT TAAGAAAGGT CGACCTAATG 240

GCAAAGTCAC ACCATAGATT AATGGTTCTC CGATACCTAG GGAAACCAAC TGGCAATGCA 300

CCTTTTAAAG TATTACGTAA TGTTGTGTTG CGGTTTACAT CTTACCCAAA GTGCTAATGC 360

GGGCACCTAC TTGGTCCCAG CACCAGCCAT CGCTGCAATT 400

(2) INFORMATION FOR SEQ ID NO: 3668:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3668:

ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG CTATGTATTC ACATATCGAT 60

AACATGACAT AACTCATGAC TGGGTTTCCC CATTCGGAAA TCTCTGGATC AAAGCTTACT 120

TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG 180

CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA AACGCGTTAT 240

TAATCTTGTG AGTGTTCTTT CGAACACTAG CGATTATTTC TTATGAATTC AAGCTTATTT 300

AAAACTCTTT ATTCACTCGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT 360

TTTCAATGTA CAATTTCTTT TTAGTCAAGC GCTCGCATAA 400

(2) INFORMATION FOR SEQ ID NO: 3669:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3669:

GAGCGCTACT TACTGGnAGG CGCTGGTGGG ATACTACCCT AGCTGTGTTG GCTTTCTAAC 120

CCGCACCACT TATCGTGGTG GGAGACAGTG TCAGGCGGGC AGTTTGACTG GGGCGGTCGC 180

CTCCTAAAAG GTAACGGAGG CGCTCAAAGG TTCCCTCAGA ATGGTTGGAA ATCATTCATA 240

GAGTGTAAAG GCATAAGGGA GCTTGACTGC GAGACCTACA AGTCGAGCAn GGTCGAAAGA 300

CGGACTTAGT GATCCGGTGG TTCCGCATGG AAGGGCCATC GCTCAACGGA TAAAAGCTAC 360

CCCGGGGGAT AACAGGCTTA TCTCCCCCAA GAGTTCACAT 400

(2) INFORMATION FOR SEQ ID NO: 3670:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3670:

ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA GCCATCTTTC 60

TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTTG CGGTCTCAAT 120

GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTCG 180

ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCGGC ATGGGAACAG GTGTGACCTC 240

CTTGCTATAG TCACCAGACA TATGAATGTA AATTATACAT TCAAAACTAG ATAGTAAGTA 300

AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAAGT CTTCCGATCG ATTAGTATTC 360

CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCCGAACCT 400

(2) INFORMATION FOR SEQ ID NO: 3671:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3671:

CACCCGAAGA TATTGCTCAG ACAAAGTCAT CATATACAGG AAAGTATTTA AAAGAAGTAC 60

TTGAACGAGA TAAACAAAAT ACTGAAGATA AATAAGATTA AAAGAAGTGA AGGATGTTAT 120

AAATTTATCC TTCGCTTCTT TTTATTAATT TAGTAATGAA TAGTAGAAAG AAAAGATGCG 180

TAAAAAGAAT TATGTTAAGA TAGGGTCAAT CTAGAGTAGT TAAACATAAA TCGAACTGGG 240

TTAGCCACAG CTATTGTGTA CTTAAAAATA GGAATGCATG AGTGCACCnA nAGGnAGAAT 360

ACTAATTTCC AAAGAAAAAG TATTCCTTAT GTTGGGGCCC 400

(2) INFORMATION FOR SEQ ID NO: 3672:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3672:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAG ATTCCATTCG AGAAAGAACG 60

TAAATTTAAT cCTGATTTAG CmCCaGGGAC aGAAAAAGTA mCmAGaGAAG GACaAAAAGG 120

TGAGAAGACA ATaACGACAC CAACACTAAA AAATCCATTA ACTGGAGTAA TTATTAGTAA 180

AGGTGAACCA AAAGAAGAAA TCACAAAAGA TCCGATTAAT GAATTAACAG AATACGGACC 240

AGAAACGATA ACACCAGGTC ATCGAGACGA ATTTGATCCG AAGTTACCAA CAGGAGAGAA 300

AGAAGAAGTT CCAGGTAAAC CAGGAATTAA GAATCCAGAA ACAGGAGACG TaGTTAGACC 360

ACCGGTCGAT AGCGTAACAA AATATGGACC TGTAAAAGGA GACTCGATTG TAGAAAAAGA 420

AGAGATTCCA TTCAAAACGT AAATTTAATC CGGATTTAGC A 461

(2) INFORMATION FOR SEQ ID NO: 3673:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3673:

CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA 60

TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA 120

ACCGCTGACC TCCTGCGTGC AAAGCAGGCG CTCTCCCAGC TGAGCTAAGC CCCCAAAnAG 180

GTATTAAATT AATGGGGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG 240

TGCGCTCTAA CCAGCTGAGC TATAGGCCCA TTAATTTGAA TGAACAAACA TTCAAAACTG 300

AATACAATAT GTCACGTTAT TCCGCATCTT CnGAAGAAGA TGTTCCGAAT ATATCCTTAG 360

AAAGGAGGTG ATCCAGCCGC ACCTTCCGAn ACGGCTACCT 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3674:

ACATGAAGAC TTAATTGAAG AATTATTAGG TATGGAAATT GAAGATGAGA TGGATAAAAA 60

GGAAAAAGAA AAACTTTCTC AACAGCAAAT TCAATTTCAA CAACGGAAAA ATCGCAACGT 120

ATCTATATAA GGAGCGAACA GCTATGTGGG AATAAGAATC GACTTACTCA AATGTTAAGT 180

ATTGAATATC CAATTATACA AGCAGGTATG GCAGGAAGTA CGACACCGAA ATTAGTTGCA 240

TCAGTAAGTA AACAGTGGTG GGTTAGGCAC AATAGGCGCG GTTACTTTAA TACGCGCCAA 300

TTGGAnGATG GAnATnGATT ATGTACGCCA TTAACGTCAA ATTCTTTTGG CGTAAATGTC 360

TTTGTACCAA GTCAACAATC ATATACCAGT AGTCCAAATT 400

(2) INFORMATION FOR SEQ ID NO: 3675:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3675:

AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCGA ACCGCCGACC 60

CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAACTGCCTG 120

GCAACGTTCT ACTCTAGCGG AACGTAAGTT CGACTACCAT CGACGCTAAG GAGCTTAACT 180

TCTGTGTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240

TAATTTATAC ATTCAAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA 300

TTTTGATTAA GTCCTCGTCG TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT 360

CGGACCTATT AACCTCATCA ACCTTGAGGG nTCTTATAAA 400

(2) INFORMATION FOR SEQ ID NO: 3676:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3676:

TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG ACATGTGGAG 60

CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC CCGTCCACCG 120

ATTGACTAAG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC CTAAGCTGAG 180

GCCGACAGCG TAGGCGATGG ATAACAGTTG ATATTCCTGT ACCACCTATA ATCGTTTTAA 240

TCGATGGGGG GACGCATAGG ATAnGCGAAn GTGCGATTGG ATTGCACGTC TAAGCAGTAA 300

GGCTGAGTAT TAGGCAAATC CGGTACTCGT TAAGGCTGAG CTGTGATnGG GAGAAGACAT 360

TGAGTCTTCG AGTCGTTGAT TTCACACTGC CGAGAAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3677:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3677:

AAAGCGCCAC ATGGTGCCAA GTCTGGAGTT AATCCAGCAA TTGCTTGTTT TAAGCTATTA 60

TATTTTTCTT CTACTTTTGT TTTTTCTGCG GCAATTTGTT GGTCAGTCGC ATCACCATTG 120

TTAATAACAT TTTGTGCATT TGTTGATTCT GTTTGACCCG CACGTTTAGC ATTTTCATAT 180

GCTTGGATTG ATGATTGTGT CATACCATCA GTAGTTACTG ATTTATTGAT TTCTTCATCA 240

AGTTTCGTCT TAGCAGTTTT TAAAGCACTA TTATCAGCTA AAGGTACTAA TTGGATTAAT 300

TGCTTGCGTT AATCGCTCAT TGACACGATT TACATTTGTT AACGCAGATT GCACTTCTTG 360

TACTGTTCTT AATGGGCTTT TGGAATAATA GCATTAGCGC 400

(2) INFORMATION FOR SEQ ID NO: 3678:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 648 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3678:

ACAGTCAATT GnTCTACCAA TTGAGCTAGG CCGGTTAAGA AATGGTTCCA GGACAGAGTC 60

GAATGCCGAC ACATGGAGCT TCAATCCATT GCTCTAACCA ACTGAGCTAC TGAACCATAA 120

AGGCGTGTTA ACCGCTACAC TACGAGACCT ATAAAATATT GCGGGAGGCG GATTTGAACC 240

ACCGTACTTC GGGTTATGAG CCCGACGAGC TACCGAACTG CTCCATCCCG CGATAATAAA 300

AAATAATGGC GGAGGAAGAG GGATTCGAAC CCCCGCGGCC CGTTAAGGCC tGTCGGTTTT 360

CAAGACCGAT CCCTTCAGCC GGACTTGGGT ATTCCTCCAT TATTATAGGT AAATCGCTAT 420

TAATTATAAA ATTAAATGGC GGTCTCGACG GGAATCGAAC CCGCGATCTC tGCGTGACAG 480

GCAGGCGTGT TAAyCGCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCGA 540

ACCCCCGCGA GCCGTTAAGC CCCTGTCGGT TTTCAAGACC GATCCCTTCA GCCGGGACTT 600

GGGGTATTCC TCCAAAATTA TATGGGACCT TGCAGGACTC GAACCTGC 648

(2) INFORMATION FOR SEQ ID NO: 3679:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3679:

CTGATCCCGT TGTGCTTCAC ACCCGATAGA TAGGGATTTA CAGATAAATT CAGGTCTCTT 60

CCACGTCATA TTTGGACCCA TCGAAAATTC GGGTTCTCAA ATCATCGAAC ATAACAAAAG 120

AAGCTAAGCA ACATGTAGGC CGTTGTCACT TAACTTCTTG TTTTTCCGAT GACAGCTTCT 180

ATTTAGAGAA TGTCATGATT ATTTTATATT CACTTCAATG TTATCAATAT TAGTGCCATC 240

TATGACATCT GCCATGCGAT TTTCTTGTAA TTTTTTGTGC AATTCAAACG TGTACTTTCC 300

ACCGTTTTTC ATTTTAATAA CAATTTTACC TGAACCAACG TTACCGTACA GATTATTTTT 360

TTCAATAAGT TGTTTTCTCA ATTTAAAATC AAGTTCTTTC 400

(2) INFORMATION FOR SEQ ID NO: 3680:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3680:

TCAATGCGGC TCATCGCATT CATTTCTTGT CTAGCAACGT TCTACTCTAG CGGAAnTAAG 60

TTAGCTACCA TCCTCGCTAA GAACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT 120

TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240

TTGACGTTTT AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA 300

CTCTAGCGGA AGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC TTGTGACAAT 360

CGCTTGGCTT CTnTCCTCTC CTTCGGnTCT CGGCTTACTC 400

(2) INFORMATION FOR SEQ ID NO: 3681:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3681:

TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGCGCTCTT 60

TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT TTGTGTTTAC 120

TTTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTCA CGGTCTCAAC TTGCCTGGCA 180

ACGTTCTACT CTAGCGGAAC GTAAGTTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT 240

TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT 300

AAACTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 360

TTTTTCTTTG TGGTTTACTT TTTATTTTGA CGGTTTAGGC 400

(2) INFORMATION FOR SEQ ID NO: 3682:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3682:

TTGAACATGT TGAATCTAAT GAAATTCTTG TTCGTCGTCT AGTTGAAGAG AACGGCGTTG 60

AGCATGAAGG TGAATTAGAT CGCTATCCAT TAGCTAAATT TAAACGTTCA AACTCAGGTA 120

CATGTTACAA CCAACGTCCA ATCGTTGCAG TTGGAGATGT TGTTGAGTAT AACGAGATTT 180

TAGCAGATGG ACCATCTATG GAATTAGGAG AAATGGCATT AGGTAGAAAC GTATAGTTGG 240

TTTCATGACT TGGGACGGTT ACAACTATGA GGATGCCGTT ATCATGAGTG AAAGACTTGT 300

GAAAGATGAC GTGTATACTT CTATTCATAT TGAAGAGTAT GAATCAGAAG CACGTGATAC 360

(2) INFORMATION FOR SEQ ID NO: 3683:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3683:

TTGGAATTTC TCCGCTACCC TCAGTTCATC CGCTCACTTT TCAACGTAAG TCGGTTCGGT 60

CCTCCATTCA GTGTTACCTG AACTTCAACC TGACCAAGGG TAGATCACCT GGTTTCGGGT 120

CTACGACCAA ATACTAAACG CCCTATTCAG ACTCGCTTTC GCTACGGCTC CACATTTACT 180

GCTTAACCTT GCATCAAATC GTAACTCGCC GGTTCATTCT ACAAAAGGCA CGCCATCACC 240

CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTC ACTCCCCTTC 300

CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGGTTCAC TATCGGTCAC TAnGAGAGTA 360

TTTAAGCCTT AnGAGATGGT CCTCCCAGAT TCCCGACGGG 400

(2) INFORMATION FOR SEQ ID NO: 3684:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3684:

GATnTATGAT GAAAAACTAT CTGACTGCTG TTTCACTTTT TATAAGACTT CTGAATGTCT 60

TCACTTATAC TTCTAGTCAC AGATTnAAAT AATCAAAAGT GCACATTATT AAAATATCAA 120

TTTCACACTC AATGCGGCTC ATCGCATTCA TTTCTTGTCT AGCAACGTTC TACTCTAGCG 180

GAACGTAAGT TAGCTACCAT CCTCGCTAAG AACCTTTcTT GACTTgTGAC AATCGCTTGC 240

TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC TACTAAACTC GTTGCGCTCT 300

TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA GCCATTTTTC TTTGTGTTTA 360

CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA CTTGCCTGGG 420

CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG TCGCTAAAGA CCTTTCTTGA 480

CTTGTGACAA TCGCTTGCTT CTnTCCTCTC CTTCGGCTCT CGGTTACT 528

(2) INFORMATION FOR SEQ ID NO: 3685:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3685:

AAATTATGGT CGATTGCGAA TGATTTAAGA GGGAnCATGG ATGCGAGTGA ATTCCGTAAT 60

TACATTTTAG GCTTGATTTT CTATCGCTTC TTATCTGAAA AAGCCGAACA AGAATATGCA 120

GATGCCTTGT CAGGTGAAGA CATCACGTAT CAAGAAGCAT GGGCAGATGA AGAATATCGT 180

GAAGACTTAA AAGCAGAATT AATTGATCAA GTCGGTTACT TCATTGAGCC ACAAGATTTA 240

TTCAGTGCGA TGATTCGTGA AATTGAAACG CAAGATTTCG ATATAGAGCA TCTAGCGACG 300

GCGATTCGCA AAGTTGAAAC ATCTACATTA GGTGAnGAAA GTGAAAATGn CTTTATCGGG 360

CTGTTCAGCG ATATGGATTT GAGTTCAACG CGGCTAGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3686:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3686:

TTAAATTATT GGTCTATCGG TTCTTGGGGT GGCCATGGTA TCTGTTCACT CTTCGGTGGT 60

GCAGTTGCGA CAACTATGGG TTGGAGATGG ATTTTCATCT TCTCAATTAT CGTTGCCGTA 120

CTTTCAATGT TACTCATCAA AGGGACGCCT GAAACGAAAT CAGAAATTAC CAATACACAT 180

AAATTTGACG TTGCAGGGCT AATTGTTCTA GTAGTTATGT TGCTAAGTTT AAACGTTGTC 240

ATTACTAAAG GTGCAGCACT TGGTTACACA TCATTATGGT TCTTTGGTTT GATTGCAATC 300

GTAATTGTAG CATTCTTTAT TTTCTTAAAT GTTGAGAAAA AAGTAGATAA TCCACTTATT 360

GATTTTAAAT TATTgAAAAT AAACCATATA CAGGTGCAAC GGT 403

(2) INFORMATION FOR SEQ ID NO: 3687:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TATGAGCCCG ACGAGCTACC GAACTGCTCC ATCCCGCGAT AATAAAAAAT AATGGCGGAG 60

GAAGAGGGAT TCGAACCCCC GCGGCCCGTT AAGGnCCTGT CGGTTTTCAA GACCGATCCC 120

TTCAGCCGGA CTTGGGTATT CCTCCATTAT TATAGGTAAA TCGCTATTAA TTATAAAATT 180

AAATGGCGGT CTCGACGGGA ATCGAACCCG CGATCTCCTG CGTGACAGGC AGGCGTGTTA 240

ACCGCTACAC TACGAGACCA TTAGTAAAAC GGAGGAAGAG GGATTCGAAC CCCCGCGAGC 300

CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC CGGACTTGGG TATTCCTCCA 360

AAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA CGGTATGAGC CGTAGCnCTA 420

ACCACTGGGC TAAAGTCCTA ATATAATTT 449

(2) INFORMATION FOR SEQ ID NO: 3688:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3688:

AAAACGTCGT AATATGCAAA TTGAAGGTGC CAAGGTTGTT ATTCAAGGTT TCnATAATGC 60

CGGAAGTTTC TTAGCTAAAT TCTTATATGA TTTAGGTGCA AAAATTGTAG GTATCTCTGA 120

TGCTTACGGT GCATTACACG ATCCAAATGG CTTAGATATA GATTATTTAT TAGACCGTCG 180

AGATAGTTTT GGTACGGTAA CAAATTTATT TGAAGAAACA ATCTCAAATA AAGAATTGTT 240

TGAATTAGAT TGTGACATTT TAGTACCAGC GGCTATTTCA AACCAAATTA CAGAAGACAA 300

TGCACATGAT ATTAAAGCTA GTATCGTTGT TGAAGCTGCT AATGGACCTA CAACACCAGA 360

AGCAACACGT ATTTTAACTG AACGTGGTAT ATTATTAGTT 400

(2) INFORMATION FOR SEQ ID NO: 3689:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3689:

CACGCTTATC AGGCGTGCGC TCTAACCAGC TGAGCTATAG GCCCATTAAT TTGAATGAAC 60

AAACATTCAA AACTGAATAC AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTC 120

CGACTTCACC CCAATCATTT GTCCCACCTT CGACGGCTAG CTCCTAAAAG GTTACTCCAC 240

CGGCTTCGGG TGTTACAAAC TCTCGTGGTG TGACGGGCGG TGTGTACAAG ACCCGGGAAC 300

GTATTCACCG TAGCATGCTG ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT 360

TGCAGACTAC AATCCGAACT GAGAACnACT TTATGGGGAA 400

(2) INFORMATION FOR SEQ ID NO: 3690:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 553 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3690:

GCnGCGTTTT AGGCCCATTC GGTTACCCCC nTTCCATAAA TGGTGCCCGG CCAGAGGACT 60

TGAACCCCCC AACTTACTGA TTACAAGTCA GTTGCTCTAC CAATTGAGCT AGGCCGGCTA 120

AGAAATGGTT CAGGACAGAG TCGAACTGCC GACACATGGA GCTTCAATCC ATTGCTCTAC 180

CAACTGAGCT ACTGAACCAT AATAAAAATG TAATGATGGC GGTCTCGACG GGAATCGAAC 240

CCGCGATCTC tGCGTGACAG GCAGGCGTGT TAACCGCTAC ACTACGAGAC CTATAAAATA 300

TTGCGGGAGG CGGATTTGAA CCACCGaCtT CGGGTTATGA GCCCGACGAG CTACCGAACT 360

GCTCCATCCC GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTCGAA CCCCCGCGGC 420

CCGTTAAGGC CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 480

ATTATTATAG GTAnATCGCT ATTAATTATA AnATTAAAAT GGCGGTCTCG ACGGGAATCG 540

AACCCGCGGA TCT 553

(2) INFORMATION FOR SEQ ID NO: 3691:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3691:

TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA 60

GTTGGCTACC ATCGACGCTA AGAACCTTTC TTGACTTGTG ACAATCGCTT GCTTCTTTCC 120

TCTTCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTTCTCGT 180

TTTGACGTTT TAGACATAAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 300

ATTTTTTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG TTCGGACTAC CATCGACGCT 360

AAGGGAGCTT AACTTTCTGT GTTCGGGCAT GGGGAACAGG 400

(2) INFORMATION FOR SEQ ID NO: 3692:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 410 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3692:

TCGAATACTG TCATGAAGTA ATTTCTCTAT TCTACGACCA GAAAATACAG ATTGAGTATA 60

TGCATATAAG ATGTTTTTAA CATCATTTTT GGATGATAGG ATGTTGCACC ACGATGATGT 120

CTGAATTCAT CGAATTCCTA TCAGGTATCG TTTCAACAAT TTCATTAACA TATCGCGAAA 180

TATCATTTTG AGAATTCTAA CGAnTTTCCT ATTGGTAGTG TAAGTTGGGG TCATGTTATA 240

ATTTTTATAC ATAAGGCACC TCTTTAATTT AGTTTAGTAG TATTTATTAA ATTATACGAG 300

GGACCCAACA CAGAAAATTC ATTTTATTGa ATTTTACATT TATGTGmCAA GTTGGGaAAA 360

ATGTCTTATT TTTTCAAAGT ATTTAAAAGT AAAaTTACAT GTTAATACGT 410

(2) INFORMATION FOR SEQ ID NO: 3693:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3693:

ACTTCATATA ATTTATGAAA TAAACCTGTC AATTTTGGAT TGATTATGCT TTGTGATTCT 60

TTTTATTTCT GCGTAATAAC GCTAAACCTA AAATGCTAAA TAATCCGCCG AACAACATGC 120

CGTTGTTTGT TGATTCTTCT CCACCTGTTT CAGTAGTTCA GATTTCTTAG ATTGTGCTTT 180

TTTAGTTGGT ACCACTGcTT TAACCTTTTC ATTGATTTCA ATAACAGGTG TTACTACTTT 240

ACCTTGTTCC ACTGGTTTAG AAGGTTTTTT AGGTTCTTCT TTAGCAGGTG GTaTTGGTTT 300

ACCAGGTTCA GTTGGTACCT CTGGCGTTGG CGGTGTTGGT GTTTCCGGCT CGCTTGGTAC 360

TTCTGGTGTC GGTGGTGTTG GGTGTTTnCC GGCTTCGCTT GGTACTTCTG GGTGTTCGGT 420

(2) INFORMATION FOR SEQ ID NO: 3694:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3694:

GCATCGTTGC CTTGGTAAGC CGTTACCTTA CCAACTAGCT AATGCAGCGG GAGTCCATCT 60

ATAAGTGACA GCAAGACCGT CTTTCACTTT TGAACCATGC GGTTCAAATn ATTATCCGGT 120

ATTAGCTACG GTTTCCCGAA GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC 180

ACCCGTCCGC CGCTAACATC AGAGAAGCAA GCTTCTCGTC CCGTTCGCTC GACTTGCATG 240

TATTAGGCAC GCCGCCAGGT TCCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG 300

ATGTTTGATT AGCTCATAAA TACTAAATAA TGTTTGTAAC TTATAGTTAC GTTTTTTGGG 360

AATTAACGTT GGACATATTG TCATTCCAGT TTTCAATGTT 400

(2) INFORMATION FOR SEQ ID NO: 3695:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3695:

ACCTAATATA TAGACAGGTT CATCACTTAA TGACTTTGCA AGTTCGGCAA TGTCCTGTGC 60

GTCGCGTTTG ACACGATAAT CACTGTCAGG GTTTGAAGCG GAATCAGGGA GTGGTTCAGT 120

TAACTCGCTT TCTCCATAAT CACGACGATC AACGGCTACA ACAGTAAAAT GGTCTTTTAA 180

CTGTTCTGCA AGAGGCAGAA AAATGTCTCC GGTACCGTTT GCACCAGGAA TAAAGATGAG 240

CACGGGTCCT TGTCCGACTT GGTGGTATCG TAATTTAGCG CCTTGTAATT CTAAAGTTTC 300

CATATTCAAT GACCTCCATT TGTTAATTGT TAGGTGATAA ACCTAATAAT TTAGCACCAT 360

TTGGTATAAC TTAATTTCnC CTTTTCCTTC ATCnGGTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3696:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3696:

TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG 60

CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT 120

CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 180

TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 240

CATTTTTATA AGTCAAACGC TCACATACGG CTTCGTTTTC ATTATTTTAA ATGCTCATTT 300

ACATAAGTAA ACTCTGCTTT AAAATAATTT AACTCATTGT CTGCTAAACG TTTTCTTTTA 360

TAAAAAGATT TAAACGCGTT GATTAAnCTG TGAGTGTTCT 400

(2) INFORMATION FOR SEQ ID NO: 3697:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3697:

CACTTTAACC AAAAAATATT TGAATGTTAA ATAAACATTC AAAACTGAAT ACAATATGTC 60

ACGTTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 120

CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC 180

TTCGACGGCT AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 240

TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA 300

TTACTAnCGA TTCCAnCTTC ATGTAGTCGA GTTGCAGACT ACAATCCGAA CTGAGAACAA 360

CTTTATGGGA TTTGCTTGAC CTCGCGGTTT CGCTnCCCTT 400

(2) INFORMATION FOR SEQ ID NO: 3698:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3698:

AAGGGAATCG AATTTTCTTT CTCTTCCTCC GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60

CCCCATTCGG AAATCTCTGG ATCAAAGCTT ACTTACAGCT CCCCAAAGCA TATCGTCGTT 180

AGTAACGTCC TTCATCGGCT TCTAGTGCCA AGGCATCCAC CGTGCGCCCT TAATAACTTA 240

ATCTATGTTT CCATCCTACA GGAAACGCGT TATTAATCTT GTGAGTGTTC TTTCGAACAC 300

TAGCGATTAT TTCTTATGAA TTCAAGCTTA TTTAAAACTC TTTATTCACT CGGTTGTGCT 360

TGGnAAAATC TATATTTTAC TTACTTATCT AGGTTTCAAT 400

(2) INFORMATION FOR SEQ ID NO: 3699:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3699:

TTTATGGCAT ACACGCATCA TAATACAGCC CAACACCACT AATGGTGCAG TTGCAAATCC 60

AAATTCTTCC GCTCCAAGCG CACATGCGTA CGCTACATCT TTACCAGTTA ATAACTTACC 120

GTCTGTTTCT AACTTAACAC GACTTCTTAA GTCATTTAGT TTTAATGTTT GATGTGTTTC 180

TGCTAAACCA ATCTCCCAAG GAACACCGGC ATGCTGAATA CTCGTTTTGG GTGAAGCCCC 240

TGTAnCACCA TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCCAGA 300

TGCAATGGTA CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT 360

CGCATTTTTC AAATCATGTA TCAGTTGCGC TAAATCTTCT 400

(2) INFORMATION FOR SEQ ID NO: 3700:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3700:

CGACGTACCA TCGACGCTAA GGAGCTTAAC TTTCGTGTGT TCGGCATGGG AACAGGTGTG 60

ACCTCCTTTG CTATAGTCAC CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG 120

TAAGTAAAAG TnATTTTGCT TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG 180

TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT 240

TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTCnC GGGGGGCTTC ATGCTTAGAT 300

GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA 400

(2) INFORMATION FOR SEQ ID NO: 3701:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3701:

AACCAAGCCC AATAATGGAC TGGCCGCCTA ATAATAAAAG CTCTAAAAGT TGTATTTTAA 60

AAATAGTTCT TTAAATTATA TACCCACCAC ATTTGGTGGA GAACCTAAAA AAAAGCACTT 120

CCCAAAAATG GAAAGTGCAA GTAGTGAGCC ATAGAGGATT CGAACCTCTG ACCCTCTGAT 180

TAAAAGTCAG ATGCTCTACC AACTGAGCTA ATGGCTCTAA TGGCTGGGCT AGCTGGATTC 240

GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA 300

TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGnTT TACAGTCCGC 360

CGCGTTTAGC CAnTTCGnTA CCCCTCCAGn TTATTCATAT 400

(2) INFORMATION FOR SEQ ID NO: 3702:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3702:

TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA 60

CGGGATTCGA ACCCGCGACC CCAACCTTGG CAAGGTTGTT ATTCTACCGC TGAACTACTT 120

CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA AGgTTAGaTC CTAAGTCTAG 180

TGCGTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG 240

ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGGCTCT TCCATGGTGC 300

CGGCCAGAGG ACTTGGAACC CCCAACCTAC TGGATTACAA GTCAGTTGGC TCTACCAATT 360

GAnGCTAAGG CCGGCAATAT GTTAAGnATn AATGGTGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3703:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3703:

CAACTAATAA ATAGTGGCGG TGGAGGGGAT CGAACCCCCG ACCTCACGGG TATGAACCGT 60

ACGCTCTAGC CAGCTGAGCT ACACCGCCTT ATATAGTTTG TAAATAATAT GGTGGAkACT 120

AGCGGGATCG AACCGCTGAC CTCCTGCGTG CAAAGCAGgC GCTCTCCCAG CTGAGCTAAG 180

CCCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTCG AACCTGCGAC CCCTTGGTCC 240

CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGCGC CCGATAGGAG 300

TCGAACCCAT AAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG CTAACGGGCG 360

CATATGTTTT TAATTGAAAT GGTGCCCGAG GACCGGAATG 400

(2) INFORMATION FOR SEQ ID NO: 3704:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3704:

CTAACGCCTA CGCGTTACAT GAAAAACGGA GAACAAGCAG AACAATTATT ACGTCAGCTT 60

ATAGAAAAAG ATGAAGCACT AGCTAAGTAT GTCATGGTTT GTGATGAAAC AGCTTGGTGG 120

TCATATATGG GTCAAGATAA TGATATTTTC AAAGATCAAT TAGGTCATCT AACTGTTCAG 180

CTAAGAAAGT ATCCCGAAGT GCTAGCCAAA AATGATACGC AACAGCTAGT GTCAATGGCA 240

GCACTCGCGG CAAATGATCG CACTTTATAT CAAATGATTT GTGGAAAAGA TAATATTTCT 300

AAAAATGATG TCATGACGTT ATTTGAAGAT ATCGCGCAAG TCTTTTTAAA GGTAACACTA 360

TCATTTATGC AATACGGCGC ATTACCCAGA GTTGCATGGT 400

(2) INFORMATION FOR SEQ ID NO: 3705:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 478 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3705:

TGACGGGGAC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT TCGAAGCAAC GCGAaGaACC 120

TTACCAAATC TTGaCATCCT TTGaCAACTC TAGaGATAGA GCTTTCCCCT TCGGGGGTAC 180

AAAGTGACAG GTGGTGCATG GTTGTCGTCA GCTCGTGTCG TGAGATGTTG GGTTAAGTCC 240

CGCAACGAGC GCAACCCTTA AGCTTAGTTG CCATCATTAA GTTGGGCACT CTAAGTTGAC 300

TGCCGGTGAC AAACCGGAGG AAGGTGGGGA TGACGTCAAA TCATCATGCC CCTTATGATT 360

TGGGgCTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGT GAGTCAAGCA 420

AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGACTAC ATGAAGCT 478

(2) INFORMATION FOR SEQ ID NO: 3706:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3706:

ATCTTAAGTC TTTGGTGAAC CGTTTTGTAG AATTAAATAA TATTACAGAG CCGCTAGCAG 60

TAACGATCCA AACGAATTTA CCACCATCAC GTGGATTAGG ATCGAGTGCA GCTGTCGCGA 120

TTGCTTTTGT TCGTGCAAGT TATGATTTTT TAGGGAAATC ATTAACGAAA GAAGAACTCA 180

TTGAAAAGGC TAATTGGGCA GAGCAAATTG CACATGGTAA ACCAAGTGGT ATTGATACGC 240

AAACGATTGT ATCAGGCAAA CCAGTTTGGT TCCAAAAAGG TCATGCTGAA ACGTTGAAAn 300

CTCAAAGTTT AGACGGCTAT ATGGTTGTTA TAGAnACTGG TGTGAAAGGT TCACCAAGAC 360

AAGCAGTAGA AGATGTTCCA TAAACTTTGG TGAGGACCCT 400

(2) INFORMATION FOR SEQ ID NO: 3707:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3707:

GTCGAACTGC CGACACATGG AGCTTCAATC CATTGCTCTA CCAACTGAGC TACTGAACCA 60

TAATAAAAAT GTAATnnTGG CGGTCTCGAC GGGAATCGAA CCCGCGATCT CCTGCGTGAC 120

AGGCAGGCGT GTTAACCGCT ACACTACGAG ACCTATAAAA TATTGCGGGA GGCGGATTTG 180

TAAAAAATAA TGGCGGAGGA AGAGGGATTC GAACCCCCGC GGCCCGTTAA GGCCCTGTCG 300

GTTTTCAAGA CCGATCCCTT CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC 360

GCTATTAATT ATAAAATTAA ATGGCGGTCT CGACGGGAAT 400

(2) INFORMATION FOR SEQ ID NO: 3708:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3708:

GTTCGCCCAT TAAAGCGGTA CCAnGCTGGG TTCAGAACGT CGTGAGCAnG TTCGGTCCCT 60

ATCnGGGGTG GGCGTAGGAA ATTTGAGAGG AGCTGTCCTT AGTACGAGAG GACCGGGATG 120

GACATACCTC TGGTGTACCA GTTGTCGTGC CAACGGCATA GCTGGGTAGC TATGTGTGGA 180

CGGGATAAGT GCTGAAACAT CTAAGCATGA AGCCCCCCTC AAGATGAGAT TTCCCAACTT 240

CGGTTATAAG ATCCCTCAAA GATGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC 300

ATGTGGAGCT GACGAATACT AATCGATCGA AGACTTAATC AAAATAAATG TTTTGCGAAC 360

AAAATCCACT TTTACTTACT ATCTAGTTTT GAATGTATAA 400

(2) INFORMATION FOR SEQ ID NO: 3709:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 424 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3709:

AATTTTATGG GCCCTTTATG GACTTTATAT TmCCTAAAAT ACTATTAAGA AGTCCTGAAA 60

AATTCACATT AGCAGTTGGA TTGTTCAACT TTATTAATGA TAAGTATGCA AATAATTTCA 120

CAGTGTTTGC AGCAGGGGCA ATTATGATTG CAGTACCTAT AGCAATCGTA TTCTTGTTCT 180

TGCAACGCTA TTTAGTATCA GGTTTAACAA CAGGTGCGAC AAAAGGTTAG TTTGAAATTr 240

GGAGTGGGGC AGAATTGATA AAGAACCACT AATGACGATA AAGATTAAAA GGAGGACGTT 300

ATGATGACGA TTAAAGTTGG AATCATTGGG TGTGGTGGTA TTGCGAATGG CAAGCACATG 360

CCAAGTTTAC AAAAAGTTGA AAATGTTGAA ATGATCGCAT TTGTGACGTG GACTTTCGAA 420

(2) INFORMATION FOR SEQ ID NO: 3710:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 559 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3710:

AGTGCTCTAC CAAGCTGAGC TACTTCCCGT ATAATTAACG CGCCCGATAG GAGTCGAACC 60

CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT 120

TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGgAT 180

TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA 240

CGGGATTCGA ACCCGCGACC CCAACCTTGG CAAGGTTGTa TTCTACCGCT GAACTACTTC 300

TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GcTkAGaTCC TgAAGTCTAG 360

TGCGTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG 420

ACCCTCTGGA TTGAAAAGTn CAGATGCTCT GACCAACTGG AGCTAATGGC TCTTCCCATG 480

GTGGCCGGCC AGAAGGACTT GGAACCCCCA ACCTGATGGA TTTACAATTC AGTTGGCTCT 540

AACCAATTTG AGCTAAGGC 559

(2) INFORMATION FOR SEQ ID NO: 3711:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3711:

AACCTTTTAG GAGCTAGCCG TCGAAGGTGG GACAAATGAT TGGGGTGAAG TCGTAACAAG 60

GTAGCCGTAT CGGAAGGTGC GGCTGGATCA CCTCCTTTCT AAGGATATAT TCGGAACATC 120

TTCTTCAGAA GATGCGGAAT AACGTGACAT ATTGTATTCA GTTTTGAATG TTTGTTCATT 180

CAAATTAATG GGCCTATAGC TCAGCTGGTT AGAGCGCACG CCTGATAAGC GTGAGGTCGG 240

TGGTTCGAGT CCACTTAGGC CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC 300

TGGGAGAGCG CCTGCTTTGC ACGCAGGAGG TCAGCGGTTC GATCCCGCTA GTCTCCACCA 360

TTATTTGTAC ATTTGAAAAC TAGATAAGTA AGTAAAATAT 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3712:

TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG 60

CGAnnTCATG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GCCTGAAACC nnGTGATCTA 120

CCCTTGGTCA GGTTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTGA 180

AAAGTGAGCG GATGAACTGA GGGTAGCGGA GAAATTCCAA TCGAACCTGG AAATAGCTGG 240

TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGG ATTATTGGAG GTAGAGCACT 300

GTTTGGACGA GGGGCCCCTC TCGGGTTACC GAATTCAGAC AAACTCCGAA TGCCAATTTA 360

ATTTAACTTG GGGAGTCAGA ACATTGGGTG ATAAGGTCCG 400

(2) INFORMATION FOR SEQ ID NO: 3713:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3713:

TTTTTAAGTC TGATGTGAAA GCCCACGGCT CAACCGTGAA GGGTCATTGG AAACTGGAAA 60

ACTTGAGTGC AGAAGAGGAA AGTGGAATTC CATGTGTAGC GGTGAAATGC GCAGAGATAT 120

GGAGGAACAC CAGTGGCGAA GGCGACTTTC TGGTCTGTAA CTGACGCTGA TGTGCGAAAC 180

GTGGGGATCA nACAGGATTA GATACCCGGT AGTCCACGCC GTAAACGATG AGTGCTAAAG 240

TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGTAAACGCA TTnAAGCACT CCGnCTGGGG 300

AGTACGnCCG CAAGTTGGAA ACTTCAAAGG AATTGACGGG GGACCCGCAC AAGCGTTGGG 360

AGCATGTGGT TTAATTTCGA AGCAACGGAG AGGAACCTGA 400

(2) INFORMATION FOR SEQ ID NO: 3714:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3714:

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60

TGTGGATTAA TATTATGCCT GGCAACGTTC TACTCTAGCG GAACGTAAnT CGACTACCAT 120

CGACGCTAAG GAGCTTAACT TCTGTGTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT 180

AGTCACCAGA CATATGAATG TAATTTATAC ATTCAAAACT AGATAGTAAG TAAAAGTGAT 240

TTTGCTTCGC AAAACATTTA TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC 300

cAtGTCACCA TGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAGG GATCTTATAA 360

CCGAAGTTGG GAAATCTCAT CTTGAGGGGG GCTTCATGTC TTAGCATTTC AGTCACTTAT 420

GCCCG 425

(2) INFORMATION FOR SEQ ID NO: 3715:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3715:

GTCCCTGCTG TTCCTATCAT ATAAATGATA GATTCAAATA GATTTGTAGG TTTGTCATGC 60

CCAGTTACAA GTTGCGTTAT CGTAGACACT AACATTAATA TGACTGGTAA TGTTGCTGTT 120

AATAAACTCA TACCAAATCC TGGCATCTCT TGATCCGTAA ATTCTTTTTG TGCACCTAAC 180

GCTGAAATAT CGCCTTCTCG TGTATACGCA GACGGAATCA TTTTTTGTGC ACTTTGTTAA 240

ATATAGGCCC TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATACA GTAATACATC 300

TCCAACATTT GCCTTTAATT CTTTTGCGAG ACTACCGGTC CTGGGATGTG GTGGTAAAAA 360

GCCATGTGTC ACTGATAAAG CTGTTACCAT AnGTAGTCCT 400

(2) INFORMATION FOR SEQ ID NO: 3716:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3716:

TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG TTTTGCTTGG TAAAATCTAT 60

GCAATATCAC TTTAACCAAA AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA 180

ATATGTCACA TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA 240

GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG 300

TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTACTCCACC GGnTTCGGGT GTTACAAACT 360

GTTCGTGGTG TGACGGGGCG GTGTGTTACA AGACCCGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3717:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3717:

AAAGGACGAC ATTAGACGAA TCATCTGGAA AGATAATTCA AAGAAGGTAA TAATCCTGTA 60

GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGGTACGAC GGAGCACGTG AAATTCCGTC 120

GGAATCTGGG AGGACCATCT CCTAAGGCTA AATACTCTCT AGTGACCGAT AGTGAACCAG 180

TACCGTGAGG AAAGGTGAAA AGCACCCCGG AAnGAGTTGA AATAGAACCT GAAACCGTGT 240

GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG 300

CGAGTTACGA TTTGATGCAA GGTTAAGCAG TAAATGTGGA GCCGTAGCAn AAnnTGTTCT 360

GAATAGGGCG TTTAGTATTT TGGTCGTAGC CCGAGAACCA 400

(2) INFORMATION FOR SEQ ID NO: 3718:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3718:

TAATTCATCT GCAGCATCTG GTTGATTTAA GCTTTCACGT AAACACATCG CTAAAGATAG 60

AATCATTCCA AATGGATTGG CAACGTTTTT ACCTGCAATA TCTGGTGCTG ATCCATGAAT 120

AGGCTCATAC AATCTTGGAC CATCGTTACT AAAACTAGCA GAAGGTGATA AACCAAGTGA 180

ACCAGGAATC ACTGAAGCTT CATCACTTAA AATATCGCCA AATAAGTTTT CACATACGAT 240

GACGTCAAAT TGTTTTGGnA TTTGTGATTA AATGCATACT ACAAGCATCA ACAAATAAGT 300

TTTACTAGAA GCTAATACAT TTCCTTATCA ACGGATGTnA 400

(2) INFORMATION FOR SEQ ID NO: 3719:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3719:

ATTTAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAAnTA AGTnGAGCTA CCATCGACGC 60

TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120

CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT 180

TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT 240

CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA 300

GTTGGGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA CTTATCCCGT 360

CCACACATAG CTACCCAGCT AGCCGTTGGC ACGACAAnGG 400

(2) INFORMATION FOR SEQ ID NO: 3720:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3720:

CGTTACACCT TCCAATAAAT TTGCTGTTGC TGGATAAGGA GAAATATTGA TATATTGTCT 60

TAAATTACTA TAATGCCAAT TTAAGTCTGG ATGATTTGTT AAGACACCAA TAGGATTATC 120

TTTTATAACC ACTTCACCCT CTTTAAATGA AACTTCGACT GTATGTCCAG TTGCATCGGA 180

AACATGATAA TGCAATGGCG GAACTTCACC GATGTCATTT AAATATACAG CTACAACATG 240

TATTTGGGAT GCTTGTTGTT TCATATCTTC AATGCTTGTT GTATATCCCA AAATCCATGT 300

CACAATTTCA TTTTGCGTAA TATTCATCGC GTCCGCTTTG TGTGTTGGAT CCATATGGAA 360

CTATAACCTC GGGAAATATT GTGGTTGAAA TGGGCACGCC 400

(2) INFORMATION FOR SEQ ID NO: 3721:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3721:

AGTCAGTTTA TAGCGATTGC TGGACTGACA GTACTTGTGC CATTATTGCC AATTTATATG 60

GCATCACTAC AAAATCTATC AGTCGTAGAA ATACAGTTGT nGAGTGGTAT AGCGATTGCT 120

GCTCCAGCTG TAACGACGAT GATAGCTTCG CCGATATGGG GGAAGCTAGG TGATAAGATC 180

AGCCGAAAAT GGATGGTGTT AAGAGCGTTA CTTGGTTTGG CGGTATGCTT ATTTTTAATG 240

GCATTGTGTA CGACACCATT ACAGTTTGTA CTTGTGGAGG TTATTGCAGG GACTATTTGG 300

TGGTGTTGTT GATGCATCAA GTGCGTTTGC GAGTGCAGAA GGCGCCACTG AnAGATCGTG 360

GGAAAGGTAT TAGGAAGACT GCAAATTnCA GTTCAGCGCA 400

(2) INFORMATION FOR SEQ ID NO: 3722:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3722:

TCTAAAAGTT GAACTACTCC CGCATAAACC TGGAGGCGGC AACCGGATTT GAACCGGTGA 60

TAAAGGTTTT GCAGACCTCT GCCTTACCAC TTGGCTATGC CGCCAATAAC TGGGCTAGCT 120

GGATTCGAAC CAACGAGTGA CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAT 180

TAATAATAAG GGCGGCTGAA GGGGATCGAA CCCTCGAATG TCGGAACCAC AATCCGATGT 240

GTTAACCACT TCACCACAGC CGCCATGGCA GGGGCAGTAG GAATCGAACC CACACCAAAG 300

GTTTTGGAGA CCTCTATTCT ACCnTTGAAC TATGCCCCTA TTAAAATGAT AAATGGAGGG 360

GGGCAGATTC GAACTGCCGA ACCCGAGGGG CGGATTTTAC 400

(2) INFORMATION FOR SEQ ID NO: 3723:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3723:

GGTTCAAGTC CTCTGGCCGG CACCATTTnT GGAGGGGTAG CGAATGGCTA AACGCGGCGG 120

ACTGTAAATC CGCTCCTTCG GGTTCGGCAG TTCGAATCTG CCCCCCTCCA TTTATTATTT 180

TTAATAGGGG CATAGTTCAA CGGTAGAATA GAGGTCTCCA AAACCTTTGG TGTGGGTTCG 240

ATTCCTACTG CCCCTGCCAT GGCGGCTGTG GTGAAGTGGT TAACACATCG GATTGTGGTT 300

CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCTTATTA TTAATGGGCT ATAGCCAAGC 360

GGTAAGGCAA CGGACTTTGA CTCCGTCACT CGTTGGTTCG 400

(2) INFORMATION FOR SEQ ID NO: 3724:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3724:

CACTTTAGCA AATGGTGACA AAGTCCGTAT TGCTACAATT TTTGACTTAA TGGCAAGTCA 60

ATATGGCGTG CGTCGTTTTG ATCATAAATT AGAATCAAAA GGATACGACG ATGCAGAATC 120

AAAATATACA CCTGCTTGGC AAGAAGCCAT TTCAGGCGTA AAACAAAGTG TTnGTCATTC 180

AAGTAGCGAA AGAATTTGCG CAAAACGCTA TCGATACTGA AGGGCGTTCA ATGATTATCA 240

TGGGTGCGGG TATTAACCAT TGGTTTAACT CAGATACGAT TTATCGTTCC AATCTTAAAC 300

TTAGTTATGT TATGTGGCTG TCAGGTGTGA ATGGTGGCGG TTGGGGCTCA CTATGTGGGG 360

ACAAGAAAAA TGTCGTCCGA TTGAAGGATG GAGTACTGTC 400

(2) INFORMATION FOR SEQ ID NO: 3725:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 476 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3725:

CGCTATCTGA ATCTGAATCG CTATCTGAAT CTGAGTCGTT GTCTGAGTCC GAATCGCTAT 60

CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTATCTGA ATCTGAGTCG CTGTCTGAAT 120

CTGAATCACT GTCTGAGTCT GAGTCGCTGT CTGAGTCTGA ATCGCTGTCA GAATCTGAGT 180

CGCTATCTGA GTCTGAATCT GAATCACTGT CTGAGTCCGA ATCGCTATCT GAATCTGAAT 240

CCGAGTCTGA ATCGCTGTCT GAGTCTGAGT CGCTGTCTGA ATCTGAATCG CTATCTGAGT 360

CTGAGTCGCT GTckGAATgC GCTGTCTGAA TCTGAGTCGC TATGCTGAAT GCTGAGTnCG 420

CTATGTGAGT CTGAATGCGC TGTGCAGAAT CTGAGTGCGC TCATCTGATG TTTCTT 476

(2) INFORMATION FOR SEQ ID NO: 3726:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3726:

ATACGACCAC TGTTTAATGC GTCCATTAAA TCTGGCCAAT TATTGAATTT AACTAATTCT 60

AGTTTATATT TCGGATGATT GTATTGTGAT AATAATTTTT TAGTCATCAT CAAATTAGCT 120

GAATGTGTAA TCGGCAAATA TCCAATTTTA ATCACTTGCT GATTTTGGGC ATTTTTAGAC 180

CGTTCTTTAG ACGTCCTTTG CCAATCACAT CCTGTAATTA TAAAGATTCC AATGATGACG 240

ATTATGCTTA ACCTTTTCAT CGTCACTCAC TCCTTATAAA TAATATTCAG GTTCAACTTG 300

ATGATGATTC AATGCAAnGT TTCCATAATT TCATTACGAA TCTTAAGTAG GTGGCTATCA 360

TTACGGACTG CGTGGATGTG AnGCTGTAAA TTCCATAnTG 400

(2) INFORMATION FOR SEQ ID NO: 3727:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3727:

ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 60

ATGGGCGAAC AGCAAACCCT TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC 120

GAGGTGCCAA ACCTCCCCGT CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG 180

GGTAGCTTTT ATCCGTTGAG CGATGGCCCT TCCATGCGGA ACCACCGGAT CACTAAGTCC 240

GTCTTTCGAC CCTGCTCGAC TTGTAGGTCT CGCAGTCAAG CTCCCTTATG CCTTTACACT 300

CTATGAATGA TTTCCAACCA TTCTGAGGGA ACTTTGAGCG CCTCCGTTnC CTTTTAGGAG 360

GCGAACGGCC CCAGTTCAAA CTGCCCGCCT GAACACTGTC 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3728:

TTGAAAAGTC ATATCAAAGC GCACATGTTT TTAAGCGTCG TCGAACACCT ATCGTGAAAG 60

GTGTGTCATT TGAGTGTCCA ATCGGTGCGA CGATTGCGAT TATCGGAGAA AGTGGTAGCG 120

GTAAATCGAC GTTGAGTCTA TTGATATTAG GTATTGAGAA ACCGGATAAA GGTTGTGTAA 180

CCTTAAATGA TCAACCGATG CATAAGAAGA AAGTGAGACG TCATCAAATT GGTGCTGTAT 240

TTCAAGATTA TACGTCATCA TTACATCCAT TTCAGACTGT TAGAGAAATC TTATTTGAAG 300

TGATGTGTCA ATGTGATGGA CAACCTAAAG AAGTTATGGA AGTCCAAGCA ATTACATTGT 360

TGGAAGAAGT CGGTCTATCT AAGGCATACA TGGGATAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3729:

ATCGAACCCC CGACCTCACG GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC 60

TTATATAGTT TGTAAATAAT ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 120

TGCAAAnAGC CGCTCTCCCA GCTGAGCTAA GCCCCCATAA TAATTACAGT ATATCGGGAA 180

GACAGGTTCG AACCTGCGAC CCCTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC 240

TTCCCGTATA ATTAACGCGC CCGATAGGAG TCGAACCCAT AACCTCTTGA TCCGTAGTCA 300

AACGCTCTAT CCAATTGAGC TACGGGCGCA TATGTTTTTA TTGAAAATGG TGCCGAGGAC 360

CGGAATCGAA CCnGTAGTGA ATCACTCACC GCAGATTTTA 400

(2) INFORMATION FOR SEQ ID NO: 3730:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3730:

ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT 60

CATCGGCTTC TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACTTAAT CTATGTTTCC 120

ACCATTTTTA TAAGTCAAAC GTTAACATGA AGTTACGTTC TTTTATAAAA AGATTTAAAC 180

GCGTTATTAA TCTTGTGAGT GTTCTTTCGA ACACTAGCGA TTATTTCTTA TGAATTCAAG 240

CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT TTACTTACTT 300

ATCTAGTTTT CAATGTACAA ATAATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT 360

GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC 400

(2) INFORMATION FOR SEQ ID NO: 3731:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3731:

TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 60

TGGAGAATGA CGGGTTCGAA CCGCCGACCC TCTGCTTGTA AGGCAGATGC TCTCCCAGCT 120

GAGCTAATTC TCCGATTTAA AACTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC 180

GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCGG CATGGGAACA GGTGTGACCT 240

CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA TTCAAAACTA GATAGTAAGT 300

AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAt GTCTTCGATC GATTAGTATT 360

CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCGAACCTA T 401

(2) INFORMATION FOR SEQ ID NO: 3732:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3732:

CATTATTAAC GGCTATGGTT TAACTGAAGC ACCTCTTGTA CTTGTTAATA CACCGGAAAA 60

TTCAAAACGT AAGCCAATGA GTATTGGTAA AGCAGTCATG TTCGTTGATG CACGTATCCT 120

AAATGTCACG CCAGGATATT GGAATAAACC AGCAGAGACT GCCAAAGCAT TTCATGGTCG 240

ATATTTATTA ACTGGTGACT TAGCGAgATG GACAACGATG GCGATATATT TATTATTGAC 300

CGCAAAaAAG AaTTAATCAT AACTGGTGGc GAAAATGTCT TACCATCCGa gTCGAAAtGC 360

TTaCtGaGCA TCCACTAGTA GACCGGTGTG TGGTCGT 397

(2) INFORMATION FOR SEQ ID NO: 3733:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3733:

AAGTAACAAT CGTTCACCGT CGTGATGAGT TACGTGCACA GCGTATTTTA CAAGATAGAG 60

CATTCAAAAA TGATAAAATC GACTTTATTT GGAGTCATAC TTTGAAATCA ATTAATGAAA 120

AAGACGGCAA AGTGGGTTCT GTGACATTAA CGTCTACAAA AGATGGTTCA GAAGAAACAC 180

ACGAGGCTGA TGGTGTATTC ATCTATATTG GTATGAAACC ATTAACAGCG CCATTTAAAG 240

ACTTAGGTAT TACAAATGAT GTTGGTTATA TTGTAACAAA AGATGATATG ACAACATCAG 300

TACCAGGTAT TTTTGCAGCA GGnGATGTTC GCGACAAAGG TTACGCCAAA TTGTCACTGC 360

CACGGCGATG GTAGTATGCC AGCGCAAGTG CCACGGAATG 400

(2) INFORMATION FOR SEQ ID NO: 3734:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3734:

GCCGTTTACT GTGGCTTCGA TTCGTAGCTT CGCAGAAGCT AACCACTCCT CTTAACCTTC 60

CAGCACCGGG CAGGCGTCAG CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT 120

TTGATAAACA GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGCGTTAA CCCTAAAGAG 180

CACCCCTTCT CCCGAAGTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG 240

CTCACCTTAG AATTCTCATC TTGACTACCT GTGTCGGTTT GCGGTACGGG CACCTATTTT 300

CTATCTAGAG GCTTTTCTCG GCAGTGTGAA ATCAACGAcT CGAAGACACA ATGTCTTCTC 360

TAGACGTGCA ATCCAATCGG CAACGCTTCG CCTAATCCTA ACTGGCGGTC CCCCCCCnAT 480

(2) INFORMATION FOR SEQ ID NO: 3735:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3735:

CGATCCCTTC AGCCGGACTT GGGTATTCCT CCAAAATTAT ATGGACCTTG CAGACTCGAA 60

CCTGCGACCG AACGGTTATG AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA 120

TAATTTTACA ACTAATAAAT AGTGGCGGTG GAGGGGATCG AACCCCCGAC CTCACGGGTA 180

TGAACCGTAC GCTCTAGCCA GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG 240

TGGAGACTAG CGGGATCGAA CCGCTGGACC TCCTGCGTGC AAACAGnCGC TCTCCCAGCT 300

GAGCTnAAGC CCCCATAATA ATTACAGTAT ATCGGGAAGA CAGGATTCGA ACCTGCGACC 360

CCTTGGTCCC CAAACCAAGT GGTTTnACCA AGTTGAGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3736:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3736:

TGAGCCCGAC GAGCTACCGA ACTGCTCCAT CCCGCGATAA TAAAAAATAA TGGCGGAGGA 60

AGAGGGATTC GAACCCCCGC GGCCCGTTAA GGCCCTGTCG GTTTTCAAGA CCGATCCCTT 120

CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC GCTATTAATT ATAAAATTAA 180

ATGGCGGTCT CGACGGGAAT CGAACCCGCG ATCTCCTGCG TGACAGGCAG GCGTGTTAAC 240

CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 300

TTAAGCCCCT GTCGGTTTTC AAGACCGATT CCTTCAGCCG GACTTGGGTA nTCnTCCAAA 360

ATTATATGGA CCTTGCAGGA CTCGAACTGC GAnCGAACGG 400

(2) INFORMATION FOR SEQ ID NO: 3737:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3737:

TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC 60

AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC 120

CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT 180

TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA 240

TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT GGAGCAGAAG 300

ACGGGATTCG AACCCGCGAC CCCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACTACTT 360

CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA 400

(2) INFORMATION FOR SEQ ID NO: 3738:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3738:

AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG 60

CTAATTCTCC GATTTAAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAAGT AATCGGAnCT 120

ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT 180

GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AAACTAGATA GTAAGTAAAA 240

GTGATTTTGC TTCGCAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG 300

CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT 360

TATAACCGAA GTTGGGAAAT CTCATCTTGG AGGGGGGCTT 400

(2) INFORMATION FOR SEQ ID NO: 3739:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3739:

CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA CCGACATCTT 120

TAATTAATTG CTnTGCACGT TTTCTATCAA ATTTATCATT ACGTGCAAGT GATGGGAATA 180

TCATGTTATC TTCAATCGTT TCACCAAACA AGTCACTTTG CTGCATCAAA TAACTGATTC 240

GTTGACGCAA TTCTTCCGGG TCATAATCAT TATAGGGTTT ACCTTTAAAA TAAAGTTCTC 300

CACTAGTTGG ACTAAACAAA TTACATATnT GCTTTTGAAA TGTACTTTTA CCACTACCTG 360

ATGGACCTAT AATGGCAATA CTCTCGCCTT TATCTACTTT 400

(2) INFORMATION FOR SEQ ID NO: 3740:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3740:

ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG 60

TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT 120

TTGTGTTTAC TTTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180

TGCGGCTCAT CGCATCCaTT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA AnTAATTGGC 240

TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT 300

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC 360

AGATtCAAAC GTTTTCACTT CGCCAAGCCA tTTTTCtTTG TGTTTGCTTT TnA 413

(2) INFORMATION FOR SEQ ID NO: 3741:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3741:

CTTAGATGCT TTCAGCACTT ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC 60

GACAACTGGT ACACCAGAGG TATGTCCATC CCGGTCCTCT CGTACTAAGG ACAGCTCCTC 120

TCAAATTTCC TACGCCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA 180

GCTCGCGTAC CGCTTTAATG GGCGAACAGC CCAACCCTTG GGACCGACTA CAGCCCCAGG 240

TAAGCTGTTA TCCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGCCCTTCC ATGCGGAACC 360

ACCGGATCAn TAAGTCCGTC TnTCGACCCT GnTGGACTTG 400

(2) INFORMATION FOR SEQ ID NO: 3742:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3742:

GTTTTGAATG TATAAATTAC ATTCATATGT CTGGTGACTA TAGCAAGGAG GTCACACCTG 60

TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC 120

CGCTAGAGTA GAACGTTGCC AGGCAGTTTT AAATCGGAGA ATTAGCTCAG CTGGGGAGAG 180

CATCTGCCTT ACAAGCAGAG GGTCGGCGGT TCGAACCCGT CATTCTCCAC CATTTATTCT 240

TACATATTGC CGGCCTAGCT CAATTGGTAG AGCAACTGGA CTTGTAATCA GTAGGTTGGG 300

GGTTCAAGTC CTCTGGCCGG CACCATGGGA AGAGCCATTA GCTCAGTTGG TAGAGCATCT 360

GACTTTTAAA TCAGAGGGTT CAGAGGTTnC GAATCCGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3743:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3743:

TCGCAATAAC CGCATCAAAT GTATTGCCTA AAAAGGCTGG ATTTTCCAAT GTGTCATCAT 60

TACGGATCTC GAAGTTCTCA TAACGCACAT CATGTAATAA CATATTCATG CGTGCTAAGT 120

TGTATGTAGT ATTGTTACGT TCTTGTCCGA AATAACGATA CACTTGCGTT TCTTTACCAA 180

CACGTAACAA CAATGAACCG GAACCACATG TTGGGTCGTA CACGTGACGT AATTTATCTT 240

TACCGTCTGT GACAATCTTC GCCAGTATCT TAGATACTTG TTGTGGTGTA TAGAACTCGC 300

CTGCTTTTTT ACCCGCTGTC GCCGCAAAGC GCCCGATTAG GAATTCATAT GCATCACCTA 360

ACATATCAAT TTCCATGGTC ACTGTGAACG AATGGGTAAG 400

(2) INFORMATION FOR SEQ ID NO: 3744:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3744:

CTACTGATTA CAAGTCAGTT GCTCTACCAA TTGAGCTAGG CCGGCAATAT GTAAGAATAA 60

ATGGTGGAGA ATGACGGGTT CGAACCGCCG ACCCTCTGCT TGTAAGGCAG ATGCTCTCCC 120

AGCTGAGCTA ATTCTCCGAT TTAAAACTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA 180

GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG 240

ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT 300

AAGTAAAAGT GATTTGCTTC GCAAAACATT ATTTGATTAA GTCCTCGATC GATAGTATCG 360

TCAGCTCCAC ATGTCACCAT GCTTCCAnCT CGnACCTATT 400

(2) INFORMATION FOR SEQ ID NO: 3745:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3745:

CATAAGTAAA CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT 60

AAAAAGATTT AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACACTA GCGATTATTT 120

CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA 180

TATTTTACTT ACTTATCTAG TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA 240

CTGCTTTATT nTCAAAAAAT CAAATGCTCA TTTACAAAAG TAAACTCCGC TTTAATTTTC 300

TTAATGCATT GTCTAACAAC CGCTTGCTTT AAAAAGAATA GATTGnCAAG CGCTCGCATA 360

AGCAATATCA CTTnAACCAA AAAATA 386

(2) INFORMATION FOR SEQ ID NO: 3746:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 677 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AAGGTGAAAA GCACCCCGGA AGGATGTTGA AATAGAACCT GAAACCGTGT GCTTACAAGT 60

AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG CGAGTTACGA 120

TTTGATGCAA GGTTAAGCAG TAAATGTGGA GCCGTAGCAk AACanGGTCT GAATAGGGCG 180

TTTAGTATTT GGTCGTACCG AnAACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG 240

TAACACTGAA TGGAGGACCG AACCGACTTA CGTTGAAAAG TGAGCGGATG AACTGAGGGT 300

AGCGGAGAAA TTCCAATCGA ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGc 360

TAGCCTCAAG TGATGATTAT TGGAGGTAGA GCACTGTTTG GaCGAgGGGC CCCTCTCGGG 420

tTACCAATTc AGACAAACTC CGAATGCCAA TTAATTTAAC TTGGGgAGTC aGAACATGGG 480

TGATAAGGTC CGTGTTCGAA AGGGAAACAG CCCAGACCAC CAGCTAAGGT CCCAAAATAT 540

ATGTTAAGTG GAAAAGGATG TGGCGTTGCC AGACAACTGA GGATGTTGGC TTAGAAGCAG 600

CCATCATTTT AAAGAGTGCG TAATAGCTCA CTAGTCGAAG TGACACTGCG CCGAAAATGT 660

GACCGGGCnT AAACnAT 677

(2) INFORMATION FOR SEQ ID NO: 3747:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 417 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3747:

GTCCAATGAT TCATATGCTT TATTATCACG GTATTGCCTT TGAATCGCAT GCACAAAATA 60

TGATGCTCAT TCATGAAAAT GGTTGGCCTA CACGTATTGC CTTAAAAGAT TTCCATGATG 120

GTGTTCGTTT TAAGCGTGAc ATTTAAGTGA AGCTGCTTCA CACCTGACAT TAAAGCCAAT 180

GCCAGAAGCA CATAAAAAAG TGAATAGTAA TTCATTTATT GAAACAGATG ACGAACGTTT 240

AGTACGCGAC TTTTTACATG ATGCATTTTT CTTTATTAAT ATCGCCGAAA TCATCTTATT 300

TATTGAAAAG CAATATGGTA TCGATGAGGA GCTGCAATGG cAATGGGkTa AAGGCATCAT 360

CGAGGCGTAT CCAGrAGcAT TTCCaGAGTT kGAATaACTA TCCAACCATT CGGTTTT 417

(2) INFORMATION FOR SEQ ID NO: 3748:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3748:

ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC CTGGCAACGT TCTACTCTAG 60

CGGAACGTAA GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG 120

AACAGGTGTG ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA 180

ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGTCTTCG 240

ATCGATTAGT ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT 300

CATCATCTTT GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA 360

TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 400

(2) INFORMATION FOR SEQ ID NO: 3749:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3749:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC 60

AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTTCTTTG TGTTTACTTT TTATTTTGAC 120

GTTTTAGGCA TAAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT 180

TGCCTGGCAA CGTTCTACTC TAGCGGAAGT AAGTTGGGCT ACCATCGTCG CTAAAGACCT 240

TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTACTCATTT 300

AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 360

GCCAAGCCAT TTTTTCTTTG TGTnTACTTT TTAATTTTGA 400

(2) INFORMATION FOR SEQ ID NO: 3750:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3750:

ATAAAAAAAA GAGACCTTGC GGTCTCAAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC 60

AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC 120

TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 240

ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA GAGACCTTGC 300

GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGGC AACGTTCTAC TCTAGCGGAA 360

nTAAnTTGGG CTACCATCGA CGCTAAGAAC CTTTCTTGGA 400

(2) INFORMATION FOR SEQ ID NO: 3751:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3751:

CACTCACCGC AGATnTTTAA GTCCTGTGCG TCTGCCAGTT CCGCCACCCC GGCACTATAA 60

AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC CTTGGCAAGG TTGTATTCTA 120

CCGCTGAACT ACTTCTGCAT ATGCGGGTGA AGGGAGTCGA ACCCCCACGC CGTAAGCTnA 180

GnATTCCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240

GGATTCGAAC CTCTGGACCC TCTGATTAAA AGTCAGATGC TCTACCAACT GGAGCTAATG 300

GCTCTTTCCA TGGTGCCCGG CCAGAGGACT TGGAACCCCC AACCTACTGA TTACAAGTCA 360

GTTGCTCTAA CCAATTGAGC TAAGCCGGGC AATATGTTAn 400

(2) INFORMATION FOR SEQ ID NO: 3752:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3752:

TTAnAnAnCC GCGACATTAT AGAGCCAATC ACTAGCCTAT CTCAGAATCA CCAACGAATC 60

CTTCATTATT AAGGAATCTA GGCATCTTTA CGGCGTGGTT CTAATCGCAT CTTTTTCAAT 120

CTAAGTGCGT TTGTGACAAC ACTTACTGAA CTTAGTGCCA TTGCAGCACC AGCAACCCAT 180

GGCGCAAGTA AGCCCAATGC AGCTATAGGG ATACCGGCAA TATTATAGCC GAATGCCCAA 240

AATAGATTTT GACGAATATT ACGAATGGTT GcTTTACTTG cATAAATGGC TTTAGGaATa 300

AGCATCAAGT cGCCACCAAG AATAGTAATA TCAGCTGCTT CAATGGGCAA CTTCTGTTAC 360

(2) INFORMATION FOR SEQ ID NO: 3753:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3753:

CCTTGCGGTC TCAATGGCGG CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA 60

GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT 120

TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 180

TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT 240

TTACTTTTTA TTTTGACGTT TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC 300

TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTGGCTACCA 360

TCGACGCTAA GAACCTTTCT TGACTGGTGA CAAnCGCTTG 400

(2) INFORMATION FOR SEQ ID NO: 3754:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3754:

CTGAGCTAAG CCCCCAAATA GGTATTAAAT TAATGGTGGG CCTAAGTGGA CTCGnACCAC 60

CGACCTCACG CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC ATTAATTTGA 120

ATGAnCAAAC ATTCAAAACT GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG 180

ATGTTCCGAA TATATCCTTA GAAAGGAnGT GATCCAGCCG CACCTTCCGA TACGGCTACC 240

TTGTTACGAC TTCACCCCAA TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGTTA 300

CTCCACCGGC TTCGGGTGTT ACAAACTCTC GTGGTGTGAC GGGCGGTGTG TACAAAACCC 360

GGGAACGTAT TCACCGTAGC A 381

(2) INFORMATION FOR SEQ ID NO: 3755:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3755:

AGCTCCCCAA AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCAAGGCAT 60

CCCCGTGCGC CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA 120

CATGAAGTTA CGTTCTTTTA TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTTCT 180

TTCGAACATA GGCGATTATT TCTTATGAAT TCAAGCTTAT TTAAAACTCT TTATTCACTC 240

GGTTTTGCTT GGTAAAAACn ATATTTTACT TACTTATCTA GTTTTCAATG TACAATTTCT 300

TTTTAGTCAA GCGCTCGCAT ACTGCTTTAT TTTCCATAAG CAATAnCACT TTAACCAAAA 360

AATATTTGGA ATGTTnAAAT AAACATnCAA AACTGAATAC 400

(2) INFORMATION FOR SEQ ID NO: 3756:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3756:

CTACTCACAC CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA 60

CGCCCTTAGA ACGCTCTCCT ACCATTGTCC AAAGGCATGC GCACAGCTTC GGTAATATGT 120

TTAGCCCCGG TACATTTTCG GCGCATGTCA CTCGACTAGT GAGCTATTAC GCACTCTTTA 180

AATGGATGGC TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCCAC ATCCTTTTCC 240

ACTTAACATA TATTTTGGGA CCTTAGCTGG TGGTCTGGGC TGTTTCCGGn GGGGnACACG 300

GACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTCGG ATTTGTCTGA 360

ATCGGTAACC CGAGAGGGCC CnTCGTCCAA ACAGTGCTCT 400

(2) INFORMATION FOR SEQ ID NO: 3757:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 458 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3757:

GGCAGATGCT CTCCCAGCTG AGCTAATTCT CCGATTTAAA ACTGCCTGGC AACGTTCTAC 60

ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT 180

TCAAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAAGT 240

CTTCGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT CGAACCTATT 300

AACCTCATCA TCTTTGAGGG aTCTTATAAC CGAArTttGG GAAtCTCATC TTGAGGGGGG 360

gCTCATGCtT AGATGCTTcA GCACTTATCC CGTCCACACA TAGCTAnCCA GCTATGCCGT 420

TnGCACGACA ACTGGTACAC CAGAnGTATG TCCATCCC 458

(2) INFORMATION FOR SEQ ID NO: 3758:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3758:

AGCGCTCGCA TACTGCTTTA TTTTCAAAAA ATCAAATGCT CATTTACAAA AGTAAACTCC 60

GCTTTAATTT TTCTTAATGC ATTGTCTAAC AACCGCTTTC TTTAAAAAGA ATAGATTGTC 120

AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAAATAT TTGAATGTTA AATAAACATT 180

CAAAACTGAA TACAATATGT CACGTTATTC CGCATCTTCT GAAGAAGATG TTCCGAATAT 240

ATCCTTAGAA AGGAGGTGAT CCAGCCGCAC CTTCCGATAC GGCTACCTTG TTACGACTTC 300

ACCCCAATCA TTTGTCCCAC CTTCGACGGC TAGCTCCTAA AAGGTTACTC CACCGGCTTC 360

GGGTGTTACA AACTCTCGTG GTGTGACGGG CGGTGTGTAC 400

(2) INFORMATION FOR SEQ ID NO: 3759:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3759:

GACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG 60

GTTATGAGCC GTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT TTTACAACTA 120

ATAAATAGTG GCGGTGGAGG GGATCGAACC CCCGACCTCA CGGGTATGAA CCGTACGCTC 180

TAGCCAGCTG AGCTACACCG CCTTATATAG TTTGTAAATA ATATGGTGGA GACTAGCGGG 240

TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC 360

AAGTGCTCTA CCAAGCTGAA GCTACTTTCC CGTATAATTA 400

(2) INFORMATION FOR SEQ ID NO: 3760:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3760:

CACTTAATGC CCGTACCACA CATAGCTACC CAGCTATGCC GTTGGCACGA CAACTGGTAC 60

ACCAGAGGTA TGTCCATCCC GGTCCTCTCG TACTAAGGAC AGCTCCTCTC AAATTTCCTA 120

CGCCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTC TGAACCCAGC TCGCGTACCG 180

CTTTAATGGG CGAACAGCAA nCCCTTGGGA CCGACTACAG CCCCAGGATG CGATGAGCCG 240

ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAACTCTTG GGGGAGATAA GCCTGTTATC 300

CCCGGGGTAG CTTTTATnCG TTGAGCGATG GnCCTTnCAT GCGGAACACC GGATCACTAA 360

GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3761:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 623 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3761:

TATGTATTTT ATAATGTACA GCTCGTTGAn TCnTATTTTT CCTTATATTA AGTGCCATTA 60

ATACAAAACC TAGCTCTCGT TTAACTTTAT TTATTCCTCG AACTGACATT CGAGTGAACC 120

CAAAATAGCC TTCATAAATC CAAAAACAGG CTCTACATCA ATTTTTCTTT GACTATAGAT 180

TTTTTTCGTT TCTGGTTCAG AAAGCTTTTG ATTAATTTGG ACTTTAAAGT ATTCCCAATT 240

ATAATTCTTC ATGATTTTCT TATTGGATTT CGAATTTGGT TTCATGCATT GATGTCTCAA 300

AGAACATGAT GAACAGTCAT CACATTCATA TAGTTTGAAG TCTCGTTTAA AACCATATCT 360

ATCATTACGG TATGCATATC TTTTAAAACC TATTCTTTTG TTATTAGGAC ATATAAATTC 420

ATCATTAAGT TCGTCATATT TCCAATTTTA AGTGTTGAAA ATGTCACTTT TAAACTTTCT 480

AATAGCCATA TAGTTTTGCT CACTACCATA ACCGGCATCA GCTACAAATA TACTCCGGTA 600

AATAACCGAG GGATTGTTGG AAT 623

(2) INFORMATION FOR SEQ ID NO: 3762:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 718 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3762:

ATTTTAAAAA TAGTTCTTTA AATTATATAC CCACCACATT TGGTGGAGAA CCTAAAAAAA 60

AGCACTTCCC AAAAATGGAA AGTGCAAGTA GTGAGCCATA GAGGATTCGA ACCTCTGACC 120

CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG GCTCTAATGG CTGGGCCTAG 180

CTGGATTCGA ACCAACGAGT GACGGAGTCA AAGTCCGTTG CCTTACCGCT TGGCTATAGC 240

CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG GAGCGGATTT 300

ACAGTCCGCC GCGTTTAGCC ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT 360

CaAAATGGTG GaGAATGACG GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC 420

TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG 480

CCGTGAAAGG GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT 540

CGAACCTTAC GACCGATCGG TTTAACAGCC GATAGCTCTT ACCACTGGAG CTACTGTGGG 600

ATTAATATTA TGCCTGGGCA ACGTTCTTAC TCTTAGCGGA ACGTTAAGTT CCGACTTACC 660

ATCCGACGCT AAGGAGCTTT AACTTTCTnG TGGTTCCGGC ATGGGGGGAA CAGGTGGT 718

(2) INFORMATION FOR SEQ ID NO: 3763:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3763:

TnCACTCACC GCAGATTTTT AAGTCCTGTG CGTCTGCCAG TTCCGCCACC CCGGCACTAT 60

AAAAATGGAG CAGAAGACGG GATTCGAACC CGCGACCCCA ACCTTGGCAA GGTTGTATTC 120

TACCGCTGAA CTACTTCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCT 180

AGGATTCGAA CCTCTGGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGGAGCTAAT 300

GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GGAACCCCCA ACCTACTGGA TTTACAAGTT 360

CAATTGCTCT AnCAATTTGA GCTAAGGCCG GGCAATATGT 400

(2) INFORMATION FOR SEQ ID NO: 3764:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 610 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3764:

TTAAAGTATT CCCAATTATA ATTCTTCATG ATTTTCTTAT TGGATTTCGA ATTTGGTTTC 60

ATGCATTGAT GTCTCAAAGA ACATGATGAA CAGTCATCAC ATTCATATAG TTTGAAGTCT 120

CGTTTAAAAC CATATCTATC ATTACGGTAT GCATATCTTT TAAAACCTAT TCTTTTGTTA 180

TTAGGACATA TAAATTCATT ATTAAGTTCG TCATATTTCC AATTTTGAGT GTTGAAAATG 240

CCACTTTTAA ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGGCGTT 300

TTATTAAAAT CATCTATAAT AGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT 360

ACAATATACT CTGGTAAATA ACCGAaGGaT TTTGAATCAT TGTTAAAAAT GGGATTAATG 420

TTCTAGTATC TGTTGGGTTT TGAAATAGGT CATAGGATAA AACAAATTGr GAATTTGTCG 480

CTATTTGgTA AATTGGTATC CTGGCTTAAG TTGGGCCATT TTTCCATATG GGCCTTCCTT 540

CCATTCTCCA TAAAAGTTGG CATCATGGAT CCAGATCCnG TTTTAGGAAA ACCTAATTCC 600

AACCTTTAAG 610

(2) INFORMATION FOR SEQ ID NO: 3765:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3765:

CTTCTTGGTG CTGCATATCC CCTACAATAA TTAAACCTTT TTTCTTATTT AAAATGTGTC 60

TTAATGCCGA TGCATCTATA CTTTTTTGAT AGTGCGGTAA AATCTTCATC TCAGAnGTTA 120

ACAATTCTGT TGCATTCAAA TCAGGTGTTA ACGGATCTCT AAATGGCAAG TTAAAATGAA 180

CACAATGGTC TCTTTACTAT CATCCGCAAT AGGCATATCG AACTCATAnC TTACATAATT 300

ATTAAACATA TTTACTTGAT TAATCGCTTG TGGTGCGCCT ACAnTTCTTA ATTCAGCGGA 360

CGGTCACTTG TTAAAACGGT TTAAGGTATT CTACTAATTn 400

(2) INFORMATION FOR SEQ ID NO: 3766:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3766:

CnTTTAACCT TTTTAAGGAA TCCTGCTAAT GCGGGTTTTG GCATTTTCGA nTnTTTrGTA 60

tCTCACGCAA tCTTGGTGGT CATTCAGTTC GTATATGGCA TCCATTAAGA CGCGAAGATC 120

AAATGGACTA TTGATGACTT CTGGAATACC ACGATCTATA TTTAGTAATT GATAAACAGC 180

TTCCATGGCA GTACGAACCG AATATTCTGT TGTAAATACA GTGTCTCGCT CTGTTTCTGC 240

AAAGTTACCA ATAAATGCTA AGTTCTGAGA TTGATGCGGG ACGACTAAAG GTCTGTCGCC 300

GATAGCACGC GTCATGAAAT AAGATGTGAT ATATGGCATA TAAACAGGgA ATCGTATTAG 360

ATGCATGTnT TGCTAAGTCT TCAATTTTGG TCAGTTGATA CACCTAAGTG GATACAGCCA 420

TTCTTGGCAT ATTTCATTAC CACTACATnC T 451

(2) INFORMATION FOR SEQ ID NO: 3767:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3767:

ACACGTGAAC GTCTTCAAAT GGAAGTACGT GACGTTCACT ACTCTCACTA TGGCCGTATG 60

TGTCCAATTG AAACACCTGA GGGACCAAAC ATTGGATTGA TTAACTCATT ATCAAGTTAT 120

GCACGTGTAA ATGAATTCGG CTTTATTGAA ACACCATATC GTAAAGTTGA TTTAGATACA 180

CATGCTATCA CTGATCAAAT TGACTATTTA ACAGCTGACG AAGAAGATAG CTATGTTGTA 240

GCACAAGCAA ACTCTAAATT AGATGAAAAT GGTCGTTTCA TGGATGATGA AGTTGTATGT 300

CGTTTCCGTG GTAACAATAC AGTTATGGCT AAAGAAAAAA TGGATTATAT GGATGTATCG 360

(2) INFORMATION FOR SEQ ID NO: 3768:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3768:

CCTACGACCG ATCGGTTAAC AGCCGATAGC TCTACCACTG AGCTACTGTG GATTAATATT 60

ATGCCTGGCA ACGTTCTACT CTAGCGGAAn TAAGTTCGTA CTACCATCGA CGCTAAGGAG 120

CTTAACTTCT GTGTTCGGCA TGGGAACAGG TGTGACCTCC TTGCTATAGT CACCAGACAT 180

ATGAATGTAA TTTATACATT CAAAACTAGA TAGTAAGTAA AAGTGATTTT GCTTCGCAAA 240

ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT CnGCTCCACA TGTCACCATG 300

CTTCCACCTC GAACCTATTA ACCTCATCAT CTTTGAGGGA TCTTATAACC GAAGTTGGGG 360

AAATCTCATC CTGnAGGGGG CTTCATGCTT AGATGCTTTC 400

(2) INFORMATION FOR SEQ ID NO: 3769:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3769:

CTTGACCGAA GTTCTTACCT ACATCACCTA AATTAATGAC ATGTCCACCA GTCATATACT 60

CTAATCCATG GTCGCCGATA CCTTCAACGA CAACATCTAC ACCACTATTT CTAATACAGA 120

ATCTTTCTnC TGCACTACCG TTAATAAATG CCTTACCACT TGTCGCACCA TAGAATGAGA 180

CGTTACCAGC AATAATTTCA TTTTGTCGTT CTTCAAAAGG TGCTTTGACA ATGACCGTAC 240

CACCAGATAA TCCTTTACCA ACATAGTCAT TCGCATCTCC AGTATGATGA ATCATTAAGC 300

CTTTCGGTGC ATATGCTGCA GGACTTTGGA CCAGCATGAC CATTCGTATA AACATTAATT 360

GTATTTTCAG GGAGGTCCTG CTTCTCCATA TTGTTTCGGA 400

(2) INFORMATION FOR SEQ ID NO: 3770:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3770:

CATTACGTAA TTAAAAGATA GTCATTAAGA GAGGnTGATA ACCATGCAAG AAGCATACAT 60

TGTAGCTTAT GGGCGTTCAG CGCAGCGAAA CAAAGCAAGG CGCATTATTC CACGAAAGAC 120

CTGATGATGT CGCAGCCAAA GTATTACAAG GCGTATTGAA ACGTATTGAC GGAAAATTCA 180

ATAAGAATAT GATTGAAGAT GTCATTGTTG GTACGGCTTT TCCAGAAGGA TTACAAGGCC 240

AAAACATTGC ACGAACGATT GCATTGCGTG CGGGATTATC TGACACGGTA CCGGTCAAAC 300

AGTGGAATCG CTACTGCTCA TCCAGGnTTT ACAAACCATT CGCGATTGCA GGCCAATCAA 360

ATTATGGCnG GTCCAAGGAG ATATACTTGT TAGCTGGTGG 400

(2) INFORMATION FOR SEQ ID NO: 3771:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3771:

ACTCTCTTGC AnTAAGGGCA GGGAATGACC GATGGGATTA AAAGATCAAG CTGTTACCTG 60

GGGAAGGTAT TTTCATCAAT TTCCAGAACT ATCCGATAAA GAATTTAAGA CTACACAAAA 120

AATTAAAGAT ATTTTAACAG AACATCATAT TAGAATATTA GACTTACCAC TTGCGACTGG 180

GCTTGTTGCT GAAGTGGGAC AAGGTCTGAG TTGTATAGCT GTTCGGGCTG ACATTGATGC 240

TTTACCGATT CAAGAGCTTG TTGAACAGGA TTTTAAATCT GAAAATGAAG GTGTTATGCA 300

TGCGTGTGGT CATGATATTC ACATGGCTAG nATTTTGGCT ACAGCTGGTA AAATTAAAAG 360

AGATTGAGGG CACTCTTACT GGGCGTGTTA AATCCATTTG 400

(2) INFORMATION FOR SEQ ID NO: 3772:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3772:

TTTATTTTGA CGTTTTAGAC ATAAAAAAAA GAGACCTTGC GGTCTCAATG CGGCTCATCG 60

GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG 180

CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 240

GTTTTCACTT CGCCAAGCCA TTTTTCTTTG TGTTTGCTTT TTATTTTGAC GTTTTAGACA 300

TAAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT TGCCTGGGCA 360

ACGTTCTACT CTAGCGGGAA CGGTAAGTTC GGACTTACCA 400

(2) INFORMATION FOR SEQ ID NO: 3773:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3773:

TTGATATTCC TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGGnATAGGC 60

GACGTGCGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG TATTAGGCAA ATCCGGTACT 120

CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT TCGAGTCGTT GATTTCACAC 180

TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCGTAC CGCAAACCGA CACAGGTAGT 240

CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA AGGAACTCGG CAAAATGACC 300

CCGTAACTTC GGGAGAAGGG TGCTCTTTAA GGTTAACGCC CAGAAGAGCC GCATGGAATA 360

GGCCCAnCGA nGTTTATTCA AAAACACAGT CTCTGCTAAA 400

(2) INFORMATION FOR SEQ ID NO: 3774:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3774:

TACTTAGACA ATCGAAAGTG TACATTATTA AATTATCATT TCCAGTTCTA CTCTAGCGGA 60

ACGTAAGTTG GCTACCATCC TCGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT 120

CTTTCCTCTC CTTCGGCTCT CACTTACTCA TTTAGCTCTA CTAAACTCGT TGCGTTCTTT 180

TCTCGTTTCG TCAGATTCAA ACGTTTTCAC TTCGCCAAGC CATTTTTCTT TGTGTTTGCT 240

TTTTATTTTG ACGTTTTAGA CATAAAAAAA AGAGACCTTG CGGTCTCAAA TGCGGCTCAT 300

GACGCTAAGG AGCTTAAACT TCTGTGTTTC GGCATGGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3775:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3775:

CGGTTTATCA AGAATGGAAA GAGTTGTACG TGAAAGAATG TCAATTCAAG ATACTGAGTC 60

TATCACACCT CAACAATTAA TTAATATTCG ACCTGTTATT GCATCTATTA AAGAATTCTT 120

TGGTAGCTCT CAATTATCAC AATTCATGGA CCAAGCAAAC CCATTAGCTG AGTTAACGCA 180

TAAACGTCGT CTATCAGCAT TAGGACCTGG TGGTTTAACA CGTGAACGGC TCAAATGGAA 240

GTACGTGACG TTCACTACTC TCACTATGGC CGGTGTGTCC AATTGAAACA CCTGAGGGAC 300

CAAACATTGG ATTGATTAAC TCATTATCAG TTATGCACGT GTAAATGGAA TTCGGCTTTA 360

TTGAAACACC ATATCGTAAA AGTTGATTTG GnTACACAGC 400

(2) INFORMATION FOR SEQ ID NO: 3776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3776:

AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 60

TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTTATAA 120

GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 180

CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT 240

AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACnTAG GCGATTATTT CTTATGGAAT 300

TCAAGCTTAT TTAAAACTCT TTATTCACTC GGTTTTGCCT GGGTAAAATC TAnATTTTAC 360

TTACnTATCT AGGTTTTCAA TGTACAAATA ATGGTGGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3777:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3777:

AATTATAAAA TTAAATGGCG GTCTCGACGG GAATCGAACC CGCGATCTCC TGCGTGACAG 60

GCAGGCGTGT TAACCnCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCGA 120

ACCCCCGCGA GCCGTTAAGC CCCTGTCGGT TTTCAAGACC GATCCCTTCA GCCGGACTTG 180

GGTATTCCTC CAAAATTATA TGGACCTTGC AGGACTCGAA CCTGCGACCG AACGGTTATG 240

AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA TAATTTTACA ACTAATAAAT 300

AGTGGCGGTG GAGGGGATCG AACCCCCGAC CTCACGGGTA TGAACCGTAC GCTCTAGCCA 360

GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG 400

(2) INFORMATION FOR SEQ ID NO: 3778:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3778:

CAAATCCTGC ACCATCAGAA AGTGGGGCAG ATGTTCCTGC AGTCATAGTG CCGTCAGCTT 60

TAAATACTGT ACGTAATTTG GCTAATGCCT CCATCGTGGT GTCAGGGCGT ATAAATTCAT 120

CTTGGTCAAA GATATTTGTG TGTACTTTTG GTCCTGCGTT TGTATATTCA ACTGAGTTTA 180

CTTGTATTGG AATAATTTCA TCTTTGAACC GACCATCACG TTGTGCGTCA TAGGCACGTT 240

GaTGACTTCT GACAGCATAA GCATCTTGaT CTTCGCGTGA TACGTCAAAT TGGGATGCTA 300

CATTTTtCAG CAGTTAAACC CATAGGATAT GACGCACCTA TATCATCAtA TTGTAAGGTT 360

GGATTGTTTG TGGGCTTCGT TnGCCACCnn TTGGTACGGC 400

(2) INFORMATION FOR SEQ ID NO: 3779:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3779:

CAATCTAAAT CGTTCAAATT TGGCACAACG ACAAATAAGG CTTCAACACG AATATATTCT 120

CTCGGTTGAA ACCTTACTTA TTCATTTATT TTTTATAAAT TAGTGACATA ACACTGTATT 180

AGCATCTGCA CGATCGGTTG AAATATATGT TACATTTTCT TGCTGCTTAA TAAATGCATC 240

ATAGTAATCA TATTGCGACG AATGATATGT GCCATTCGAT GTATCATTTG GGTTTAGCAA 300

ACAGCCATAA CCTTCGTCAT ATAAATGTTC ACnGAGCATA AGGGGCGTCA TGTTTTAGAA 360

CCACCTTACC TACATAAAAT TnGCCTCCAT AGGGATCATA 400

(2) INFORMATION FOR SEQ ID NO: 3780:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3780:

ATGGnCGGTC TCGACGGGAA TCGCAACCCG CGATCTCCTG CGTGCACACn CAGGCGTGTT 60

AACCGCTACA CTACGAGACC ATTAGTAAAA CGGAGGAAGA GGGATTCGAA CCCCCGCGAG 120

CCGTTAAGCC CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 180

AAAATTATAT GGACCTTGCA GGACTCGAAC CTGCGACCGA ACGGTTATGA GCCGTTAGCT 240

CTAACCAACT GAGCTAAAGG TCCTAAATAT AATTTTACAA CTAATAAATA GTGGCGGTGG 300

AGGGGATCGA ACCCCCGACC TCACGGGTAT GAACCGTACG CTCTAGCCAG CTGAGCTACA 360

CCGCCTTATA TAGTTTGTAA ATAATATGGT GGAGACTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3781:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3781:

AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC CGCCTGATTC 60

TCTAGCACGT TCATAAATAG TTACTTGATA TCCTAGTAGA TTAAGTTCTT CAGCAGCAGC 120

TAATCCTGCT GGACCGCTTC CAACGATTGC CACTTTTTCA TCTCTACGGC GACTCGGAAC 180

TTTCGGCGCT ACCCAACCAT TTTCAAAAGC TTCATCAATA ATTGTGCGTT CAATACCTTT 240

TACACGCCCT GTAAAGTCAG GAAAGTTATT TGTTTCGCTT AAGCGTCATA AGCAGTTTTA 360

AAATCTTGAT GATACACCAA GTCGTCCAnT CAGGATGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3782:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3782:

ACATGATGCG TGTGGTATTG GTTTTTATGC GAATATGGAT AATAAAAGGT CTCACGACAT 60

CATTGATAAA TCGCTTGAAA TGTTGCGACG CTTAGATCAC AGGGGCGGGG TCGGCGCAGA 120

TGGCATCACT GGTGATGGCG CAGGTATTAT GACTGAAATA CCTTTTGCAT TTTTCAAACA 180

ACATGTAACG GACTTTGATA TCCCAGGTGA AGGTGAATAT GCCGTGGGGT TATTTTTTTC 240

CAAAGAACGC ATTTTAGGTT CTGAACATGA AGTAGTTTTT AAAAAATATT TTGGAAGGCG 300

AnGGGTTATC AATTCTTGGT TAACGTAATG TACCAGTTAA TAAAAGATGC CATTGCCTAA 360

ACCATGTAGC AGATACGATG GCCAGTCATT CCACCAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3783:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3783:

AATCGGGTGA TGTTGGACGA TGATACGCAG GGAACGTTGC GTTATTCGTA TATGAAATAT 60

TGGATAACTG TTTTAACAAT GATGGTAGAG ATATTTCATC ATTTGTAACA TCGTCAATTT 120

TGATATTGTG ATGATTTAAC ATAACGACAT CATCGATATT GAATTGGTAT GAAAAACCTG 180

CTGTTGCTGA ATCTGTTAAT TTGGCTCCAA TATTTAAAAT TAAATCGCTG TTGTCCACAT 240

AATCTCGTAT TTTATCTTCG GCAATTTTCC CATCGTAAAT ACCCATATAA TATGGATTTT 300

CCTCATTAAA AGCACCTTTT CCTAATGAAA GTTGTGCTAC TGGGTATCTG TGTTTGAnTT 360

ACAAAATCTT CnAAGTCCTG GATGGAGGTG AAAACTGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3784:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3784:

GGTACTAAGA TGTTTCAGTT CTCCGGGTGT GCCTTCTGAT ATGCTATGTA TTCACATATC 60

GATAACATGA CATAACTCAT GCTGGGTTTC CCCATTCGGA AATCTCTGGA TCAAAGCTTA 120

CTTACAGCTC CCCAAAGCAT ATCGTCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180

GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 240

CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 300

TTTAAAATAA TTTAACTCAT TGTCTGCnAA ACGTTTTCTT TTATAAAAAG AnTTTAAACG 360

CGTTAATGAA GCTGTGAGTG TTCCTTCGAA CACGAGnnGA 400

(2) INFORMATION FOR SEQ ID NO: 3785:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3785:

TACTGGAATG ACATCAGATA CATGTGCACC ACCAATCCAT TTCTTTTCAC CATTGATAAC 60

CCAAGTATCG CCTTGnCGTT CAGCGACTGT TTCAAGACCT CCCGCAACGT CCGAACCGTG 120

TTCTGGTTCA GTTAAAGCAA AGCATGTACG CAGTTCATGT GACTGTAATT TAGGTACATA 180

TTTCGCAATT TGTTCTTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG 240

AACACCGAGT AGGGTAGCTA AGGAAATATC AAATCGCGCG AGTAGGTAAG ACATGAAAAA 300

CTGAAATAGT TGACTAGGCA TTTTGGCGTT TGGACGATCC TTGTAAAGTA ATGGATTGTT 360

AAAATAATTT AATTCTCCCA GTCTTTAAAT AGTCCTCGGG 400

(2) INFORMATION FOR SEQ ID NO: 3786:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCATTTGACG AATTTCATTG TTATTCAAAA TTCTATCTAA TCGTGCTTTT TCAACATTTA 60

ATATCTTACC TCGTAATGGT AAAATCGCCT GCGTTCTAGA GTCACGACCA GATTTTGTAG 120

ACCCCCCGGC AGAGTCCCCT TCGACTAAGA AAATCTCACA TTCTTCAGGA CTTTTACTAG 180

AGCAATCGGC TAATTTACCT GGAAGCTTGC TACATCTAAC GCTGATTTAC GACGTGTTAC 240

TTCACGCGCT TTTTTCGCAG CAACACGTGC ACGGCCCGCC ATAATACCTT TTTCAACCAC 300

TGTACGTGCG ACTTGTGGGA TTTTCATATA AAAATCGTTC AAAGTGCTCT GAGAATAATT 360

TATCTACAAC TTGACGCACT TCAGAATTAC CTAATTTTGT 400

(2) INFORMATION FOR SEQ ID NO: 3787:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3787:

TCTCTTCCCG TTTCGCTCGC CGCTACTAAG GGAATCGAAn TTTCTTTCTC TTCCTCCGGG 60

TACTAAGATG TTTCAGTTCT CCGGGTGTGC CTTCTGATAT GCTATGTATT CACATATCGA 120

TAACATGACA TAACTCATGC TGGGTTTCCC CATTCGGAAA TCTCTGGATC AAAGCTTACT 180

TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG 240

CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTTAT AAGTCAAACG 300

TTAACATGAA GTTACGTTCT TTTATAAAAA GATTTAAACG CGTTATTAAT CTTGTGAGTG 360

TTCTTTCGGA CACTAGCGAT TATTTCTnAT GATnCAAGCT 400

(2) INFORMATION FOR SEQ ID NO: 3788:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3788:

ATTCTCTGCT TTCATCTCAT TTGGTGACTA ATACCCTGAT TTTGTCCAAG TAAATGCTTC 60

ATAAAGTATT CTTGACCTTT TGCAGAACTT GAAATTAAGT TTGAACGCCA TATATAATGA 120

TTTTGGATGA TTCTTTTTCA AATCAGGATC TCTATTGCAA ATTGTGTTTG TnTTGATTTC 180

TCTTCTGCAA ACAACAAACT ATTTTTATTA AATTGTGGAT ATGATGGTAA CCAACCAAGT 300

CTAGCTGCTA AnACATTATA ATCAGCTGGA TGTTGATGCT TTAACTCCTC TGTTTTAGCT 360

AATGGAGATT TTAAACGATC TACATTTGAC TCTTCATAAT 400

(2) INFORMATION FOR SEQ ID NO: 3789:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3789:

CGGTTTCTTA ATTATGAACG CAACTATGAA TGGCTTATTA ACTATCACGG GCACATTGGC 60

AAAAGATCAG CTTGCACAAA ATGGACAAGG CATGGTGCTC GGTATACAAA CGGTTGAAAC 120

CGGTGTTTTT GGCGGGATTA TCACAGGTAT TATGACCGCA ATACTTCACA ACAAATATCA 180

CAAAGTGGTA TTACCACCGT ATTTAGGTTT CTTTGGTGGC TCTAGATTTG TCCCTATTGT 240

CACAGCATTT GCCGCAATCT TTTTAGGTGT ATTGATGTTT TTCATTTGGC CAAGCATACA 300

nGCCGGCATT TATCATGTTG GTGGGATTTG TAACGAAAAC AGGTGCCATC GGTACTnTTG 360

TTTATGGGTT CATCTTTAGG ATTGTTAGGT CCACTCGGTT 400

(2) INFORMATION FOR SEQ ID NO: 3790:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 716 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3790:

ATAATGGACT GTGCCGnGTA ATAATATnGn TCTCTAAAAG TTGTATTTTA AAAATAGTTC 60

TTTAAATTAT ATACCCACCA CATTTGGTGA kGAACCTAAA AAAAAGCACT TCCCAAAAAT 120

GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA 180

GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG 240

AGTGACGGAT CAAAnGTCCG TTGCCTTACC GCTTGGCTAT AGCCaATATA TAGATGGTGG 300

AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC 360

ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 420

CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGTGnTCTT 540

AACCGtTGAC CAAGGAGCCA TGGCTCaCcA GGTAgGACTC GAACCTACGA CCGATCGGTT 600

TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGGATTA ATATTATGCC TGGCAACGTT 660

CTACTCTAGC GGAACTAAAG TTnGAACTnA CCATCGACGC TAAAGGAGCT TAACTT 716

(2) INFORMATION FOR SEQ ID NO: 3791:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3791:

TGTCATGACG TTATTTGAAG ATATCGCGCA AGTCTTTTTA AAGGTAACAC TATCATTTAT 60

GCAATACGGC GCATTACCAG AGTTGCATGG TCAAAATATA TTGTTGTCAT TTGAAGATGG 120

ACGTGTACAA AAATGCGTGT TACGTGATCA TGATACTGTC AGAATTTATA AACCATGGCT 180

AACAGCACAT CAGCTTTCAT TGCCGAAGTA TGTCGTCAGA GAAGATACAC CTAATACGCT 240

AATTAATGAG GATTTGGAAA CATTCTTTGC nTGATTTTCA AACATTAGCT GTGATCGGTA 300

AATCTATATG CCATTATTGA TGCAATTCCA AGATTTATTT GGTGTGAAGT GnAGCATGAA 360

CTTATGTCGT TGTTAAAACA AATTTTGAAA AAAGGAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3792:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3792:

TTTTCACACA ATACATGGAC ACCATGGTTC AATGCTTCTA TAGAAAGATC AGCATGGAAT 60

TTATTAGGTG TACAAATGAC CACCGCATCA ACAAGTTTAA ACAGCTCGCT AGGTGTCTCA 120

ACTGCATGAG GTATATTAAA GCGCTTCGCA ACATCAATCA TCTGCACTGT ATTAATATCT 180

TGTACTGCAA CTAATGAGAC TGTGTCTTTG AGTTTCAGCA ATGCTGGAAT ATGACGGTCT 240

TGTGCAATAC CACCAACACC TATCACACCA ACTTTTAATT TTGTCATGAT GTGCCTCCTT 300

ACCGTATGAT GTtATTCAAA GTAAATTGCT TTGCCTGATT TkGCAGACTG ATaAATyGCT 360

TACCA 425

(2) INFORMATION FOR SEQ ID NO: 3793:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3793:

GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG 60

AGTGACGGAG nAAAGGTCCG TTGCCTTACC GCTTGGCTAT AGCCCAATAT ATAGATGGTG 120

GAGGGGGGCA GATTCGAACT GCCGAACCCG AAGGAGCGGA TTTACAGTCC GCCGCGTTTA 180

GCCACTTCGC TACCCCTCCA GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG 240

ACGGGTTCGA ACCGCCGACC CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT 300

CTCCAAAATA ATGACTCCTA CGGGACTCGA ACCCGTGTTA CCGCCGTGAA AGGGCGGTGT 360

CTTAACCGCT TTGACCAAGG AGCCATGGCT CCACAGGTAG 400

(2) INFORMATION FOR SEQ ID NO: 3794:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3794:

ATCAGCAGGG TTGAAAGTAC CTGCTGCAAC AGTAATACCA TTATTAGTTC CAGCAATACC 60

TGCTACAGTT GCTGCAGATG CTTCTTTCAC CCATGGACTC GTATTATTGC GACGTGTAAA 120

TGTnTCACAA CGTTACCATT ACGTTTAATA ACTAATTTAT CAGCGTATGT CGTTACGTTA 180

CCGGCATGTG TATTCACTGT TTGGTTTGCT CCAGGTGCAA TTGTAATCGC TCCTGCCGCT 240

GTTTCAGTCA CAGTTGGTTT CGCTGGTTGC ACATCTTTTA CTACAAATTT CGCTGGTAAA 300

GATGTTGCAA AAGTATGTCC GTTATAGATG ACGTCCATAT TTTGCGTTAA CGACTTTAGC 360

CACATTCGGT TTATTCATAG CGGACCAGTT TGCGTCCATT 400

(2) INFORMATION FOR SEQ ID NO: 3795:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3795:

GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACAA 60

TGGTAGGAGA GCGTTCTAAG GGCGTTGAAG CATGATCGTA AGGACATGTG GAGCGCTTAG 120

AAGTGAGAAT GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT 180

AAGGTTTCCA GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCCTAAGC TGAGGCCGAC 240

AGGCGTAGGC GATGGATAAC AGGTTGATAT TCCTGTACCA CCTATAATCG TTTAATCGAT 300

GGGGGGACGC AGTAGGATAG GCGAACGTGC CATTTGATTG CACGTCTAAA GCAGTAAAGC 360

TGAGTATTAG GCnAATCCGG TACTCGTTnA AGGCTGAACT 400

(2) INFORMATION FOR SEQ ID NO: 3796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3796:

GCACATGTTG CCATgCTTGA GCTAAATTAC CTTGCATCAT TGCTAGCTTT TCTTGTATTA 60

ACTGATATTT ACTAATTGGT TTGCCGAATT GCTTACGCTC AGTGACATAA TCTAATGTGG 120

CACGTAAAGC GCCACCATAC CACCTGTAGC CATATAAGCA ACGsCTGCTC TCGTTGAATA 180

AAGAATTTTG GCAATATCTT TAAAGCTTGT TATGTTTTGT AAGCGATCCG CTTCATCTAC 240

TTTGACATTA GTTAATTTAA TTAGGGCGTT AGGAACAATG CGAAGTGCGA TTTTATTATC 300

AATGACTTCA ATATCGACGC CATCTTGTTC TGGTCTGACT ACAAAGCAAT GGGGTTTGCC 360

AGTTTCnGTT ATTTACTGCG AATACTGGGG GGGnGnGGTT 400

(2) INFORMATION FOR SEQ ID NO: 3797:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3797:

GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG ACGCTGATGT GCGAAACGTG 120

GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT AAACGATGAG TGCTAAGTGT 180

TAGGGGGTTT CCGCCCCTTA GTGCTGCAGC TAACGCATTA AGCACTCCGC CTGGGGAGTA 240

CGACCGCAAG TTGAAACTCA AAGGAATTGA CGGGGACCCG CACAACGGTG GGAGCATGTG 300

GTTTAATTCG AAGCAACGnA GAGAACCTTA CCAATCTTTG ACATCCTTTT GACACTCTAG 360

GAGATAGAGC CTTCCCTTCG GGGGGACnAA GTGACAGTTG 400

(2) INFORMATION FOR SEQ ID NO: 3798:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3798:

CACAAAACAA GCCAAGCAAA ACAAACGCAT ATAACGTAAC AACACATGGA AACGGCCAAG 60

TATCATATGG CGCTCGCCCA ACACAAAACA AGCCAAGCAA AACAAATGCA TACAACGTAA 120

CAACACATGC AAACGGTCAA GTGTCATACG GAGCTCGCCC GACATACAAG AAGCCAAGTA 180

AAACAAATGC ATACAATGTA ACAACACATG CAGATGGTAC TGCGACATAT GGGCCTAGAG 240

TAACAAAATA AGTTTGTAAC TCTATCCAAA GACATACAGT CAATACAAAA CATTACGTAT 300

CTTTACAACA GTAATCATGG CATTCTATGG ATGCTTCTAA CTGGAATTAA AGCATCGGAA 360

CAATCGGGAn GCATATTTCT AAAATTATTT ATTCCATTAT 400

(2) INFORMATION FOR SEQ ID NO: 3799:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3799:

CTTCGCCGAT ATGGGGGAAG CTAGGTGATA AGATCAGCCG AAAATGGATG GTGTTAAGAG 60

CGTTACTTGG TTTGGCGGTA TGCTTATTTT TAATGGCATT GTGTACGACA CCATTACAGT 120

TTGTACTTGT GAGGTTATTG CAGGGACTAT TTGGTGGTGT TGTTGATGCA TCAAGTGCGT 180

TTGCGAGTGC AGAGGCGCCA CTGAAGGATC GTGGAAAGGT ATTAGGAAGA CTGCAAAGTT 240

TTTTAGTGCG TTACTGATGA GTATTGCCGT TATTACTTTT ATTGTCTGTn TTTTCGGTGC 360

CATTAAAATG ATTGAAACGA CACATATGGC CAAAnnCACA 400

(2) INFORMATION FOR SEQ ID NO: 3800:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3800:

GGAATCTATT ATATTAGATG TAAAAAATTT CGCGCAAAAT GTGTTAGGTA AAGGTGTCAT 60

TGTCGTCAAT GATGTGCCTG GCTTTGTCGC AAATAGAGTC GGCACGCAAA CAATGAATGA 120

TATTATGTAT CGCGCCGAGC AACACAAGAT AAGCATTGTA GATGTGGATG CTTTAACTGG 180

GCAAGCGATT GGTCGTCCTA AAACAGGTAC ATATGCGCTA TCTGACCTAG TCGGTTTAGA 240

TATTGCAGTG TCTGTAAATT AAAGGCATGC AACAAGTACC TGAAGAAACA CCTTATTTTC 300

ATGATGTCAA AATGTAAATA CGTTGTTTGA CCATGGGCGC ACTCGGACGT TAAnnCGnAA 360

ACCAAGGGTT TTTACCAAAA AGGGTTAAAG GGnAACTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3801:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3801:

TGCAGGCGTT TCTGGTCTGC ATAGTTTACG CATACGACCT GCGCGATCCT TATCTGGTAA 60

TAAATTGTAA AACGATAGTT CCCGTTGTTC CTAATAGTTG TATTCTATCT GACGCATAAT 120

GTGAAAAATA ACCTGCCATC TCTAAGCCCG GTCTTGATAT ATCAGCATTT TTAATTGGCT 180

TCGATAGTCC TTCTTCACCA GCGATTAAAT CTAACTTTAA TGTTTCAACT AGTTTTTCTG 240

TCGTTAACAT GGGTTCACCT CAATTGTATT TACCCTACTC TTACATCTCT TCTTATCATA 300

TCAAAAATAT AACACCAATC TACATTGAAA AGCTAAAnTA AATATTAATG TTCATTATTG 360

TTATnATTTT ACAAGTCAAT ATCATCATAA TTTATTGCTG 400

(2) INFORMATION FOR SEQ ID NO: 3802:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: doubl
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3802:

TTTCACTTTT GAACCATGCG GTTCAAAATG ATTATCCGGT ATTAGCTCCG GTTTCCCGAA 60

GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC ACCCGTCCGC CGCTAACATC 120

AGAGAAGCAA GCTTCTCGTC CGTTCGCTCG ACTTGCATGT ATTAGGCACG CCGCCAGCGT 180

TCATCCTGAG CCAGGATCAA ACTCTCCATA AAAATTATGA TGTTTGATTA GCTCATAAAT 240

ACTAAATAAT GTTTGTAACT TATAGTTACG TTTTTTGGAA TTAACGTTGA CATATTGTCA 300

TTCAGTTTTC AATGTTCATT TTTCTTACCG ACAAGAATTA ATTATACATT TTATTAACAT 360

TTAAGTCAAT AACTTTnTTT ATCCTGTCCA TTTnATTTTT 400

(2) INFORMATION FOR SEQ ID NO: 3803:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3803:

TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAAC TAGATAGTAA GTAAAAGTGA 60

TTTTGCTTCG CAAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 120

CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 180

AACCGAAGTT GGGAAATCTC ATCTTGAGGG GGGCTTCATG CTTAGATGCT TTCAGCACTT 240

ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC GACAACTGGT ACACCAGAGG 300

TATGTCCATC CCGGTCCTCT CGTACTAAGG ACAGCTCCTn TCAAATTTCC TACGnCCAnG 360

ACGGATAGGG ACCGAACTGT TTTCACGACG GTnCTGAACC 400

(2) INFORMATION FOR SEQ ID NO: 3804:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 457 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AGTnCACTCA CnCCAGATGT TTAAGTCCTG TGCGTCTGCC AGTTCCGCCA CCCCGGCACT 60

ATAAAAATGG AGCAGAAGAC GGGATTCGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAt 120

TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 180

TTAGwATCCT AAGTCTAGTG CGTCTGCCAA TTCCGCCACA CCCGCAAATG GTGAGCCATA 240

GAGGATTCGA ACCTCTGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG 300

GCTCTTCCAT GGTGCCGGCC AGAGGACTTG AACCCCCAAC CTACTGATTA CAAGTCAGTT 360

GCTCTtACCA ATTGaGCTAG GCCGGCAATA TGTaAGAATA AATGGTGGAG AATGACGGGT 420

TTCGAAACCG CCGnACCCTC TGGCTTGTTA AGGGCAG 457

(2) INFORMATION FOR SEQ ID NO: 3805:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3805:

ACTTTTTATT TTGACGTTTT AGACATAAAA AAAGCTCACG GTCTCAACTT GCCTGGCAAC 60

GTTCTACTCT AGCGGAACGT AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120

GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180

CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT 240

TTCTTTGTGT TTACTTTTTA TnTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300

TCAATGCGGC TCATCGCATC CATnTTTTGC CGGGCAACGT TCTACTCTTA GCGGAACGTA 360

AGTTGGCTAC CATCGTCGCT AAAGACCTTT TTGGACTGTG 400

(2) INFORMATION FOR SEQ ID NO: 3806:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3806:

GTTATGAAAG TCGCGCTTAA AATGCGTTAA TGTGACAAGG ATAATTCAAC ATCGTTTCAT 60

TTTACTGAGT CATTGCACTT ATCATACACA TTATATTTAG CATGAGTTAT ATTACTAAAA 120

TCATTGGCTT AATATTTACA GCGCTTGGTA TTGCAGGTGC CGTATTACCT TTACTGCCAA 240

CGACCCCTTT TTTACTCGTA GCAGTTTTTT GCTTTGCTCG AAGTTCAGAT CGCTTTTACA 300

ATTGGGCnnA TTAATCAAAA AATTTATAAA GAATATGTAG AAAACCTTTn TTTGACATCG 360

AGGCTACACG CTACAACAGA AAATTGAAAA TTTAATTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3807:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 388 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3807:

AGGAGAACAT GCTGTTACAT TTGGAGAGCC TGCTATTGCA GTGACCGTTT AACGCAGGTA 60

AAATCAAAGT TTTAATAGAA GCCTTAGAGA GCGGGAACTA TTCGTCTATT AAAAGCGATG 120

TTTACGATGG TATGTTATAT GATGCGCCTG ACCATCTTAA GTCTTTGGTG AACCGTTTTG 180

TAGAATTAAA TAATATTACA GAGCCGCTAG CAGTGAACGA TCCAAACGAA TTTACCACCA 240

TCACGTGGAT TAGGATCGAG TGCCAGCTGT CGCGGTTGCT TTTGTTCGTG CAAGTTATGG 300

ATTTTTTAGG GnAAATCATT AACGAAAGnA AGAACTCATT GGAAAAGGCT nATTGGGCCA 360

GAAGCAAATT GCCACATGGT AAAACCAA 388

(2) INFORMATION FOR SEQ ID NO: 3808:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3808:

ATGCGCAGAG TATATGGAGG AACACCAGTG TCGAAGCGCA CTTTCTGGTC TGTAACTGAC 60

GCTGATGTGC GAAACGTGkG GGATCAAACA GGATTAGATA CCCTGGTAGT CCACGCCGTA 120

AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCTTAG TGCTGCAGCT AACGCATTAA 180

GCACTCCGCC TGGGGAGTAC GACCGCAAGT TgAAAACTCA AAGGrATTGA CGGGGACCCG 240

CAcAAGCGTG GGAGCATGTG GtTTAATTCG AaGCAACGnn GAGGAACCTT ACCAAATCTT 300

GACATCCTTT GACAACTCTA GAGATAGAGC CTTCCCCTTC nGGGAACAAA TGACAGGTGG 360

ACCCTTAAGC TTATTTGCCA TCATTAA 447

(2) INFORMATION FOR SEQ ID NO: 3809:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3809:

CCAACTGAGC TACTGAACCA TAATAAAAAT GTAATGACTG GCGGTCTCGA CGGGAATCGA 60

ACCCGCGATC TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACACTACGA GACCTATAAA 120

ATATTGCGGG AGGCGGATTT GAACCACCGA CCTTCGGGTT ATGAGCCCGA CGAGCTACCG 180

AACTGCTCCA TCCCGCGATA ATAAAAAATA ATGGCGGAGG AAGAGGGATT CGAACCCCCG 240

CGGCCCGTTA AGGCCCTGTC GGTTTTCAAG ACCGATCCCT TCAGCCGGAC TTGGGTATTC 300

CTCCATTATT ATAGGTAAAT CGCTATTAAT TATAAAATTA AATGGCGGTC TCGACGGGAA 360

TCGAACCCGC GATCTCCTGC GTGACAGGCA GGCGTGTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3810:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3810:

TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA ATAATGGTGG 60

GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT AACCAGCTGA 120

GCTATAGGCC CATTTTTTTG AATGTTAAAT AAACATTCAA AACTGAATAC AATATGTCAC 180

GTTATTCCGC ATCTTCTGAA GAAGATGTTC CGAATATATC CTTAGAAAGG AGGTGATCCA 240

GCCGCACCTT CCGATACGGC TACCTTGTTA CGACTTCACC CCAATCATTT GTCCCACCTT 300

CGACGGCTAG CTCCTAAAAG GTTACTCCAC CGGCTTCGGG TGTTACAAAC TCTCGTGGTG 360

TGACGGGCGG TGTGTACAAG ACCCGGGAAC GnATTCACCG 400

(2) INFORMATION FOR SEQ ID NO: 3811:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3811:

GCTTCATGCT TAGATGCTTT CAGCACTTAT CCCGTCCACA CATAGCTACC CAGCTATGCC 60

GTTGGCACGA CAACTGGTAC ACCAGAGGTA TGTCCATCCC GGTCCTCTCG TACTAAGGAC 120

AGCTCCTCTC AAATTTCCTA CGCCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTC 180

TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCTTGGG ACCGACTACA 240

GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCGTCGAT GTGGAACTCT 300

TGGGGGAGAT AAGCCTGTTA TnCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGnnCTTCC 360

ATGCGGGAAC CACCGGGATT 380

(2) INFORMATION FOR SEQ ID NO: 3812:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3812:

GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA TGCTTAGATG 60

CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTAGC ACGACAACTG 120

GTACACCAGA GGTATGTCCA TCCCGGTCCT CTCGTACTAA GGACAGCTCC TCTCAAATTT 180

CCTACGCCCA CGACGGATAG GGACCGAACT GTCTCACGAC GTTCTGAACC CAGCTCGCGT 240

ACCGCTTTAA TGGGCGAACA GCAACCCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA 300

GCCGACATCG AGGTGCCAAA CCTCCCCGTC GnTGTGAACT CTTGGGGGAG ATAAGCTGTT 360

ATCCCCGGGT GAGnTTTnTC CGTTGA 386

(2) INFORMATION FOR SEQ ID NO: 3813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3813:

CTTGGTACTT CTGGTGTTGG TGGCGTTGGT GTTTCCGGCT CACTTGGTAC TTCTGGTGTC 120

GGTGGCGTTG GTGGCACGAT TGGAGGTGTT GTATCTTCTT CAATCGTTTG TTGACCTTCA 180

TTTTGGCCGC TTACTTTTGG AAGTGTATCT TCTTCAAAGT CAACACTATT GTGTCCACCG 240

AATTGATAAC TTGGTTTATC TTTATTTGTA TCTTCTTCAA TAATTTCAGT GTGCTTATTG 300

AATCCGTGAA TATGTGGCAC nTGGTCGAAG TCGATATCAA TGATGTTACC GCCATGTTCA 360

TACTTAGGTT TGTCTTTTTC TGTAnCTTCC TCGAATGACT 400

(2) INFORMATION FOR SEQ ID NO: 3814:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3814:

TAATTGGGCT ACCATCGTCG CTAAAGACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60

TCCTCTCCTT CGGCTCTCGC TTACTCATTT AGCTCnACTA AACTCGTTGC GCnCTTTTCT 120

CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180

TATTTTGACG TTTTAGGCAT AAAAAAAAGA GACCTTGCGG TCTCAATGCG GCTCATCGCA 240

TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGGCT ACCATCGTCG 300

CTAAAGACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 360

TTACTCATTT AGCTCTACTA AACTCGGTGC GCTCTTTTCT 400

(2) INFORMATION FOR SEQ ID NO: 3815:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3815:

TTCTTTCATA TGATTTTTTA GATTTTAGTA AGTCAATAAA GCCAATTTTC TCCAACGATT 60

GAATGTAACG TTGATTGATA AATGTATTTC TTGGTAAATC ACCACCCGCT AAAATTGTGG 120

CGATATTTAA GGCAATATGA TAATCATGGT CGCTAATAAA ATGACCCCGT CTTTGCGCAT 180

CTAATTGTCC TTGGATCAAT GCTTTGAAGT CTTCACCTAA AGCGATATAT TGATGTCTAG 240

GTTGTGCTGT ATTGAAAATA ATCGTATCTG GTATCACGTA AATnACCATA ACGACGTGCC 360

TCCAAAGGCA TTTGGTAnGA GCCTTCGGCA ATGCCGATAA 400

(2) INFORMATION FOR SEQ ID NO: 3816:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3816:

CCAATATTTA TATTAATGAA AATAAGATGT TATATTCATT GTTAATTTAA CACATAGTAA 60

GAnAAACAGT CATAAATTGA TTTCTAATTG AAATCATCTT ATGACTGCTT TTTATTATAC 120

TTTACATTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TCTTTCTTTG 180

TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT CTCAATGCGG 240

CTCATCGCAT CCACTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA GTCGGACTAC 300

CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG GAACAGGTGT GACCTCCTTG 360

GCTATAGTCA CCAGACATAT GAATGTAAAT TCATACATTC 400

(2) INFORMATION FOR SEQ ID NO: 3817:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3817:

TGTTATTGTT CAAAATCATG ATCAAGATCA GTATATCGGG GGGnATTATG AAGCGATGCA 60

TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120

ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180

GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240

TACCGAACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300

TCATGATAAT TTCTTTGAAT TAGGTGGCCA TTCATTAAAA GCAACGTTAT GGnTGGAATC 360

GGATAGAGGC ATCTACTGGG GAAACGATTA CCAATTGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3818:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: d uble
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3818:

TCGGAATCTG GGAGGACCAT CTCCTAAGGC TAAATACTCT CTAGTGACCG ATAGTGAACC 60

AGTACCGTGA GGAGAAGGTG AAAAGCACCC CGGAAGGAAG TTGAAATAGA ACCTGAAACC 120

GTGTGCTTAC AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA 180

CCGGCGAGTT ACGATTTGAT GCAAGGTTAA GCAGTAAATG TGGAGCCGTA GCAnAACATG 240

TTCTGAATAG GGCGTTTAGT ATTTGGTCGT AGCCGnAAAC CAGGTGATCT ACCCTTGGTC 300

CAGGTTGAAG TTCAGGTAAC ACTGGAATGG AGGACCGAAC CGACTTACGT TTGAAAAGTG 360

AGCGGATGAA CTGAAGGTAG CGGAGAAATT CCCAATCGAA 400

(2) INFORMATION FOR SEQ ID NO: 3819:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3819:

CAACGAGAGA CTCGGTGAAA TCATAGTACC TGTGAAGATG CAGGTTACCC GCGACAGGAC 60

GGAAAGACCC CGTGGAGCTT TACTGTAGCC TGATATTGAA ATTCGGCACA GCTTGTACAG 120

GATAGGTAGG AGCCTTTGAA ACGTGAGCGC TAnTTACGTG GAGGCGCTGG TGGGATACTA 180

CCCTAGCTGT GTTGGCTTTC TAACCCGCAC CACTTATCGT GGTGGGAGAC AGTTTCAGGC 240

GGGCAGTTTG ACTGGGGCGG TCGCCTCCTA AAAGGTAACG GAGGCGCTCA AAGGTTCCCT 300

CAGAATGGTT GGAAATCATT CATAGAGTGT AAAGGCATAA GGGACTTGAC TGCGAGACCT 360

ACAAGTCGAG CAGGTCCAAA AACGGACnTA GTGATnCGGT 400

(2) INFORMATION FOR SEQ ID NO: 3820:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TGGCTCGAAC CACCGACCTC ACGCTTATCA GGCGTCGCTC TAACCAGCTG AGCTATAGGC 60

CATTAATTTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT ATTCCGCATC 120

TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC GCACCTTCCG 180

ATACGGCTAC CTTGTTACGA CTTCACCCCA ATCATTTGTC CCACCTTCGA CGGCTAGCTC 240

CTAAAAGGTT ACTCCACCGG CTTCGGGTGT TACAAACTCT CGTGGTGTGA CGGGCGGTGT 300

GTACAAGACC CGGGAACGTT ATTCACCGTA GCATGCTGAT CTACGATTAC TAnCGATTCC 360

AGCTTCATGT AGTCGAGTTT GCAGACTACA ATnCGAACTG 400

(2) INFORMATION FOR SEQ ID NO: 3821:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3821:

TATTAAATTA ATGGTGGGCC TAAnTGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT 60

GCGCTCTAAC CAGCTGAGCT ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAAACTGA 120

ATACAATATG TCACGTTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA 180

AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC 240

ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT CGGGTGTTAC 300

AAACTCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC ACCGTAGCAT 360

GCTGATCTAC GATTACTnAG CGnTTCCAGC TTCCATGnTA 400

(2) INFORMATION FOR SEQ ID NO: 3822:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3822:

TCTACCAACT GAGCTAATGG CTCTAATGGC TGGGCTAGCT GGATTCGAAC CAACGAGTGA 60

CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAA TATATAGATG GnGGAGGGGG 120

GCAGATTCGA ACTGCCGAAC CCGAAGAGCG GATTTACAGT CCGCCGCGTT TACCACTTCG 180

GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCAAAA 300

TAATGACTCC TACGGACTCG AACCCGTGTT ACCGCCGTGA AAGGGCGGTG TCTTAACCGC 360

TTGACCAAGG AGCCATGCTC CACAGTAGGA TTCGAACTAA 400

(2) INFORMATION FOR SEQ ID NO: 3823:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3823:

AACTTGCCTC TTTAGGTACA GCATGAGGCC CTAGGAAAGT ATGTTTCATG TCTAAATCAT 60

ATTTCTCAGC TAAACGATTA GACACTTTCA ATTGCTTCAG TTCATTTTCT CTATCTAATC 120

CATAACCACT CTTACTTTCA ACTGCAnGCA CGCCGTGTTT AATCATAGTA AGCAAATCAT 180

GCTCTGCTTT TTTAAACAAG TCATCTTCGG ATGTTTCTCT AGTAGCATTA ACGGTAGATA 240

ATATGCCACC ACCCATTTCT AATATTTCAA GGTAAGACTT ACCTGGACGT TTTAATGACA 300

TCTCATGTTC TCGAGATCCA CCAAATGTnA AATGGGGTAT GTGGCATCTA CTAAGCCGGG 360

GGACACTAnC TTTCCCACTA GGCATCAATC G 391

(2) INFORMATION FOR SEQ ID NO: 3824:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3824:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT CTCTGGATCA 60

AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120

GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA 180

ACGCGTTATT AATCTTGTGG AGTGTTCTTT CGAACACTGA GCGATTATTT CTTATGAATT 240

CAAGCTTATT TAAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300

ACnTATCTAG TTTTCAATGT ACAATTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC 360

TTTGAACCAA AAAAGATTGG AAGGTGAAAT AAACATTCAA 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3825:

ATCGATAACA TGACATAACT CATGCTGGGT TTCCCCATTC GGAAATCTCT GGATCAAAGC 60

TTACTTACAG CTCCCCAAAG CATATCGTCG TTAGTAACGT CCTTCATCGG CTTCTAGTGC 120

CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT TTCCATCCTA CAGGAAACGC 180

GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 240

TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATnTT ACTTACTTAT 300

CTAGTTTTCA ATGTACAATT TCTTTTTAGT CAAGCGCTCG CATAAGCAAT ATCACTTTAA 360

CCAAAAAATA TTTGAATGTn AAATAAACAT TCAAAACTGA 400

(2) INFORMATION FOR SEQ ID NO: 3826:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3826:

TCACTCACCG CAGATTTTTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA 60

AAAATGGAGC AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT 120

ACCGCTGAAC TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGnCT 180

TAGATCCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240

GGATTCGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT CTACCAACTG AGCTAATGGC 300

TCTTCCATGG TGCCGGCCAG AGGATTTGAA CCCCCAACCT TATTGGTTAC AAGTCAGTTG 360

CTCTTACCAA TTGAGCTAGG nCGGCAATAT GTTAAGATTA 400

(2) INFORMATION FOR SEQ ID NO: 3827:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3827:

AGTGGTGGAA TGGTCTTAAA AGTTGGTGGT CTAACTTTAG AGAAGACCAA AAGAAGAAAA 60

GTGATAAATA CGCTAAAGAA CAAGAAGAAA CAGCTCGTAG AAACAGAGAA AATATAAAGA 120

AATGGTTTGG AAATGCTTGG GACGGCGTAA AAACTAAAAC TGGTGAAGCC TTTAGTAAAA 180

TGGGCAGAAA TGCTAATCAT TTTGGCGGCG AAATGAAAAA AATGTGGAGT GGAATCAAAG 240

GAATTCCAAG CAAATTAAGT TCAAGTTGGA GCTCAGCCAA AAGTTCTGTA GGATATCACA 300

CTAAGGCTAT AGCTAATTAG TACTGGTAAA ATGGTTTGGA AAAGCTTGGC CAATCTGTTA 360

AATTCGACTA CAGGAAGTAT TTACATTCAA ACTAGGCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3828:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3828:

TCTCAGTTCC AGTGTGGCCG ATCACCCTCT CAGGTCGGCT ATGCATCGTT GCCTTGGTAA 60

GCCGTTACCT TACCAACTAG CTAATGCAGC GCGGATCCAT CTATAAGTGA CAGCAAGACC 120

GTCTTTCACT TTTGAACCAT GCGGTTCAAA ATATTATCCG GTATTAGCTA CGGTTTCCCG 180

AAGTTATCCC AGTCTTATAG GTAGGTTATC CACGTGTTAC TCACCCGTCC GCCGCTAACA 240

TCAGAGAAGC AAGCTTCTCG TCCGTTCGCT CGACTTGCAT GTATTAGGCA CGCCGCCAGC 300

GTTCATCCTG AGCCAGGATC AAACTCTCCA TAAAAATTAT GATGTTGAnT AGCTCATAAA 360

TACTAAATAA TGTTGTAACT TATAGTACGT TTTTnGAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3829:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3829:

CAAGCGCCAT GACATCATAA CTTTCTTGCA CAAGATATGT GAACGGCGGT GTTGATCCTA 60

GATTCGTGGC ATGCATACGC AAACCATTTT CTTCAATTAC TTCACCAAGG CGTTTAAAAT 120

ATTGATAAAA CCTTGATGTG TTTCGTGTCA ATGACATACC ATATCGACTA GGTACCTTTT 240

TAGAATGTTG ATTAATCACA ACAAATATCA TGGCAAGGTC ATCTTCAAAA TGATTCGATT 300

CAAGTGGGAr sGGCATATGA CGTCTCATCA CtATACCCTt TnTnCCCATT CTGCAAATnC 360

ACCCATAAAT ACTACGGGAC GGAGAACCCG TACCCATTTC 400

(2) INFORMATION FOR SEQ ID NO: 3830:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3830:

GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60

CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCGG AAATCTCTGG ATCAAAGCTT 120

ACTTACAGCT CCCCAAAGCA TATCnCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180

GGATCCACCG TGCGCCCTTA ATAACTTAAT CTATGTTTCC ACCATTTTTA TAAGTCAAAC 240

GCTCACATAC GGCTTCGTTT TCATTATTTT AAATGCTCAT TTACATAAGT AAACTCTGCT 300

TTAAAATAAT TTAACTCATT GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTTAAACGCG 360

TTATTAATCT TGTGAGTGGT CCTTCGAACA CTAGCGATnA 400

(2) INFORMATION FOR SEQ ID NO: 3831:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3831:

AAATGCGGCT CATCGCATCC ATTTTTTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 60

TTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT 120

CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAAACT CGTTGCGCTC TTTTCTCGTT 180

TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240

TTGACGTTTT AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA 300

TTTTTTGCCT GGGCAACGTT CTACTCTAGC GGAACGTAAT TGGGCTACCA TCGACGCTAA 360

(2) INFORMATION FOR SEQ ID NO: 3832:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3832:

AGCTTATTTT AAAACGTCGT TTATTCACTC TGGTTTTGCT TGGTAAAATC TATATTTTAC 60

TTACTTATCT AGTTTTCAAT GTACAATTTC TTTTTAGTCA AGCGCTCGCA TAAGCAATAT 120

CACTTTAACC AAAAAATATT TGAATGTTAA ATAAACATTC AAAACTGAAT ACAATATGTC 180

ACATTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 240

CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC 300

TTCGACGGCT AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 360

TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTTCA 400

(2) INFORMATION FOR SEQ ID NO: 3833:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3833:

TTTTCTTCTG GTAAAATATC TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT 60

TGAGCAGTGT TTTTATTATC GCCAGTTAAC ATGGCAACTT CAATGCCCAT ATCATGCAAT 120

TGTATTATAG CATCTTTGGC ATGATCTTTG ACAGTATCTG CCACTGCnAT GATACCAGTT 180

AATGAATAAT TAACAGCAAT GAGCATAGCA GTTTTACCAT CTCGTTCATA ATGTGTTAAA 240

TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG CCATTAATnT ACGGGTTACC 300

AACCAATATA TGGTGATGAT CAATCCGTGG CTTCAATACC ATGGCCAGGT ACCGCTTnAA 360

AGTTGTTGTC TCAGTTAATA TTAATTGCTT TCCTTTTGCA 400

(2) INFORMATION FOR SEQ ID NO: 3834:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3834:

nAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA CGGTTATGAG CCGTTAGCTC 60

TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TnGCGGnnGA 120

GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 180

CGCCTTATAT AGTTTGTAAA TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC 240

TGCGTGCAAA GCAGGCGCTC TCCCAGCTGA GCTAAGCCCC CATAATAATT ACAGTATATC 300

GGGAAGACAG GATTCGAACC TGCGACCCCT TGGTCCCAAA CCAAGTGCTC TACCAAGCTG 360

AGCTACTTCC CGTATAATTA ACGCGCCCGA TAGGAGTCGA 400

(2) INFORMATION FOR SEQ ID NO: 3835:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3835:

AATAACAATT GCGCCACTAA AACTCAAAAT TTCCACCACC AACATCCAAA TTATCAACAT 60

CGCAACATAA CCAAATGTTA TAATAAATCT ATTACACAAA GAGATAAATT ACTTATGCAA 120

AGGCGGAGGA ATCACATGTC TATTACTGAA AAACAACGTC AGCAACAAGC TGAATTACAT 180

AAAAAATTAT GGTCGATTGC GAATGATTTA AGAGGGAACA TGGATGCGAG TGAATTCCGT 240

AATTACATTT TAGGCTTGAT TTTCTATCGC TTCTTATCTG AAAAAGCCGA ACAAGnATAT 300

GCAGATGCCT TGTCAGGTGA AGACATCACG TATCnAGAAG CGTGGGCAGA TGAAGAATAT 360

CGTGAAGACT TnAAAAGCAG GAATTAATTG GTTCAAGTCG 400

(2) INFORMATION FOR SEQ ID NO: 3836:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3836:

CTAATCGCAT CTTTTTCAAT CTAAGTGCGT TTGTGACAAA CTTACTGAAC TTAGTGCCAT 60

ATTATAGCCG AATGCCCAAA ATAGATTTTG ACGAATATTA CGAATGGTTG CTTTACTTGC 180

ATAAATGGCT TTAGGAATAA GCATCAAGTC GCCACCAAGA ATAGTAATAT CAGCTGCTTC 240

AATGGCAACT TCTGTACCTG TACCAATGGC GATACCGATA TCAGCTTTAA CTAAATGCAG 300

GTGCATCATT TACACCGTCA CCAACCATCG CAACCTTCTT ACCTGTTGGC TGTAGTTTCG 360

CAATTGTGGC AGCTTTTTnC TTCCGGnGAA AATATCnGGC 400

(2) INFORMATION FOR SEQ ID NO: 3837:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3837:

AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC CCCTCCAGCT TATTCATATA 60

ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC GCCGACCCTC TGCTTGTAAG 120

GCAGATGCTC TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC 180

CGTGTTACCG CCGTGAAAGG GCGTGTCTTA ACCGCTTGGA CCAAGGAGCC ATGGCTCAAC 240

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 300

TGTGGGATTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGGAAGTAAn TCGGACTACC 360

ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3838:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3838:

AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC TACTAAACTC 60

GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA GCCATTTTTC 120

TTTGTGTTTA TTTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180

ATGCGGCTCA TCGCATCCAT TTTTTGCCTG GCAACGTTCT ACTCTAGCGG AAGTAATTGG 240

GCTACCATCG ACGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 300

TCAGATCCAA ACGTTTTCAn TCGnCCAAGC CAATTTGCCT 400

(2) INFORMATION FOR SEQ ID NO: 3839:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 416 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3839:

TTACGGCCGC CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGTAGAcrC GACTCCTCTT 60

AACCTTCCAG CACCGGGCAG GCGTCACCCT gATAcATCAC CTTACGGTTT AGCAGAGACC 120

TGTGTTTTTG ATAAACAGTC GCTTGGGCCT ATTCACTGCG GCTCTTCTGG GCGTTAACCC 180

TAAAGAGCAC CCCTTCTCCC GAAGTTACGG GGTCATTTTG CCGAGTTCCT TAACGAGAGT 240

TCGCTCGCTC ACCTTAGAAT TCTCATCTTG ACTACCTGTG TCGGTTTGCG GTAGGGcACC 300

TATTTTCTAT CTAGAGGCTT TTCTCGGCAG TGTGAAATCA ACGACTcGAg GACACAATGT 360

CTTCTCCCCA TCACAGtTCA GCCTTgAACG rGTaCCGGAT TTGnCTAATG ATTCAG 416

(2) INFORMATION FOR SEQ ID NO: 3840:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3840:

AAGTTAGGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60

TCCTCTCCTT CGGCTCTCGC TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120

CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180

TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT CTCAAACTTG CCTGGCAACG 240

TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 300

GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 360

CTCGTTGGnG CTCTTTTTCT CGGTTTnGTC AGAnTTCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3841:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3841:

CGCGACTGAn GAATACAATG nCTACGATAA CTAAACCCAA TCAATCTTTT CATTCTATCA 60

ATTCCTTTCA AAATCTTCAC TATATATCAT TAATGTCTAC GTATGAATCT AGCTAGAACA 120

TTCCCTAGCG TTTGAATCAC TTGGACAATA ATGACTAATA CAATAACGGT AATAATAATG 180

ACCGTCGTAT CAAATCTTTG ATAACCATAC ACTAAAGCTA AGTCTCCTAT ACCACCACCG 240

CCAACAGCTC CTGCCATCGC CGTACTTCCA ATAAGTCCAA TAATCGCAGT GGTAATTGCT 300

AATACTAACG AACCTAAAGC TTCAGGAATT AAAAAATATC TAATGATTTG TAGTGGTGAA 360

GCGCCCATCG CTTTCGCCGC TTCAATAATC CCCTCGTCTA 400

(2) INFORMATION FOR SEQ ID NO: 3842:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3842:

TCGCGATTCG CGTGTTCAGA AATCATCGGC ATCGCGTCAT TCAATGATTC ATATGCATCT 60

AAAGCAATAG AAGATAATGT GTCTGGCACA TATACCCATG CCAACGTATC AGTAGACGTA 120

TGATGTTCTG CTACCGCAAA AACAGTTGTC TCTGGAATAT ACACACCTGA TTGTTTTAAT 180

CCTTGTCTGA CATTTGGACG ATTACATATC ATCGCTAATA ACTTAGCATT AAAACCGCTT 240

GATGCGCCAC CACAAGCCCC ACATTCAAGT GATGCATGAT GTGGATTATT GTGAGAATGA 300

CTAGCATGAC CTGCTAACAC AACGAACGGC GCAAATGCTT CGGkTAAATC CATCAATTTC 360

AACGCTgTAA CGCGAATCAA TTGCTCTGCT CAGTAAATCC 400

(2) INFORMATION FOR SEQ ID NO: 3843:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3843:

GCCAACATCC TAGTTGTCTG GGCAACGCCA CATCCTTTTC CACTTAACAT ATATTTTGGG 120

ACCTTAGCTG GTGGTCTGGG CTGTTTCCCn GTCGAACACG GACCTTATCA CCCATGTTCT 180

GACTCCCAAG TTAAATTAAT TGGACATTCG GAGTTTGTCT GAATTCGGTA ACCCGAGAGG 240

GGCCCCTCGT CCAAACAGTG CTCTACCTCC AATAATCATC ACTTGAGGCT AGCCCTAAAG 300

CTATTTCGGA GAGAACCAGC TATTTCCAGG TTCGATTGGG AATTCTCCGC TAACCTCAGT 360

TCATCCGnTC ACTTTCAACG TAAnTCGGGT CGGGTCTCCA 400

(2) INFORMATION FOR SEQ ID NO: 3844:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3844:

ACTTTTACTT GCTGCGCCTC CAGCCAAACC TGCTGTTCCA GCACCGATCG CTGCACCTTT 60

TTTGCCATTA TGATGATCTT TAGACTTATC TTGAGACGCT TTATCCTCAG TCGAGTTATT 120

CGCCTTGCCA GAATTACTTT TGTTTTGAGC GTCATTTGAA TGTTTCTTAG CTTTAGAAGC 180

AGCCATTGCA CCAGCTGCAC CTGCAACACC TGCTGTTCCA GCACCAATAG CTGCTGCTTT 240

TTTACCATTA TGATGTTCTT TAGGTTCATC TTGATCTTGT TTTACAGAAT CATTATCATG 300

TTCATTTTTT GATGTTTCTG ATTGGTTAGC ACCTGTTGTA AAATATGGTT TAGGTTGCTG 360

AGATTGTTCA GCTTCACTCT TATCAGAAAC TGTTGAATGC TCAGTGTTAT TTTCTGCATT 420

TTTAATAGTA TCGTGTTTAn CCATTGTCCT CGAATGGGTT CnGGATGTG 469

(2) INFORMATION FOR SEQ ID NO: 3845:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3845:

GCTTCACTAC CAAGTGAAGA AGTTGCTGAA ACTCCTGCAG CACCTGCAnC AGTAACATTA 60

GAAGGCGACT TCCCAGAAAC AACTGAAAAA ATCCCTGCTA TGCGTAGAGC AATTGCGnAA 120

CATGGnTTTA ACTCTAAGCA TACTGCACCT CATGTAACAT TAATGGATGA AATTGATGTT 180

TTAACATTCT TACCTTATGT TGTTAAAGCA CTTGTTTCTG CATTGAAAAA ATACCCAGCA 300

CTTAACACTT CATTCAATGA AGAAGCTGGT GAAATCGTTC ATAAACATTA CTGGGAATAT 360

CGGTATTGCA GCAGACACTG ATAGAGGATT ATTAGTACCT 400

(2) INFORMATION FOR SEQ ID NO: 3846:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3846:

TTAAGCTACC ATCCTCGCTA AGAACCTTTC TTGACTTGTG ACAATCGCTT GCTTCTTTCC 60

TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTTCTCGT 120

TTCGTCAGAT TCAAACGTTT TCACTTCGCC AAGCCATTTT TCTTTGTGTT TACTTTTTAT 180

TTTGACGTTT TAGACATAAA AAAAGAGACC TCACGGTCTC AACTTGCCTG GCAACGTTCT 240

ACTCTAGCGG AACGTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT GACTTGTGAC 300

AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCnTACT CATTTAGCTC TACTAAACTC 360

GTTGGCGCTC TTTTCTCGGT TCGTCAGATT CAAACGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 3847:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3847:

ATCGTCAACT TATTATTAGA CGATGTACAA GTTACATTAG ACAAAAAAGG TATTACGATG 60

GACGTTTCTC AAGATGCGAA AGATTGGTTA ATTGAAGAAG GCTATGATGA AGAATTAGGT 120

GCACGTCCAT TAAGACGTAT TGTTGAACAG CAAGTACGTG ACAAAATTAC AGATTACTAT 180

TTAGATCATA CAGACGTTAA ACATGTGGAT ATAGATGTTG AGGGATAACG AATTAGTCGT 240

AAAAGGTAAA TAACGACACT TTAACATATC GCGCATCAAA AATGAGCATC AGGTCGCCCT 300

TGCCTGTGGC TCATTTTTTT GAATTATTTC CCTGGGAAAA TGATTCGCTG TGTGCTGTTC 360

TGTTnCCACA ACAATCACGA TTGAATGTGC ACATGTGACC 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3848:

TTTAAAACTC TTTATTCACT CGGTTTTGCT TGGTAAAATC TATATTTTAC TTACTTATCT 60

AGTTTTCAAT GTACAAATAA TGGTGGGCCT AAGTGGACTC GAACCACCGA CCTCACGCTT 120

ATCAGGCGTG CGCTCTAACC AGCTGAGCTA TAGGCCCATT TTTTTGAATG TTAAATAAAC 180

ATTCAAAACT GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA 240

TATATCCTTA GAAAGGAGGT GATCCAGCCG CACCTTTCCG ATACGGCTAC CTTGGTnACG 300

ACTTCACCCC AAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTACTCCACC 360

GGCTTCGGGn GTTACAAACT CTCGTGGGTG TGACnGGCGG 400

(2) INFORMATION FOR SEQ ID NO: 3849:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3849:

GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC 60

TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT 120

TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT 180

TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA 240

AAAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT CCATTTTTTG CCTGGCAACG 300

TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 360

GACAATCGCT TGCTTCTTTC CTnTCCTTCG GCTCTCGCTT 400

(2) INFORMATION FOR SEQ ID NO: 3850:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3850:

GTCTACTAAT GTTACAACCA CACCTGATTa ATTGCTTTTT TAGCAGTAAT TGCCACATCT 60

GTGTGACGAT AATGATATGC GACAGTTAAT AATTTGTGAT TTTTATTAGC CGCTTCAATC 120

ATGCGATCAC ACTCTTCCGT CGTCATCGCC ATTGGCTTTT CACACAATAC ATGGACACCA 180

TGGTTCAATG CTTCTATAGA AAGATCAGCA TGGAATTTAT TAGGTGTACA AATGACCACC 240

GCATCAACAA GTTTAAACAG CTCGCTAGGT GTCTCAACTG CATGAGGTAT ATTAAAGCGC 300

TTCGCAACAT CAATCATCTG CACTGTATTA ATATCTTGTA CTGCAACTAA TGAGACTGTG 360

TCTTTGAGTT TCAGCAATGC TGGAATATGA CGGTCTTGTG CAATACCACC AACAACTATG 420

CACACCAACT TTTAAnTTTG TnCATGATGT GCCnGCTTnA CCG 463

(2) INFORMATION FOR SEQ ID NO: 3851:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 628 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3851:

TATGCTCTAA TGCTGGGCTT AGTGGATTCG ACCAACGAGT GACGnAGTCA AAGTCnGTTG 60

CTTTACGCTT GGCTATAGCC CCAATATATA GATGTTGGAG GGGGCAGATT CGAACTGCCG 120

AACCCGAAGG AGCGGATTTA CAGTCCGCcG CGTTTAGCCA CTTCGCTACC CCTCCAGCTT 180

ATTCATATAA TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT 240

GCTTGTAAGG CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG 300

ACTCGAACCC GTGTTACCGC CGTGAAAGGG CGtGTcTTAA CCGCTTGACC AAGGAGCCAT 360

GGCTCaCAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG CTCTACCACT 420

GAGCTACTGT GGaTTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTtCG 480

GACTrACCAT CGACGCTgAA GGAGCTTAAa CTTCTGTGTT CgGCATGGGa ACAGGTGTGA 540

CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTGAATTT GATGACATTG CAAAAnTAGn 600

TTAGTAAGTA AAAGTGGATT TTGGnTTn 628

(2) INFORMATION FOR SEQ ID NO: 3852:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3852:

TAAAGATTTA AAAGTAGCTG TTATTGGnAC AGGTCGAATT GGCCGTGTAG TAGCCGATAT 60

ATTTGCCAAT GGTTATCAAA GTGATGTGGT CGCATACGAC CGTTTCCTAA TGCTAAAATT 120

GCAACGTATG TCGATTACAA AGATACGATT GAGGAAGCGG TTGAAGGTGC TGATATCGTG 180

ACATTACATG TACCTGCAAC GAAATATAAT CATTATCTAT TTAATGCTGA ATTATTTAAA 240

CATTTTAAAA AGGGCGCnTA TTTGTCAATT GTGCGAGAGG TTCTTTAGTA GGATACTAAG 300

GCGTTATTAG ACGCATTAGA CAATGGTGTG ATTAAAGGTG CAGCACTTGn TTACGTATGG 360

ATTTGGAACG GCAAACTTTT TCCCAAGTGG TCCAAAGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3853:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3853:

TCTTAAACAT TAGCCACAGC TAATTGTGAC TTAAAAATAG GAATACATGA GTAAAACTCA 60

TCATAAGAAA TACTAATTTC TATAGAAAAA GTATTACTTT ATCGTTGTCC CACCCCAACT 120

TGCACATTAT TGTAAGCTGA CTTTCCGCCA GCTTCTGTGT TGGGGCCCCG CCAACTTGCA 180

CATTATTGTA AGCTGACTTT TCGTCACTTG CTGTGTTGGG GCCCCGCCAA CTTGCACATT 240

ATTGTAAGCT GACTTTTCGT CACTTnCTGT GTTGGGGCCC CGCCAACTTG CATTGTCTGT 300

AGAAATTGGG AATCCAATTT CTGCTATGTT GGGGCCCACA CCCCAACTnC GCATTGCCTG 360

TAGAATTTCT TTTCGAAATT CTCTGTGTTG GGGGCCCACA 400

(2) INFORMATION FOR SEQ ID NO: 3854:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3854:

GTGCAATCTG CGTTAACAAA TGTAAATCGT GTCAATGAGC GATTAACGCA AGCAATTAAT 60

GAAATCAATA nATCAGTAAC TACTGATGGT ATGACACAAT CATCAATCCA AGCATATGAA 180

AATGCTAAAC GTGCGGGTCA AACAGAATCA ACAAATGCAC AAAATGTTAT TAACAATGGT 240

GATGCGACTG ACCAACAAAT TGCCGCAGAA AAAACAAAAG TAGAAGAAAA ATATAATAGC 300

TTAAAACAAG CAATTGCTGG ATTAnCTCCA GACTTGGCAC CATTACAAAC TGCAAAAnCT 360

CAGTTGCAAA TGnTATTGTC AGCCACGAGT ACGGCTGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3855:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3855:

TGTGTGAAAA ACCAATGGCT GAAAACGACA GCAGAAGCTC AAAAAATGAT AGATACAGCT 60

AAATCAACAG GTAAAAAATT AACAATAGGT TATCAAAATC GTTTCCGAGC AGATAGTCAA 120

TTTTTACATC AAGCAGCGCA ACGTGGCGAC TTAGGAGACA TTTACTTCGG AAAGGCACAT 180

GCCATTCGTC GTCGAGCAGT ACCAACATGG GGTGTCTTTC TAGACGTAGT AAGCTCAAGG 240

TGGAGGACCA TTAATCGATA TCGGTACACA CGCTTTAGAT TTAACGTTAT GGATGATGGA 300

TAnTTATGGA ACCAGAATCA GTGATGGGTT TCAACATTCC ATAAATTnAA TAAACAGCCT 360

CATGCGGGCA AACGCTTGGG GTTTCAGGnG TTCCAGATGG 400

(2) INFORMATION FOR SEQ ID NO: 3856:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3856:

CGTTCTCAAT AGAATGATTT AAATCTTCGA TTTCTTTATC TAAATGACTA CCAATTAAAT 60

CTATTTCTTC TATTGTTAAA TCGCTATCTC CATCTTCTTT TATCTCTGGT ATTATTTTTT 120

CTTCAACTAA GTCACGATAT AATGTTTTTG AATTTTCGTT CAATTTCGAT TCGTGATTTT 180

GAATACTTTT CTTCCACACA AATGTATATC TATTGGCATT AGCTTCTACT TTTGTACCAT 240

CAATAAAAAT TGAATTATTA TCAATAAGAT TTTGCTTTAA ACATTGACTA TGGAACTGAA 300

TATAAGAAGG nGGTTGGAnC nTGAGCGAAC CACAnCATCC 400

(2) INFORMATION FOR SEQ ID NO: 3857:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3857:

GGCATACCAT GGTCAAACGC GTGATGATCA AGTAACATCA CATGTTCAAC ATATTTTTGA 60

AGTTGTGAAT GCACATGGTA AACATTTTTG TGCATTACCA CGTGAAGATG AAGATATTGC 120

AAAATGGCAG GCACAAGGTG TACAAACATT TATTTTAGGT GATGATCGCG GAAAAATATA 180

TCGCCATTTA AGTGCATCTC TAGCGACGTC TAAACAGAAA GGGGATGAAG GCTAATGCGT 240

AAAGTTCAAC CTGTTATTGA ACAATTAAAA GCACAATCTC ATCCAGTTTG TCATTAnATC 300

TATGATTTAG TCGGACTGGG ACATCATTTG CAnCATATTA CATCGnCCTT GCCGAGTAAT 360

TGTCAAATGT ACTATGCAAT G 381

(2) INFORMATION FOR SEQ ID NO: 3858:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3858:

GCATGAAGCC CCCCTCAAGA TGAGATTTCC CAACTTCGGT TATAAGATCC CTCAAAGATG 60

ATGAGGTTAA TAGGTTCGAG GTGGAAGCAT GGTGACATGT GGAAGCTGAC GAATACTAAT 120

CGATCGAAGA CTTAATCAAA ATAAATGTTT TGCGACAATT CACTTTTACT TACTATCTAG 180

TTTTGAATGT ATAAATTACA TTCATATGTC TGGTGACTAT AGCAAGGAGG TCACACCTGT 240

TCCCATGCCG AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC 300

GCTAGAGTAG AACGTTGCCA GGCAAAAAAT GGATGCCGAT GGAGCCGCAT TGAGACCGCA 360

GGnCTnTTTG TTTTTTATGT CTAAAACGTC CAAATTAAnA 400

(2) INFORMATION FOR SEQ ID NO: 3859:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3859:

GTTTATTAAT CGTGTCATTA GCATCTTTAT AATTGCTTCT AATCGTATTC AAATCACCTA 60

ATGTTAAATC TGTTTTAACA TTATTTTGAA TTTCATTCAT GCATCTGAAT CTGAATCGCT 120

ATCTGAATCT GAGTCGTTGT CTGAGTCCGA nTCGCTATCT GAnTCTGAGT CGCTGTCTGA 180

ATCTGAATCG CTATCCGAGT CTGAGTCGCT ATCTGAGTCT GAGTCGCTAT CTGAATCTGA 240

ATCGCTGTCT GAGTCTGAAT CGCTATCTGA GTCTGAATCG CTGTCCGAAT CTGAGTCGCT 300

ATCTGAATCT GAATCGCTAT CTGAATCTGA GTCGTTGTCT GAGTCCGAAT CGCTATCTGA 360

ATCTGAGTCG CTATCTGAGT CTGAGTCGCT ATCTGAATCT GAGTCGCTGT CTGAATCTGA 420

ATCACTGTCT GAGTCTGAGT CGCTGTCTGA AGTCTGAATC GCTGTCAGAA TCTGAGTCGC 480

CAACTGAGTC TGAATCTGAA TCACTGGTCT GAGTCCGAAT CGCnATCTGA ATCnGAATCG 540

CnAACCGAGT CCGAAGCCGC nAATCCGAAT CTG 573

(2) INFORMATION FOR SEQ ID NO: 3860:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3860:

GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GATCGAACCG 60

CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA 120

CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT 180

ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT 240

CTTGATCCGT AGTCAAACGC TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGnA 300

AAATGGTGCC GAGGnACCGG GAATCGGAAC CGGTACGGTT GATnCACTCA CCGGCAGGAT 360

TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGnGC 400

(2) INFORMATION FOR SEQ ID NO: 3861:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3861:

TGTTGCGACT AAACCATTAC CTATCGCACA TATGACGAAA CCAATGATAA CTGCAATGAC 60

ATATTGTGAT GCCAATAATT GAGTCATGCT AATAATAGTG ATGCCGATGA CAGGGAACAA 120

CGGACCAATG ATGAGCATCA ATTTGCCACC GAAACGTAAT GTTGCTTTTT CACCTAAACG 180

AATCATCGCA ACTGCCACAA TGGCATATGG CAATGTAACA nGTCCAGATT GCGCACTGAT 240

AAACCAAGGT GTGTTTGAGC ATATATGAAA AAGACCACTG TTACGCCTAG ACCGCTATTT 300

AAAACAAAGT TATTTAAAAA TGCACCAATG GAACGGACGG TTGCGTAATA CTGGAGAAnT 360

CAATAAAAGG TACTTCCATG TCCGACGTTC CGATGGATGG 400

(2) INFORMATION FOR SEQ ID NO: 3862:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3862:

GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGA ATTAGGGATC 60

GGTACTTTAT ATGAAGACGT GCTGCTTCCA TTAAATGAGT GATGCGATTT TGGCATGAAG 120

GTCACCTTAA ATGTACATTG TTGTAATAAA ATTGCCTATA AATTTTTAGC ACATAAAATA 180

AGAGGAGCCA ACCATTGTTA GACTATAACA ACGGTTGGCT CTTTAATTGT AAAAAGAAAA 240

CCATACGCTA TGCGTATGGT TCAGAAAAGG TCTACCATTG TCACCAAAAA TGCATCTCTA 300

CGTGCTAGAA TAAATATTGG TCAGCCAACC AAAATAATCC ACACGGGGAG ATGCTATTTA 360

ATGTCCTCCT GACACCAACA GTTAGCACCA TACAAAATGG 400

(2) INFORMATION FOR SEQ ID NO: 3863:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3863:

TCGGCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA 60

CTAGCGGAAC GTAAGTTGGC TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC 180

GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG 240

CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTTCTTTG 300

TGTTTGCTTT TTATTTTGAC GTTTTAGACA TAAAAAAAAG AGACCTTGCG GTCTCAAATG 360

CGGCTCATCG CATnCATTnT TGCCGGCAAC GTTCTACTCT 400

(2) INFORMATION FOR SEQ ID NO: 3864:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3864:

GTACTATAGA ATTAAAGAAT TATAAAAATA TAATCCTGAT TAGCTTGTTG TCAAGTCATC 60

GTTCATAATG AAGATATCAC GTTCAATTGT ATTGTTTGTT TATGGGAAAT GAATTAATGT 120

AATAGTATAT GTATGCGGTT ACATAAAAAG CGAACATCTA ACCTGATATT TAAATGAACC 180

TGACGCTCAA TCAACTAATT TACAACCGTA TTTTTATAAT CAACCATAAA GGAGGAGATA 240

GAAAATGAAT AGTGCAAAAT TGATTGATCA CACTTTATTG AAGCCTGAGT CAACACGTAC 300

GCAAATCGAT CCAAATCATC GATGAAGCGA AGCATACCAT TTTAAATCTG TATGTGTGAA 360

TCCAACGCAT GTTAAAnGTG CCAGCAGAGC GACTAGCTGG 400

(2) INFORMATION FOR SEQ ID NO: 3865:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3865:

GCAGCACGTC TTCATATAAA GTACCGATCC CTAATTCAAC GCATGTAGTA CCACATCTTC 60

AAAGCTTGAT AGTTCCCATG CGCACACCAC GTTTCATACT AGCTATGCGA GCTCAACTTG 120

GTTCATAAAC TCTTTAATAT AAGTCAATGT TTCAACCATC GCTGGTGGTC TTGGCACATG 180

TCCTTCTGCC ATTTGATAAA ATGTTTCATG CGTGGCACCT TTTAACTCTA GTTGGTCCGC 240

TAAATAATAC GCATGATGAA TACCAACTTG CTGGTCTTTC CCTCCATGTA CAATTAATAT 300

TTTTTTCGGA TGACCAATCA TTCTTCGTAG CATGCCTCTT 400

(2) INFORMATION FOR SEQ ID NO: 3866:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3866:

AAGTCAATAA CTTTTTTTAT CTTGTCCATT TTATTTTTTA ACCAAAATTT GATTAAAAAA 60

CTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTCGA nCTACCATCG ACGCTAAGGA 120

GCTTAACTTC TGTGTTCGGC ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA 180

TATGAATGTA ATTTATACAT TCAAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA 240

AACATTTATT TTGATTAAGT CTTCGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300

GCTTCCACCT CGGAACCTAT TAACCTCATC ATCTTTGGAG GGGATCTTAT AACCGGAGGT 360

TGGGGnAAAT CTCATCTTGA GGGGGGGCTT CCAGGCTTAG 400

(2) INFORMATION FOR SEQ ID NO: 3867:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3867:

CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT GnCGATTGGA 60

TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC 120

TGTGATGGGG AGAAGACATT GTGTCTTCGA GGTCGTTGAT TTCACACTGC CGAGAAAAGC 180

CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC AGGTAGTCAA GATGAGAATT 240

CTAAGGTGAG CGAGCGAACT CTCGTTAAGG AACTCGGCAA AATGACCCCG TAACTTCGGG 300

AAGAAGGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC ATGAATAGGC CCAAGCGACT 360

GTTTAnTCAA AACACAGTCT CTGCTAAACC TAAGGATGTA 400

(2) INFORMATION FOR SEQ ID NO: 3868:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 383 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3868:

TTCTTTGGAA ATAGTAACGT TGAAGTTGTA CTCACTGGTG ATACATTTGA TCACTGTTTA 60

GCTGAAGCTT TAACTTATAC AAGTGAACAT CAAATGAnCT TTATAGATCC ATTCAATAAT 120

GTTCATACAA TTTCTGGACA AGGTACGCTT GCTAAAGAAA TGCTAGAACA AGCAAAGTCT 180

GACAATGTTA ACTTTGATTA TCTATTTGCC GCAATTGGTG GTGGCGGTTT AATTTCAGGT 240

ATTAGTACTT ACTTTAAAAC CTATTCACCT ACCACGnAAA TTATAGGTGT TGAACCTTCA 300

GGTGCCAAGT AGTATGTGAT GGAATCTGTT GTGAAATATT CAGGTAGTCA CATTGCCCTA 360

AnTCGATAAA TTTGTGGACG GTG 383

(2) INFORMATION FOR SEQ ID NO: 3869:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3869:

CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA CTTAACCCAA CATCTCACGA CACGAGCTGA 60

CGACAACCAC CACCTGTCAC TTTGTCCCCC GAAGAAGnGC TCTATCTCTA GATTGTCAAA 120

GGATGTCAAG ATTTGGTAAG GTTCTTCGCG TTGCTTCGAA TTAAACCACA TGCTCCACCG 180

nTTGTGCGGT TCCCCGTCAA TTCCTTTGAG TTTCAACCTT GCGGTCGTAC TCCCCAGGCG 240

GAGTGCTTAA TGCGTTAnTG CCAGCACTAA GGGGCGGAAA CCCCCTAACA CTTAGCACTC 300

ATCGTTTACG GCGTGGACTA CCAGGGTATC TAATCCTGTT TGATCCCCAC GGTTTCGCAC 360

ATCAGCGTCA TTTACAGACC AGAAAGTCGn CTTCGGCAAT 400

(2) INFORMATION FOR SEQ ID NO: 3870:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3870:

GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC TCATGCTGGG 120

TTTCCCCATT CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 180

GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC CCTTAATAAC 240

TTAATCTATG TTTCCATCCT ACAGGAAACG CGTTATTAAT CTTGTGAGTG TTCTTTCGAA 300

CATGAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 360

GCTTGGTAAA AGCnnGn 377

(2) INFORMATION FOR SEQ ID NO: 3871:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3871:

ATAACGTTGC CCCTCCCATG TATATCCTAC CCAAACATGA CCATCTTGTA ACATCACTTC 60

TGTATAATCA CAATACCCAC CAGGTTGGAA CTGATAACCC ACTGGACAAG ATAAGAATGG 120

CCCCACTTTT CTTACTGTGA TTGGTTGATT GCCGTTTGTG AATCTAGCAC TTTCTTCCAT 180

GTAGTAAGTA CCATATTTAT TACGTTTCCA TGCACTTGCA ACTGGTTTAA CTGTATTACT 240

TGAAGCGCTT GACTCATTAG AGACAGTGGC AACCGGTATT TTACCATCCA TGTACGCCCT 300

AAATCTGCTT GATAAAGTAG TCTTTTAAGT TGCAACCGCT TGTCTTCTGG GCAATAGACC 360

GCGAGTTACn GGGGTCCAAA CCCnTGGTGT AAAAnCGAAC 400

(2) INFORMATION FOR SEQ ID NO: 3872:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3872:

CGCTACACTA CGAGACCATT AGTAAAACGC AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 60

TTAAGCCCCT GTCGGTTTTC AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120

ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG TTATGAGCCG TTAGCTCTAA 180

CCAACTGAGC TAAAGGTCCT AAATATAATT TTACAACTAA TAAATAGTGG CGGTGGAGGG 240

GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GGATCGAACC GCTGTACCTC 360

CTGCGTGCAA ACGGGCGCTC TTCCCAGCTG nAGCTAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3873:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 584 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3873:

ACAGCTCACG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 60

CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCTTCG 120

GTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGTT TCGTCAGATT 180

CAAnnGTTTT CAtTCGCCAA GCCATTTTTC TTTGTGTTTA CTTTTTATTT TGACGTTTTA 240

GGCATAAAAA AAAGAGACCT TGCGGTCTCA AnTGCGGCTC ATCGCATCCA TTTTTTGCCT 300

GGCAACGTTC TACTCTAGCG GAAnTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 360

GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 420

TACTAAACTC GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA 480

GCCATTTTTC TTTGTGTTTA CTTnTnATTT TGACGTTTTA GACATAAAAA AAAGAGACCT 540

TGCGGTCCAA ATGCGGGCTC ATCGCATCCA TTTTTTGCCT GGGC 584

(2) INFORMATION FOR SEQ ID NO: 3874:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3874:

TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAnTTGG CTACCATCGT CGCTAAAGAC 60

CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 120

TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180

TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA 240

GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300

GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT 400

(2) INFORMATION FOR SEQ ID NO: 3875:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3875:

TCTGCTAATT TAAAAATGAT ATTTTCTATC TTTTCTTTAT TATTAACGTC TAATGCACTG 60

GTCGATTCAT CTAATAAAAG AATATCCGGT GTATACATCA GTTGGCGCGC TATAGCAATT 120

CTTTGCCGCT CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA 180

CCGACATCTT TAATTAATTG CTTTGCACGT TTTCTATCAA ATTTATCATT ACGTGCAAGT 240

GATGGGAATA TCATGTTATC TTCAATCGGT CACCAAACAA GTCACTTTGC TGCATCAAAT 300

AACTGATTCG TTGACGCCAA TTCTTCCGGG GCATAATnCA TATAGGGGTT ACCTTAAAAA 360

TAAAGGTCCT CCACTAGTTG GCCTAnACnA ATTACATAAn 400

(2) INFORMATION FOR SEQ ID NO: 3876:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3876:

AGATAGACTT TCTGGTGAAG ATACACGTGA AGGTATGACA GCAATTATAT CTATCAAACA 60

TGGTGATCCT CAATTCGAAG GTCAAACGAA GACAAAATTA GGTAATTCTG AAGTGCGTCA 120

AGTTGTAGAT AAATTATTCT CAGAGCACTT TGAACGATTT TTATATGAAA ATCCACAAGT 180

CGCACGTACA GTGGTTGAAA AAGGTATTAT GGCGGCACTG CACGTnTTGC TGCGAAAAAA 240

GCGCGTGAAG TAACACGTCC GTAAATCAGC GTTAGATGTA GCAAGCCTTC CAGGTAAATT 300

AGCCGATTGC TCTAGTAAAA GTCCTGAAGA ATGTGAGATT TCTTAGTCGA AGGGGCTCTG 360

CCGGGGGGTC TACAAAATCT GGTCGTGACT CTAGACCGCA 400

(2) INFORMATION FOR SEQ ID NO: 3877:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3877:

ACCAATTTCT CCTTTGTATC CGCCATCTTT AAATAATTTT ACTGCTCTAG CATGAGCCAC 60

CATCATGTTA TGTGATTGGA ATACTTTTTC AAAATCATAT TTAATACCTG GAGGGAATTT 120

ACCTACTAAA TATTGACCAT CACCAATAGG TCCAATTTCA TTGAATGTAG TCCAATATTT 180

TACTTCTGGG AATTCTTTAA AACAATATTC AGCATAATCT ACAAAGTAGT CAATCGTTTT 240

ACGnTTTAGA AAATCGCCAT CTTTGGTGGT ACACTTCTGG GnGTATCAAA ATGnTGCAAT 300

GTTACAAATG GTTCAACATG ACGGTTTATG GnCACTCTGC AAATAACCTT ATGGTAATAC 360

TCAACACCTT AGGGGTTAAC TTCGGCCATA TCCCTTTTGG 400

(2) INFORMATION FOR SEQ ID NO: 3878:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3878:

ATTAAAGCAG TTTCTGGATC TGGTAAAAAT GGTCGTATTA CAAAAGAAGA TGTAGATGCA 60

TACTTAAATG GTGGTGCACC AACAGCTTCA AATGAATCAG CTGCTTCACT AACAAGTGAA 120

GAAGTTGCTG AAACTCCTGC AGCACCTGCn GCAGTTAACA TTAGAAGGCG ACTTCCCAGA 180

AACAACTGGA AAAAATCCCT GGCTATGCGT AGAGCAATTG CGAnAACATG GGTTTAACTC 240

TAAGCATACT GCACCTCATG TAACATTAAT GGATGAAATT GGATGTTCAA GCATTATGGG 300

GATCACCGTA AGAAATTTAA AGAAATCGCG GCTGAACAAG GTACTAAGTT AACATTCTTA 360

CCTTATGTTG TTAAnGCACT GTTTTCGGCA TGGnAAAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3879:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3879:

TTGTGTTTAC TTTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 120

TGCGGCTCAT CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 180

GCTACCATCG ACGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 240

CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCGCTCTTT TCTCGTTTCG 300

TCAGATTCAA ACGTTTCACT TCGCAAGCCA TTTTTCTTTG TGTTGCnTTT ATTTGACGTT 360

TAGACATAAA AnAAGAnCCT TGCGGnCTCA ATGCGGCCAT 400

(2) INFORMATION FOR SEQ ID NO: 3880:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3880:

TAGGTGTAAA TCCTGCGATT CGATCTGGAC CATATTTTTT TATTGTATAC AGTAATTGTG 60

CTGCGATTAT CTCTGTAACG TCTTTCCAAT TTGAACGCAC GTGCCCTCCC ATACCTCGGG 120

CTTGCTTATA TTGTTTGGCT TTGTCTTCAT TTTCAACAAT AGACGCCCAT GCAGCAACGC 180

GATTACCATT GTTTTCTTCT AATGCTTCAG TCCATAAATC CCAGAGTTTT CCACGAATAT 240

ATGGATATTG ATTCGAAGCG GACTGTATCA TACCAAGAGA ATGACGCACT CGTGGACATC 300

CTCTCGGTCA TATTCAGGCA TATCCGGACA CAACTTGGAT AGCAGTTGTG ATTTCCCAGG 360

AATCACACCA TTTCACAAAC TTCCAGACAT GGCTGACAGT 400

(2) INFORMATION FOR SEQ ID NO: 3881:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3881:

TGAGTAGCGA AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAGGTTT CCAGAGGAAG 60

GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA AGCTGAGGCC GACAGnGTAG GCGATGGATA 120

ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCAGTAGGA 180

TAGGCGAACG TGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC 240

TCACACTGCC GAGAAAAGCC TCTAAGATAA GAAAATTAGG TGCCCGTACC GCAAACCGAC 360

ACAGGTAGTC CAAGATGGAG AnTCTnAAGG TGGAGCGAGC 400

(2) INFORMATION FOR SEQ ID NO: 3882:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 609 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3882:

CATCCCCAAC TTGCACATTA TTGTAAGCTG ACTTTTCGTC ACTTCTGTGT TGGGGCCCTC 60

ACCCCAACTC GCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG GGGCCCCTGA 120

CTAGAATTGA AAAAAGCTTG TTACAAGCGC ATTTTCGTTC AGTCAACTAC TGCCAATATA 180

ACTTCGTAGA GCATAGAATA TTGATTTATG TCCCAGCCTG AGTTAATTTT CTATAAAAGT 240

ATATTTAATT TGCGTTTATA CCGTCAAACT TCACTTTAGC TTTGTCAAAC CCCTTTCTAT 300

TAAGTTTTCA GAAATAAACC TATCTTAAAA TATAAAAAAA TCGAGAATTC GTAGTTTAAT 360

AACGAAATTC TCGTTCTTAT CCTTTTGaAT aTACTCAATT TTCCACAAAA ACAAACAAGT 420

AGTATATCTG TTCTAGCTAC TAGAATGACA TACTACTTGT TATTAAAATA CTTAACTAAA 480

CTTTATTAGT TATCTTTnTT CTCTATATTT CTACGTGGAC TGACGCTTTT CAnGAATGTC 540

AGATTCATAA TCTTCTTGGT TGGACTCCTG GATATATTCT TGGTAAGCGG ATGGTTTATT 600

CGGAGTCAA 609

(2) INFORMATION FOR SEQ ID NO: 3883:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3883:

ATATATTGGC GGACATAACG ATGTACTAGC AGGTGTCGTA ACCGTCAAAG ATGAATCACT 60

CGCGCAACAG TTGTTTGATT TTCACAACAT GACTGGCGCA ACACTTTCAC CAATAGATAG 120

TTATTTGTTG TTACGTGGAC TTAAAACTTT GCATTTACGC ATTGAGCGTG CGCAATCAAA 180

CGCTAGAAAA CTTGCTAAAA AATGTCAGTC ACTTCAAGCA ATTGACGAAt ACTaTATAGC 240

GAAAATTTAG ACATTTGcAT TTTTGCAGAA AGTTTAGGAg GTACkGAAAC ATTAGTGACC 360

TTCCCTTACA CCCAAACACt GTTGATATGC CAGT 394

(2) INFORMATION FOR SEQ ID NO: 3884:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3884:

CGATTAATGA ATTAACAGAA TACGGACCAG AAACGATAAC ACCAGGTCAT CGAGACGAAT 60

TTGATCCGAA GTTACCAACA GGAGAGAAAG AGGAAGTTCC AGGTAAACCA GGAATTAAGA 120

ATCCAGAAAC AGGAGACGTG TTAGACCACC GGTCGATTAG CGTAACAAAA TATGGACCTG 180

TAAAAGGAGA CTCGATTGTA GAAAAAGAAG AAATTCCATT CAAGAAAGAA CGTAAATTTA 240

ATCCTGATTT AGCACCAGGG ACAGAAAAAG TAACAAGAGA AGGACAAAAA GGTGAGAAGA 300

CAATAACGAC GCCAACACTA AAAAnTCCAT TAACTGGAGA ATTATTAGTA AAGGTGATCG 360

AAAGAGGAAT CACAAAAGTT CCnTTTATGA TTAACAGATA 400

(2) INFORMATION FOR SEQ ID NO: 3885:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3885:

TGAGCGGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG 60

CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120

CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG TGCGCTCTAA CCAGCTGAGC 180

TATAGGCCCA TTTTTTTGAA TGTTAAATAA ACATTCAAAA CTGGAATACA ATATGTCACG 240

TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG 300

CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 360

GACGGCTAGC TCCCAAAAGG GTACTnCCAn CGGGnTTCGG 400

(2) INFORMATION FOR SEQ ID NO: 3886:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3886:

TACGGTAGGT GGCAAGCAGT TATCCnGGAA TTATTGGGCG TAAAGCGCGC GTAGGGGTTT 60

TTTTAAGTCT GATGTGAAAG CCCACGGCTC AACCGTGGAG GGTCATTGGA AACTGGAATn 120

CTTGAGTGCA GAAGAGGAAA GTGGAATTCC ATGTGTAGCG GTGAAATGCG CAGAGATATG 180

GAGGAACACC AGTGGCGAAG GCGACTTTCT GGTCTGTAAC TGACGCTGAT GTGCGAAACG 240

TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG AGTGCTAAGT 300

GTTAGGGGGT TTCCGCCCCT TTAGTGCTGC AGCTAACGCA TTTAAGCACT CCGCCTGGGG 360

GAGTTACGAC CGCAAAGTTT GGAAACTCAA AGGGAATTGG 400

(2) INFORMATION FOR SEQ ID NO: 3887:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3887:

ATTTTTTAAT TTTCATGCAA ATTTTTAAGC ACCATATAAT GCCTACCAAA TTTCAATAAT 60

CTTTGTTGCC GTTTAAATAA TGTGAATGTC AATAAATTCT CCAAACTAGT CGAAAATAAA 120

GGGAGTnGGA CATAAATCCC TAAAAAAACA GCAGTAAGAT AATTTTCAAT TAGAAAATAT 180

CTTACTGCTG TTCTCTATTT ATACAATACT TCGTATTGAA TGGCTTCGCT TTCCnAGGGT 240

GCCGTCTCAG CCTCGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAATACT 300

ACGTATTAAC ATGGAATTTT ACTTTTACAT ACTTTAAAAA ATAAGnCACT TTGGCCAACT 360

TACACTACCA TAGGAACCCT GGTAGGAATC CCCCAAATGn 400

(2) INFORMATION FOR SEQ ID NO: 3888:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATACGACAAT CACAGCAATA ATAATTGCTT TAGAAAGTCG TGCCGAACTG GAACTTACAA 60

GTCTAGTTCG AACACACACT GATGTGAGTG GTTTTATTTA TTTTAAACAT GAACAATCAG 120

ATAAGTTACT AGCATTAGCA AATATTATTA AATCAAAGGG CTTCGATTCA TAAAATTAAA 180

ACAATGATTA AAATTAGACG TGTAAATGTT AAATTCTAAA ACGGAAATAA CCACCATCCC 240

ATTAAACCAC TTTnATnGTT CAATCACTAT ATTTCACACA GCTTCATTAA TAAAACGACT 300

TGCTTCAACC CGCTTCAACT TCAACTGGCT TCAACTTCAG CCTACTTCAT TCAATnACAA 360

AACGAATCCG CTTCATCCAA AATCAnCCAT TCTAACGCAC 400

(2) INFORMATION FOR SEQ ID NO: 3889:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3889:

CCATGCnAGA CGCATACATT GTaGCTTATG GgCGTTCAGC gCAGCGAAmG aAAGCAAGGC 60

GCATTATTCC ACGAAAGACC TGATGATGTC GCAGCCAAAG TATTACAAGG CGTATTGAAA 120

CGTATTGACG GAAAATTCAA TAAGAATATG ATTGAAGATG TCATTGTTGG TACGGCTTTT 180

CCAGAAGGAT TACAAGGCCA AAACATTGCA CGAACGATTG CATTGCGTGC GGGATTATCT 240

GACACGGTAC CGGGTCAAAC AGTGAATCGC TACTGCTCAT CAGGATTACA AACCATCGCG 300

ATTGCAGCCA ATCAAATTAT GGCTGGTCAA GGAGATATAC TTGTAgCTGG TGGCGTTGAA 360

TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA ACAATCCaAC CTTwACAATA 420

tGaTGATATA GGTGCGTCCA TATnCCTATG GGTTTnAAnT GCTGGAAAAT GTTAGCCTnC 480

CCAAT 485

(2) INFORMATION FOR SEQ ID NO: 3890:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3890:

AGGCAGATGC TCTCCCAGCT GAGCTAATTC TCCAAAATAA TGACTCCTAC GGGACTCGAA 60

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 180

TGTGGGATTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGAAnTGAAT TCGGACTACC 240

ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT 300

ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTG AAGTAAAAGT 360

GGTTTTGCnT CGCAAAACAT TTATTTTGn 389

(2) INFORMATION FOR SEQ ID NO: 3891:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3891:

CAGATGTTTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA AAAATGGAGC 60

AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT ACCGCTGAAC 120

TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGCTn AGATCCTAAG 180

TCTAGTGCGT CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG GATTCGAACC 240

TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGG AGCTAATGGC TCTTCCATGG 300

TGCCGGCCAG AGGACTTGAA CCCCCAACCT ACTGGATTTA CAAGTCAGTT TGCTCTACCA 360

ATTGGAGCTA GGGCCGGGCA ATATGGTAAG AATAAATTGG 400

(2) INFORMATION FOR SEQ ID NO: 3892:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3892:

CTCTCGGTGG TCGTGCTACA ACTGGTAAAA ATGTACATGT AGGGGCTGGC GCAGTATTAG 60

CAGGTGTGAT TGAACCCCCT AGTGCTTCAC CGGTTATAAT CGAGGATGAT GTATTAATCG 120

GTGCAAATGC AGTTATTTTA GAAGGTGTAC GTGTTGGTAA AGGTGCTATT GTTGCAGCTG 180

GCGCGATTGT GACACAAGAT GTACCAGCTG GTGCAGTTGT TGCTGGTACA CCTGCAAAAG 240

TGATTAAGCA AGCTTCTGAA GTACAAGATA CTAAAAAAGA GATTGTAGCA GCATTAAGAA 300

CCACCnTAAT GGTnTAGCAT TGAATAAACT TATGnnCCCC 400

(2) INFORMATION FOR SEQ ID NO: 3893:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3893:

GAATGTAGTT GTGGTAAATA CAAACGTGTT CGCTACAAAG GCATGGTCTG TGACAGATGT 60

GGAGTTGAAG TAACTAAATC TAAAGTACGT CGTGAAAGAA TGGGTCACAT TGAACTTGCT 120

GCTCCAGTTT CTCACATTTG GTATTTCAAA GGTATACCAA GTCGTATGGG TATTATTACT 180

TGACATGTCA CCAAGAGCAT TAGAAGAAGT TATTTACTTT GCTTCTTATG TGTTGTAGAT 240

CCAGGTCCAA CTGGTTTAGA AAAGAAAACT TTATTATCTG AAGCTGAATT CAGAGATTAT 300

TATGATGAAA TACCCAGGTC AATTCGTTGC CAAAAATGGG TGCCAGAAGG TCATTAAAAG 360

ATTTACTTGA AGnnGATTGA TnCTTGACGA GGGAACTTnA 400

(2) INFORMATION FOR SEQ ID NO: 3894:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3894:

CACGTGAAGT TAGAGATACT TCATTACGTG TACCTCACGG CGCTGGCGGT ATCGTTCTTG 60

ATGTAAAAGT ATTCAATCGT GAAGAAGGCG ACGATACATT ATCACCTGGT GTAAACCAAT 120

TAGTACGTGT ATATATCGTT CAAAAACGTA AAATTCATGT TGGTGATAAG ATGTGTGGTC 180

GACATGGTAA CAAAGGTGTC ATTTCTAAGA TTGTTCCTGA AGAAGATATG CCTTACTTAC 240

CAGATGGACG TCCGATCGAT ATCATGTTAA ATCCTCTTGG TGTACCATCT CGTATGAACA 300

TCGGACAAGT ATTAGAGCTA CACTTAGGTA TGGCTGCTaA AAATCTTGGT ATTCACGTTG 360

cATCACCAGT ATTTGaCGGT GCaAACGrTG aCGATGTATG GTCAnCAATT GAAGAAGCTG 420

GTATGGCTCG TGATGGTAAA ACTGTACTTT ATCGATGGAC GTACCAGGTG ACCCnTCCGA 480

TAACC 485

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 507 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3895:

GAACAACATA CCTTTGTTTG TTGATTCTTC TCCACCTGTT TCAAGTAGTT CAGATTTCTT 60

AGATTGTGGT TTTTTAGTTG GTGCCACTGc TTTAACCTTT TCATTGATTT CAATAACAGG 120

TGTTACTACT TTACCTTGTT CCACTGGTTT AGAAGGCTTT TTAGGTTCTT CTTTGGCAGG 180

TGGTACTGGT TTACCAnGTT CAGCTGGTAC CTCTGGTGTT GGCGGTGTTG GAGTTTCTGG 240

CTCACTCGGC ACTTCTGGTG TCGGTGGTGT TGGTGTTTCC GGCTCACTTG GTACTTCTGG 300

TGTTGGTGGc GTTGGTGTTT CCGGCTCACT TGGTACTTCT GGTGTCGGTG GCGTTGGtGG 360

CACGATTGGA gGTGTTGTAT CTTCTTCAAT CGTTTGTTGA CCTTCATTTT GGGCCGCTTA 420

CTTTTGGGAA GTGTATCTTC TTCAAAGTCA ACACTAATGT GGTCCACCGG AATTGATAAC 480

TGGGGTTAAC CTTAAATTGG AACCTCC 507

(2) INFORMATION FOR SEQ ID NO: 3896:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3896:

CTAGCGGAAG TAATTGGCTA CCATCGTCGC TAAAGACCTT nGGnGACTTG TGACAATCGC 60

TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 120

CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTTGTG 180

TTTACTTTTT ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGGT CTCAATGCGG 240

CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnGTA ATTGGGCTAC 300

CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 360

GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 400

(2) INFORMATION FOR SEQ ID NO: 3897:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3897:

TTGAAGAAGA TCGCGATGAC TATACAATCA ATATCGAGTA TAATACCGAT TTATATCACT 60

CAGAAACAGT TCGTCACATG GGTAATCAAT GTATGATTAT GATTGATTAT ATTTTGAAGC 120

ATCAAGATAC ACTACAAATT TGTGATATAC CAAACGGCAC GAGGAACTTC TAAATTGGGT 180

CAATACGCAT GTTAACGATC GAATGCTTAA TGTCCCGGGA AATAAATCTA TCATAAGTTA 240

CTTTAATGAA GTTGTCTCAC GACAAGGTAA TCATGTTGCG CTAGTCATGA ATGAnTTGAC 300

AATGACGTAT GAAACATTAC GCAACTATGT GGGATGCCAT TGCGCACATG CTCCTATCAA 360

ATGGTGTGGG CAATGGTCAA CGGGTTGCCT TGGTGTACAG 400

(2) INFORMATION FOR SEQ ID NO: 3898:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3898:

GAAATCAGTA TTAAAGCAGT TAATCCACAA GGGAAAGTGG TTAATACAGT TGGCTCTGGT 60

GATAGTACAG TTGCAGGCAT GGTGGCTGGA ATTGCTTCAG GTTTAACGAT TGAAAAAGCA 120

TTCCAACAAG CAGTCGCATG CGGTACTGCC ACGGCATTTG ATGAGGACTT AGCAACACGG 180

GACGCTATAG AAAAAATAAA ATCACAAGTT ACGATTAGCG TACTTGATGG GGAGTGAAAA 240

TAATGAGAGT AACAGAGTTA TTAACAAAAG ATACAATAGC AATGGATTTA ATGGCAAATG 300

ACAAAAATGG TGTTATTGAT GAGTTAGTAA ATCAATTAGA CCAAGCAGGT AAATTAAGTG 360

ATGTCGCGTC ATTTAAnGGA AGCGATTCAC CATCGnGATC 400

(2) INFORMATION FOR SEQ ID NO: 3899:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3899:

CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 120

GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG 180

CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTTCTTTG 240

TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAAGA nACCTCACGG TCTCAACTTG 300

CCTGGCAACG TTCTACTTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC TnAAAGACCT 360

TTCTTGGACT TGTGGACAAT CGGCTTGGCA nTCTTTnCTC 400

(2) INFORMATION FOR SEQ ID NO: 3900:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3900:

TGCACGCGTA TCTGATGGTT GCTCAGTTGC ATCTACCCAA GGTAACCATT CCCTAAGTGA 60

ATTTCTTGAA CGATTGACTA AATTGAAAAG CGCTTCTGTG TCATGAGCTT CTAAAATTTT 120

TAATGTTATT TGTTCATTCA CTTTCATTCC AAACATACCA TCACATCCTC ATTCATTTTT 180

CATATAATTC TGTAAATTAT CATTATAATA ACATATTAAT GTTACGCATT GTATCTTAAA 240

TTTGTTGTCC TTCCCCAACT TGCATTGCTT GTAGAATTTC TTTTCGAAAT TCTCTATGTT 300

GGGGCCCGCn AACTTGCATT GTCTGTAGAA ATTACGGACC CAATTTCTCT AGGTGGGGCC 360

CATCCCCAAC TTGCACATTA ATnGCAAGCn GACTTTCCGT 400

(2) INFORMATION FOR SEQ ID NO: 3901:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3901:

TACTGCTGTT CACTTTTTAT AATACTTCTG AATGTCTTCA CTTATACTTC TAGTCACAGA 60

TTTAAATAAT CAAAAGTGCA CATTATTAAA ATATCAATTT CACACTCAAT GCGGCTCATC 120

GCATTCATTT CTTGTCTCAA CGTTCTACTC TAGCGGAAGT AAGTTAGCTA CCATCCTCGC 180

TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT 240

TTTCACTTCG CCAAGCCATT TTTCCTTGGT GGTTTACCTT TTAATTTGGA CGGTTTAGAC 360

ATnAAAAAAG GGGACCTCAC GGGCCCAACT TGGCCTGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3902:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3902:

TTATTTTGAC GTTTTAGACA TAAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60

TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120

GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180

CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT 240

TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300

TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGGCAACG TTCTACTCTA GCGGGAACGT 360

AAGTTGGGCT ACCAnCGGCG GCTAAAGACC TTTCCTGGAC 400

(2) INFORMATION FOR SEQ ID NO: 3903:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3903:

TTGTTATAAC GAAAACCATT AATAGATTTT TATTTGGTGA TTTCAAATCA TGAGACTGGG 60

ACAGAAATGA TGTTTTCATA AAAATTATTT CGTTGTTCCA CTCTCATGAT TTTTTTGATG 120

AAACATAATT ACATGATTGA TTGCATCATT TTGTTAAACA AGTGATTGCA AACCTGCCAT 180

TTCACACTGA AAATTTACAT AATAAGTGAC GATATTTTAC AAGTCATATA CAAATAACAT 240

ATATTGTTAA ATAATTTTAC CTAATCTTAA CATTAAATTT ACAATTATAA GCGATAATCT 300

AAATATAAAG CTTATTTGAG GTGAAATAAT GGAAATGTCG GTTACAGAAG TCATTTTCTC 360

CTTTTTAGGT GGGTTTAGGG AATTTCCnTT ACGGCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3904:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3904:

CATAAGACAT AATCGCTAGT GTTCGAAAGA GCACTCACAA GATTAATAAC GCGTTTCCTG 60

TAGGATGGAA ACATAGATTA AGTTATTAAG GGCGCACGGT GGATGCCTTG GCACTAGAAG 120

CCGATGAAGG ACGTTACTAA CGACGATATG CTTTGGGGAG CTGTAAGTAA GCTTTGATCC 180

AGAGATTTCC GAATGGGGAA ACCCAGCATG AGTTATGTCA TGTTATCGAT ATGTGAATAC 240

ATAGCATATC AGAAGGCACA CCCGGAGAnC TGAAACATCT TAGTACCCGG AGGAAGAGAA 300

AGAAAATTCG ATTCCCTTAG TAGCGGCGAG CGAAACGGGA AGAGCCCAAA CCAnCAAGCT 360

TGCTTGTTGG GGTTGTAGGG CACTCTATAC GGAGTTACAA 400

(2) INFORMATION FOR SEQ ID NO: 3905:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3905:

AACTAACATT ACAACATGCA TGTGAACAAT TAAAAACATA TTTTAAGTAG GTGAATGAAA 60

TGgTAAATGA ACAAATCATT GATATTTCAG GTCCGTTAAA GGGCGAAATA GAAGTGCCGG 120

GCGATAAGTC AATGACACAC CGTGCAATCA TGTTGGCGTC GCTAGCTGAA GGTGTATCTA 180

CTATATATAA GCCACTACTT GGCGAaTtCG TCGTACgATG GaCATTTTCC gACTGTTAGG 240

TGTAGAAATC AAAGAAGATG ATGAAAAATT AGTTGTGACT TCCCCAGGAT ATCAATCTTT 300

TAACACGCCA CATCAAGTnT TGTnTACAGG TAATTCCGGG TACGACAACA CGATTGATAG 360

TTTGGTTAAT GGGTTAAGTA TTGAAAGTGT TTTGTCCGG 399

(2) INFORMATION FOR SEQ ID NO: 3906:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTCTTTAAAA ATAAACGCCT ATnCGTTATC GGTGGTGGTG ATTCAGCAGT AGAAGAGGGA 60

ACATTCTAAA CTAAATTTGC TGACAAAGTA ACAATCGTTC ACCGTCGTGA TGAGTTACGT 120

GCACAGCGTA TTTTACAAGA TAGAGCATTC AAAAATGATA AAATCGACTT TATTTGGAGT 180

CATACTTTGA AATCAATTAA TGAAAAAGAC GGCAAAGTGG GTTCTGTGAC ATTAACGTCT 240

ACAAAAGATG GTTCAGAAGA AACACACGAG GCTGATGGTG TATTCATCTA TATTGGTATG 300

AACCATTAAC AGCGCCATTT AAnGCTTAGG TATTACnAAT GATGTTGGTT ATATTGTGAC 360

AAAGGTGGAT TGGCCAC 377

(2) INFORMATION FOR SEQ ID NO: 3907:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3907:

AATTAGGTAA TTCAAAATAA TATTAGCGCG GGATGGAGCA GTTCGGTAGC TCGTCGGGCT 60

CATAACCCGA AGTCGGtGGT TCAAATCCGC CTCCCGCAAT ACATAGTTTT TAATTTAATA 120

GGTCTCGTAG TGTAGCGrTT AACACGCCTG CCTGTCACGC AGAGATCGCG GGTTCGATTC 180

CCGTCGAGAC CGCCATTATT ATTACCATTA CGGTTCAGTA GCTCAGTTGG TAGAGCAATG 240

GATTGAAGCT CCATGTGTCG GCAGTTCGAC TCTGTCCTGa ACCATTCTTA ATTCATGGCG 300

GTTGTGGTGA AGTGGTTAAC ACATCGGATT GTGGTTCCGA CATTCGAGGG TTCGATCCCC 360

TTCAGCCGCC CCATAATCGT TTACATTAGC GGGTGTAGTT TAATGGcAAA ACCTCAGCCT 420

TCCAAGCTGA TGTTGTGGGk TtCGrTTCCC AtCAmCCnGy TCCaTaATTT CnAAnAATTC 480

CAACAGTAGC CGCAAGTnGG TA 502

(2) INFORMATION FOR SEQ ID NO: 3908:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3908:

AAAAAATGCA TCTCTACGTG CTAGAATAAA TATTGGTCAG CCAACCAAAA TAATCAACAC 60

TAAGTATCAT ATTGTCTTTG CACCTAAATA CAGAAGACAA GTGATATATG GAAAAATAAA 180

AAAAGATATA GGGATTATAT TGCGTCAATT ATGTGAAAGA AAAGGTGTAG AGATAATTGA 240

AGCAGAGGCA TGTAAAGATC ATATCCATAT GTTAGTTAGT ATACCACCCA AACTTGGGGG 300

TATCATCATT TGTTGGGCTA TTTAAAAGGG AAAAAGTAGT TTAATGGATA TTTGGATAGA 360

CATGGCTAAC TTAAAGTATA GATATGGGAA ATAGGAAAGT 400

(2) INFORMATION FOR SEQ ID NO: 3909:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3909:

GGTTTAACTA TTGAAGAAAA TGTGCCGACA ATTAACAAGA TAAAAAATGC GGTATATTCA 60

GCAGATAAAG CTTTACCTAA GATTAATGAC TTTGCGAATA AAATTGTATA TTTGAATAAC 120

CACCAAGCGG ATTTAGATAA ATATGCCAAT GATTTTAGAA AACTAGGAAA TTATAAAGGT 180

GATATTTTAG ATGCTCAGAA AAAATTAAAC GAGTCAATGG TGCTATTCCG CAACTTAATG 240

AAAAGGCTAA GTTGGATATT AGCTTTTAAA TAATTATATG CCGGAAAATT GGAAAAAGCG 300

TTTAAATTTT GCAGCTGGAT GACGTGCCAC GCnGTTCCCT AAAATTAATC CAGGGCTTAA 360

CATTGCGAGT CCAGGTATTG GnTCCAAGCT AATGGGGCCG 400

(2) INFORMATION FOR SEQ ID NO: 3910:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3910:

TTACCCGATA TCGGGAAGGT ATCCACGAAG GTGAAATTGT AAAATGGTTT GTTAAAGCTG 60

GAGATACTAT TGAAGAAGAC GATGTTTTAG CTGAGGTACA AAACGATAAA TCAGTAGTAG 120

AAATCCCATC ACCAGCATCT GGTACTGTAG AAGAAGTTAT GGTAGAAGAA GGTACAGTAG 180

CTGTAGTTGG TGACGTTATT GTTAAAATCG ATGCACCTGA TGCAGAAGAT ATGCAATTTA 240

AAGGTCATGA TGATGATTCA TCATCTAAAG AAGAACCTGC GAAAGAGGGA AGCGCCACAG 300

GCCATGCCTT CCAGTTACGT TAAATACGCA CGTGGAAAAG 400

(2) INFORMATION FOR SEQ ID NO: 3911:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3911:

CGTGTAnCTC AAGTTATGGG TCCTGTAATT GATGTTCGAT TTGAACATAA CGAATTCCTA 60

AAATTAATAA CGCCTTGGTT ATTGATGTGC CTAAAGAAGA AGGTACAATA CAACTAACAT 120

TAGAAGTTGC GCTGCAATTA GGTGACGACG TTGTTCGTAC AATTGCGATG GATTCAACTG 180

ATGGTGTCCA AAGAGGCATG GATGTAAAAG ATACAGGCAA AGAAATTAGT GTACCTGTTG 240

GTGACGAAAC ATTAGGTCGT GTATTTAATG TACTAGGTGA AACAATTGAC CTTAAAGAAG 300

AAATTAGTGA TTCTGTTCGC CGCGATCCTA TCCATCGTTC AAGCACCAGC ATTCCGATGG 360

AACTTTTCAA CAGAAGTTCC AAATTTTTAG GnACAGGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3912:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3912:

TTGTACAAGT TGAAGAAAAA TCAACACAAC CAAAAGGTAG AAAATTCAAA GATTTCACTA 60

GTAAATTTAA TATAGCATCA GAAGCTAAAG AAAATGAACC TATATCAGTC ATTGGTTATC 120

CAAATCCTAA TGGAAATAAA CTACAAATGT ATGAATCAAC TGGTAAAGTA TTATCAGTGA 180

ATGGGAATAT AGTGTCATCG GATGCAATTA TTCAGCCTGG TAGCTCTGGT TCACCTATAT 240

TAAATAGTAA ACACGAnGCT ATTGGTGTAA TCTATGCCGG TAATAAGCCA TCAGGTGAAA 300

GCACCAGAGG GATTTGCTGT TTATTTCTCT CCTGAAATTA AGAAATTCCA TTGCAGATAA 360

TTTAGATAAA TnATTAAGAC CTAnGACATT CACCCAATCC 400

(2) INFORMATION FOR SEQ ID NO: 3913:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3913:

ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 60

TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGACATAA 120

AAAAAAGAGA CCTTGCGGTC TCAATGnGGC TCATCGCATC CATTTTTTGC CTGGCAACGT 180

TCTACTCTAG CGGAAGTAAG TTGGCTACCA TCGACGCTAA GAACCTTTCT TGACTTGTGA 240

CAATCGCTTG CTTCTTTCCT CTTCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAAACT 300

CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT 360

CTTTGGGGTT TGCnnTTTGA ATTTGGACGT TTTAGACATA 400

(2) INFORMATION FOR SEQ ID NO: 3914:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3914:

TGGAATGAGC GGATATAAGC ATCTTTAGAT AATGCACCAT CAACTAATGG ATATTTATGT 60

CCAGTTGGAC GCCAGAAATC ATAAACGTCT TCAGTGTAAG CAACAGCATC TTCATTTAAT 120

GCCAAAATGC TTGGATTATG TGCAATAACC ATCGCAACTG nGCCACACCT TGTGTTGGCT 180

CGCCGCCTGA ATTCAATCCA TAACGTGCTG TATCTGTAGC AATAACTAAT ACTTTTTCAT 240

TCGGTCTAGT TGCTAAATAA TCTTTAGCTA ATTGAATTGC TGGTGTTGCA GCATAACAAG 300

CTTCTTTCAT TTCAAAGCAG CGTGCAAAAG GTTGGnATAC CTAATAAGTT GTGGAATTTG 360

nACAGCGGCT GCTTTACGAA TTCCAACTGC TGATTCCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3915:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3915:

TCTTTATTTA TCCAGTTTCA TAGTCAATGT TTAAAGCAAA ATCTTATTGA TGGTACAAAA 120

GTAGAAGCTA ATGCCAATAG GTATACATTT GTGTGGAAGA AAAGTATTCA AAATCACGAA 180

TCGAAATTGA ACGAnAATTC AAAAACATTA TATCGTGACT TAGTTGAAGA AAAAATAATA 240

CCAGAGATAA AAGAAGATGG AGATAGCGAT TTAACAATAG AnGAAATAGA TTTAATTGGT 300

AGTCATTTAG ATAAAGAAAT CGAGGTTTAA ATCATTCTAT TGAGACGnGA TAGTACTCAA 360

ATTAGAAACA G 371

(2) INFORMATION FOR SEQ ID NO: 3916:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3916:

ACCATGGACG ACGGTTAGGT TTATGAATGT TATTCCAAAT AGGTTCATCT ATAAAATAGC 60

TTTAGTTGGA AAAGATGAGA AAAAATATAA AGATGGACCT TACGATAATA TCGATGTATT 120

TATCGTTTTA GAAGACAATA AATATCAATT GAAAAAATAT TCTGTCGGTG GCATCACGAA 180

GACTAATAGT AAAAAAGTTA ATCACAAAGT AGAATTAAGC ATTACTAAAA AAGATAATCA 240

AGGTATGATT TCACGCGATG TTTCAGAATA CATGATTACT AAGGAAGAGA TTTCCTTGAA 300

AGAGCTTGAT TTTAAATTGA GAAAACAACT TATTGAAAAA CAGATCTTTA CGGTAACATG 360

GGTTCAGGAC AATCGTATTA AATGAAAACG GGGGAATATA 400

(2) INFORMATION FOR SEQ ID NO: 3917:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3917:

GAGGAAATTA TTAACCTTnC GCATCGTATG GGCCnTGAAG GAATAACAaC CTTTAGACCT 60

GGAGATTGAG CTAAAATACC TTCTAAGTTA TCTGCGTGTA ATTCTGGTGT GTGTACGCCA 120

CCACCAAATG GGCTACGAAT TGTTACAGGT GCAGTTTTAG TACCGCCTGA ACGGAAACGA 180

GTACGTGCAA TTTGTCCAGC AATCGCATCA AATACTTCGA ATACGAAACC TAAGAATTGT 240

GATTCAGCTA AAGGTGTATC GAATACTCTA TCTTCACCAA ATTCTTTTTG TAGTCCTTCA 360

GTAACACGGA AAACACCGCC GTTAACACCA ACGTCTTCAC CAnAATnAAA AC 412

(2) INFORMATION FOR SEQ ID NO: 3918:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3918:

ATAGATTGCT GAGTGACAAT ACTTCAGGAn TCGCATATGC AGGCCCAATA CCCATAATTT 60

TCGGGTCAAC GCCTACTGCC TTAAAACCAA CGAATCGTGC AATAGGTGTC ACGCCGAGTT 120

CTTTCACTTT ATCTCCAGAC ATTAAAACTA CAAATCCTGC ACCATCAGAA AGTGGGGCAG 180

ATGTTCCTGC AGTCATAGTG CCGTCAGCTT TAAATACTGT ACGTAATTTG GCTAATGCCT 240

CCATCGTGGT GTCAGGGCGT ATnAAATTCA TCTTGGTCAA AGATATTTGT GTGTACTTTT 300

GGTCCTGCGT TTGTATATTC AACTGAGTTT ACTTGTATTG GGATnATTTC ATCTTTGGAA 360

CCGACCATCA CGGTGTGCGT TCATAGGCAC GTTGATGnAC 400

(2) INFORMATION FOR SEQ ID NO: 3919:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3919:

CAAGGGCAAC AAGGTGGCAA CGGCAATTAT TTAGAACAAA TTGGTCGTAA CCTTACnAAG 60

AAGCACGTGA CGGTTTATTA GATCCAGTCA TTGGTCGTGA TAAAGAAATT CAAGAAACTG 120

CTGAAGTTTT AAGTAGACGA ACTAAAAACA ATCCTATATT AGTTGGAGAA GCTGGTGTTG 180

GTAAAACTGC GATTGTTGAA GGTTTAGCAC AGGCAATCGT TGAAGGAAAT GTACCAGCAG 240

CAATCAAAGA CAAAGAAATT ATTTCTGTAG ACATTTCATC ATTAGAAGCT GGAACGCAAT 300

ATCGTGGTGC TTTTGAGGAA AATATTCCAA AATTAATCGA GGTGTTAAnC TTCACAAATG 360

CCGTACTATC TTTGATGAAn CCATCAATTA TCGGTTCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3920:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3920:

CTTATCCCGT CCACACATAG CTACCCAGCT ATGCCGTTGG CACGACAACT GGTACACCAG 60

AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACAGCTC CTCTCAAATT TCCTACGCCC 120

ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 180

ATGGGCGAAC AGCCAAGnCC TTGGGACCGA CTACAGCCCC AGGATGCGAT GAGCCGACAT 240

CGAGGTGCCA AACCTCCCCG TCGATGTGAA CTCTTGGGGG AGATAAGCCT GTTATCCCCG 300

GGGTAGCTTT TATCCGTTGA GCGATGGCCC TTCCATGCGG GAAnCAACGG ATTCACTAAA 360

GTCCGTCTTT TCGAACCTGG CTCGGACTTG TAGGTCTCGG 400

(2) INFORMATION FOR SEQ ID NO: 3921:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3921:

CGGGTTGGGC AGGTATGTTG TATTACCGTT CACAGCAGCA TCACTTTGAA CAACATTTGT 60

TAACGGATTA TTTGGCAATT CGGTTAGTTG TCGAACAATT GCTAGTTGGT GATGAGTTTA 120

AGTCAGTCGC TAAAGATTGT GAAAGTAGAT CGGAAAATTG GTTTAAGCAA ACTGTTGCAT 180

CATGGTGTTA CTACAGTGGA TATGCCTAGC GATGTATTAC TACAACATGA CGTCAATGAA 240

ATTCAAACGT TTATTCATTT TGGCAGCAAC TATGGAATAA AAATGTATTT AAAATTTATG 300

GCTnAATTGC CnGGGGAAAT GACATACGGG ATCTCAGTTT AAAACAAAAA TTAAAGCAGG 360

TCATGGAAAG TGTGGCGGGC GCCTTAGGTG TnAACCCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3922:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GTGCGCTCTA ACCAGCTGAG CTATAGGCCC ATTTTTTTGA ATGTTAAATA AACATTCAAA 60

ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 120

TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC 180

CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTACTCCACC GGCTTCGGGT 240

GTTACAAACT CTCGTGGTGT GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT 300

AGCATGCTGT ATCTACGTTT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC 360

AATnCGAACT GAGGAACAAC TTTTATGGGG TTTGnTTTGn 400

(2) INFORMATION FOR SEQ ID NO: 3923:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3923:

AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA ATAAAGAGTT TTAAATAAGC 60

TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAGAACTC CACAAGATTA ATAACGCGTT 120

TCCTGTAGGA TGGAAACATA GATTAAGTTA TTAAGGGCGC ACGGTGGATG CCTTGGCACT 180

AGAAGCCGAT GAAGGACGTT ACTAACGACG ATATGCTTTG GGGAGCTGTA AGTAAGCTTT 240

GATCCAGAGA TTTCCGAATG GGGAAACCCA GCATGAGTTA TGTCATGTTA TCGATATGTG 300

AATACATAGC ATATCAGAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGAGAAG 360

AGAAAGAAAT TCGnTCCCTA GTACCGCGAn CGAAACGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3924:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3924:

ATGCGATACG TAGCACAGCT GCAACAATCC ATGCTAGTAA AATCGGAGAC ATCTCTGTAC 60

CTTCAAACTA GCAATTGTAT TTCCGACACC GCCGTCAATT AATACTTGTT TAATGTACCG 120

CCACCGCCAA TAATCAATAA CATCATTCCG ATTGGATAAA TCGCATTCGT CACTGATTCC 180

GCTATTAGCA TGGCTGTCCC TGCTGTTCCT ATCATATAAA TGATAGATTC AAATAGATTT 300

GTAGGGTTGT CATGCCCAGT TACAAGTTGC GTTGATCGTn GACACTAACA TTAATATGAC 360

TGGTAATGTT GCTGTTAATA AACTCATACC AAnTCCGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3925:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 525 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3925:

GGCTGGGCTA GCTGGATTCG AACCAACGAG TGACGGAnAn AGGTCCGTTG CCTTACCGCT 60

TGGCTATAGC CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG 120

AGCCGGATTT ACAGTCCGCC GCGTTTACCA CTTCGCTACC CCTCCAGCTT ATTCATATAA 180

TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG 240

CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG ACTCGAACCC 300

GTGTTACCGC CGTGaAAGGG CGTGtgCTTA ACCcTTGGAC CAAGGAGCCA TGGCTCaCAG 360

GTAGGACTCG AACCTACGAC CGATCGGTTA AcAGCCGATA GCTCTACCAC TGGAGCTGAC 420

TGTGGATTAA TATTATGCCT GGCAACGTTC TGAnnCTAGC GGAAnTGAAT TCGGACTGAC 480

CATCGACGCn AAGGAGCTGA ACTTCTGTGT TCGGGCATGG GGAAC 525

(2) INFORMATION FOR SEQ ID NO: 3926:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3926:

TGTTATTGTT CAAAATCATG ATCAAGATCA GTATATCGTT GCTTATTATG AAGCGATGCA 60

TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120

ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180

GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240

TACCGnACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300

TCCGGATAGA GGCATCCACT GGGGAACGGT TACCAATTGG 400

(2) INFORMATION FOR SEQ ID NO: 3927:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3927:

TATCGATCAA TTTCTATCGA GTTGGACAAT GCCGAACGTG ACAAAGTTTT TACCATGCAT 60

GGTTGCATTT AGCGCAACAT GACCATAGTT TTACTAAAGC ACAGCGCGCA AGTGATTAAA 120

GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT TAACTCATTT TTCAATAGAT 180

CAGGAAGACT ACCAAGCTTA TGTTGAAGGA CATCTTTTGG CGTTACCGGG TTGGGCAGGT 240

ATGTTGTATT ACCGTTCACA ACAGCATCAC TTTGGAACAA CATTTGTTAA CGGATTATTT 300

GGCAATTCGG TTAGTTGTCG AACAATTGCT AGTTGGTGGA TGAGTTTAAG TCCATCGCTA 360

AAGATGTGGA AATAGnCCGG AAAATGGTTT TAAGCAAACT 400

(2) INFORMATION FOR SEQ ID NO: 3928:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3928:

GTGCACCTAA CGCTGAAATA TCGCCTTCTC GTGTATAGCA GACGGAATCA TTTTTTGTGC 60

AnTTTGTTAA ATATAGGCCC TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATACA 120

GTAATACATC TCCAACATTT GCCTTTAATT CTTTTGCGAT GACTACCGGT CCTGGATGTG 180

GTGGTAAAAA GCCATGTGTC ACTGATAAAG CTGTTACCAT AGGTAGTCCT AGTTTTAACA 240

CTGAAACATT TGCGCGTTTT GCTACTGTAA ATACTAATGG AATCAGTAAG ACTAAACCTA 300

CTTCAAAGAA CAATGCAATA CCGACGATAA ATGCTGGCAA CAAGCATTGC CCCATTGGTA 360

CATGGTTTTT GGACCAAATT TTTGGAATCA ACGTGTCTGG 400

(2) INFORMATION FOR SEQ ID NO: 3929:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3929:

CTCAAGGTGT TGCCTATACA GCTAAAAAAC TTAATTTAAA CGCTGTTATC TTTATGCCAG 60

TCACTACACC TTTACAAAAG GTAAATCAAG TAAAGTTCTT TGGAAATAGT AACGTTGAAG 120

TTGTACTCAC TGGTGATACA TTTGATCACT GTTTAGCTGA AGCTTTAACT TATACAAGTG 180

AACATCAAAT GAACTTTATA GATCCATTCA ATAATGTTCA TACAATTTCT GGACAAGGTA 240

CGCTTGCTAA AGAAATGCTA GAACAAGCAA nGTCTGACAA TGTTAACTTT GCATTATCTA 300

TTTGCCGCAA TTGGTGGTGG CGGTTTAATT TCAGGTATTT CGTACTTACT nTTAAAACCT 360

ATTCACCTAC CACGnAAATT ATAGGTGTTG AACCCCnAGT 400

(2) INFORMATION FOR SEQ ID NO: 3930:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3930:

ATATGATCCT ATGAAGCAAT TTTATGTAGT AAGTGGTTCT AAACATGACG CCCTTATGCT 60

CTGTGAACAT TTATATGACG AGGTTATGGC TGTTTGCTAA nCCCAAATGA TACATCGAAT 120

GGCACATATC ATTCGTCGCA ATATGATTAC TATGATGCAT TTATTAAGCA GCAAGAAAAT 180

GTAACATATA TTTCAACCGA TCGTGCAGAT GCTAATACAG TGTTATGTCA CTAATTTATA 240

AAAAATAAAT GAATAAGTAA GGTTTCAACC GAGAGAATAT ATTCGTGTTG AAGCCTTATT 300

TGTCGTTGTG CCAAATTTGA ACGnTTTAGA TGGCAATAAG CATGACCATA CAGATTGTGT 360

ATTATTTCCA TGnA 374

(2) INFORMATION FOR SEQ ID NO: 3931:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3931:

TGCTTCTTTC GCTAGCCTCG TATGGGCATC TTTATCAATA ATATACTCGC CATGACTATC 120

TTTCGCTTTT AAGTCAATTT CATCAAACTC TTTCCCACCT GTTAACGGTG CACCACTATG 180

TCGTTTCCGA CCAAATGTAG CCTCTTGTTC TTCCAGCGCA GTACGATCCC ACGTTTCAAT 240

GTGTATTTGA ATACGTCTGA CAACGCAATA AGTTCCATGT TTCGCCCATC CGTCATCAAT 300

AAACACATAA TCTTTAAGTT GATTATTCTT CCTAGGATTA ATTGTTCCAC TTTAAAATGC 360

CATTnAAATT CTAGGTGTTT CCnTAnC 387

(2) INFORMATION FOR SEQ ID NO: 3932:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3932:

AAGGTAATAA TCCTGTAGTC GAAAATGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG 60

AGCACGTGAA ATTCCGTCGG AATCTGGGAG GACCATCTCC TAAGGCTAAA TACTCTCTAG 120

TGACCGATAG TGAACCAGTA CCGTGAGGAG AAGGTGAAAA GCACCCCGGA AGGTAGnTGA 180

AATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG 240

CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTTAAGCAG TAAATGTGGA 300

GCCGTAGCnG AAGnAnGTTC TGAATAGGGC GTTTAGTATT TGGTCGTAGC CGATAACCAG 360

GTGATTCTAC CCTTTGGTCA GGTTGAAGTT CAAGTAACAT 400

(2) INFORMATION FOR SEQ ID NO: 3933:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3933:

GCGATGGTTG AAACATTGAC TTATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60

TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120

CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180

CGATTTTGGC ATGAAGGTCA CCTTAAATGT ACATTGTTGT AATAAAATTG CCTATAAATT 240

AATTGTAAAA AGAAAACCAT ACGCTATGTG nTGCCAAGGA AAAGGTTCTA CCATTGTCAC 360

nAAAAATGCA TCTCTACGTG CTAGGAATAA ATATTGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 3934:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3934:

TTTGACGTTT TAGACATAAA AAAAGAGACC TTGCGGTCCA GATGGGGCTC ATCGCATCCA 60

CTTTTTGCCT GGCAACGTTC TACTCTAGCG GAAnTAATCG AACTACCATC GACGCTAAGG 120

AGCTTAACTT CTGTGTTCGG CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC 180

ATATGAATGT AAATTATACA TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA 240

AACATTTATT TTGATTAAGT CTTCGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300

GGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAnG GATCTTATAA CCGAATTGGG 360

AAnCTCATCT GAAGGGGGCT CAGCTAGATG CTTCAnACTT 400

(2) INFORMATION FOR SEQ ID NO: 3935:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3935:

TGTTCTTTTT GGGCAGTGGG ACACAAATGG ATATTTTCGG CAAAATTTAT TTCGTTCGnT 60

CCCACCCCAA CTTGGCACAC TATTGTAAGC TGACTTTTCG CCAGCTTCTG TGTTGGGGCC 120

CCGCCAACTT GCCATTGTCT GTAGAAATTG AGGAGCTAAT TTCTCTGTGT CGGGGCTCCA 180

CCCCAACTTG CACACTATTG TAAGCTGACT TTCCGCCAGC CTCTGTGTTG GGGCCCCGCC 240

AACTTGCACA CTATTGTAAG CTGACTTTCC ACCAGCCTCT GTGTTGGGCC CCGACTATTT 300

TTGAAAAGAG CGTGTTACAC GGGCATTGTT TTACAGTCAA CTACTGCTAA AATAAAATTA 360

ACGAGCTTAA GGCTTTGGnT TCTGTCCCAA GCC 393

(2) INFORMATION FOR SEQ ID NO: 3936:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3936:

AAAAAGAAGA CAACCAAGCC CAATAATGGA CTGGCCGCGT AATAATnGTG GCTCTAAAAG 60

TTGTATTTTA AAAATAGTTC TTTAAATTAT ATACCCACCA CATTTGGTGG AGAACCTAAA 120

AAAAAGCACT TCCCAAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT 180

GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC 240

TAGCTGGATT CGAACCAACG AGTGACGGAn TCAAAAGTCC GTTGCCTTAC CGCTTGGCTA 300

TAGCCCAATA TATAGATGGT GGAAGGGGGC AGATCGAACT GCCGAACCCG AGGAGCGGAT 360

TTACAGTCCG CCGCGTTTAG CACTTCGCTA CCCTCCAGCT 400

(2) INFORMATION FOR SEQ ID NO: 3937:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 609 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3937:

GGTTTAACAC GCCTGCCTGT CACGCAGGAG ATCGCGGGTT CGATTCCCTG TCGAGACCGC 60

CATTATTATT ACCATTACGG TTCAGTAGCT CAGTTGGTAG AGCAATGGAT TGAAGCTCCA 120

TGTGTCGGCA GTTCGACTCT GTCCTGAACC ATTCTTAATT CATGGCGGTT GTGGTGAAgT 180

GGTTAACACA TCGGATTGTG GTTCCGACAT TCGAGGGTTC GATCCCCTTC AGCCGCCCCA 240

TAATCGTTTA CATTAGCGGG TGTAGTTTAA TGGCAAAACC TCAGCCTTCC AAGCTGATGT 300

TGTGGGTTCG ATTCCCATCA CCCGCTCCAT TATTTTCTAT TATTCCACAG TAGCTCAGTG 360

GTAGAGCTAT CGGCTGTTAA CCGATCGGTC GTAGGTTCGA GTCCTACCTG TGGAGCCATG 420

GCTCyTTGGt CAAGCGGTTA AGACACCGCC CTTTCACGGC GGTAACACGG GTTCGAGTCC 480

CGTAGaGTyC ATACAAGCAG AAGTGnAAAT ATCGCTTCTG TTTTTTTaTT ACATAwTTAA 540

TkGTTGgAGG aAGtTGTcCG AgCyGGGCCG AAGGaGCACG CCTGGAAATG TGTAAGCGTT 600

CACAAGCTT 609

(2) INFORMATION FOR SEQ ID NO: 3938:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3938:

TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC TACATGAAGC TGGAATCGCT 60

AGTAATCGTA GTCAGCATGC TACGGTGAAT ACGTTCCCGG GTCTTGTACA CACCGCCCGT 120

CACACCACGA GAGTTTGTAA CACCCGAAGC CGGTGGAGTA ACCTTTTAGG AGCTAGCCGT 180

CGAAGTGGGA CAAATGATTG GGGTGAAGTC GTAACAAGGT AGCCGTATCG GAAGGTGCGG 240

CTGGATCACC TCCTTTCTAA GGATATATTC GGAACATCTT CTTCAGAAGA GCGGAATAAC 300

GTGACATATT GTATTCAGTT TTGAATGTTT GTTCATTCAA ATTAATGGGC CTATAGCTCA 360

GnGGTTAnAG CGCACCCTGA TnAACGTGAA GTCGGTGGTT 400

(2) INFORMATION FOR SEQ ID NO: 3939:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3939:

AGTTTTGAAT GTATAAATTA CATTCATATG TCTGGTGACT ATAGCAAGGA GGTCCACCTG 60

TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC 120

CGCTAGAGTA GAACGTTGCC AGGCATAATA TTAATCCACA GTAGCTCAGT GGTAGAGCTA 180

TCGGCTGTTA ACCGATCGGT CGTAGGTTCG AGTCCTACCT GTGGAGCCAT GGCTCTTGGT 240

CAAGCGGTTA AGGACACCGC CCTTTCACGG CGGTAACACG GGTTCGAGTC CCGTAGAGTT 300

CATTATTTTG GAGAATTAGC TCAGTAGGGA GAGCATCTGC CTTACAAGCA GAGGGTCGGC 360

GGTTTCGAAC CCTnCATTTT CCACCATTTG GTTATTAAAn 400

(2) INFORMATION FOR SEQ ID NO: 3940:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ACACAACAGC TGTTTCAAAA ATGATTGGTA CAACTGCTGG TTATGTTGGT TATGATGACA 60

ATTCAAATAC GTTAACTGAA AAAGTACGCC GTAATCCATA CTCAGTCATT CTATTTGATG 120

AAATCGAAAA AGCAAATCCA CAAATTTTAA CATTGTTATT ACAAGTAATG GATGATGGTA 180

ATTTGACTGA TGGTCAAGGT AATGTCATCA ACTTTAAAAA TACAATTATT ATTTGTACAT 240

CAAATGCTGG CTTTGGCAAT GGCAATGACG CTGAAGAAAA AGATATTATG CACGAAATGA 300

AAAAATTCTT CCGCCCTGAA TTCCTTAACC GCTTCAACGG CATCGTGAAT TnCTTACATT 360

TAGATAAGGT GCCnTGCAGG TATCGTCCAA CTATTATTAG 400

(2) INFORMATION FOR SEQ ID NO: 3941:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3941:

ATACAATTTT AAATCTGTAT GTGTGAATCC AACACATGTT AAATATGCAG CAGAGCGnCT 60

AGCTGATTCA GAGGTGCTCG TTTGTACGGT AATAGGATTC CCATTAGGTG CGTCGACAAC 120

TGCAACGAAA GCATTTGAAA CAGAAGATGC AATTCAAAAT GGTGCAGATG AAATTGACAT 180

GGTCATCAAC ATCGGCGCAT TAAAAGATGG ACGTTTTGAT GATGTACAAC AAGACATTGA 240

AGCAGTGGTT AAAGCTGCGA AAGGTCACAC AGTAAAAGTG ATTATTGAGA CGGTATTGTT 300

GGACCATGAC GAAATTGTAA AAGCGAGTGA TTAACAAAAG CGGCTGGTGC GGACTTCGTT 360

AAAAACTTCA GCAGGTTTTG CCAGTGGCnG TGCGACTGCA 400

(2) INFORMATION FOR SEQ ID NO: 3942:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3942:

CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 60

TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 120

CATTTTTATA AGTCAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG ATTTAAACGC 180

TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATTTT ACTTACTnAT 300

CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA TCCGAACCCG CTGACCCnAC 360

CnGCGTGCAA AGCAGGCGCT CTACCCAGCT TGAGCTAAGG 400

(2) INFORMATION FOR SEQ ID NO: 3943:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3943:

CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 60

TTAAGCCCCT GTCGGTTTTC AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120

ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG GTTATGGAGC CGTTAGCTCT 180

GAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA 240

GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 300

CGCCTTATAT AGTTTGTAAA TnAnnATGGT GGGAGACTAG CGGGGTTCGA ACCGCTGGAC 360

CTCCTGCGTG CCAAAGCAGG CGGCTTCTAC CCAGCTGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3944:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 406 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3944:

CCAAAATTGC ACCTTGTCGT TTATTCGGAA AATCAATATn GnTAGGGGGT ATAAGATGCA 60

CCTACTTTAA CTGTCGCCAA CATCGCCGCA ATCATTTCAA AACTACGTTC TGTAAACAAG 120

GCAACCCGTT GACCATTGCC CACACCATTT GATAGGAGCA TGTGCGCAAT GGCATCCACA 180

TAGTTGCGTA ATGTTTCATA CGTCATTGTC AAATCATTCA TGACTAGCGC AACATGATTA 240

CCTTGTCGTG AGAAACTTCA TTAAAGTAAC TTATGATAGA TTTATTTCCC GGGACATTAA 300

GCATTCGATC GTTAACATGC GTATTGACCC AATTTAGAAG TTCCTCCGTG CCGTTTGGTA 360

TATCACAAAT TTGTAGTGTA wCtTGaTGCT TCmAAATAtC AATCAn 406

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3945:

CAATGACAAC AGCAACTGAG ACAGTGTCAA ACGCTTAATA ATAATGATGT AGTGTCGAAT 60

AATACCGCAT TAAATGTACC AACTAAAACA AATGAAAATG GTTCAGGAGG ACATCTAACT 120

TTAAAGGAAA TTCAAGAAGA TGTTCGTCAT TCTTCAAATA AACCAGAGCT AGTTGCAATT 180

GCTGGAACCA GCATCTGAAT AGACCGAAAA AGAGAAGTTA GACGTGCGGC ACCGGCAGAT 240

CCTGAATGCC AACTCCAGCA GATCCAGCGG CTGCAGCGGT TAGGAAACGG TGGTGCACCA 300

GTTGCAATTA CAGCGCCATA TACGCCAACA ACTGATCCTA ATGCCATGAn GCCAGGACAA 360

ATGGCACCTA ACGAnGCTTG TTCATTTGAT GGACAnGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3946:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3946:

CTCGCTGCGA TAAAGTACCA GTTCATAGCA ACGTTTGTnT TAATAGGnTC TGAAACGATA 60

CGTGTTGCCG GTTCTGTAAA TGAATAGACC AAAGCATCTT GCATACCAAC AACTATATTT 120

GCTGCAAATC CTCCAACAGC GGAAnATATG CCATCGTTAG TCCAGCGATA GGGTGATAGC 180

CAATTTTAAT AAAAAGCATT GCTGCAACGG CCGGCAAGAT AATTGTCGCA GCATCGCCGG 240

CTGTACTACC TAAAATACCA ATTAATATAA TAGTCGGTAA AATTAAGAAA CGTGGTGCGC 300

GATTCACAAC AGAAATCATT AACTTATCGA AGTATCCTGT TTTCTCTGCA ACACCAATAC 360

CAATCATCAC TGCTAGGTAC TAAGCCTAAT GCTGGGnACT 400

(2) INFORMATION FOR SEQ ID NO: 3947:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3947:

GCCGGCCAGA GGACTTGGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT 60

GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCG AACCGCCGAC 120

CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 180

GGCAACGTTC TACTCTAGCG GAAnTAATTC GnACTACCAT CGACGCTAAG GAGCTTAACT 240

TCTGTGTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 300

TAATTTATAC ATTCAAAACT AGATAGTAAG TAAAAGTGAT TTTGCnTTCG CAAAACATTT 360

A 361

(2) INFORMATION FOR SEQ ID NO: 3948:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3948:

TTCCGTCAGA CCCTGACATG GTTCATGGGT TCATATTGCA TAGGACCGAA ATCTTCAAAC 60

ACTACGTGCT TTGGGCAGAC TTCGCAAAAA TACGGCCTCA ACAAAGGAAT TAAGCCTCGC 120

ATAAAGCGGA TTTCGAGTAC AGGGAACCGC TACCTCCCCA CCTAGCACGG CAAGATATAT 180

ATTACTATAT TTTAATAGTT AATTGCAAGT ATAAATCATT TATATCATTG TTTACTTTAT 240

ACGACGTCTT GAGAAGTCAT TAATTTAAAT TCATTTGCAA GATGTTTTGA AATATTATAT 300

TGAAACGGCA TTGTATTTTC TAAATACACA nTACTTCGAA CTGTTGCnGA ATAGGCCACC 360

GATACATCAC CAACAATTGG nA 382

(2) INFORMATION FOR SEQ ID NO: 3949:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3949:

GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAAGA 60

GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT 120

TTGCTTCTTT CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 240

CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTTGTG 300

TTTGCTTTTT AnTTTGACGT TTTAGACATA AAAAAAAGAG ACCTTGCGGn CTCAATGnGG 360

GCTCATCGCA TCCAATTTTT GGCCTGGCAA CGGTTCTACT 400

(2) INFORMATION FOR SEQ ID NO: 3950:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3950:

ACTCGGTTTT GCTTGGAAAA TCTATATTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 60

CTTTTTAGTC AAGCGCTCGC ATACTGCTTT ATTTTCATAA GCAATATCAC TTTAACCAAA 120

AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA ATATGTCACG TTATTCCGCA 180

TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC 240

CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC 300

TCCTAAAAGG nTACnCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGCGGT 360

GTGTACAAGA CCCGGGAACG nATTCACCG 389

(2) INFORMATION FOR SEQ ID NO: 3951:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3951:

AAAGCTCGAC TTGTTTACGA TGTTGAAAAA CAAGATTATG TACCTGTATC GCAACCACAA 60

TTACCAATTT TAAATGAATT TAATAAAGAC TTAGTGCATA ACCTTGATAC CATATTCAAT 120

GCGCAAGACG AnCGGGACTA TTTTTATGGG AGACATTACG TAATAATTTC TATTACTCTG 180

CTATCAATGT ACCTAAAGCT ACCGATGATT TCCGAGACAT AGACCGTGCG CTTGTCTGGG 240

GGTTCAACTG GAAACTTGGT CCATTCCAAT TATGGGATGC AATGGGATAC GAACGTGTTA 300

AAACAnTGAT GGGAAGACGA ACTTGGGAGA CTTACCACAA TGGGATTAGT GAnTTAGATG 360

(2) INFORMATION FOR SEQ ID NO: 3952:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3952:

CAAAGGGCAG CGAAACCGCG AGTCCAGAGC AAATCCCATA AAGTTGTTCT CAGTTCGGAT 60

TGTAGTCTGC AACTCGACTA CATGAAGCTG GAATCGCTAG TAATCGTAGA TCAGCATGCT 120

ACGGTGAATA CGTTCCCGGG TCTTGTACAC ACCGCCCGTC ACACCACGAG AGTTTGTAAC 180

ACCCGAAGCC GGTGGAGTAA CCTTTTAGGA GCTAGCCGTC GAAGTGGGAC AAATGATTGG 240

GGTGAAGTCG TAACAAGGTA GCCGTATCGG AAGGTGCGGC TGGGATCACC TCCTTTCTGA 300

AGGATATATT CGGGAACATC TTCTTCAGAA GAGCGGGAAT AACGTGACAT ATTGTATTCA 360

GnTTTGGAAT GTTTnnTTAA CATTnCAAAA AAATGGGGCC 400

(2) INFORMATION FOR SEQ ID NO: 3953:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3953:

TGATTTTGAC GTTTTAGACA TAAAAAAAAG AGACCTTGCG GTCTCAAATG CGGCTCATCG 60

CATCCATTTT TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAATTGGCT ACCATCGACG 120

CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTTCTT CGGCTCTCGC 180

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 240

TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTGCTTTT TATTTTGACG TTTTAGACAT 300

AAAAAAAAGA GACCTTGCGG TCTCAATGCG GGCTCATCGC ATCCATTTTT TGCCTGGCAA 360

CGTTCTACTC nAGCGGGAAG TGAAGnCGGA CTGACCAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3954:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3954:

AAACTACATA ATGAAAATGC CGTTTTAATC GGTAAATTAA ATATGGATGA GTTTGCAATG 60

GGTGGTTCAA CAGAAACATC TTATTTCAAA AAAACAGTTA ACCCATTTGA CCATAAAGCA 120

GTGCCAGGTG GTTCATCAGG TGGATCTGCA GCAGCAGTTG CAGCTGGCTT AGTACCATTT 180

AGCTTAGGTT CAGACACAGG TGGTTCAATT AGACAACCGG CTGCATATTG TGGCGTTGTC 240

GGTATGAAAC CAACATACGG TCGTGTATCT CGATTTGGAT TAGTGCTTTG CATCTTCATA 300

GACCAAATTG GGCCATGACT CGAATGTAAA GTAATGCCAT CGTATTAGAA GCTATTCTGG 360

TGCAGATGnT AATGACTCTA CCAGTGCACC AGTGATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 3955:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3955:

TCGATTGGCA TTTCTCCGCT ACCCTCAGTT CATCCGCTCA CTTTTCAACG TAATCGGTTC 60

GGTCCTCCAT TCAGTGTTAC CTGAACTTCA ACCTGACCAA GGGTAGATCA CCTGGTTTCG 120

GGTCTACGAC AAATACTAAA CGCCCTATTC AGACTCGCTT TCGCTACGGC TCCACATTTA 180

CTGCTTAACC TTGCATCAAA TCGTAACTCG CCGGTTCATT CTACAAAAGG CACGCCATCA 240

CCCATTAACG GGCTCTGACT ACTTGTAAGC ACACGGTTTC AGGTTCTATT TCACTCCCCT 300

TCCGGGGGTG CTTTTCACTT TTCnCTTCAA GGTATGGGTT CACTATCGGT nACTAGAGAG 360

TAATTAGCTT AGGnGATGGT CCTCCCAGAT TCGGAAGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3956:

GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG AACCGGTAGT 60

ATAAAAATGG AGCAGAAGAC GGGATTCGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 180

TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 240

CTTAGGATCC TAAGTCTAGT GCGTCTGCCA ATTCCGCCAC ACCCGCAAAT GGTGAGCCAT 300

AGAGGATTCG AACCTCTGGA CCCTCTGGAT TAAAAGTCAG ATGCTCTACC AACTGGAGCT 360

AATGGCTCTT TCCATGGTGC CGGGCCAGAG GACTTTGAAn 400

(2) INFORMATION FOR SEQ ID NO: 3957:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3957:

CAGACATGTG TTATACGGGA AATTGGGCGA ACCGCAACTA TTATACATTG ATTTACACCT 60

TATACATGAA GTTACTTCTC CTCAAGCATT TGAAGGACTT AGGCTTCAAA ACAGAAAATT 120

AAGACGCCCA GATTTAACAT TTGCAACACT CGATCACAAT GTTCCTACTA TTGATATATT 180

CAATATTAAA GATGAAATTG CAAACAAACA AATCACAACA TTACAAAAAA ACGCCATAGA 240

TTTTGGGGTG CATATTTTTG ATATGGGTTC TGATGAACAA GGTATTGTTC ACATGGTAGG 300

ACCTGAGACA GGACTTACAC AGCCTGGCnA GACCATCCGT nTGTGGGTGA CTCTCACACA 360

GCCACACATG GnGCCTTTT 379

(2) INFORMATION FOR SEQ ID NO: 3958:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3958:

TGTTAAAATA CGGTACATCT AAATTAATGT TAACTGATTT TCAAAAAGAG AATTAAATAA 60

ATATATTCAA GGTCAGAnAC AACGCGTGAT ATTTGAAAAT GGCCATTTTG TCTAATTGAT 120

AGTGAATATA ATTAGAGTAA GAGGCTGGGA CATAAATCCC TAAAAAACAG CAGTAAGATA 180

ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT CGTATTGAAT 240

GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT GCTCCCTCAG 300

AATAAGACAT TTGnCCAACT TGACACTACC ATTAAAAACT 400

(2) INFORMATION FOR SEQ ID NO: 3959:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3959:

GAGCCGCAGT GGAATGAGGC CCAAGCGACT GTTTATCAAA AACACAGGTC TCTGCTAAAC 60

CGTAAGGATG TGTTATAGGG GCTGACGGCT GCCCGGTGCT GGAAGGTTAA GAGGAGTGGT 120

TAGCTTCTGC GACGTACrGA ATCGAAGCCC CAGTAAACGG CGGCCGTAAC TATAACGGTC 180

CTAAGGTAGC GAAATTCCTT GTCGGGTAAG TTCCGACCCG CACGAAAGGC GTAACGATTT 240

GGGCACTGTC TCAACGAGAG ACTCGGTGAA AATCATAGTA CCTGTGAAGA TGCAGGTTAC 300

CCGCGTACAG GACGGAAAGn CCCCTGGAGC TTTACTGTAG CCTGATATTG AAATnCGGCA 360

CAGTTTGTAC AGGATAGGTT AGGAGCCTTG GAAACGTGTG 400

(2) INFORMATION FOR SEQ ID NO: 3960:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3960:

TGGTCCCAAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA 60

TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120

GGCGCATATG TTTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTGAnTnC 180

ACTCACCGCA GATTTTAAGT CCTGTGCGTC TGCCAGTTCC GCCACCCCGG CACTATAAAA 240

ATGGAGCAGA AGACGGGATT CGAACCCGCG ACCCCAACCT TGGCAAGTTG TTATTCTTAC 300

CGCTGGAACT ACTTCTGGCA TATGCGGGTT GAAGGGGAGT CGAACCCCCA CGCCGTAGGC 360

TTAAGATTCC TGAAGTCTAG TGCGTCTGGC CAATTTCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3961:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3961:

TTTTGATACA TAATCTAAAT TTCTCAAAGC GCCAATAACA GAGGACCATC TCCTAAGGCT 60

AAATACTCTC TAGTGACCGA TAGTGAACCA GTACCGTGAG GGAAAGGTGA AAAGCACCCC 120

GGAAGGGAGT GAAATAGAAC CTGAAACCGT GTGCTTACAA GTAGTCAGAG CCCGTTAATG 180

GGTGATGGCG TGCCTTTTGT AGAATGAACC GGCGAGTTAC GATTTGATGC AAGGTTAAGC 240

AGTAAATGTG GAGCCGTAGC GAAAGCGAnG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA 300

GACCGGAAAC CAGGTGATCT ACCCTTGGTC AGGTTGAAGT TCAGGTAACA CTGAATGGAG 360

GACCGAACCG ACTTACGTTG AAAAGTGAGC GGATGAACTG 400

(2) INFORMATION FOR SEQ ID NO: 3962:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3962:

TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTn CGACCCCTTG GTCCCAAACC 60

AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAnTTAAC GCGCCCGATA GGAGTCGAAC 120

CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTG 180

TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA 240

TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAnAAAT GGATCAGAAG 300

ACGGGATTCG AACCCGCGAC CCCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACTACTT 360

C 361

(2) INFORMATION FOR SEQ ID NO: 3963:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3963:

AAGTGTCTTA TTTTTTTAAA GTATTTCAAA GTAAAATTAC ATGTTAATAC GTAGATTAAT 120

GGCGAGACTC CTGAGGGAGC AGTGCCAGTC GAAGCCGTAG GCTGAGACGG CACCCTAGGA 180

AAGCGAACCA TTCAATACGA AGATnTnATn AAATAGAGAA CAGCAGTAAG ATATTTTCTA 240

ATTGAAAATT ATCTTACTGC TGTTTTTTAG GGATTTATGT CCCAGCCTCT TACTCTAATT 300

ATATTCACTA TCAATTAGAC AAAATGGCCA TTTTCAAATA TCACGCGTTG GTTTCTGACC 360

TTGGAATATA TTTAT 375

(2) INFORMATION FOR SEQ ID NO: 3964:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3964:

AAAATGGCCT TGATAGACTT GCTCAATGCA GGGTTGCCAC AAACCAATGA TGCACTTACA 60

ATTTTAAATA GATTTTTAAG ACCTTGTTGG TTTTGTACAA TTAATGTGAC ATGACTAGGT 120

CTTGCACGTT TATATGCATC TTCATTACTG AGTTTTTTGT TGATTTCGTT ATGATTTAAT 180

ACGCCTAATT CTTTCATTTG TTGAACCATT TTTATGAAAA TGTAAGCTGT TGCTTCTGTA 240

TCATAAATGG CACGGTGATG TTGCGTTAAT TCTACGCCAT ATTTTTTAGC CAAGAAATTC 300

AAACCATGTT TACCATATTC AGTATTAATC GTACGAGGAT AATTCTAAAG TATCGATAAC 360

ACCATTCGTT GGATGGTCCA AACCCAAGAC GTTCATATCC 400

(2) INFORMATION FOR SEQ ID NO: 3965:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3965:

ACTTTTAATT TTGTCATGAT GTGCCTCCTT ACCGTATGAT GTTATTCAAA GTAAATTGCT 60

TTGCCTGATT TTGCAGACTG ATAAATCGCT TCAAGAATTT TTGTAACTAC CATTGCTTGT 120

TCCGGTTTCA CAACTGGTTC AGTATCATTT ACAACTGCAT CAATCCAAGC TTTTGCTTCT 180

TCTTCAGCTT CATCCACTTC ATTACCTTCA TAAAAGTCGA CGCCTTTGTT TTCCAATTCA 240

TCAGCACCTG CTTTAGGTTC CTGATAATGA ACATTTTGGC CTCATCCACT TCTAAAnGAA 360

TTAATCGCCC AAGnGGGATT CCAAAAAGGA n 391

(2) INFORMATION FOR SEQ ID NO: 3966:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3966:

CGCTATCAGG TATTGTTTCA ACAATTTCAT TAACATATCG TGAAATATCA TTTTGAGGGA 60

TTCTAACAGA AGTTTCTATT GGTAGTGTAG TTGGGGCATG TTATAATTTT TATACATAAG 120

GCACCTCGTT AATTTAGTTT AGTGGTATTT ATTAAATTAT AAGAAGGGAC CCAACACAGA 180

AAATTCATTT TATTGAATTT TACATTTATG TGCAAGTTGG GCAAAGTGTC TTATTTTTTA 240

AAAGTATTTC AAAGTAAAAT TACATGTTAA TACGTAtATa ATGGcGAGAC TCCTGAGGGA 300

GCAGTGCCAG TCGAAGcCAA GGCTGAGACG GCACCCtAGG AAAGCGAcnC ATTcAATACG 360

AAGATTGTAT AAATAGAGAA CAGCAGTAAG ATATTTTC 398

(2) INFORMATION FOR SEQ ID NO: 3967:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3967:

GCTATAGAAA AAATAAAATC ACAAGTTACG ATTAGCGTAC TTGATGGGGA GTGAAAATAA 60

TGAGAGTAAC AGAGTTATTA ACAAAAGATA CAATAGCAAT GGATTTAATG GCAAATGACA 120

AAAATGGTGT TATTGATGAG TTAGTAAATC AATTAGACAA AGCAGGTAAA TTAAGTGATG 180

TCGCGTCATT TAAGGAAGCG ATTCACAATC GAGAATCACA AAGTACAACT GGTATCGGCG 240

AGGTATTGCC ATTCCACATG CCAAAGTGGC CGCAGTTGAA GTCACCAGCT ATTGCGTTTG 300

GTAAATCTAA AGCAGGCGTG GATTATCAAn TTTGGnTATG CAACCAGCAC ACTTnTTCTT 360

TGTGGTTGGC AGCG 374

(2) INFORMATION FOR SEQ ID NO: 3968:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3968:

ACCCCGGCAC TATAAAAATG GAGCAGAAGA CGGGATTCGA ACCCGCGACC CCAACCTTGG 60

CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC 120

CACGCCGTAA nCTGAGGATC CTAAGTCTAG TGCGTCTGCC AATTCCGCCA CACCCGCAAA 180

TGGTGAGCCA TAGAGGATTC GAACCTCTGG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC 240

AACTGAGCTG AATGGCTCTT CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTGACT 300

GGATTACAAG TCAGTTGCTC TACCAATTGA GCTAAGGCCG GGCAATATGT AAGAATAAAT 360

GGTGGAGAAT GACGGGTTTC GAAnCGCCGA CCCTCTGCTT 400

(2) INFORMATION FOR SEQ ID NO: 3969:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3969:

GCGAGTTGGG GTGTGGGCCC CAACATAGAG AAATTGGATT CCCAATTTCT ACAGACAATG 60

CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC ATTAnCAATA ATGTGCAAGT 120

TGGCGGGGCC CCAACACAGA AGCTGACGAA AAGTCATTAn CAATAATGTG CAAGTTGGCG 180

GGGCCCCAAC ACAGAAGCTG GCGGAAAGTC AGCTTACAAT AATGTGCAAG TTGGGGTGGG 240

ACAACGATAA AGTAATACTT TTTCTATAGA AATTAGTATT TCTTATGCAT GAGTTTTACT 300

CATGTATTCC TATTTTTAAG TACACATTAG CTGTGGCTAA TGTTTAAGAC CCACTACATA 360

ATAAATCATT AGTGGCTCTn TATCATTTCT GTCCCACTCC 400

(2) INFORMATION FOR SEQ ID NO: 3970:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 419 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GATAAGATCA GCCGAAAATG GATGGTGTTA AGAGCGTTAC TTGGTTTGGC GGTATGCTTA 60

TTTTTAATGG CATTGTGTAC GACACCATTA CAGTTTGTAC TTGTGAGGTT ATTGCAGGGA 120

CTATTTGGTG GTGTTGTTGA TGCATCAAGT GCGTTTGCGA GTGCAGAGGC GCCACTGAkA 180

GATCGTGGAA AGtATTAGGA gACTGCAAAT TCAGTCAGCG CAGGtCTCTT GTGGGGCCAT 240

TAATTGGCGG TGTTACAGCT TCGATATTAG GTTTTAGTGC GTTACTGATG AGTATTGCCG 300

TTATTACTTT TATTGTCTGT ATTTTCGGTG CATTAAAATg ATTGAAACGA CACATATGCC 360

AAaATCACAA ACACCAAATA TTAATAAAGG TnTTCGCCGT TCCAnTTnCA ATGTCTAAT 419

(2) INFORMATION FOR SEQ ID NO: 3971:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3971:

AAACTTGGGA GACTTCAATA ACAGATTTAG GTTTATCTAA AAATCAGGCA TATAATTTCT 60

TAATTACATC TAGTCAAAGA TGGGGCCTTA ATCAAGGGAT AAATGCAAAT GGCTGGATGA 120

GAACTGACTT GAAAGGTTCA GAGTTTACTT TTACACCAGA AGCGCCAAAA ACAATAACAG 180

AATTAGAAAA AAAAGTTGAA GAGATTCCAT TCAAGAAAGA ACGTAAATTT AATCCGGATT 240

TAGCACCAGG GACAGAAAAA GTAACAAGAG AAGGACAAAA AGGTGAGAAG ACAATAACGA 300

CACCAACACT AAAAAATCCA TTAACTGGAG TAATTATTAG TAAAGGTGAA CCnnAAGGAG 360

GGGTTTCCAn AGTCCGTTAT G 381

(2) INFORMATION FOR SEQ ID NO: 3972:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3972:

GGGTTCAGAA CGTCGTGAGA CAGTTCGGTC CCTATCCGTC GTGGGCGTAG GAAATTTGAG 60

AGGAGCTGTC CTTAGTACGA GAGGACCGGG ATGGACATAC CTCTGGTGTA CCAGTTGTCG 120

TGCCAACGGC ATAGCTGGGT AGCTATGTGT GGACGGGATA AGTGCTGAAA GCATCTAAGC 180

GAnGTTAATA GGTTCGAGGT GGAAGCATGG TGACATGTGG AGCTGACGAA TACTAATCGn 300

TCGAnGACTT AATCAAAATA AATGTTTTGC GACCAAATCA CTTTACTTAC TATCTAGTTT 360

GAATGATAAA TACATCATAT GCTGGnGCCA TACCAAGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3973:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3973:

TCTTTTAATT ACGTAATGGC TTACCAGTTT TTAACATATG TGCAATTCTT TCATATGATT 60

TTTTAGATTT TAGTAAGTCA ATAAAGCCAA TTTTCTCCAA CGATTGAATG TAACGTTGAT 120

TGATAAATGT ATTTCTTGGT AAATCACCAC CCGCTAAAAT TGTGGCGATA TTTAAGGCAA 180

TATGATAATC ATGGTCGCTA ATAAAATGAC CCCGTCTTTG CGCATCTAAT TGTCCTTGGA 240

TCAATGCTTT GAAGTCTTCA CCTAAAGCGA TATATTGATG TCTAGGATTC GGAATATAGT 300

TTGTTTCTGC TTCATATTTC GCACGTGTGA GCGCAACTTC GACACGnTGG TGCCTGGATT 360

nGAAAATAAA CCGGAnCCnG GGATCCACGG GAAATAACCC 400

(2) INFORMATION FOR SEQ ID NO: 3974:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3974:

TGCCATGTTC ACCTTGTTTA AAATCAAGGT TTGTAATGTT TCCTTGTGTC ACGATAATAG 60

GCGTAATATC ACTCTTTGCA TGATTGCGGA TGTAGTCTAA ATCAAAGTTG ATTAATAAAT 120

CACCTTGTTT AACTTCTTGA CCTTCCTCAA CATGTAAAGT AAAGCCTTCT CCGTTTAATT 180

TAACAGTGTC TAAACCGATG TGGATTAATA GTTCTAAACC ACTATCTGAA TACAAGACCA 240

ATTGCATGTT TTGTTGGGAA AATCATTTGT TACTTTACCG TTGAAATGGT GCACGAAACT 300

TCACCTTGTG AnGTTTTTGG ATAGCGATAC CGTCACCCCA TCCATTTTTT TTCGCTGAAA 360

CACTTGGATC AnGGCACTTC TGAATAAATG GTGGTTAACT 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3975:

CCTTTGCAGC GCCTCCGTTA CCTTTTAGGA GGCGACCGCC CCAGTCAAAC TGCCCGCCTG 60

ACACTGTCTC CCACCACGAT AAGnGCGGGn GTTTAGAAAG CCAACACAGC TAGGGTAGTA 120

TCCCACCAGC GCCTCCACGT AAGCTAGCGC TCACGTTTCA AAGGCTCCTA CCTATCCTGT 180

ACAAGCTGTG CCGAATTTCA ATATCAGGCT ACAGTAAAGC TCCACGGGGT CTTTCCGTCC 240

TGTCGCGGGT AACCTGCATC TTCACAGGTA CTATGATTTC ACCGAGTCTC TCGTTGAGAC 300

AGTGCCCAAA TCGTTAACGC CTTTCGTGCG GGTCGGAACT TACCCGACAA GGAnTTTCGC 360

TAACTTAGGA CC 372

(2) INFORMATION FOR SEQ ID NO: 3976:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3976:

AGGGAATCGA ATTTTCTTTC TCTTCCTnCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60

GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120

CCCATTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180

GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AAATAACTTA 240

ATCTATGTTT CCACCATTTT TATAAGTCAA ACGCTCACAT ACGGCTTCGT TTTCATTATT 300

TTAAAGCTCA TTTACATAAG TAAACTCTGC TTTAAATGAT TTAACTCATT GTCTGCTAAA 360

ACGGTTTnTT TTATGAAAAG GTTTGAAACG GGTTn 395

(2) INFORMATION FOR SEQ ID NO: 3977:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3977:

TTGGTCCCAA ACCAAGTGCT CTACCAAGCT GAGCTACTTC CCGTATAATT AACGCGCCCG 60

ATAGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120

GGCGCATATG TTTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTnnTTCA 180

CTCACGCAGA TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT 240

GGAGCAGAAG ACGGGATTCG AACCCGCGAC CCCAACCTTG GCAAGTTGTT ATTCTACCGC 300

TGAACTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA GGCTTAGATC 360

CTTAAGTCTA AGTGCGTCTG GCCAATTTCC GCCAnACCCG 400

(2) INFORMATION FOR SEQ ID NO: 3978:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3978:

AAGTGGTTAA ATATTATAGA AAACATCAAA GGATGTTAAG AAATACAATT TATTACCCAG 60

CATTTAATAA TGGTGCTATA GAAGGAATTA ATAATAAGAT AAAATTAATC AAGTGAATTT 120

CTTTTGGTTA CAGAAATTTC AACAACTTTA AAGCACGTAT AATGATGATT TTCAGCTTGT 180

ACAAAGGAGA AAAAAAGAAG ACAACCAAGC CCAATAATGG ACTGGCCGCC TAATAATAAA 240

AGCTCTAAAA GTTGTATTTT AAAAATAGTT CTTTAAATTA TATACCCACC ACATTTGGTG 300

GAGGAACCTA AAAAAAAGCA CTTCCCAAAA ATGGGAAAGT GCAGTnAGTG GAGCCATAGA 360

GGATTCCGAA CCTCGGACCC TCnGAnT 387

(2) INFORMATION FOR SEQ ID NO: 3979:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3979:

TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG TATTCTACCG 60

CTGAACTACT TCTGCATATG CGGGTGAAGG GAGTCGAACC CCCACGCCGT AAnTTAGCAT 120

CGAACCTCTG GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTT 240

CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTT CAGTTGCTCT 300

ACCAATTGAG CTAGGCCGGn CAATATGTAA GAATAAATGG TGGAGAATGA CGGGTTTCGA 360

ACCGCCGAAC CCTCTGCTTG TnAAGGGCAG ATGGCTCnTC 400

(2) INFORMATION FOR SEQ ID NO: 3980:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3980:

TTACCACGTA TTTAGGTTTC TTTGGTGGCT CTAGATTTGT CCCTATTGTC ACAGCATTTG 60

CCGCAATCTT TTTAGGTGTA TTGATGTTTT TCATTTGGCC AAGCATACAA GCCGGCATTT 120

ATCATGTTGG TGGATTTGTA ACGAAAACAG GTGCCATCGG TACTTTTGTT TATGGCTTCA 180

TCTTAAGATT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTACTTACCG TTTTGGCAGA 240

CGGCACTTGG TGGTACTTTA GAAGTCAAAG GGCACTTAGT TCAAGGTACG CAGAACATCT 300

TCTTTGCTCA ACTTGGTGAT CCAGATGTGA CGAnTATTAT TCCAGGTGTG TCACGCTTTA 360

nGTCAGCCGT TTTAATACGA GGATGTTCGG CTAnGTGGTG 400

(2) INFORMATION FOR SEQ ID NO: 3981:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3981:

CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC 60

GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG 120

CTGGAACTAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GATACAATTC 180

AAGTTGTTGC AACGCAAGGG AAGCGGAGAG ACAGTGTAGT GGATGGAGCA ACGTATAGTT 240

GGATTTCACA GTTGTCGCAC CACAACCGAA CCAAGCGACT GACTGAAGAT TTGGCAAAAT 300

GGnCATATTG ATATCACGCC TAATGAnTCC ATTCAGGACA TTTAATTAAT CCAACTCAAG 360

(2) INFORMATION FOR SEQ ID NO: 3982:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3982:

TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 60

TAATGTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAGCAAA 120

GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTC 180

AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG AAAATTATAG GTGTTGAACC 240

TTCAGTGCAA GTAGTATGTA TGAATCTGTT GTGGTAAATA ATCAGGTAGT CACATTGCCT 300

AATATCGATA AATTTGTGGG ACGGTGCATC TGTAGCTAGA GTTGGCGATA TTACATTGGA 360

AATTGCCAAA GAAAAGTAGA GGATTACGTT CCAGTAGAGn 400

(2) INFORMATION FOR SEQ ID NO: 3983:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3983:

CCACCATTAT TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT TTACCAAGCA 60

AAACCGAGTG AATAAAGAGT TTTAAATAAG CTTGAATTCA TAAGAAATAA TCGCTAGTGT 120

TCGAAAGAcG CGACAAGATT AATAACGCGT TTAAATCTTT TTATAAAAGA AAACGTTTAG 180

CAGACAATGA GTTAAATTAT TTTAAAGCAG AGTTTACTTA TGTAAATGAG CATTTAAAAT 240

AATGAAAACG AGGCCGTATG TGGAGCGTTT GACTTATnAA AAATGGTGGG AAACATAGAT 300

TCAAGTTATT GAAGGGCGCA CGGTGGGATG CCTTGGGCAC TAGnAAGCCG nTGGAAGGAC 360

GTTACTAACG ACGATATGCC TTGGGGGAGC 390

(2) INFORMATION FOR SEQ ID NO: 3984:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3984:

GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTTGC CTTGTATCTG CAAATGTTTT 60

GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC ACAAATTCAA ATGTATCAGG 120

CGTTTCTTTT ATCCATTTCA ATATATTTCT TTCCGGTTGT ATCGCATAGT ATGTCGCATC 180

TAATTCGACA ACCGGAAAAT GTCCAGCATA TGTTTTAAGT TTATCGGTTT GGCGTTCTAA 240

ATCTTCATAT AATGAATAGT GATCACCCCA ACCTGTTAAT CCGATGTTTT ATCATATATA 300

TCACCAATGT CATCATACCA TATAACTTTT ATCATnATCA TTTCAGCGAA CTTTAGGTTT 360

GnAGGTTTTT TGGCCTGGAT TAAAnATCTT TCGGGCGGAT 400

(2) INFORMATION FOR SEQ ID NO: 3985:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3985:

GCATTTGCTT ATATCTTTAA AAAAGATTTT GAAGATATTG AAAGAAAAAC TAAAGAAATT 60

ATTTCTGATA TTGAAAGTAA AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT 120

AAAAAnCAGC AGTAAGATAA TTTTCAATTA GAAAATATCT TACTGCTGTT CTCTATTTAT 180

ACAATACTTC GTATTGAAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTTGGTCTTC 240

GACTGGCACT GCTCCCTCAG GAGTCTCGCC ATTGAATACT ACGTATTAAC ATGTnAATTT 300

TACTTTGGAA ATACTTTTAA AAAATAAGAC ACTTTGCCCA ACTTGGCACA TAAATGTTAA 360

AATnCAATGA AATGAATTTT CTGTGTTGGG TCCCCTnCTA 400

(2) INFORMATION FOR SEQ ID NO: 3986:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3986:

TTCGTTCAAA GTCATCTAGG TCACATTATT CTATTTGGGA TTCTTAGTGC TGTTCTTATT 60

ATGACAATAC AAAACGTAAA AAAGTCGCAG TGATCGGTAG TATTTTAGTA TTTATCATTA 180

GTATTCCAGC AACCTTATCT TTTGGTATCT TAAAAGATGT AAGATTCGGT GCGGGAACGA 240

TTTTTGATAA TATGGATTTC ATCGTTTCGA ATGTATTGAT GCCATTAGGC GCATTAGGTA 300

CTACGCTTGT CGTAGGnCAA TTATTAGnTA AAAAATTATT ACAnCAATAT TTTGGTAAAG 360

AnCGATTTAG GATTATTCAG TGGTTGGTAT TACTTAATTA 400

(2) INFORMATION FOR SEQ ID NO: 3987:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3987:

GGATTCGAAC CCCCGCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC 60

CGGACTTGGG TATTCCTCCA AAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA 120

CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC 180

TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC 240

TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAA TAATATGGTG GGGACTAnCG 300

GGATCGGAAC CGCTGGACCT CCTGCGTGGC AAAGCAGGCC GCTCTCCCAG CTGGAGCTAA 360

GnCCCCCATA ATAATnACAG TATATCnGGG AAGACAGGAT 400

(2) INFORMATION FOR SEQ ID NO: 3988:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3988:

CAGCTGATAA ACAAGTTGAT CTGGTCCCGA TTTGTTGGGT AAACGGTTGA TTAATGnAAA 60

ATGTTCGCCG AAGGATTCAT AATCCGAGAG GTCTAATTCA ACGTATCATT AATCAAGATG 120

CGCCTATTTA TCAATCTGAA ACAAATTATC ATTCGAAAGA TCGCGGTAAG TCTAAAAATG 180

GTATTCAAAT GGTGTATCAA CATTTAATGA ACGGTGTATC GTTTATGGnT CCTTTTATCG 240

TAGTTGGTGG ACTCCTTATC GCCATCGCGC TGACTCCTAG GCGGTGAACG ACCATCCAAA 300

CCTTTAAATT AATGGTCCCA TACCAGnCGG GATAAACGCT 400

(2) INFORMATION FOR SEQ ID NO: 3989:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3989:

CCAGAGATTT CCGAATGGGG GAAACCCAGC CATGAGTTAT GTCATGTTAT CGATATGTGA 60

ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA 120

GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCAAACGG GAAGAGCCCA AACCAACAAG 180

CTTGCTTnGn GGTnTGTAGG ACACTCTATA CGGATTACAA AGGACGACAT TAGACGAATC 240

ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT CGAAAATGTT GTCTCTCTTG 300

AGTGGATCCT GAGTACGACG GAGCACGTGG AAATTCCGTC GGAATCTGGG AGGACCATCT 360

CCT 363

(2) INFORMATION FOR SEQ ID NO: 3990:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3990:

TTTCCAAGAA CATGAGCCTG TACAGTTAAC ACCATGTnTG nTTCTTACTT CTTTATCGTG 60

GCTCCAACGT TCTCTGTACA TTTTTTCCCA TTCTCTACTT TTACTTTCTA GGATCGACCA 120

ATTCCCATTA AATTTTTCTG TTGGCTTAAA GAAATTCAAT CCAAATTTTC CCATATTTAT 180

ATCCTCCTAC GTATAAAAAT ACGATGTGTA GATGTCGTGT TTTTAAATAC TTTAAAATGC 240

CCAAGACTAT TGCTTTAATT AGATTGTACA TTTTTTCACA AACATAAAAT ATTAGGGAAT 300

CACCTAATTA CTTAAGGnAT TCCCTATCAA TAACGGGATT TCATTGAAAT AATACACAAT 360

CAGTAnGGTC AGCCTAATGC CAGGCTAAAT CGTTCAAATT 400

(2) INFORMATION FOR SEQ ID NO: 3991:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3991:

AAAGTGGTTA AATATTATAG AAAACATCAA AGGATGTTAA GAAATACAAT TTATTACCCA 60

GCATTTAATA ATGGTGCTAT AGAAGGAATT AATAATAAGA TAAAATTAAT CAAGTGAATT 120

TCTTTTGGTT ACAGAAATTT CAACAACTTT AAAGCAnGTA TAATGATGAT TTTCAGCTTG 180

TACAAAGGAG AAAAAAAGAA GACAACCAAG CCCAATAATG GACTGGCCGC CTAATAATnn 240

GAGCTCTAAA AGTTGTATTT TAAAAATAGT TCTTTAAATT ATATACCCAC CACATTTGGT 300

GGAGAACCTA AAAAAAAGCA CTTCCCAAAA ATGGAAAGTG CAAGTAGTGA GCCATAGAGG 360

ATTCGAACCT CTGACCCTCT GATTAAAAGT CAGATGCTCT 400

(2) INFORMATION FOR SEQ ID NO: 3992:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3992:

AGTGTATGGT TATCAAAGAT TTGATACGAC GGTCATTATT ATTACCGTTA TTGTATTAGT 60

CATTATTGTC CAAGTGATTC AAACGCTAGG GAATGTTCTA GCTAGATTCA TACGTnGACA 120

TTAATGATAT ATAGTGAAGA TTTTGAAAGG AATTGATAGA ATGAAAAGAT TGATTGGGTT 180

AGTTATCGTA GCACTTGTAT TAATTAGCAG CGTGTGGTGG TAACAATGAT AAAAAAGTAA 240

CAATTGGTGT CGCATCAAAT GACACTAAGG CTTGGGGAGA AGGTTAAAAG AATTAGCTAA 300

AAAAAGATGG ATnTTGATGT GGGAGATTAA GCACTTCCTC nGGATTACAA TTTACCGGAT 360

TAAAGCCTTn AAATGGATGG TGATATTGAT AATGAATGCC 400

(2) INFORMATION FOR SEQ ID NO: 3993:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3993:

TTATCAGAAG AACAATTCGA CATTTTACTG AATCATCCAT TAATCGATGA AGAAGTAGCC 120

AATAGTTTAA TTGAAAATGT CATCGCGCAA GGnGCATTAC CCGTTGGATT ATTACCGAAT 180

ATCATTGTGG ACGATAAGGC ATATGTTGTA CCTATGATGG TGGAAGAGCC TTCAGTTGTC 240

GCTGCAGCTA GTTATGGTGC AAAGCTAGTG AATCAGACTG GCGGATTTAA AACGGTATCT 300

TCTGAACGTA TTATGATAGG TCAAATCGTC TTTGATGGCG TTGACGATAC TGAAAAnTnT 360

CCGCCGGCAT TGAGAGCCTT AGA 383

(2) INFORMATION FOR SEQ ID NO: 3994:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3994:

GGTACTATGA TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGCCTTTCGT 60

GCGGGTCGGA ACTTACCCGA CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC 120

GCCTTTACTG GGGCTTCGAT TCGTAGCTTC GCAGnnAAAC CnACTCCTCT TAACCTTCCA 180

GCACCGGGCA GGCGTCACCC TGATACATCA CCTTACGGTT TAGCAGAGAC CTGTGTTTTT 240

GATAAACAGT CGCTTGGGCC TATTCACTGC GGCTCTTCTG GGCGTTAACC CTGAAAGAGC 300

ACCCCTTCTC CCGAATTACG GGGTCATTTG CCGATTCCTT AACGAGATTC GCTCGCTCAC 360

CTTAGA 366

(2) INFORMATION FOR SEQ ID NO: 3995:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3995:

AGATATTTTA CATGTGAATC AAGTAGGTAT TCATGATAAT TTCTTTGAAT TAGGTGGCCA 60

TTCATTAAAA GCAACGTTAT GnTGAATCGG ATAGAGGCAT CTACTGGGAA ACGATTACAA 120

ATTGGTGATT TATTACAAAA GCCAACTGTA TTTGAACTAG CACAAGCGAT TGCTAAGGTT 180

CAAGAACAAA ACTATGAAGT GATTCCAGAA ACTATAGTTA AAGATGATTA TGTGCTGAGC 240

GTACCTTTTT TATGGCGGTT ATnCATCAGA ACTTAATGTA GCTCAnTGCG ACAAGCATG 359

(2) INFORMATION FOR SEQ ID NO: 3996:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3996:

CAATTATTGG TATTCAACTT AAAGATCATG ATGATTTAAT ACAACTCAAA CAACGTTnAA 60

ATCATTTCGA TCCTTCCAAT ATTTATATTA ATGAAAATAA GATGTTATAT TCATTGTTAA 120

TTTAACACAT AGTAAGAAAA ACAGTCATAA ATTGATTTCT AATTGAAATC ATCTTATGAC 180

TGCTTTTTAT TATACTTTAC ATTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA 240

AGCCATCTTT CTTTGTGTTT GCTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTT 300

GCGGTCTCAA ATGCGGCTCA TCGCATCCAC TTTTTGCCTG GGCAACGTTC TACTCTAGGC 360

GGAAnGTAAG TGGGACTTAC CATCGACGGn TAAGGGGCTT 400

(2) INFORMATION FOR SEQ ID NO: 3997:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3997:

GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC TTATCGTGGT GGGAGACAGT 60

GTCAnGCGGG CAGTTTGACT GGGGCGGTCG CTCCTAAAAG GTAACGGAGG CGCTCAAAGG 120

TTCCCTCAGA TGGTTGGAAA TCATTCATAG AGTGTAAAGG CATAAGGGAG CTTGACTGCG 180

AGACCTACAA GTCGAGCAGG GTCGAAAnCG GACTTAGTGA TCCGGTGGTT CCGCATTGAA 240

GGGCCATCGC TCAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG 300

TTCACACGAC GGGGAGGTTT GGCACCTCGA TGTCGnCTCA TCGCATCCTG GGGCTGTA 358

(2) INFORMATION FOR SEQ ID NO: 3998:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3998:

TAGGAGGAAT TTATATGACA TTTGAAAAAG AAACGGTCTT AAAAACATTA TTTCCTGAAG 60

ATGTACTTAG TATTGCTAAA GGTTTAACAG ACGGTGAAGT CGAATTTTTA CAACAAGTAG 120

ATTCATTGCT AGAAAGTAAG TACCGTGAAA ATATTAATCA ACATTGGATA GACGCTACTG 180

TACCCGAGGA CTATTTTAAA GATCTGGGAG ArTTAAATTA TTTTAACArT CCATTACTTT 240

ACAAGGATCG TCCAAACGCC AAAATGCCTA GTCAnCTATT TCAGTTTTTC ATGTCTTACC 300

TACTCGCGCG ATTTGATATT TCCTTAGCTA CCCTACTCGG TGTTCACCAA GGTTAGGGCA 360

TAACACTTTC TATTTCGGAG GTAGCAAAGA CAAATTGCGA 400

(2) INFORMATION FOR SEQ ID NO: 3999:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3999:

CGCCCCTTAG TGCTGCAcTA ACGCATTAAG CACTCCGsCT GGGGAGTACG ACCGCAAGTg 60

AAACTCAAAG GAATTGACGG GGACCCGCAC AAGnGTGGAG CATGTGGTTT AATTCGAGGC 120

AACGGtAGAA CCTTACCAAA TCTTGACATC CTTTGACAAC TCTAGAGATA GAGCTTTCCC 180

CTTCGGGGAC CAAAGTGACA GGTGGTGCAT GGTTGTCGTC AGCTCGTGTC GTGAGATGTT 240

GGGTTAAGTC CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATTA AGTTGGGCAC 300

TCTAAGTTGA CTGCCGGTGA CAAACCCAGG AAGGTTGGGG ATGACGTCAA ATCATCATGC 360

CCCTTATGGn TTTGGGTTAC ACAAGTGGTT ACAATGGG 398

(2) INFORMATION FOR SEQ ID NO: 4000:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4000:

TGTTCTTGCA ACGCTATTTA GTATCAGGTT TAACAACAGG TGCGACAAAA GGTTAGTTTG 60

GACGTTATGA TGACGATTAA AGTTGGAATC ATTGGGTGTG GTGGTATTGC GAATGGCAAG 180

CACATGCCAA GTTTACAAAA AGTTGAAAAT GTTGAAATGA TCGCATTTTG TGACGTAGAC 240

ATTTCGAAAG CAGCGaGTGC GGCAGAAGCA TACGGAACTG ACAATGsCAA aGtTTATGAT 300

GATTACmAAG CaTTGTTAAA AGATGACACG ATTGATGTTA TCCATGTTTT GTACCCCCAA 360

TGGACCCCGC ATTGTGG 377

(2) INFORMATION FOR SEQ ID NO: 4001:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4001:

TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACATGTAG GCCGTTGTCA 60

CTTAACTTCT TGTTTTTCCG ATGACAGCTT CTATTTAGAG AATGTCATGA TTATTTTATA 120

TTCACTTCAA TGTTATCAAT ATTAGTGCCA TCTATGACAT CTGCCATGCG ATTTTCTTGT 180

AATTTTTTGT GCAATTCAAA CGTGTACTTT CCACCGTTTT TCATTTTAAT AACAATTTTA 240

CCTGAACCAA CGTTACCGTA CAGATTATTT TTTTCAATAA GTGTTTTCTC AATTTAAAAT 300

CAAGTTCTTT CAAGGAAATC TGTTCTTTAG TAATCTTGAA TTCTGAAACA TCATGGGnGA 360

TTGTACCGTA TnATCTTnCC TAGTAAT 387

(2) INFORMATION FOR SEQ ID NO: 4002:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4002:

CTATTACGAT TGCTGCGAAA GAAGGTATTA AAAATATACA AATAGGCATG GCTCACCGTG 60

GACGTTTAAA CGTTTTAACG CATGTCTTAG AAAAACCGTA CGAAATGATG ATTTCAGAAT 120

TTATGCATAC AGATCCAATG AAATTCTTAC CTGAAGATGG TAGCTTGCAG TTAACTGCTG 180

GATGGACTGG TGATGTGAAA TATCACTTGG TGGGCATTAA AACTACTGAT TCATACGGTA 240

CAATGCAGCG TATTGCACTG GCTAACAATC CAAGTCACTT GGAAATTGTT GCACCTGTTG 300

TCCATCATAA AnGCAATGnC CATTGTTGAT ACATGGCGAT 400

(2) INFORMATION FOR SEQ ID NO: 4003:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4003:

AGAAATATAT GCATTTCGGA TATCATGGTA AAGAGAATGG ATTAAGCGGT AAATCACGTG 60

ATGAAGTGCG AGCGAAATGA AACAAAATTT AGATGTCATG CGAGACGATA ATCAAAGGGA 120

CGACAGGTGA TGGGGTTGAA AGTGTAACGn GCTACACTGG TCATGATGCT GCTAAACTAC 180

GTGATTATAA TGAAACACAT CATGCTTTGT CTGGATATGA AATGATTGAC GCAGCAAAGG 240

TGCCATTGCA ACAAATGAAG TCAATGCTGC GATGGGTATT ATTTGTGCAC GCCAACAGCT 300

GGTTCCTCGG GTACCATTCC CGGTGCACTT TTTAAATTAG GAAAAAACAC ATGATTTAAC 360

AGAAGAGCAA ATGATTTGAT TTCTTATTCA CTTCAGCATT 400

(2) INFORMATION FOR SEQ ID NO: 4004:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4004:

TGAAATAGAA CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC 60

GTGCCTTTTG TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT 120

GGAGCCGTAG CGAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GACCGAAACC 180

AGGTGATCTA CCCTTGGTCA GGTTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA 240

CTTACGTTGA AAAAGTGAGC GGATGAACTG AGGGTAGCGG AGAAATTCCA ATCGACCTGG 300

AGGATAnTGG TTCTCTCCGA ATAGTTTAGG GCTAGCCTCA AGTGTGATTA TTGAGGTAGA 360

nACTGTTTGA CGAGGGGCCC TCTCGGGTAC CGAATTCAGG 400

(2) INFORMATION FOR SEQ ID NO: 4005:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 415 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4005:

ATACTAAGGC GTTATTAGAC GaTTAGACAA TGGTGTGATT AAAGGTGCAG CACTTGATAC 60

GTATGAATTT GAACGCAAAC TTTTCCCAAG TGATCAAAGG GGCAAAACAC TGAACGATCC 120

ATTGTTAGAA TCGTTGATTG ACAGGGAAGA TGTCATATTA ACACCACATA TTGCGTTTTA 180

TACTGAAGCT GCAGTTAAAA ATCTAATTGT CGATGCATTA GATGCAACAT TAGATGTATT 240

GGCAGACTGG AGATACTAGG TTACGAGTAA ATTAAAAATC GAACTGATGA GATAATTTGG 300

ATTGTTGGGG ATTCTGCATC CAGTTCGATT TTTTTAATTT GGTGTTGGAT GACGTTGnAA 360

TGTTGCCTAA TTTAAACGAC ATCGTAAACC nTGGATCCTC CAATGGCGTC CTTnC 415

(2) INFORMATION FOR SEQ ID NO: 4006:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 444 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4006:

CTAACAGAAG CTAGTATAGG AAATCGGTAC TCGTTAAGGC TGATCTGTGA TGGGGAGAAG 60

ACATTGTGTC TTCGAGTCGT TGATTTCACA CTGCCGAGAA AAGCCTCTAG ATAGAAAATA 120

GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG 180

AACTCTCGTT AAGGAACTCG GCAAAATGAC CCCGTAACTT CGGGAGAAGG GGtGCTCTTT 240

AGGGTTAACG CCCAGAAGAG CCGCAGTGAA TAGGCCCAAG CGACTGTTTA TCAAAAACAC 300

AGGTCTCTGC TAAACCCGTA AGTGATGTAT AGGGGCTGAC GCTGCCCGGT GCTGGAAAGT 360

TAAnGAGAGT GGGTTACTTC TTGCGACTTA nCGAAATCGA GnCCCCAGTA AACGGCGGGC 420

CGTAACTATA ACnGTCCTAA GGTA 444

(2) INFORMATION FOR SEQ ID NO: 4007:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTTGAACTCT ATCAAAGCAT CAGCAATCAA AACATACGTA TCTTTACAAC AGTAATCATG 60

CATTCTATGA TGCTTCTAAC TGAATTAAAG CATCGAACAA TCGGAAGCAT ATTTCTAAAT 120

TATTTATTCA TTATAGTCTT AAACATAACA TGACCTAATA TATTACTAAC CTATTAAAAT 180

AAACCACGCA CATCTAAGTG ATATACGACA ATCACAGCAA TAATAATTGC TTTAGAAAGT 240

CGTGCCGAAC TGGAACTTAC AAGTCTAGTT CGAACACACA CTGATGTGAG TGGTTTTCTT 300

TATTTTAAAC ATGAACAATC AGATAAGTTA CTAGCATTAG CAAATATTAT TAAATCAAGG 360

GCTTCGnTTC ATAAATTTAA AACATGTTAA ATTAGACGTG 400

(2) INFORMATION FOR SEQ ID NO: 4008:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4008:

TATACTTGTT TTTACAAACC ACAAAAAGCT CTAAACATTA GTTTAAACCA ATGCTTAGAG 60

CTTTCTAATT ATTTTATGCT TTAAAAGATA CTGTGTTATC TACGATGACC TTACCGTCTT 120

TAATAACTTT TTCTGCGTGA TTGATACCAA AATGATATGG AATATATTCA TGATTTGGTG 180

CATCCCAAAT TACTAAATTA GCCTTATCAC CTGTGTTAAT TGTACCCGCG TTAATGTCTA 240

TTGCTTTAGA GCCATTGACC GTAACAGCAT TCCAAACTTC ATTAGGTGAT AGCTTTAATT 300

TCAAGGCTGC AATCGCCATA ACAAGTTGTA AGTTGTTTGT GGACACTACT ACCAGGGTTA 360

TAATCAGTTG GCTAATGCCA TCGGCACCGG TTAATGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4009:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4009:

ACAAACATTG AAATTAGAGG TATATAAAAA ATGCTTCTGC AATAGATGCA ATAAACATGC 60

AATACAATAT GGAGGCGAAG TAAATGAAAA GTATTACGTT TGAAGAACAT TATGTCATTG 120

AAGATATTCA AAAAGAAACG ATGAATGCGA TATCAGCAGA TCCTAAAGGT GTACCGATGA 180

ATCATGATGA ACGTATCCAA TTTATGAATA ATCAAGACGT TCAAATTCAA GTCTTATCTT 300

ATGGAAATGG TTCTGCTTCA AATTTGGTTG GTCAGAAAGC CATTGAATTA TGTCCAAAAG 360

GCAAATGATC CATTGGGCAA ACTATATTGC ACCATATCCC 400

(2) INFORMATION FOR SEQ ID NO: 4010:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4010:

ACTAGAGAAG GTATGTTACG TGACAATGAA TTACTAAATG GTATTTATTC ATCGAGTTAC 60

ATCTATAGTT TATTAAAATC AGAATACGAC CAAAAATGAC AAATTAGACT TACAAAAGAG 120

TGATGACATT TAAAATGGCA GCGCTCTTTT ATTTAATTTT TGAAAATAAA AGGTTGTTGA 180

CAGTATTATT TTATAACAAT ATAATGATTT TGATAATTAT TATCAACTAG ATGATGTTTA 240

TGGGAGGATG CTTTAAAACA GCCGTTTTAA GTGTAATGTA TTATTTTAGC GTGTAGGGAT 300

GCGAAAATAT ATTTATAGGA CACATCTTGG GGATAATnGA TTTCTATAAT GAGGTGTCAA 360

ATGGAAAAGT TACCACGCTA TTATTAGCCn CCACGTTATT 400

(2) INFORMATION FOR SEQ ID NO: 4011:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4011:

TnTCAATTAG AAAATATCTT ACCGCTGnCT CTATTTATAC AATCCTCGTA TTGAATGGnT 60

CGCTTTCCTA GGGTGCCGTC TCAGCATCGG CTTCGACTGG CACTGCTCCC TCAGGAGTCT 120

CGCCATTAAT ACTACGTATT AACATGTAAT TTTACTTTGA AATACTTTAA AAAAATAAGA 180

CACTTTGCCC AACTTACACT ACCAATAAAA ACTTCTGTTA GAATTCCTCA AAATGATATT 240

TCGCGACATG TTAATGAAAT TGTTGAAACG ATACCTGATA GCAAATTCGA TGAATTCAGA 300

CATCATCGTG GCGCAACATC CTATCATCCA AAGATGATGT TAAAAATCAT CTTATATGCA 360

TATACTCAAT CTGTATTTTC TGGTCGTAGA ATAGAGAAAT TACTTCATGA CAGTATTCGA 420

GAATCCnAAT ACTG 494

(2) INFORMATION FOR SEQ ID NO: 4012:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4012:

TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGACATA 60

AAAAAAGAGA CCTCACGGTC CAACTTGCCT GGCAACGTTC TACTCTAGCG GAAGTAATTG 120

GCTACCATCG TCGCTAAAGA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTC 180

CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCGCTCTTT TCTCGTTTCG 240

TCAGATTCAA ACGTTTTCAC TTCGCCAAGC CATTTTTCTT TGTGTTTACT TTTTATTTTG 300

ACGTTTTAGG CATAAAAAAA AGAGACCTTG CGGTCCCAAT GCGGGCTCAT CGCATCCATT 360

TTTTGGCCTG GGCAACGTTC TnATnCCAGC GGAAnTnAAT 400

(2) INFORMATION FOR SEQ ID NO: 4013:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4013:

CGAACTGCCG AACCCGAAGA GCGGATTTAC AGTCCGCCGC GTTTACCACT TCGCTACCCC 60

TCCAGCTTAT TCATATAATT TAATAATCAA AATGGTGGAG AATGACGGGT TCGAACCGCC 120

GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGACT 180

CCTACGGGAC TCGAACCCGT GTTACCGCCG TGAAAGGGCG GTGTCTTAAC CGCTTGACCA 240

AGGAGCCATG GCTCCACAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG 300

CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTTA CTCTnAGCGG 360

AACGTGAATT CGACTTACCA TCGACGnTAA GGAGCTTnAC 400

(2) INFORMATION FOR SEQ ID NO: 4014:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4014:

ATTAGGACCT CAAGACGATA TTACTAAATT TGAATACTTA AAAAAATCTT CTCAAAATAC 60

AGGTACTTCA TTATTGGTAT TCAACTTAAA GATCATGATG ATTTAATACA ACTCAAACAA 120

CGTGTGAAAT CATTTCGATC CTTCCAATAT TTATATTAAT GAAAATAAGA TGTTATATTC 180

ATTGTTAATT TAACACATAG TAAGAnAAAC AGTCATAAAT TGATTTCTAA TTGAAATCAT 240

CTTATGACTG CTTTTACATT ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTC 300

ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA 360

nGnGACCTGC GGTCTCAATG CGGCTTCATC GCATCCACTT 400

(2) INFORMATION FOR SEQ ID NO: 4015:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4015:

GAATGAAAAG CTCTAAAAGT TGTATTTTAA AAATAGTTCT TTAAATTATA TACCCACCAC 60

ATTTGGGGAG GAACCTAAAA AAAAGCACTT CCCAAAAATG GAAAGTGCAA GTAGTGAGCC 120

ATAGAGGATT CGAACCTCTG ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT 180

AATGGCTCTG AATGGCTGGG CTAGCTGGAT TCGAACCAAC GAGTGACGGA GnAAAGGTCC 240

GTTGCCTTAC CGCTTGGCTA TAGCCCAATA TATAGATGGT GGAGGGGGGC AGATTCGAAC 300

TGCCGAACCC GAGGAGGCGG ATTTACAGTC CGCCGCGTTT AGCCCACTTC GnTACCCCTG 360

CCAGnTTATT CATATGA 377

(2) INFORMATION FOR SEQ ID NO: 4016:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4016:

ATGACGCACC TGACATCCTC TCGGTTCATA TTCAGGCATA TCCGGACCAC AACTTGGATA 120

GTCAGTTTGT TGATTTTCCC AGGTAATCAC ACCATTTTTC ACAAATACTT TCCAAGAACA 180

TGAGCCTGTA CAGTTAACAC CATGTGTTGT TTCTTACTTC TTTATCGTGG CTCCAACGTT 240

CTCTGTACAT TTTTTCCCAT TCTCTACTTT TACTTTCTAG GATCGACCAA TTCCCATTGA 300

AATTTTTCTG TTGGCTTAAA GAAATCAATC CAAATTTCCC ATATTTATAT CCTCCTACGG 360

GTGAAAAATA CGGTGTGTAG AnGTCGTGGT TTTTnAAATA 400

(2) INFORMATION FOR SEQ ID NO: 4017:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4017:

CTTTGAGCGC CTCCGTTACC TTTTAGGAGG CGACCGTCCC AGTCAAACTG CCCGnCTGAC 60

ACTGnCTCCC ACCACGATAA GGGCGTGGGT TAGAAAGCCA ACACAGCTAG GGTAGTATCC 120

CACCAGCGnC TCCACGTAAG CTAGCGCTCA CGTTTCAAAG GCTCCTACCT ATCCTGTACA 180

AGCTGTGCCG AATTTCAATA TCAGGCTACA GTAAAGCTCC ACGGGGTCTT TCCGTCCTGT 240

CGCGGGTAAC CTGCATCTTC ACAGGTACTA TGATTTCACC GAGTCTCTCG TTGAGACAGT 300

GCCCAAATCG TTACGTCTTT CGTTGCGGGT CGGAACTTAC CCGACAAGGA ATTTCGTTAC 360

CTTAGGACCT TATAGTTACG GCCGnCTTTA ATTGGGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4018:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4018:

TGTCGATTTA AGAGGCATGC TACGAGGAAT GATTGGTCAT CCGAAAAAAG ATCGAGCGGC 60

ATATGAGGCA CGCCAAGCGA TTCCAAACAT TAATGAAAAC AGTCCGCCAA TATTAATTGT 120

ACATGGAGGG AAAGACCAGC AAGTTGGTAT TCATCATGCG TATTATTTAG CGGACCAACT 180

AGAGTTAAAA GGTGCCACGC ATGnAAACAT TTTATCAAAT GGCAGAAGGA CATGTGCCAA 240

CGCATAGCTT AGTTATGGAA ACGTGGTGTG CGCATGGGGA ACTATTCAAG CTTTGGAGGA 360

TGTGGTACTT ACATGCGTTG GAATTAGGGG TCCGGTTACT 400

(2) INFORMATION FOR SEQ ID NO: 4019:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4019:

GGAGGTTTGG CACCTCGATG TCGGCTCATC GCATCCTGGG GCTGTAGTCG GTCCCAAGGG 60

TTGGGCTGTT CGCCCATTAA AGCGGTACCA AGCTGGGTTC AGAACGTCGT GAGACAGTTC 120

GGTCCCTATC CGTCGTGGGC GTAGGAAATT TGAGAGGAGC TGTCCTTAGT ACGAGAGGAC 180

CGGGATGGAC ATACCTCTGG TGTACCAGTT GTCGTGCCAA CGGCATTAGC TGGGTAGCTA 240

TGTGTGGACG GGATAAGTGC TTGAAACATC TTAAGCATGA AGCCCCCCTC CAAGATGGAG 300

ATTTCCCAAC TTCGGTTTnT AAGATCCCTC CAAAGnTGAT GGAGGTTTAA TAGGTTTCGA 360

GGTGGGAAGC AnGGTGGACA GTTGGGAGCT GGACGAnTAC 400

(2) INFORMATION FOR SEQ ID NO: 4020:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4020:

GAAGATGTTC GTCATTCTTC AAATAAACCA GAGCTAGTTG CAATTGCTGA ACCAGCATCT 60

AATAGACCGA AAAAGAGAAG TAGACGTGCG GCACCGGCAG ATCCTAATGC AACTCCAGCA 120

GATCCAGCGG CTGCAGCGGT AGGAAACGGT GGTGCACCAG TTGCAATTAC AGCGCCATAT 180

ACGCCAACAA CTGATCCTAA TGCCAATAAT GCAGGACAAA ATGCACCTAA CCGAnTnTTG 240

TCATTTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAA CAGTTAAACG 300

TTTGTTAATA ACTTGCCGGG CTTCACACTA ATCAATGGTG GGCAAAGTAn GGGTGTTTAG 360

TCATGCAATG GGTAAGAACG AGCATGTTTG GATTTCAGGG 400

(2) INFORMATION FOR SEQ ID NO: 4021:

(A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4021:

CTAAGTCATG AATGGGAAGT GGCTCGCGTT GAAGAAGGAC TGACTACTGC TGCCACACAG 60

CTTGCTAAAC AATTATCAGA ATTAGATTTA GCGTCACATC CTTTTGTGAT GTCAGAGCAG 120

TTTGCAAGTn TAAAAGATCG TCCATTTCAT CCATTAGCTA AAGAAAAAAG AGGATTAAGA 180

GAAGCGGATT ATCAAGTGTA TCAAGCTGAA TTAAATCAAT CATTTCCTTT AATGGTTGCA 240

GCAGTTAAAA AGACACATAT GATTCATGGC GATACTGCAA ATATCGATGA ATTAGAAAAT 300

TTGACAGTAC CTATAAAAGA ACAAGCGACA GACATGTTAA AATGATCCAA GGTTATCAnT 360

AGATGACTAT GTACCATTCC GGTACnTCCT GGCCAT 396

(2) INFORMATION FOR SEQ ID NO: 4022:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4022:

GATTGGTCTG nAAGAAGAAT TAATGGAAAA GCTACGTGAA AAATTAGAAG CGGCATTTGA 60

TACGATTTAC GAATTGTCTC AAAACCGAAA AATAGATATG AGACTTGCAG CATATATCAT 120

AGGTATTAAA CGTACAGCAG AAGCAGCTAG ATATCGTGGT TGGGCATAAT TAATTATCAT 180

ATGTGATTTA ACGAGCTTGG GACAGAAAAC AAAGCCCTAA GCTCGTTAAT TTTATTTTAG 240

CAGTAGTTGA CTGTAAAACA ATGCCCGTGT AAACGCTCTT TTCAAAAATA GTCGGGGCCC 300

CAACACAGAG GCTGGTGGGA AAGTCAGCCT ACAATAGnGT GCAAGTTGGC nGGGGCCCCA 360

ACACAGAGGC TGGCGG 376

(2) INFORMATION FOR SEQ ID NO: 4023:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CAAATGGTGG AGCCATAGGA GGATTCGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT 60

CTACCAACTG AGCTAATGGC TCTTCCATGG nGCnGGCCAG AGGACTTGAA CCCCCAACCT 120

ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC GGCAATATGT AAGAATAAAT 180

GGTGGAGAGT GACGGGTTCG AACCGCCGAC CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG 240

CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTC TACTCTAGCG GAAnTAATTC 300

GGACTACCAT CGACGCTAAA GGAGCTTAAC TTCTGTGTTC CGGCATGGGA ACAGGTGTGA 360

CTCCTTGCTA TATCACCAGA C 381

(2) INFORMATION FOR SEQ ID NO: 4024:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4024:

GCCCCTTATG ATTTGGGCTA CACACGTGCT ACAATGGACA ATACAAAGGG CAGCGAAACC 60

GCGAGTCGAA GCAAATCCCA TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC 120

TACATGAAGC TGGAATCGCT AGTAATCGTA GATCAGCATG CTACGGTGGA ATACGTTCCC 180

GGGTCTTGTA CACACCGCCC GTCACACCAC GAGAGTTTGT AACACCCGAA GCCGGTGGGA 240

GTAACCTTTT AAGGAGCTAG CCGTCGAAGG TGGGGACAAA TGGATTGGGG TGAAGTCGTG 300

AACAAGGTAG CCGTGATCGG AAGGTGCGGC TGGGATCACC TCCTTTGCTG AAGGATGATG 360

ATTTCGGnAA CATCnTTCTT CCAGAAGATG CCGGTAATAA 400

(2) INFORMATION FOR SEQ ID NO: 4025:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4025:

CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGGG TGAGAATCCC GTCCACCGAT 60

TGCTAAGGTT TCCAGAGGAA GGCTCGTCCG CTCTGGGTTA GTCGGGTCCT AAGCTGAGGC 120

CGACAnGTAn GGCGATGGAT AACAGGTTGA TATTCCTGTA CCACCTATAA TCGTTTTAAT 180

GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT 300

GTGTCTTCGA GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AA 352

(2) INFORMATION FOR SEQ ID NO: 4026:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4026:

TGGGGCTCTT CCCGTTTCGC TCGCCGCTAC TAAGGGAATC GAATTTTCTT TCTCTTCCTC 60

CGGGTACTAA GATGTTTCAG TTCTCCGGGT GTGCCTTCTG ATATGCTATG TATTCACATA 120

TCGATAACAT GACATAACTC ATGCTGGGTT TCCCCATTCG GAAATCTCTG GATCAAAGCT 180

TACTTACAGC TCCCCAAAGC ATATCGTCGT TAGTAACGTC CTTCATCGGC TTCTAGTGCC 240

AAGGCATCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 300

AnGTTAACAT GAAGTTAGGT TCTTTTATAA AAGGATTAAA nGGGTTATTA ATCTTGTGnG 360

TGTTCTTTCG 370

(2) INFORMATION FOR SEQ ID NO: 4027:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4027:

TCATGTTTCG CTTGGTTTAA TGCTGTTAAT GCGTTATCGA CACGATGTTT TTCATCTGAA 60

ATTTGTTGTG CAGTTGCATC GCCATTGTCA ATAACACGTT GAGCTGCAGT TATTTCAGTT 120

TCTGCTTCCG CTTCTTCGCA TTATAGTTAT CAATACTTTG TTGCGTCATA CCAGCAGTTG 180

ATGGTACTTG GTTCACAGAA CTTTGTAAGT TATTTTTAGA CGTTACTAAT TGGCTATTAT 240

CTTCTTTATT TTGAAGTAAT GCTTTACTTG GATCAATCTT AGTTTGTGCG CACGAACTTT 300

AGTTAGTGCG TGCAGAAACT TGTTGTGGTG TTGCACGCTC ATTnATGAAG CACTGTTGGT 360

GCCTCCGTTT TCGCATAnTG GATTGTTGTT GCGCATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 4028:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4028:

CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC 60

CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 120

GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA 180

TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT 240

TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC 300

CTGGGCAACG TTCTACTCTA GCGGGAACGn AAGTTGGGCT TACCATCGAC GCTAAGAACC 360

TTTCTTGGAC TTGGTGGACA AACGGnGTGG CTGCTTTTCC 400

(2) INFORMATION FOR SEQ ID NO: 4029:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4029:

AGGACTTGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC 60

GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCG AACCGCCGAC CCTCTGCTTG 120

TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTC 180

TACTCTAGCG GAAnTAATTC GGACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTCG 240

GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG TAATTTGATA 300

CATTCAAAAC TAGATAGTnA AGTGAAAAGT GATTTTGGnT TCGCAAAACC ATTTGATTTT 360

GATTGAAGTC CTTCGATCGA TTGAGTGATT CGTGCAGCTn 400

(2) INFORMATION FOR SEQ ID NO: 4030:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GATGATAAAT CATGTTTTTC ATACCAAGTC GCTGCCGGCA AAACAATGTC AGAATATAAC 60

GGTGTTGCCG TCATTCTGAA GTCTAAAGAG ACCACTAAAT CTAACTTACC TGTTGTTTCT 120

TCACGCCACG TAATTTCTTC TGGCTTTTCA TCTTCATTTG GTGTAGCTAA TAACCCTGAT 180

TTTGTGCCAA GTAAATGCTT CATAAAGTAT TCTTGACCTT TTGCAGAACT TGAAATTAAG 240

TTTGAACGCC ATATAAATAA TGATTTTGGA TGATTCTTTT CAAATCAGGA TCTTCTATTG 300

CAAATTGTGG TTTGTnTTGG ATTTCACnTC ATCAATTGCA CGTTGCAAAA TCGCTTCATG 360

TGAATCTATA CCCTGCATCT TGTAGCnTCC 390

(2) INFORMATION FOR SEQ ID NO: 4031:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4031:

TGGTTCGAAT CCAGCTAGCC CAGTTATTGG CGGCATAGCA AGTGGTAAGG CAGAGGTCTG 60

CAAAACCTTT ATCACCGGTT CAAATCCGGT TGCCGCCTCC AGGTTTATGC GGGAGTAGTT 120

CAACTTTTAG AACACGTTCC TTCCCGGAAn GAGGTATAGG TGCAAATCCT ATCTTCCGCT 180

CCATAATTTA ATAATAATGC GGGAGTATTT CAACTCTTAG AATACATTCC TTCCTGGAAT 240

GAGGTATAGG TGTAAATCCT ATCTTCCGCT CCATAATTTA ATATTTGCGG GGAGTAGTTC 300

CAACTTTTAG AACACGTTCC TTCCCGGGAA GGAGGTATAn GTGTATCCTA TCTTCCGCnC 360

CATAATGCCT TCCAAAGGGG AATTTTTTGG TTTnACCATT 400

(2) INFORMATION FOR SEQ ID NO: 4032:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4032:

GTATCGATGA GTTTCTTCGG TGCGTCTTCG ACAGCCATTT TGACTTCGAC AAAATGCATC 60

ACATCGGGAT GACCATTAAT TGCATTAAAC GTGTCTTGTA AATCTTTTGA TGATTCAACG 120

TCATGAATTT CAACATTTTT ACCACCAAAT ACAGCTGGTA AAGCTTTATA ATCCCACATG 180

TTATTAATCA CCAATAATAC CGGGTTAATA TGCTGTCTAA TCATAGTTGG AAATAGCTTG 300

AACAGTTAGT TGGCCATGAG CCATCACCCA TTTAATAATA AGTTACGACG GATCTTTGGT 360

CTGCCAATTG GGGGAnCnCA ATGTTGCAGG GnAATGGTAT 400

(2) INFORMATION FOR SEQ ID NO: 4033:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4033:

CACGACGTTC TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCTTgGG 60

ACCGACTACA GCCCCcAGGA TGCGATGAGC CGACATCGAG GTGCCAAACt CCCCGTCGAT 120

GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCGGGGTA GCTTTTATCC GTTGAGCGAT 180

GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 240

AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTCC AACCATTCTG 300

AGGGAACTTT GAAGCGCTCC GTACCTTTTA AGAnGGCGAC CGGCCCAGTC AAACTGGCCG 360

CTGACACTGT CTTCCAACAC GATAAGTGGT GCGGGTTAGA 400

(2) INFORMATION FOR SEQ ID NO: 4034:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4034:

AATTCCATGT GTACGGTTGA AATGCGCAGA GATATGGAGG AACACCAGTG nCGAAGCGAC 60

TTTCTGGTCT GTAACTGACG CTGATGTGCG AAACGTGGGG ATCAAACAGG ATTAGATACC 120

CTGGTAGTCC ACGCCGTAAA CGATGAGTGC TAAGTGTTAG GGGGTTTCCG CCCCTTAGTG 180

CTGCAGCTAA CGCATTAAGC ACTCCGCCTG GGGAGTACGA CCGCAAGTTG GAAACTCAAA 240

GGAATTGACG GGGACCCGCA CAAGCGTGGn AGCATGTGGT TTAnTTCGAA CAACGCAGAG 300

AACCTTACCA AATCTTGACA TCCTTTGACA ACTCTAGAGA TAAAGCCTCC CCTTCGGGGA 360

CAAATGACAG TGGTGCAnGT TGTCCTCACT CGTGTCGTGA 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4035:

TTCGCTTTGC CCGTCTGTCA CATTACTGTA AAATTCTATA AATAGAATTT TTGATGACGG 60

GTCCCTTCCT AGGGTGCCGT CTCAGCCACC CCAACCGGCA CATTGTTGTA AGCTGACTAT 120

ATGTCACTTC TGTGTTGGGG CCCCTGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC 180

CATTAATACT ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACATTAAAGC CCAAATTAAT 240

CAAAAGCTTT CTGAACCAGA AACGAAAAAA ATCTATAGTC ATAGAAAAAT TTATGTAGAG 300

CCTGTTTTTG GATTTATGAA GGCTATTTGG GGTTCACTCG AATGTCAGTT CGAGGAATAA 360

TnAAGTnAAC GAGAGCCAGG TTTGTAATTA TGGCACTnAT 400

(2) INFORMATION FOR SEQ ID NO: 4036:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4036:

TAAATGTTGA AAAAGCACGA TTAGATAGAA TTTTGAATAA CAATGAAATT CGTCAAATGA 60

TCACAGCATT TGGTACAGGA ATCGGTGGCG ACTTTGATCT AGCGAAAGCA AGATATCACA 120

AAATCGTCAT TATGACTGAT GCCGATGTGG ATGGAGCGCA TATTAGAACA TTGTTATTAA 180

CATTCTTCTA TCGATTTATG AGACCGTTAA TTGAAGCAGG CTATGTGTAT ATTGCACAGC 240

CACCGTTGTA TAAACTGACA CAAGGTAAAC AAAAGTATTA TGTATACAAT GATAGGGGAC 300

TTGATAAACT TAAATCTGAA TTGAATCCAA CACCAAAATG GCTATTGCAC GTACAAAGGC 360

TTGGAGAATG AATGCAGTCC ATTTGGGAAC ACATGACCTG 400

(2) INFORMATION FOR SEQ ID NO: 4037:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4037:

TCGTCGCTAA AGACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT CTCCTTCGGC 60

TCTCGCTTAC TCATTTAGCT CTACTAAACT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT 120

CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT 180

AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA TTTTTTGCCT 240

GGCAACGTTC TACTCTAGCG GAAnTAAATT GGGCTACCAT CGACGCTAAG AACCTTTCTT 300

GACTTGTGAC AATCGCTTGC TTCTTTCCTC TTCTTCGGCT CTCGCTTACn CATTTAGCTC 360

TACnAAACTC GTTGCGCTCT T 381

(2) INFORMATION FOR SEQ ID NO: 4038:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4038:

CTGTTTGTCA TACTTCATAA ATCCTTTAAA TTCACCCATC GTATCTCCCC CTTTCCTTAA 60

TACACAACGG CTGGTTTATG TTTAGCATCG ATTGTTTTAC TGTCATCGTA AAATGCAGCT 120

AACATCGCTT CATCTTCATT GTCATGTAAT GATTTGTGCA AATGAATTTT TTGCATCATT 180

AATTGATAAT CTTTAGGAAT AACTTTAACG ACGACATCTT CAATGCGATC AAAATGTTTT 240

AACACATGAA TCGCTCTCGT ACTATTCGTG TGTGACACAT GTnCTTCCAG CATTTGCTTA 300

ATGAATGCTT TTnCTTCTTG GTGTTTAATC TTTGTAAACG AAAGCGTATC TAGTGATAnG 360

(2) INFORMATION FOR SEQ ID NO: 4039:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4039:

AGTGCGAACC CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC 60

GCATATGTTT TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAG TGAnTGCACT 120

CACCGCAGAT TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG 180

GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GCTnAGGATC 300

CTAAGTCTAG TGCGTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC 360

GAACCTCTGG ACCCTCTGGA TTAAAAAGTC AGATGCTCTA 400

(2) INFORMATION FOR SEQ ID NO: 4040:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4040:

CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 60

TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 120

TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAG 180

AGACCTCACG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 240

CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC 300

GGCTCTCGCn TACTCATTTA GCTCnACTAA ACTCGTTGCG CTCTTGTTCT CGTTTCGGGC 360

AGATTCAAAC GnTTGTCA 378

(2) INFORMATION FOR SEQ ID NO: 4041:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4041:

GTACCTTAAC AATATCTCGA AATGGACGAA CTAAATTATG AACCGCATGA AAGGATACTT 60

GCGAATCATT TGAGCATGCT TGAATCATAA TATCACCATC GCTGTAATCG TCTATTAACT 120

GATCATTCGG AAAATGCGGT AAATCTTTAA AGGCATCGGG AATTTTACTA GATAACCCAA 180

TTTTCTTCAT CAAAGACTTA CTAATCCCAA AGGTAATCGT TAACTTGCTT GCACCTAATC 240

CTATCGATTC ACCGGTATCT ACTGGTGGGC ATTAAAGGAT TGTTACTCGG GCTTGGCCAA 300

CTGTATCACC ATCCATCATA CGATTCAGCC ATAACGGTCC ACTTTTTTAA ACATTGGCTT 360

TATTGGCACC CnAACCTTTG GACTTCnAAT CTAACGGCCA 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4042:

GACTTGCAAA CGTTGTGATG ACGGTCAAGA AAACTGGTAA CACACCAGAC GGACGTAAAG 60

CTGGCGAACC ATTTGCTCCA GGTGCAAACC CAATGCATGG CCGTGACCAA AAAGGTGCAT 120

TATCTTCATT AAGTTCTGTA GCTAAGATCC CTTACGATTG CTGTAAAGAT GGTATTTCAA 180

ATACATTCAG TATCGTACCA AAATCATTAG GTAAAGAACC AGAAGATCAA AACCGTAACT 240

TAACTAGTAT GTTAGATGGT TACGCAATGC AATGTGGTCA CCACTTAAAT ATTAACGTAT 300

TTAACCGTGA AACATTAATA GATGCAATGG AACATCCAGA AGGAATATCC ACAGTTAACA 360

ATCCGTGTAT CTGGTTACGC TGTTAACTTC ATTAAATTAA 400

(2) INFORMATION FOR SEQ ID NO: 4043:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4043:

CTATTTTATC TAAAGTTAAA CCTGACCCAC CTAGAATTGA CGCAAACTCT GTGACATATA 60

AAGCAGGTCT TACAAACCAA GAnATTAAAG TTAATAACGT ATTAAATAAC TCGTCAGTAA 120

AATTATTTAA AGCAGATAAT ACACCATTAA ATGTCACAAA TATTACTCAT GGTAGCGGTT 180

TTAGTTCGGT TGTGACAGTA AGTGACGCGT TACCAAATGG CGGAATTAAA GCAAAATCTT 240

CAATTTCAAT GAACAATGTG ACGTATACGA CGCAAGACGA ACATGGTCAA GTTGTTACAG 300

TAACAAGAAA TGAATCTGTT GATTCAAATG ACAGTGCACA GTGAACAGTG GACACCACAA 360

TTGACAAGCC AACTACTGAA GGCGCnGTGn TTATTAAAAG 400

(2) INFORMATION FOR SEQ ID NO: 4044:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4044:

AAAATGGCTT GATTTGAAAA ACGACCAGCA TGCGCTACTG GnATAATAGC GAGGCTACCA 60

TGTTGTTTCA TCGTAGnCGC ATGTTAGTTA ATCCAGGGAT ACAAGCATCA TGATCAATAT 120

TAAAGCCATA TTCAAACAAT TGACCATAAG GTTCAATGTA AGCAGCGCCG GTGCACTTGC 180

ATTCCAGCTG AATTAGAGCG ACGTGCAGCA TAAGCCAAGT CTTCTTTTGT AATATAGCCT 240

TCTTTTGTTG ATGTGTTTAC GGTCCATTGG GTGGATAATA CAAAGCGATT CGAAATTTTG 300

ATGCCATTAG GTAAGTGGAT TGATTGTAAA AGTGGTTTGT ATCGGTACAT ACTATGATTC 360

CnTTTCCATT GCAAT 375

(2) INFORMATION FOR SEQ ID NO: 4045:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4045:

GTTCCAATGA AGATAGCTAG AAATGATATC CAAAACACAT GATGCATCAC TGGTGATGCT 60

CGACTAATTG TATTCCATGA TGCATTAATA ATAATGACCA ATACACATAA AATAAGCAGC 120

CATTTATCGT TTATTTTAAA AATATAATGC AGCAAAAATC CCAAAATGAT TAATTGCACA 180

ACTGCTCGTA ATGTCGCAAC AATTAAATCT TTAATAATAT GTAAACCTTC TTTATATGAA 240

ATGATAATCG GAATGACTAA AAGCAATGCC GTCAATCCAA GTGCCGTATT ACTCATGTnG 300

ATTCAACTCC TCTGTATTAG AAATTTGACC ATCAACAATT GTTATACGCT TTTTGnAAGT 360

GGTCGCATAC TTTGGGGCAT CGCTGTGGGG TAGGGGGnCn 400

(2) INFORMATION FOR SEQ ID NO: 4046:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4046:

CGAGTCTGAG TCGCTGTCTG AATCTGAATC GCTGTCTGAG TCCGAATCGC TATCTGAATC 60

TGAGTCGCTG TCTGAGTCTG AATCGCTATC TGAATCTGAG TCGCTATCTG AGTCTGAGTC 120

TGAGTCTGAG TCGCTATCTG AGTCTGAGTC GCTGTCTGAA TCTGGAGTCG CTGTCTGAAT 240

CTGGAATCGC TGTCTGGAGT CTGAATCGCT ATCTGAGTCT GGAATCGCTA TCTGAGTCTG 300

AATCACTGGT CTGGAGTCCG AGTCACTGTC TGAATCTGAC TGCACTnACn GGATTCTGAG 360

TCGCTAACnG GAATC 375

(2) INFORMATION FOR SEQ ID NO: 4047:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4047:

ATGGGTAAAA AGGCATTAGA GTCAATCATT GATAACGCTG ATGAAACAAC TCAAGAGCGT 60

TTACGTTCAG GATATGAAGA TGCTGTAGAT TATAACCGTT ATGTCGGTAA TATTTATACT 120

GGATCATTAT ATTTAAGCCT AATATCATTA CTTGAAAATC GAGATTTACA AGCTGGTGAA 180

ACAATCGGTT TATTCAGTTA TGGCTCAGGT TCAGTTGGTG AATTTTATAG TGCGACATTA 240

GTTGAAGGCT ACAAAGATCA TTTAGATCAA GCTGCACATA AAGCATTATT AAATAACCGT 300

ACTGAnGTAT CTGTTGGATG GCATATGGAA ACATTCTTCC AAACGTTTTG GATGACGGTG 360

GAATTTGACG GnGGACCAAG ATGCnTGTTC CAGGAGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4048:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4048:

CAAACCATCT GACATAATAT ACACTTGGAT GTTAGATAAG GGTTTGCCAA TTGGAATCGT 60

CTCAGGTATC AATCACCACA ATGATGTGAC CAATACGATG TGATGACTGT TGACTCAGAT 120

GGTCCATAGG CATTGAAATA CGTGCCACAA TGCTTCTCAA TATATTTAAC AAAGGATGCC 180

GTACTAGTTG CCCCGCCTGT AATCAACTTT TCAATATAAA AGTCTTCCAT AACACTACAC 240

ATCTGTAACG GAATCGACGC AACCGTCACA CGATGCTTAT TAATGAGTTG TTGTAACTGT 300

TCTGGATTAA CACGnTCCTC TCTATCTGGA nTCACAAGCG TATGACCATT AACAAACAAC 360

(2) INFORMATION FOR SEQ ID NO: 4049:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4049:

TCTGCATGTT CTCGAGATCC ACCAAATGTT AAATGGGTAT GTGCATCTAC TAATGCTGGG 60

GACACTACCT TCCCACTAGC ATCAATCGTC TCAGTCGCAT CGTAGTCATC TGTATGTGTT 120

CCAGCATATA CAATTTTGGC CATCTTTAAT GACAACTGTA CCATTTTTCA CAACATTTGA 180

ATTCATCTAA TTCCTTACCC TTCAAAGGTT TATCTGTTGA TCTCGGTAAA ATTAATTGCT 240

GCTATATGAT TAnTATTAAA TCATTCATTA CTATCACCTG CTTATCAATC ATGGAATAGA 300

ATACCTTTTC nTTAGCGTTT GAATAGCGAG TCATAGCCAG CATCAACATG TCGGGCAACA 360

CCCATACCGG GGTCATCGTC CAATACACGT TCCAAnCTnC 400

(2) INFORMATION FOR SEQ ID NO: 4050:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4050:

ATCACCCATG TTCTGACTCC CAAGTTAAAT TAATTGGCAT TCGGAGTTTG TCTGAATTCG 60

GTAACCCGAG AGGGGCCCCT CGTCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG 120

GCTAGCCCTA AAGCTATTTC GGAGAGAACC AGCTATTTCC AGGTTCGATT GGAATTTCTC 180

CGCTACCCTC AGTTCATCCG CTCACTTTTC AACGTAAGTC GGTTCGGTCC TCCATTCAGT 240

GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACAAATA 300

CTAAACGCCT ATTCAGCTCG nTTCGTACGG CTCCACATTT ACTGCTAAnC TTGCATCAAT 360

CGTACTCGCG GTCAATCTAC AAAAGnACGC ATCACCAnTA 400

(2) INFORMATION FOR SEQ ID NO: 4051:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4051:

AGTGAAAATG ACTTTATCGG GCTGTTCAGC GATATGGATT TGAGTTCAAC GCGACTAGGT 60

AACAATGTCA AAGAACGTAC TGCTTTAATC TCTAAAGTCA TGGTTAATCT TGACGACTTA 120

CCATTCGTTC ACAGTGACAT GGAAATTGAT ATGTTAGGTG ATGCATATGA ATTCCTAATC 180

GGGCGCTTTG CGGCGACAGC GGGTAAAAAA GCAGGCGAGT TCTATACACC ACAACAAGTA 240

TCTAAGATAC TGGCGAAGTT GTCACAGACG GTAAAGATnA ATTACGTCAC GTGTAACGAC 300

CCAACATGTG GGnTCCGGTT CATTGTGGTA ACGTGTTGGT AAAGAACGCA AGTGTATCGT 360

TAATTCGGAC nAAGAACGTA ACAATACTAC nTACGACTTA 400

(2) INFORMATION FOR SEQ ID NO: 4052:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4052:

TCCTACAACC CCAACAAGCA AGCTTGTGGT GTTGGGCTCT TCCCGTTTCG CTCGCCGCTA 60

CTAAGGGAAT CGAATTTTCT TTCTCTTCCT CCGGGTACTA AGATGTTTCA GTTCTCCGGG 120

TGTGCCTTCT GATATGCTAT GTATTCACAT ATCGATAACA TGACATAACT CATGCTGGGT 180

TTCCCCATTC GGAAATCTCT GGATCAAAGC TTACTTACAG CTCCCCAAAG CATATCGTCG 240

TTAGTAACGT CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGGC CCTTAATAAC 300

TTAATCnATG TTTTCCACCA TTTTTTATAA GTnCAAAGGC TTCACATACG GCTTCGGTTT 360

TTCATTAATT TTAAATGGCn CAATTTAACA 390

(2) INFORMATION FOR SEQ ID NO: 4053:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4053:

AACATACCGA TGTATATAAT CTATACACAA AGGATAATTA CTTATGCAAA GGCGGAGGAA 60

GTCGATTGCG AATGATTTAA GAGGGAACAT GGATGCGAGT GAATTCCGTA ATTACATTTT 180

AGGCTTGATT TTCTATCGCT TCTTATCTGA AAAAGCCGAA CAAGAATATG CAGATGCCTT 240

GTCAGGTGAA GACATCACGT ATCAAGAAGC ATGGGCAGAT GAAGAATATC GTGAAGACTT 300

AAAAGCAGAA TTAATTGATC AAAGTCGGTT ACTTCATTGA GCCACAAGAT TTATTCAGTG 360

CGATGATCGT GAAATTGAnA CGCAnGATTT CCGATATAGA 400

(2) INFORMATION FOR SEQ ID NO: 4054:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4054:

GTAAGACCAT CGTACTTGAG TCTTCAAGTG TTCTTGATAA AACGGAACGA GAGACTTGGT 60

ATTTTTCGAA CAAATCTTTC ATTAACACAC CGACCATAAT AATTACAATC GAAGCAACAC 120

CTGCAGCGAA TACAAGCGCA ATACAACAAA TAACAGTAAT ACATATTAAA CTTCCTACAG 180

AATGGATGCC TTTAGAAATA GTAGTTAATA AGACTTCTAA ACATCCTGCT TTTTCTACAA 240

TACCTGCAAA TGCATATCCG CAAAATATCG TTACTAATAT TTGGGnCATA CTCATCATAC 300

CACCCTGTTC TAACAAGCTT TCACACTGGA TGAATATGAG nTGATGTATC ATTGATCGTT 360

AAACCCTAAT GTGCTTTGAA CCATCGTCAT TTGAATGTGA 400

(2) INFORMATION FOR SEQ ID NO: 4055:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4055:

CGTCTACAAG TTCAAAATTC AAGTCTTCCA TAATTGGTTT AACAATCACT TCTACTTGTT 60

CTGTAATTTT ACTCATACAG GCCTCCCTTT TTGGCAAATA GAAAAGAGCG GGAATCTCCC 120

ACTCTTCTGC CTGAGTTCAC TAATTTTTAA GCAACTTAAT TATAGCATAA GTTTATGCTT 180

GAAACAAATG ACTTCACTAT TAATCAGAGA TTCTTGTAAA AGTTTGTTCC TTTATTTCAC 240

CATTACATTT GAATAGACTC GTAAGACATT GAAAAGAAAT ACGGGCATAA TTTTGTGTCC 300

TCATTTTACA TATCAAATAT CGGAAGTTGA GCTTTATCTG 400

(2) INFORMATION FOR SEQ ID NO: 4056:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4056:

ATTTTGGTTT ACTTCATGTT GAGTTTTAGA CATTTTAACC ATCTCCAATA TAAAAATAAA 60

TTAAATTAAA TTCTCAGGGA CTTGCATGAC GCCACCTGTA TTTGCGCTAG TTACTAGGGC 120

AGTATAACGA GCTAGATAAC CTGTTTTTAC TTTCGCTTTA AATGGTGTTA AAGATTCTCG 180

GCGACGCGCT AGAACATCTT CAGGCTGGTT TACGTTTAAT GTACGATTTG TTAAATCAAT 240

AGTAATCTCA TCACCATCTT CAATTAAgGc AATTGGTCCA CCAGATGCAG CTTCAGGGGA 300

AATATGaCCA ACTGcAATAC CTCTTGTGGc ACCGGtAAAA ACGCCCATCA GTkAATTAAT 360

GCaACATCTT TACCTAAGCC GCGaCCAACA ATAGAGGAAG TAGGTGCTAA CATTTTCAGG 420

nCATACCTGG GTCCACCTTT TAGGTGCCTT TCAnTATCTn ATGGACAACG ACGTGGGCCT 480

G 481

(2) INFORMATION FOR SEQ ID NO: 4057:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4057:

TTTTTGCCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT GGCTACCATC GTCGCTAAAG 60

ACCTTTCTTG ACTTGTGACA ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC 120

ATTTAGCTCT ACTAAACTCG TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA 180

CTTCGCCAAG CCATTTTTCT TTGTGTTTAC TTTTTATTTT GGACGTTTTA GACATAAAAA 240

AAAGAGACCT TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTTGCCTG GCAACGTTCT 300

ACTCTAGCGG AAGTAAATTG GGCTACCAnC GACGCTAAGA ACCTTTCTTG GACTGTGACA 360

ATCGGCTGCn TCTGTnCCT 379

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4058:

CTGCATCACT GCCATAAAAA CTACCGTCAG CAGCGATAGn CGGCCAATCA TACCAGGAAC 60

AAGACCGGGC TTGTCAGCGA TACTAACAGC GATATATCCA GCTAGTATTG GAACCATAAA 120

TTTAAAGGCT AAACTACCAA TGTTTTCAAT GGATTTCCAA AATGAATCAT CTGGGATGAC 180

TAATCCTTTT GATGTCGTTT CACCGCCTAG AGTCAGCGCG ATGGCGATAA GGAGTCCACC 240

AACTACGATA AAAGGAACCA TAAACGATAC ACCGTTCATT AAATGTTGAT ACACCATTTG 300

AATACCATTT TAGACTnACC GCGATCTTTC GAATGATAAT TTGTTTCAGA TGGTTAAATA 360

GGCGCATTTG ATTTAATGAT ACGTGGATTT GGACCCTCGG 400

(2) INFORMATION FOR SEQ ID NO: 4059:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4059:

TTAAAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAACTA AGTnGAnCTA CCATCGACGC 60

TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120

CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT 180

TCGCAAAACA TTTATTTTGG ATTAAGTCTT CGATCGATTA GTATTCGTCA GCTCCACATG 240

TCACCATGCT TCCACCTCGG AACCTATTAA CCTCATCATC TTTGGAGGGA TCTTATAAAC 300

CGAAATTGGG GAAATCTCAT CTTGAGGGGG GCTTnCATGC TTAGATGCTT TCCAGCACTT 360

ATCCCGT 367

(2) INFORMATION FOR SEQ ID NO: 4060:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4060:

TTCCGnACTC ACATAGCGAC TCAGGATTCA GACAGCGCAT TCAGATTCAG ACACCGCATT 60

CAGATTCAGC ATAGCGATTC AGCATTCCGC ACAGTGACTC AGnATTCCGA CAGTGACTCG 120

GATTCAGATA GCGATTCAGA TTCCGACAGT GACTCAGATT CCGACAGTGA CTCAGACTCA 180

GACAGTGATT CGGATTCAGC GAGTGATTCG GATTCAGATA GTGATTCCGA CTCCGACAGT 240

GACTCGGATT CAGATAGCGA CTCAGACTCG GATAGCGACT CGGATTCAGA TAGCGATTCG 300

GACTCAGATA GCGATTCAGA ATCAGACAGC GATTCAGATT CAGACAGCGA CTCAGACAGT 360

GACTCAGATT CAGA 374

(2) INFORMATION FOR SEQ ID NO: 4061:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4061:

AAAATCATAA TATTTGGCAA TTTTTTCAAC TTGACTCTGG TCCTTCTGCA TAACTGCCGT 60

AAATAATTCA CCTTCATCAC ACGCTGTACC TACCAATAAT CCCTCACGAT ATTCATCTAA 120

CAATGAACGT GGAATTCGAG GTGTACGGTA GAAATACTTC ACCAATGATG CACTTACAAT 180

TTTAAATAGA TTTTTAAGAC CTTGTTGGTT TTGTACAATT AATGTGACAT GACTAGGTCT 240

TGCACGTTTA TATGCATCTT CATTACTGAG TTTTTkGTtG ATTTCGTTAT GATTTAATAC 300

GCCTAAwTCy TTCATTTGTT GAACCATTTT TATGAAAATG TAAGCTGTTG CTTCTGTATC 360

ATAAATGGCA CGGTGATGTT GCGTTAATTC TACGCCATAT TTTTTAGCCA AGAAATTCAA 420

ACCATGTTTA CC 432

(2) INFORMATION FOR SEQ ID NO: 4062:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4062:

TATCTTCGTT CTCAATAGAA TGATTTAAAC CTTCGATTTC TTTATCTAAA TGACTACCAA 60

TTTTTTCTTC AACTAAGTCA CGATATAATG TTTTTGAATT TTCGTTCAAT TTCGATTCGT 180

GATTTTGAAT ACTTTTCTTC CACACAAATG TATACCTATT GGCATTAGCT TCTACTTTTG 240

TACCATCAAT AAGATTTTGC TTTAAACATT GACTATGAAA CTGGGATAAA TAAAGAnTCA 300

ATTAACGCAT CAGTATTAGG GAnTCACTCT AATACGATTA ATAGTTTTTA TAAGAAGGTG 360

nTTGGATTTG GAGCTAACCA CATCCA 386

(2) INFORMATION FOR SEQ ID NO: 4063:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4063:

TAGGAGAGCG TTCTAAGGGC GTAGCATGAT CGTAAGGACA TGTGGAGCGC TTAGGAGAAT 60

GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT AAGGTTTCCA 120

GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCCTAAGC TGAGGCCGAC ACGTAGGGCG 180

ATGGATAACA GGTTGATATT CCTGTACCAC CTATGAATCG TTTTAATCGA TGGGGGGACG 240

CATAGGTATA GGCGAGGTGA CGATTGGGAT TGCACGTCTT AAGCAGTAAG GCTGAGTATT 300

AGGCAAATCC GGTACTCGTT nAAGGCTTGA GCTGTGGATG GGGAGAAGAC ATnGAGTCTT 360

CGAGTTCGTT GGnTTTCACA ATGGCC 386

(2) INFORMATION FOR SEQ ID NO: 4064:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4064:

TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTC 60

TACTCTAGCG GAACGTAAGT TGGAGCTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT 120

CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT 180

ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA 240

AGTCTTCGAT CGAnTAGTAT TCGTCAGCTC CACATGTCAC CATGCTTCCA CCTCGAACCT 300

AGGGGGGGCT TCATGCCTTT AGAATG 386

(2) INFORMATION FOR SEQ ID NO: 4065:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4065:

AATTCTTTCG CTACTTGAAT GACAACACTT TGTTTTACGC CTGAAATGGC TTCTTGCCAA 60

GCAGGTGTAT ATTTTGATTC TGCATCGTCG TATCCTTTTG ATTCTAATTT ATGATCAAAA 120

CGACGCACGC CATATTGACT TGCCATTAAG TCAAAAATTG TAGCAATACG GACTTTGTCA 180

CCATTTGCTA AAGTGACTTG TCGAGTTGGA ATTGGACGAT TGAATATCCC ATCTCCATCA 240

CTATCAAAGT ATGGGAATTG AATTGTTTCT AATTCGTATC CACCTTCTGT CATTGATAAT 300

GTAGGGTTAA TTTTAGAACC ATCTTCTGTT TCTAGTTTTA AGTTCCACTT CTTACCTTCT 360

TCCCAACGTG GACCCATGGT GCCATTAnGn ACTACTAAAC 400

(2) INFORMATION FOR SEQ ID NO: 4066:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4066:

ATTTTGAAAT TGAGAAAACA ACTTATTGAA AAACATAATC TTTACGGTAA CATGGGTTCA 60

GGAACAATCG TTATTAAAAT GAAAAACGGT GGGAAATATA CGTTTGAATT ACACAAAAAA 120

CTGCAGAGCA TCGTATGGCA GACGTCATAG ATGGCACTAA TATTGATAAC ATTGAAGTGA 180

ATATAAAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA TCGGAAAAAC AAGAAGTTAA 240

GTGACAACGG TTTACATGTT GCTTAGCTTC TTTTATTATG CGTAATGATG TAAAAAGACG 300

nATATTCATT TGTTTGTAAA AGTGGCATTC TATGTCTTAA AGTGACGnAA CTTCCAATGT 360

GCCCAGTGTT TGATTCACAT CAAATCCATT TTTATTTAAC 400

(2) INFORMATION FOR SEQ ID NO: 4067:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4067:

CCTCATTCCA GGAAGGAATG TATTCTAAGA GTTGAAATAC TCCCGCATTA TTATTAAATT 60

ATGGAGCGGA AGATAGGATT TGCACCTATA CCTCGTTCCG GGAAGGAACG TGTTCTAAAA 120

GTTGAACTAC TCCCGCATAA ACCTGGAGGC GGCAACCGGA TTTGAACCGG TGATAAAGGT 180

TTTGCAGACC TCTGCCTTAC CACTTGGCTA TGCCGCCAAT AACTGGGCTA GCTGGATTCG 240

AACCAACGAG TGACGGAGTC AAAGTCCGTT GCCTTACCGC TTGGCTATAG CCCATTAATA 300

ATAAGGGCGG CTGAAGGGGA TCGAACCCTC GAATGTCGGA ACCACAATCC GATGTGTTAA 360

CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC 400

(2) INFORMATION FOR SEQ ID NO: 4068:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4068:

TATCTAATAG TTTTACTTTA AGTCCAGCAT TCACAAAAAG TGCTGCCAGT TGAGCGCCCA 60

TTGTGCCTGC GCCAAGAACG GTTACTTTAT TAATTGTCAT AGTGATTCCT CCAATTTAGT 120

TGAGGATAAG ATAACCATTA AGATAATTGG AATAACGTTG CTATTTTATA AAATTAATTA 180

AGTATCTTTG ACAGTCATCT TAGCCTCTTA TTTAAGGAAA AAGCTTTATG CTTAAAATAA 240

GTCTTTTTTA GTGAAATTAA TGCATCTCAT ATAATTATTT GCTATTTATA CGAAAGCAGA 300

ATCTCCAGTC AAAGCGCGTC CAnTACTAAG GCATTAATTT CATGTGTACC TCGTACGTGT 360

AAATCGnTTC TGCATCAGnG AGGAAACGTG CAATATCATA 400

(2) INFORMATION FOR SEQ ID NO: 4069:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4069:

AAAAAGAAGA ATTGAAACGC CATATAAAGT AACGTTAAAT AATAACGAAA AAAGGGCACT 120

ATTCAAACAA TTAGCGTATG TTGAAGGGTT TGAAAAATAT CTTCATAAAA ACTTCGTTGG 180

TGCAAAGCGT TTTTCAATTC nCGGGGTAGA CGCACTTGTA CCGATGTTAC AACGTACTAT 240

TACGATTGCT GCGAAAGAAG GTATTAAAAA TATACAAATA GGCATGGCTC ACCGTGGGAC 300

GTTTAAACGT TTTTAACGCA TGTnCTTAGA AAAAACCGTA CGAAATGATG ATTTCn 356

(2) INFORMATION FOR SEQ ID NO: 4070:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4070:

AAACGTTTAG GGAAAATTAT CACACAGATA CAACAATACA CAGATATTGA TTACCCGATA 60

GCGATTGTCT TTCAAGCATC GTGTTTTAAC GAGTTTGTTG TTAAGGGGCG TTTAAGTAAT 120

ATTATTTCAA AATTGCAACA CTATTCAATT GAGGCGAAAC CAGGTATATG TATTATAGGG 180

GAAGTTGTTG ATTATACTGA AAACACTCCT AAATCATATG ATCCTATGAA GCAATTTTAT 240

GTAGTAAGTG GTTCTAAACA TGACGCCCTT ATGCTCTGTG AACATTATAT GACGAAGGTT 300

ATGGCTGTTG CTAAACCCCA ATGATACATC GAATGGGCAC CATTATCCAn TCGTCGCAAT 360

AATGGATTAC CCAAGGATGC CATTTAnTTA AGCCnGCCAn 400

(2) INFORMATION FOR SEQ ID NO: 4071:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4071:

CCTCTGGAAA CCTTAGTCAA TCGGTGGACG GGATTCTCAC CCGTCTTTCG CTACTCACAC 60

CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA CGCCCTTAGA 120

ACGCTCTCCT ACCATTGTCC AAAGGnATnC CCACAGCTTC GGTAATATGT TTAGCCCCGG 180

TACATTTTCG GCGCATGTGC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGGATGG 240

CTGCTTCTAA GCCAACATCC TAGTTGTCTG GGnAACGCCA CATCCTTTTC CACTTAACAT 300

T 361

(2) INFORMATION FOR SEQ ID NO: 4072:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4072:

ATGGTGACAA AAACATCGCA TTATTACTAG GTGTCGGCAC AGGCGTTTGT GGTGCTGCTG 60

CTATTGCCGC AGTCGCTCCA ATATTCAAAT CACGTGAAAA GGATACAGCT ATTAGTATCG 120

GTATCATCGC ATTGATTGGT ACGATATTTT CACTTATATA TACAGCTATC TACGCTATCT 180

TTTCAATGAC GACAAATGTT TATGGCGCTT GGTCTGGTGT TAGTCTTCAT GAAATTGnCA 240

CACGTTGTCT TAGCTGGTGG CTTTGGTGGT AGTGATGCAC TTAAAATTGC ACTTCTTGGT 300

AAACTTGGTA GGAGTATTCT TACTGGATTC CCATTAACCA TCGTACTTAA TTTTAAATAT 360

GCGGTTnCCG TTnCATCAGG AnTCATCTAG GCAAGGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 4073:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4073:

GCGACGATCA TTTTAGAATC CGCTTGGGCG ATTAATTCTT TAGAAGTGGA TGAGGCAAAA 60

TGTTCATTAT CAGGAACTAA AGCAGGTGCT GATATGAAAG ATGGTCTACG TATTCATGGT 120

GAAGACATGG GTACACTTTA TACCAAACAC GTTGAATTGG AAAACAAAGG CGTCGACTTT 180

TATGAAGGTA ATGAAGTGGA TGAAGCTGAA GAAGAAGCAA AAGCTTGGAT TGATGCAGTT 240

GTAAATGATA CTGAACCAGT TGTGAACCGG AACAAGCAAT GGTAGTTACC AnAATTCTTG 300

AAGCGATTTA TCCGTCTGCC AAATCCAGGC CAAAGCCATT TACTTTGGAA TAACATCnTA 360

CCGGTAAGGG GGCnCATCCT GGACCAAATT TAAAAGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 4074:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4074:

TCTTCCTAAT ACCTTTCCAC GATCTTCAGC TGGCGCCTCT GCACTCGCAA ACGCACTTGA 60

TGCATCAACA ACACCACCAA ATAGTCCCTG CAATAACCTC ACAAGTACAA ACTGTAATGG 120

TGTCGTACAC AATGCCATTA AAAATAAGCA TACCGCCAAA CCAAGTAACG CTCTTAACAC 180

CATCCATTTT CGGCTGATCT TATCACCTAG CTTCCCCCAT ATCGGCGGAG TTATGCATCG 240

TCGTTACAGC TGGAGCAGCA ATCGCTATAC CACTCCACAn CTGTATTTCT ACGGACTGAT 300

AGGATTTTGT AGTGATGnCC ATGATGAAAT GGGCAATAAT GGGCACAAGT ACTGTTCAGT 360

CCAGCCAATC GTTATGAAAC TGGACTGGGG CCATnAAATG 400

(2) INFORMATION FOR SEQ ID NO: 4075:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4075:

GGTTCAGAAC GTCGTATGnA GTTCGnTCCC TATCCGTCGT GGGCGTAGGA AATTTGAGAG 60

GAGCTGTCCT TAGTACGAGA GGACCGGGAT GGACATACCT CTGGTGTACC AGTTGTCGTG 120

CCAACGCATA GCTGGGTAGC TATGTGTGGA CGGGATAAGT GCTGAAACTC TAAGCATGAA 180

GCCCCCCTCA AGATGAGATT TCCCAACTTC GGTTATAAGA TCCCTCAAAG ATGATGAGGT 240

TAATAGGTTT CGAGGTGGAA GCATGGTGAC ATnTGGAGCT GACGAATACT AATCGATCGA 300

AGACTTAATC AAAATAAATG TTTTGCGACA AATCCACTTT TACTTACTAT CTAGTTTGAA 360

TGATAAATTA CATCCATATG 380

(2) INFORMATION FOR SEQ ID NO: 4076:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4076:

TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC 120

CTACTGCGTC CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA 180

TCCATCGCCT ACGCCTGTCG GCCTCAGCTT AGGACCCGAC TAACCCAGAG CGGACGAGCC 240

TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC AnCCGTCTTT CGCTACTCAC 300

AnCGGCATTC TCACTTCTAA GCGGTCCACA TGTCTTACGA TCATGCTTnA AGGCCTTAGG 360

AAGGTTCCTA CCATGGTCAA 380

(2) INFORMATION FOR SEQ ID NO: 4077:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4077:

GCAGGTCTGA CTCTAGAGGA TnCCCACGCG CGCAAGATTT AAATCGAAGA AACCAGCAAC 60

AGATTCCTCA AAATAGCGCG GCGAACAACG AAACATCAAA TAGTGCACCT GCAGCTGGTA 120

ATGGTGTAGC ATCAACGCCA CCAAGTGCAC CAAGTGGCGA TACTGCACCA AATAATAATG 180

TTACGCAAAA TACCGCACCA AATAGTAATA ATGCGCCTGT ATCGACTACA CCACAAAGTA 240

CAAGGCGGGA AnAAAGATGG TCAAAGTTTT GTAGATATAA CAACAACACA AGTCAGCACA 300

GCTAACGAGA ACACACAAAA CATTACAGAT AAAGATGTTA AATCAATGGA AGCGGCATTA 360

ACGGGCTCTT 370

(2) INFORMATION FOR SEQ ID NO: 4078:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4078:

AAACATTTTA TCAAATGGCA GAAGGACATG TGCCAAGACC ACCAGCGATG GTTGAAACAT 60

TGACTTATAT TAAAGAGTTT ATGAACCAAG TTGAGTCGCA TAGCTAGTAT GAAACGTGGT 120

GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGG AATTAGGGAT 180

CGGTACTTTA TATGAAGACG TGCTGCTTCC ATTAAATGAG TGATGCGATT TTGGCATGAA 240

TAAGAGGGGC CAACCATTGT TAGAnATAAC AACGGTTGGC TCTTTAAnTG T 351

(2) INFORMATION FOR SEQ ID NO: 4079:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4079:

TTGAAGTAAC TAAATTAATA TTATGTTGTT CAATTAAAAG CTTCATACAA ACCTAATCTA 60

TTTGCACTCC ACCGCTAACA CCGAACACTT GTCCGGTTGT ATAACTTGAT TCTTCTGACG 120

CTAATAGCAC ATAAGTTCCA CATAACTCAA CAGGTTGACC TGCACGACCT AAAGGTGTTT 180

TTTGACCAAA TGTTGGGATT TTACTTTGAG GTTGTCCACC AGAAATTTGT AATGGTGACC 240

AGAATGGACC AGGCGCTACA CAGTTCACTC TAATTCCTTT TGGTCCTAAT TCTTCTGAAA 300

AACTTTTAGT TAATGAAATA ATTGCTGCCT TTTGAAGGGG CATAATCCAT GAAGAATAnG 360

GCCAGGGAnT AAAACCCTGG ACnAAAGAAG CCGTGGAAAT 400

(2) INFORMATION FOR SEQ ID NO: 4080:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4080:

TCGTTGGACA CAATCTGAAA AATAAATAGA TATAAATTCG CGAGATATAT TCGTATTTAT 60

AGTAAAATTA AATAAAGAGA TTATATAACA CGAGGAGTAG TAAGTATGAA ATTTGAGAAA 120

TATATAGATC ACACTTTATT GAAGCCTGAG TCAACACGTA CGCAAATCGA TCAAATCATC 180

GATGAAGCGA AACATTACAA TTTTAAATCT GTATGTGTGA ATCCAACACA TGTTAAATAT 240

GCAGCAGAGC GACTAGCTGA TTCAGAGGTG CTCGTTTGTA CGGTAATAGG ATTCCCATTA 300

GGTGCGTCGA CAACTGGCAA CGAAAGCATT TGAAACAGAA GATGCAATTC AAAATGGTGC 360

AGATGAATTG GACATGGTCA TCCACATCGG CGCATTAAAA 400

(2) INFORMATION FOR SEQ ID NO: 4081:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4081:

CGACTAGTGA GCTATTACGC ACTCTTTAAA TGATGGCTGC TTCTAAGCCA ACATCCTAGT 60

TGTCTGGGCA ACGCACATCC TTTTCCACTT AACATATATT TTGGGACCTT AGCTGGTGGT 120

CTGGGCTGTT TCCCTnCnCG AACACGGACC TTATCACCCA TGTTCTGACT CCCAAGTTAA 180

ATTAATTGGC ATTCGGAGTT TGTCTGAATT CGGTAACCCG AGAGGGACCC CTCGTACCAA 240

ACAGTGCTCT ACCTCCAATA ATCATCACTT GGAGGCTAGC CCTAAAGCTA TTTACGGAGA 300

GAACCAGCTA TCTCCAGGTT CGATTGGAAT TTCTCCGCnA CCCTCAGTTC ATCCGCTCA 359

(2) INFORMATION FOR SEQ ID NO: 4082:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4082:

TTTGACATTT AGTGTAAGCG TnTTACAAAT AAAGCGTGTT GTTTTTGAAT TAAATGCATT 60

TCACATTAGT ATTCATATTA TTTTTAGGAG GAATTTATAT GACATTTGAA AAAGAAACGG 120

TCTTAAAAAC ATTATTTCCT GAAGATGTAC TTAGTATTGC TAAAGGTTTA ACAGACGGTG 180

AAGTCGAATT TTTACAACAA GTAGATTCAT TGGCTAGAAA GTAAGTACCG TGGAAAATAT 240

TAATCAACAT TGGATAGACG CTACTGTACC CGAGGACTAT TTTAAAGATC TGGGGAGAAT 300

TAAATTATTT TAACAATCCA TTACTTTACA AGGGATCGTC CAAACGCCAA AnGGCCTAGT 360

CCAACTATTT nCAGTTTTT 379

(2) INFORMATION FOR SEQ ID NO: 4083:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4083:

TTGAAACAGC CAGAGGTGTT TTATACCCAG GTGTTTCAGA TATGTATGAT GCGAAACAAT 60

TTGGAACATA TGGTCCTAAC AAAGATGTTG TAGGCATATC TACTCGTCTT ATTAGAGTGA 180

CATATGATAA TAGACAAACA GAAGATTTAA CTATTTTATC TAAAGTTAAA CCTGACCCAC 240

CTAGAATTGA CGCAAACTCT GTGACATATA AAGCAGGTCT TACAAACCAA GAAATTAAAG 300

TTAATAACGT ATTAATTAAC TCGTCCGTGA AATTATTTAA GCCGATAATA CACCATTAAA 360

TGTnCnCAAT ATTACCCnGG GTAGCGGGTT TTAGTTCCGG 400

(2) INFORMATION FOR SEQ ID NO: 4084:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4084:

AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCnAGGCAT CCACCGTGCG 60

CCCTTAATAA CTTAATCTAT GTTTCCATCC TACAGGAAAC GCGTTAGTAA TCTTGTGAGT 120

GTTCTTTCGA ACATAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC 180

ACTCGGTTTT GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAT 240

TTCTTTTTAG TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 300

TAAATAAACA TTCAAAACTG AATACAATAT GTCACATTAT TCCGCCATCT nCTGAAGAAG 360

ATGTTnCCGA ATATnATCCT TAGAAAGGAG GTGGATCCCA 400

(2) INFORMATION FOR SEQ ID NO: 4085:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4085:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60

CCTCCTGCGT GCAAAGCAGG CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA 120

TTAATGGTGG GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT 180

GAACCAGCTG GAGCTATAGG CCCATTAATT TGGAATGAAC AAACATTCAA AACTGGAATA 240

CAATATGTCA CGTTATTCCG CATCTTCTGG AAGAAGATGT TTCCGAATAn ATCCTTAnGA 300

AAGCATTTGT TCCCACCTTC GACGGCTGAG CTCCTAAAAG 400

(2) INFORMATION FOR SEQ ID NO: 4086:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4086:

GTCATTGGAA ACTGGAGnAC TTGAGTGCAG AAGAGGAAAG TGGAATTCCA TGTGTAGCGG 60

TGAAATGCGC AGAGATATGG AGGAACACCA GTGGCGAAGC GACTTTCTGG TCTGTAACTG 120

ACGCTGATGT GCGAAACGTG GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT 180

AAACGATGAG TGCTAAGTGT TAGGGGGTTT CCGCCCCTTA GTGCTGCAGC TAACGCATTA 240

AGCACTCCGC CTGGGGAGTA CGACCGCAAG TTGnAAACTC CAAAGGAATT GACGGGCGCA 300

CAAGCGTGGG AGCATGTGGT TTAATTCGAA CCAACGnATA GAACCTTACC AAATCTTGGA 360

C 361

(2) INFORMATION FOR SEQ ID NO: 4087:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4087:

GACCTTGCAG GACTCGAACC TGCGACCGAA CGGTTATGAG CCGTTAGCTC TAACCAACTG 60

AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA 120

CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT 180

AGTTTGTAAA TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TGCGTGCAAA 240

GCAGnCGCTC TCCCAGCTGA GCTAAAGCCC CCATAAATAA TTACAGTATA TCGGGAAGAC 300

AGGATTCGAA CCTGCGACCC CTTTCCCAAA CCAAGTGCTT TTACCAAGTT GGTACTTCCn 360

GTATAATTTA ACGGGCCCGA TAGGAGTTCG GAACCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4088:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4088:

AGCTATTATT TTTGACAGAT TCCATATCGT TCAACATTTA AATAGAGAAC TTAATAAGTA 60

TCGTGTACAA GTTATGAATG AATACCGTAA TAAAAAAGGA CCTGATTATA CAATTTTTAA 120

GAATAACTGG AAAGTCCTAT TGATGGATAC TAGTAAAACC ATATTTAGTA AATACAGATG 180

GAATAAATCT TTTAAGGCTT ATAAACGCTC ATCTGACATT GTAGGAATTC ATGCTTTCAA 240

AAGACGATAT ACTACGACAC TCCTACGAAC TTGTCCCAAG GGATTACGGA AAAGGCCCTA 300

AGGGTTATGT TAATTGGCCC TAAATTTATT AAATGCGTTT GAAATTCAGT TAGTTAAAAA 360

GTCTGTGAGT GAnGGGTGTA TGGGAAAGTG GTTAAAATAT 400

(2) INFORMATION FOR SEQ ID NO: 4089:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4089:

ATCGTTTTAG ATAAGACGGG TACATTACAA ATGGTCGTCC AGTCGTGACA GATTATCATG 60

GTGACAATCA AACGCTACAA CTACTTGCTA CTGCTGAAAA AGATTCTGAA CACCCATTGG 120

CAGAAGCCAT TGTCAATTAT GCAAAAGAAA AGCAATTAAT ATTAACTGAG ACAACAACAT 180

TTAAAGCAGT ACCTGGGCCA TGGTATTGAA GCAACGATTG GATCATCACC ATATATTGGT 240

TGGTAACCGT GAAATTAATG GCTGACAATG GATATTAGCT TGCCTAAGCA TATTTnnGGA 300

TGGATTTAAC ACATTATGAA CGAGATGGTA AAACTGCTAG CTCATTGCTG TTGAATTATT 360

nCATAACGGT ATCA 374

(2) INFORMATION FOR SEQ ID NO: 4090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4090:

TTAATAACGT ATTAAATAAC TCGTCAGTAA AATTATTTAA AGCAGATAAT ACACCATTAA 120

ATGTCACAAA TATTACTCAT GGTAGCTGTT TTTGTTCGGT TGTGACAGTA AGTGACGCGT 180

TACCAAATGG CGGAGTTAAA GCAAAATCTT CAATTTCAAT GAACAATGTG ACGTATACGA 240

CGCAAGACGA ACATGGTCAA GTTGTTACAG TAACAAGAAA TGAATCTGTT GATTCAAATG 300

ACAGTGCACC AGTAACAGTG ACACCACAnT TACAAGCAAC TACTGAAGGC GCTGTATTTA 360

TTAAGTT 367

(2) INFORMATION FOR SEQ ID NO: 4091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4091:

TAATATTATA TTGCTAGTAG TTGACTGAAT GAAAATGCGC TTGCAACAAG CTTTTTTCAA 60

CTCTAGTCAG GGGCCCCAAC ACAGAGAATT TCGAAAAGAA ATTCTACAGG CAATGCGAGT 120

TGGGGTGTGG GCCCCAACAC AGAGAATTTC GAAAAGAAAT TCTACAGGCA ATGCGAGTTG 180

GGGTGTGGGC CCCAACACAG AGAATTTCGA AAAGAAATTC TACAGGGCAA TGCGAGTTGG 240

GGTGTGGGCC CCAACATGAG AGAAATTGGA TTCCCAATTT CTGACAGACA ATGCAAGTTG 300

GCGGGGGCCC CAACACAGAA GCTGGACGAA AATCCTTGAA CGAATGAATG TGGCAATTGG 360

CGGGGGCCCA ACACAGAAGn TGACGAAAAT nCTnGAACCA 400

(2) INFORMATION FOR SEQ ID NO: 4092:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4092:

GCATTTCTCA TAACACAAGG AATTTCAACA AGTCCGGCTA CTGGATCACA AACTAAACCT 60

AATAAATTAC TTATCGCTAA TGCCATAGCG TGCCCGGATG CTTCTGGTGA TCCTCCGAAT 120

ATAGCTACTG CTGCAGCTGC GGCCATTGCA GATGCTGAAC CAACTTCAGC TTGGCAGCCA 180

CCTGTTGCAC CAGCTACACT TGCATTGTTT GCTACGACAC GCCCAAACAA TGCTGAAGTG 240

CCGGGAATGG TAnCCGAGGG AAnCAGCTGT GGGCGTTGCA CAAATAATAC CCCATCGCAG 360

CATTTGACCT TCATTTGGTT GCAATGGGAA CCTTTGACTG 400

(2) INFORMATION FOR SEQ ID NO: 4093:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4093:

TGACTTACGT ACTGTTCAAC CAATCGATGT TGACACAATT GTAGCTTCAG TTGAAAAAAC 60

TGGTCGTGCA GTTGTAGTTC AAGAAGCACA ACGTCAAGCT GGTGTTGGTG CAGCAGTTGT 120

AGCTGAATTA AGTGAACGTG CAATCCTTTC ATTAGAAGCA CCTATTGGAA GAGTTGCAGC 180

AGCAGATACA ATTTATCCAT TCACTCAAGC TGAAAATGTT TGGTTACCAA ACAAAAATGA 240

CATCATCGAA AAAGCAAAAG AAACTTTAGA ATTTTAATAC ATTTTAAAAG TTAACGAATT 300

AGCGTATTTT AGTCTCATTG ATTAAnATGA AATGnGnTAA TTTACGGAAT CCTA 354

(2) INFORMATION FOR SEQ ID NO: 4094:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4094:

CGTTAACATG AAGTTACGTT CTTTTATAAA AAGATTTAAA CGCGTTATTA ATCTTGTGAG 60

TGTTCTTTCG AACACTAGCG ATTATTTCTT ATGAATTCAA GCTTATTTAA AACTCTTTAT 120

TCACTCGGTT TTGCTTGGTA AAATCTATAT nTTACTTACT TATCnAGTTT TCAATGTACA 180

AATAATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TGCGTGCAAA GCAGGCGCTC 240

TCCCAGCTGA GCTAAGCCCC CAAATAGGnA TTAAATTAAT GGTGGGCCTA AGTGGACTCG 300

AACCACCGAC CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT A 351

(2) INFORMATION FOR SEQ ID NO: 4095:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4095:

ATTGTTGCGA CTGGCACACC CGAAGATATT GCTCAGACAA AGTCATCATA TACAGGAAAG 60

TATTTAAAAG AAGTACTTGA ACGAGATAAA CAAAATACTG AAGATAAATA AGATTAAAAG 120

AAGTGAAGGA TGTTATAATT TATCCTTCGC TTCTTTTTAT TAATTTAGTA ATGAATAGTA 180

GAAAGAAAAG ATGCGTAAAA AGAATTATGT TAAGATAGGG TCAATCTAGA GTAGTTAAAC 240

ATAAATCGAA CTnGGAGTGG GACAGAAATG ATAAAGAATC ACTAATGATT TATTATGTAG 300

TGGTTCTTTG TCATTAGCCA CAGCTATTTG TGTACTTAAA AnTAGGTATG CCAGTGTGCA 360

CTCCTTGAGA GGAAATACTn ATTT 384

(2) INFORMATION FOR SEQ ID NO: 4096:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4096:

CTGCATCTTC ACAGGTACTA TGATTTCACC GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60

TTACGCCTTT CGTGCGGGTC GGAACTTACC CGACAAGGAA TTTCGCTACC TTAGGACCGT 120

TATAGTTACG GCCGCCGTTT ACTGGGGCTT CGATTCGTAG CTTCGCAGAA AGAGCCGACT 180

CCTCTTGAAC CTTCCAGCAC CGGGCAGGCG TCACCCTGAT GACATCACCT TACGGTTTAG 240

CAGAGACCTG TGTTTTTGAT AAACAGTCGC TTGGGCCTAT TCACTGCGGC TCTTCTGGGC 300

GTTAACCCTn AAAGAGCACC CCTTCTCCCG AAATTnACGG GGTCATTTTG GCCGAGTTCC 360

TTAACGAGnA TTCGCTCGGT GCAACTT 387

(2) INFORMATION FOR SEQ ID NO: 4097:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4097:

CCACTCACAT TCACACATCG ATTCACACAC CGCACTCAGC ACTCAGnATA CCGCATTCAG 60

TCAGATAGCG ACTCAGATTC GGATAGCGAC TCAGACTCAG ATAGCGATTC AGATTCAGAT 180

AGCGATTCGG ACTCAGACAG TGATTCAGAT TCAGACTCAG ATAGCGACTC AGATTCTGAC 240

AGCGATTCAG ACTCAGACAG CGACTCAGAC TCAGACAGTG ATTCAGATTC AGACAGCGAC 300

TCAGATTCAG ATnGCGACTC AGACTCAGAT AGCGACTCAG ATTCAGATAG CGATTCGGAC 360

TCAGACAACG ACTCAGATTC AGATAGCGAT TCAGATTCAG 400

(2) INFORMATION FOR SEQ ID NO: 4098:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4098:

TCGTACCTGA ACTACTTTGT ATTAAAATAG TTACAACGAT ACCTGCAATA ACACCTAATA 60

CTGGATTTGA TGTAAATTTG TTTAAAATAT CTCGTAGCCT GTCTCCTGCT GATGCTTGAA 120

GCCCGTCTCC CATGATTTTT AAGCCGTAAA GGAAAATACC TAAACCACCT AAAAAGGAGA 180

AAATGACTTC TGTAACCGAC ATTTCCATTA TTTCACCTCA AATAAGCTTT ATATTTAGAT 240

TATCGCTTAT AATTGTAAAT TTAATGTTAA GATTAGGTAA AATTATTTAA CAATATATGT 300

TATTTGTATA TGACTTGTAA AATATCGTCA CTTATTATGT AAATTTTCAG TGGTGGnAAT 360

GGCCAGTTTG CCAAGCACTG GTTTGACCAn ATGGnGGCAn 400

(2) INFORMATION FOR SEQ ID NO: 4099:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4099:

ATCCTTTTCC ACTTAACATA TATTTTGGGA CCTTACCTGG TGGTCTGGGC TGTTTCCGGA 60

CCGAACACGG nACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTCGG 120

AGTTTGTCTG AATTCGGTAA CCCGAGAGGG CCCCTCGTCC AAACAGGGCT CTACCTCCAA 180

TAATCATCAC TTGAGGCTAG CCCTAAAGCT ATTTCGGAGA GAACCAGCTA TCTCCAGGTT 240

CGATTGGAAT TTCTCCGCTA CCCTCAGTTC ATCCGCTCAC TTTCAACGTA ATCGGTTCGG 300

(2) INFORMATION FOR SEQ ID NO: 4100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4100:

TAGAACTTGT TGCCAAACAG CATGCTTAAT TTCAATATCT TCTTTGACTG CTTCGATATA 60

TAAATCAGCA TCATCATTTA CCAAGTCATC ATCAAAATTA CCATATGTTA AATGACTCGC 120

TAGATTTAAG TCGAATAGTA GCGGCCGTTT CTTATCTGTA ATTTTATCGT AAGATTTTTT 180

CGCAATGAGA TTTGGATCGT TTTTGTCCAC TACAATATCT AATAGTTTTA CTTTAAGTCC 240

AGCATTCACA AAAAGTGCTG CCAGTTGGAG CGCCCATTGT GCCTGCGCCA AGAACGGnTA 300

CTTTATTAAT TGGTCATAGT GAnTCCnCCC ATTTAGTTGA GGGATAAGAT AACCATT 357

(2) INFORMATION FOR SEQ ID NO: 4101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4101:

TAACTCAGGC TGGGGACATA AATCAATATT CTATGCTCTA CGAATTATAT TGGCAGTAGT 60

TGACTGGnCG AAAATGCGCT TGTAACAAGC TTTTTTCAAT TCTAGTCAGG GGCCCCAACA 120

CAGAGAATTT CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGAGGG CCCCAACACA 180

GAAGCTGACG AAAAGTCAGC TTACAATAAT GTGCAAGTTG GGGATGGGCC CCAACAAAGA 240

GAAATTGGAT TCCCAATTTC TACAGACAAT GCAAGTnGGG GTGGGACGAC GnGATAAATT 300

TTGCGAAAAT ATCATTTCTG TCCCACTCCC ATCAAAAGAA TGACAT 346

(2) INFORMATION FOR SEQ ID NO: 4102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AATGATGAAA ATCAATTAGA CAAAGCAGGT AAATTAAGTG ATGTCGCGTC ATTTAAGGAA 60

GCGATTCACA ATCGAGAATC ACAAAGTACA ACTGGTATCG GCGAAGGTAT TGCCATTCCA 120

CATGCCAAAG TGGCCGCAGT TAAGTCACCA GCTATTGCGT TTGGTAAATC TAAAGCAGGC 180

GTAGATTATC AAAGTTTGGG ATATGCAACC AGCACACTTA TTCTTTATGA TTGCAGCGCC 240

AGAAGGTGGC CCCAAACACA TTCTAGATGC TTTACTAAAG TTGnCTGGTA TTTTAATGGG 300

ATGAAAATGT ACGTGAGGAA ATTnTTACAT GGCTTCATCA nCTGAAGAAG TACTAGCGAT 360

CAT 363

(2) INFORMATION FOR SEQ ID NO: 4103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4103:

GAGTGCAGCG GATAACATTA AACCGACGAC AnCTTTTTTA TGTTCAGGTT TAGCTGTGTG 60

ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC GGCCTGACAT 120

AAAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGa TCACCAAGTT GAGCAAAGAA 180

GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC CAAGTGCCGT 240

CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA ATCTTAAGAT 300

GAAGCCATAA rCAAAAGTAC CsGTTGGcAC CTGTTtTCGT TACAAATCCA CCAACATGtk 360

AaTGCCGGTT TGTATGGTTG GCCCAAnTGA nAACATCATA 400

(2) INFORMATION FOR SEQ ID NO: 4104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4104:

AATTGAGAAT TTGTCGCTAT TTGTAAATTG TATCCTGGCT TAAGTTGGCC AAAGTGTCTT 60

ATTTTTTTAA AGTATTTAAA AGTAAAATTA CATGTTAATA CGTATATTAA TTGGCGAGAC 120

TCCTGAGGGA GCAGTGCCAG TCGAAGCAGG GGCCCCAACA CAGAAGCTGA CATATAGTCA 180

CAAAAATTCT ATTTATAGAA TTTTACAGTA ATGTGCCAGA TGGGCATAGC GACCCATTCA 300

ATACGAnTAT nTGAnTAAAT AGAGAACAGC AGTAAGATAT TTTCTAATTG AAAATTAT 358

(2) INFORMATION FOR SEQ ID NO: 4105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4105:

GACGCGTTAC CAAATGGCGG AATTAAAGCA AAATCTTCAA TTTCAATGAA CAATGTGACG 60

TATACGACGC AAGACGAACA TGGTCAAGTT GTTACAGTAA CAAGAAATGA ATCTGTTGAT 120

TCAAATGACA GTGCAACAGT AACAGTGACA CCACAATTAC AAGCAACTAC TGAAGGCGCT 180

GTATTTATTA AAGGTGGCGA CGGTTTTGAT TTCGGACACG TGGAAAGATT TATTCAAAAC 240

CCGCCACATG GGGCAACGGT TGCATGGCAT GATAGTCCAG ATACATGGAA GGAnTACAGT 300

CGGTAACACT TCATAAAACT GCGGTTTGTn ACCATTACCT AATnGTCAAG GGTACGGCGT 360

TAATGTTTGA AGGTTCCCGT TCCAAGGTTT TTTCCCGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4106:

GAAGTTAAGC TCCTTAGCGT CGATGGTAGT CGAACTTACG TnCCGCTAGA GTAGAACGTn 60

TGCCAGGCAG TTTTTTAATC AAATTTTGGT TAAAAAATAA AATGGACAAG ATAAAAAAAG 120

TTATTGACTT AAATGTTAAT AAAATGTATA ATTAATTCTT GTCGGTAAGA AAAATGAACA 180

TTGAAAACTG AATGACAATA TGTCAACGTT AATTCCAAAA AACGTAACTA TAAGTTACAA 240

ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTCATGGGA GAGTTTGGAT 300

CCTGGGCTCA GGATGGAACG CTGGGCGGCG TGCCCTAATA CATGGCAAGT CnGAGCGAAC 360

GGGACGAGAA GGCTTTGCTT CTCCTGGATG TTAACCGGCn 400

(2) INFORMATION FOR SEQ ID NO: 4107:

(A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4107:

GATTGTGCCA CGCTTTTAAC CGAAATACAA CATCATCATT GACAATTTGT TGATTTGAAA 60

AATCTTTCTC TTCAATAAAT ACATACGTTT GCATCGTATG TGCTTTCATG TAACTCAATA 120

TTGGTTTTAA ATGCATTTCA GGAATTAAAT AATGTTTACT AGAACCTGCT GTCGCTACAA 180

GTCCTATTAC CTTGTCACGA AACGCATTGA CTGGAAGTAG ATCAAACACA TTTnnCAAAG 240

CACCAGGGAT GGAAAGCTTG AAAAATTGGA AAACCAATAA AAATCACATC AGCCTGCATT 300

AACGACGTCG TTAATTTATA TACATCTCCT GTAGTATCTA GnT 343

(2) INFORMATION FOR SEQ ID NO: 4108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4108:

ATACAAAACA CCAGGTCGTG AAGATAAACA ATCACAAGCG GCTACTGCTT CAGCAACTGA 60

ATTACCATAT GCAGTATTAG AAGCTATGGG TGGCAAAGCA AACATTAAAC ATTTAGACGC 120

TTGTATCACA CGTCTACGGT TGAAGTTAAC GACAAATCTA AAGTTGATGT TCCTGGTTTG 180

AnAGATTTAG GCGCATCTGG TGTATTAGAA GTCGGCAATA ATATGCAAGC AATTTTTGGT 240

CCTAAATCTG ACCAAATCAA ACATGAAATG CAACAGATTA TGAnTGGTCA AGTAGTAGAA 300

AATCCTACTA CTATGGAAGA CGATnAAGAC GAAACTGTTG TGGGTTGGCA G 351

(2) INFORMATION FOR SEQ ID NO: 4109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4109:

CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60

CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGnAT CACACCTTCT 180

GCGGCACCAC GGAATAATAC ACCATGTGGG AGTACGACTG CnATGGTACC TTCATCGTCT 240

AAGGTAATGT ACCCTGTGGT TGAATAAAGG CAAAATCTGC TTTGGGATTT TGGCGCAACT 300

TTGCCCGTAA CCACTGAATC GTTCATCATT TTCAAATTTT TGAATCnGCT GGTCCATTCG 360

CACTGTA 367

(2) INFORMATION FOR SEQ ID NO: 4110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4110:

GTCGTCCGAT TGAAGGATGG AGTACTGTCG CATTTGCGAA AGACTGGCAA GGACCACCAC 60

GTTTGCAAAA CGGAACAAGT TGGTTCTATT TTGCAACAGA CCAATGGAAA TATGAAGAGT 120

CAAATGTAGA TCGTTTAAAA TCTCCATTAG CTAAAACAGA GGAGTTAAAG CATCAACATC 180

CAGCTGATTA TAATGTTTTA GCAGCTAGAC TTGGTTGGTT ACCATCATAT CCACAATTTA 240

ATAAAAATAG TTTGTTGTTT GCAGAAGAAG CTAAAGATGA AGGTATAGAT TCAAATGAAG 300

CGATTTTGCC ACGTGCAATT GATGAAGTGA ATCAAAACCA AACACCATTT GCCATAnGAA 360

AATCCTGATT TGGAAAAGGA TCCTnCCAAA ATCCAnnATT 400

(2) INFORMATION FOR SEQ ID NO: 4111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4111:

TCAGATGAAG CTAAAAGTAA AGGTATTACA TGTGCAAGTG CAGGTAATCA TGCTCAAGGT 60

GTTGCCTATA CAGCTAAAAA ACTTAATTTA AACGCTGTTA TCTTTATGCC AGTCACTACA 120

CCTTTACAAA AGGTAAATCA AGTAAAGTTC TTTGGAAATA GTAACGTTGA AGTTGTACTC 180

ACTGGTGATA CATTTGATCA CTGTTTAGCT GAAGCTTTAA CTTATACAAG TGAACATCAA 240

ATGAACTTTA TAGATCCATT CAATAATGTT CATACAATTT CTGGACAAGG TACGCTTGCT 300

AATTGGTGGT GGCGGTTTAA TTTCCAGTAT TAGTACTAAC 400

(2) INFORMATION FOR SEQ ID NO: 4112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4112:

GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTTATAA GTCAAACGCT CACATACGGC 60

TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120

ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180

GAGTGTTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT 240

TATTCACTCG GnTTTGCTTG GGAAAATCTA TATTTTACnT ACTTATCTAG TnTTCAATGT 300

ACAAATAATG GTGGGCCCAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGGCGTGC 360

GG 362

(2) INFORMATION FOR SEQ ID NO: 4113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4113:

CAGGTGGTTT TGCGAAAAGT GAAGTATGGC GTCAAATGAT GTCAGATATA TTTGACACAG 60

AGTTAGTGGT TCCTGAAAGT TATGAAAGTT CATGCTTAGG TGCCTGCGTG CTCGGACTTA 120

AAGCTGTAGG TGACATTGAA GATTTTTCAA TCGTTTCATC GATGGTCGGT GCCACAAACA 180

ATCATACGCC GATTGAAGAA AATGTCACTG TTTACCAAGA GATCGTATCC ATTTTTATCA 240

ATTTAAGTCG TTCTTTAACA GAGAATTATG ACAAATTGCA GATTTCAACG CCACATATCG 300

CTGAAATAAA ACnCCATAAA TACGnCACTC AAGCATCTTA GATAAAGTTG TnGGCCATGC 360

TAC 363

(2) INFORMATION FOR SEQ ID NO: 4114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4114:

GGTCTGGGCT TGGTTCCGGT TCTGGGTCTG GACTTGGTTC TGGATCTGGC GTTGGTTCTG 60

GTTCTGGGTC TGGACTTGGT TCTGGGTCAA CCGGCGGCCC TGGAGTTGGG TCTTTCGGAT 120

TTACTGCTGA ATCACCATCA GCACTTCCAC CACCATAACG TACAACATTC TCATTATTCC 180

AACCGAAAAT ACTGTAGTCT CTATTTGTTA CAGGATCAAC ATTTTCTTGA ATAACCTGAG 240

TTTTTAAGTT CTTACCTGTA TTGTCGTAAT GCCCTTCTAC TAATACTACA TATGTTTTAG 300

TAATATCACC AAATTAATAC TAGCTACATT GGATGCnCAT AATAGATCTA TTTTAAATGG 360

nCTGTACTCC TTAAGGTAGA GCATTGGACT GCAn 394

(2) INFORMATION FOR SEQ ID NO: 4115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4115:

GGCGATTATA TTAAAAAGCC AATTACAGAA TGTAGTGGTA ATGAAATATG CCAAGAATGG 60

CTGTATCACT TAGGTGTATC AACTGACAAA ATTGAAGACT TAGCAAAACA TGCATCTAAT 120

ACGATTCCTG TTTATATGCC ATATATCACA TCTTATTTCA TGACGCGTGC TATCGGCGAC 180

AGACCTTTAG TCGTCCCGCA TCAATCTCAG AACTTAGCAT TTATTGGTAA CTTTGCCAGA 240

AACAGAGCGA GACACTGTAT TTACAACAGA ATATTCGGTT CGTACTGCCA GGGAAGCTGT 300

TTATCAATTA CTAAATATAG ATCGTGGTAT TCCAGAAGTC ATCAATAAGT CCATTGGATC 360

TTnCGCGTnC TTAATGGGAT GGCCATATAC GAACTGGATG 400

(2) INFORMATION FOR SEQ ID NO: 4116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4116:

TTAAAGGGCG AAATAGAAGT GCCGGGCGAT AAGTCAATGA CACACCGTGC AATCATGTTG 120

GCGTCGCTAG CTGAAGGTGT ATCTACTATA TATAAGCCAC TACTTGGCGA ATGTCGTCGT 180

ACGATGGACA TTTTCCGACT GTTAGGTGTA GAAATCAAAG AAGATGATGA AAAATTAGTT 240

GTGACTTCCC CAGGATATCA ATCCTTTAAC ACGCCACATC AAGTATTGTA TACAGGnAAA 300

TTCnGGGTAC GACAACACGA TTATAGGTTG TTAAGTGGGT TAGGTATTGA AAGTGGTTTG 360

GTCnGGGCGA ATGTTTTCCA ATTGGGTAAA AGGCCCATGG 400

(2) INFORMATION FOR SEQ ID NO: 4117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4117:

AATAAAAAGG AACAAAACGA TGGCTATTGA TATGGACACA AATCATAAAT AGCTGCTTTG 60

TTCCTTTTTT AATTTATATA TTTAnAATAC ACATATTCAA GAGCCTCGAG ATATAAGTCA 120

ATGTACTAGG CCACACAATT TAATATTGAC AGTAATTACC CGAACGAAAA TGCGCCCCGG 180

GGCCCCAACA TGGGGAATTT CGAAAAGAAA TTCTACAGAC AATGCAAGTT GGCGGGGCCC 240

CAACATAGAA GCTGGCCAAT AGTTAGCTTT CAATAATGTG CCAGTTGGGG TAAGGGCCCC 300

AACACAGAAG CTGGCCAATA GTCAGCTTTC AATAATGTGC CAAGTTGGGG TAAGGGGCCC 360

CCACCACAGG GAATTTCGAA AGAAATnCT 389

(2) INFORMATION FOR SEQ ID NO: 4118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4118:

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60

TGTGGATTAA TATTATGCCT GGCAACGTTC TACTCTAGCG GAAnTAAGTT GACTACCATC 120

GACGCTAAGG AGCTTAACTT CTGTGTTCGG CATGGGAACA GGTGTGACCT CCTTGCTATA 180

GTCACCAGAC ATATGAATGT AATTTATACA TTCAAAACTA GATAGTAAGT AAAAGTGATT 240

ACATGTCACC ATGCTTCCCA CCTCGAACCT ATTAAACCTC AnCATCTTTG AAGGGGATCT 360

TATnAACCGA A 371

(2) INFORMATION FOR SEQ ID NO: 4119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4119:

GCACTATTAG CCCAGTTAGA GAAAGATTGA CCTAATCTAT CCAACCAATC AGCCGACCAT 60

TGAAACAGTG GTGCTAATTG CGGTGAATAC ATTGACTAAT CCGTCACCAA AACCACCTGC 120

AGCACTTAAT AGCTTGTTAA ATACCGAAAC ACCCGTTGTA TTCATCATAT TAAAGAATCT 180

TGAAGCTACA CTGCTATTTT CAGCCCATTn AAGCACGCTT TGAGACGCTT CTTCCATTCC 240

TCTTGAAATA CCACTAAAAA ACGGnTGTAA GCTCTGCATT GCAGTTTTAA CAGTATTTAA 300

ACCATTTGCA AGAGTTGTGA AGnTAGCGGA TTGATTTTGC T 341

(2) INFORMATION FOR SEQ ID NO: 4120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4120:

GGTTGAGAAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCCTCCAC GTAAGCTAGC 60

GCTCACGTTT CAAAGGCTCC TACCTATCCT GTACAAGCTG TGCCGAATTT CAATATCAGG 120

CTACAGTAAA GCTCCACGGG GTCTTTCCGT CCTGTCGCGG GTAACCTGCA TCTTCACAGG 180

TACTATGATT TCACCGAGTC TCTCGTTGAG ACAGTGCCCA AATCGTTACG CCTTTCGTGC 240

GGGTCGGAAC TTACCCGACA AGGAATTTCG CTACCTTAGG ACCGTTATAG TTACGGCCGC 300

CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGAnAAACG CACTTCCTGT TAAACCTTTC 360

CAGCACCGGn CAGGCGTTCA CCCTnATTAC ATCAACTTTA 400

(2) INFORMATION FOR SEQ ID NO: 4121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4121:

AATAAATCTT GCTTTATTCT TTTTACCAGT AATATCTAAA TGAGTTGGAT ATTTAACTTT 60

CGCATTAATT TCAATATTAA ATTGCGTTAC CGCGACAAGC GCAAACACAA CATACATAAT 120

AAGATTGGCT AAAAAGATAT AGTTAAAGCT AAATTCTGCG ACAAAGCCGC CCATTGCAGC 180

ACCGACAGCC ACACCAATAT TTTGCGCTAA GTATATCGCA TTAAACGTTT GTCTTCCGCC 240

ATTTGGCCAC ACTGCTCCAG CCATAGCGTA TATCGCAGGA ATAATCATTC CGCCACCAAA 300

CCCTAACATT ACCAGGCCAT ACCAGCATAC CCAGGGCCAC CCGnGGAAGG AAATTAAGTA 360

GCGGTGGTAC TACCAAnGAC CAGTGGAAGG TnCCAATTAA 400

(2) INFORMATION FOR SEQ ID NO: 4122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4122:

GATAACTAAT AAAGTTTAGT TAAGTATTTT AATAACAAGT AGTATGTCAT TCTAGTAGCT 60

AGAACAGATA TACTACTTGT TTGTTTTTGT GGAAAATTGA GTATATTCAA AAGGATAAGn 120

ACGAGAATTT CGTTATTAAA CTACGAATTC TCGATTTTTT TATATTTTAA GATAGGTTTA 180

TTTCTGAAAA CTTAATAGAA AGGGGTTTGA CAAAGCTAAA GTGAAGTTTG ACGgTATAAA 240

CGCAAATTAA ATATACTTTT ATAGAAAATT AACTCAGGCT GGGACATAAA TCAATATTCT 300

ATGCTCTACG GAGGTATATT GGCAGTAGTT GACTGAACGA AAnGCGCTTG TnACCAGCTT 360

TT 362

(2) INFORMATION FOR SEQ ID NO: 4123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4123:

CGCGAGGTGG TTTACAAGGA TTGTTGACAT TTCAAGACTT ACCAGTAACA AGTTATACAA 120

TCTGGGGTGG TGTCTCAGAT ATTGATTTAA TGTATGAAGA ACGTGTCGAT TTAAGAGGCA 180

TGCTACGAAG AATGATTGGT CATCCGAAAA AAGATCGAGC GGGCATATGA GGCACGCCAA 240

GCGATTCCAA ACATTAATGA nAACAGTCCG CCAATATTAA TTGTACATnG GAGGGGAAAG 300

ACCCAGCAAG TTGGGTATTn CATCATGCGT ATTATTTTAA GCGGACCAAC TA 352

(2) INFORMATION FOR SEQ ID NO: 4124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4124:

AACCAGGTGA TCTACCCTTG GTCAGGTTGA AGTTCAGGTA ACACTGAATG GAGGACCGAA 60

CCGACTTACG TTGAAAAGTG GAGCGGATGA ACTGAGGGTA GCGGAGGAAA TTCCAATCGA 120

ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGC TAGCCTCAAG TGGATGATTA 180

TTGGGAGGTA GAGCACTGTT TGGACGAGGG GCCCCTCTTC GGGTTTACCA ATTTCAGACA 240

AACTTCCGAA TGCCAATTAA TTTGAACTTn GGAGTTCAGA ACATGGGTGA TAAGGTCCnT 300

GTTTCGnAAn GGGAAACAGC CCAGACCACC AGTTAAGGTC CCCAAATGTA TGTTTAAGTG 360

GAAAAGGGTT TTGGCGTTGC CCCGACAACT AGGATGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 4125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4125:

GGCTTATTAA TCAAAAAATT TATAAAGAAT ATGTAGAAAA CTTTTATTTA CATCGAGGCT 60

ACACGCTACA ACAGAAAATT AAAATTTTAA TTAGCTTATA CATTGTAATA GGTTTTTCAA 120

TTTATATGGT GGATGTTCTT GCAGTCCGTG TAGGATTAAT CATAATGGTT ATCATACAAA 180

CCGCTGTACT CTTTACATTT GTAAAAACAT TACCCAAATC AAATCATAAA ATAGAGGAGT 240

GATTGCCCAT GTTTATGGCA GAAAATAGAT TACAATTACA AAAAGGCAGT GCGGAAGAAA 300

TTGTCACTAA AACATTAAAT ACCGGGATAC AGCCGAGTAA 400

(2) INFORMATION FOR SEQ ID NO: 4126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4126:

AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTTA GTCAAGCGCT 60

CGCATAAGCA ATATCACTTT AACCAAAAAA TATTTGAATG TTAAATAAAC ATTCAAAACT 120

GAATACAATA TGTCACATTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA TATATCCTTA 180

GAAAGGAGGT GATCCAGCCG CACCTTCCGA TACGGCTACC TTGTTACGAC TTCACCCCAA 240

TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGGTT ACTCCACCGG CTTCGGGTGT 300

TACAAACTCT CGTGGGTGTG GACGGGGCGG TGTGGTACAA nGACCCGGGG AACGTnATTC 360

AnCGGTAGCA TGGCTGGATC TAACGATTTA CTAnGCGGAT 400

(2) INFORMATION FOR SEQ ID NO: 4127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4127:

CGAAATTTGT AGTAAAAGAT GTGCAACCAG CGAAACCAAC TGTGACTGAA ACAGCGGCAG 60

GAGCGATTAC AATTGCACCT GGAGCAAACC AAACAGTGAA TACACATGCC GGTAACGTAA 120

CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC 180

GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG 240

CTGGAACTAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GGATACAATT 300

CCAAGTTGGT TGCAACGCCA AGGAAGCGGA GAGACCAGTG AAGTGATTGA GCCACCGTAA 360

TGGTTGGnTT CCCCAGTTTG TCGGCAnCCA CAACCGGAAC 400

(2) INFORMATION FOR SEQ ID NO: 4128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4128:

GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT GGAGATTATC TGTCGTCTTC 60

AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC CATGTCAAAG TACCATTTGC 120

AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GCCTACGCGT TACATGAAAA ACGGAGAACA 180

AGCAGAACAA TTATTACGTC AGCTTATAGA AAAAGATGAA GCACTAGCTA AGTATGTCAT 240

GGGTTGTGAT GAAACAGCTT GGTGGTCATA TATGGGTCCA GATAATGATA TTTTCCAAGA 300

TCCATTAnGG CCATCTAACT GTTCCAGCTA AGGAAAGTAT CCCCGAAGTG GCTAAGCCCA 360

AAAATGATTA CGCCAACCAG CTAGTGGTCC ATnGGCCAGC 400

(2) INFORMATION FOR SEQ ID NO: 4129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4129:

AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA TAGATGGnGG AGGGGGGCAG 60

ATTCGAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC 120

CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC 180

GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGG AGCTAATTCT CCAAAATAAT 240

GACTCCTGAC GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGTGTTC TTGAACCGCT 300

TGGACCAAGG GAGCCATGGC TCCAACAGGT GAGGGACTCG AACCTnACGG ACCGATTCGG 360

TTnAACAGCC GGAT 374

(2) INFORMATION FOR SEQ ID NO: 4130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4130:

ATTAAATTTC AGTTGTTGCA ATTTCTTCAT CTGTAGGTAC ATCATCGTTA AGGCCAACAA 120

GTGCTTCAGA AACATTTCGT GAATGATAAC CGATACGTTC AAGAACrCsA ATCATATCGA 180

TATATAGTAA TCCGCCTTTT GTTGTACATT CACCACGATT AAGGCGTTTA ATATGACCTT 240

TGCGTAGTTT ATGTTCAATA TTAAATGATT CTCTACTACG TTCTACAATT TCATCTTTTT 300

TCGTTTTGTC ATAAACATCT AACATGTCGA TGGCTTTATC AAATGACTCA GCAACATGGT 360

TGGAATAAnT TATCCATACC GCGTTGTGCA TCTnCTGGTA ATGCGAATAT CTTCATCATG 420

TTGGCGGTTT T 431

(2) INFORMATION FOR SEQ ID NO: 4131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4131:

TTTAGTTGAA GGCGGTGTTG TCGCATTTGC TGTTTGTTGC GGTGCTTCTA CTTTAGTTGA 60

GGGCGGTGTT GTCGCGTTTG GTTTTGATTG CGGTGCTTCT ATTTTAGTTG AGGGCGGTGT 120

TGATGTGGTG CTTCCACTTT AGGnAAnTGA GTGTTGTCGC GTTTGCTGCT TGCGTTGTCG 180

TTGTGATTAC ACCTGTTGTT AAAAGGCCTA GTGCTAAACT TGTTTTAGCA ATCGTTGTTA 240

TTTTCATAGT TGTATGCTCC ATTCGTAATT ATTAGATTTG TTCGATACAT TCATTGAATC 300

ATACAGCTTT ATTATAGAGG CGTATTGCTC CATTCACATT AAACCTGTnT AACCAGATTG 360

GAAGCAGCGT TGAATnAAAT GAAGAAAGCC AGAAGTTCGT 400

(2) INFORMATION FOR SEQ ID NO: 4132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4132:

CCATTCACTG TATGTCTTTG GCCACCACCT TGACGTTGTT GTTGCTGTTG TTGATTTTGA 60

TTAGCTTGTT GTTGATTTTG ATTATTTTGT GCTTGATTGT TCGCTTGATT AGCGTTGTTT 120

TGATCATTAT CAGATTCATC TTTAGTCGCT TTGTCTTGAT CCTCTTTTGA TTTATCACTG 180

TCAGCATTAT TTTTATTTGT ATTCGCGATT TTATTTTCTT TTGTACCATT ATTATGATTG 300

TTTAATGCCA TGCCTCCAAA TATCGCTAAA TGCACCGATA AATnAGTACA GCTGCAATGA 360

ATGGTAACAA TACTTTGGGC CAGnCACCGT TTTTACGGTn 400

(2) INFORMATION FOR SEQ ID NO: 4133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 417 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4133:

TTGAATACTT TTCTTCCACA CAAATGTATA TCTATTGGCA TTAGCTTCTA CTTTTGTACC 60

ATCAATAAAA ATTGAATTAT TATCAATAAG ATTTTGCTTT AAACATTGAC TATGGAACTG 120

AATAAATAAA GATTCAATTA ACGCATCAGT ATTAGGATTC ACTCTAAAAC GATTAATAGT 180

TTTATAAGAA GGTGTTTGAT TTTGAGCTAA CCACATCATT CGAATACTGT CATGAAGTAA 240

TTTCTCTATT CTTCGACCAG AAAATACAGA TTGAGTATAT GCATATAAGA TGATTTTTAA 300

CATCATTTTT GGGATGATAG GATGTTGCGC CACGATGATG TCTGAATTCA TCGAATTCGC 360

TAnCGGGTAC CGTTCCACCA ATTCCATTAA CATATCGCGG AATATCATTT TGAGGAA 417

(2) INFORMATION FOR SEQ ID NO: 4134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4134:

GGTTTAATAT GGACCTTTGC CGTnTTTATG TTCAATATTA AATGGATTCT CTACTACGTT 60

CTACAATTTC ATCTTTTTTC GTTTTGTCAT AAACATCTAA CATGTCGATG GCTTTATCAA 120

ATGACTCAGC AACATGGTTG nAATAATTTA TCCATACCGC GTTGTGCATC TTCTGTAATG 180

CGnAATATCT TCATCATGTT GGTCGTTTTA ATTGAGCGAC ATACTCTTCT GTTAGCTCTG 240

CTACTTTTAA AATAGAGCGA TTGACATCAA ACATAACTGC TAAACGCTCA ACGTCTGCCT 300

TCGTAATGGC TTTTGTAGAA ATTCTAACTA AATAATTTCG AATGCTATCA TTGT 354

(2) INFORMATION FOR SEQ ID NO: 4135:

(A) LENGTH: 400 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4135:

CTGGGATCGC CACCTTTAAG TCTAACAACC TTGTTATATC GACGCGCTGC TTCCACGATA 60

CAGTCATTTA TTTTTTCTTG CTGAATATGT TTTGCATACG GCTTTTTACC AACATCGATA 120

ATTTCAGTAG TCAAATTCGC ATATTGTAAA ATTAACGGAT TCACTAATCG ATCATATAGA 180

ATGACATCCG CTTCACGTAT TAAACGCTCA GCCTTTTTCG TCAAATAATT CGGATTACCT 240

GGACCCGCAC CTATCAAGTA AACCTTGCCA TATTCCTCTA CAGACATATA TATACGGTCC 300

CGTCTGTAAC TTCTACCTCA TAAACATCTA CACAACCTTC ATCAGGTCTG GACAATACCT 360

GnATTAAACA ATTTTTGATC GTGGGGGGGC AAATACATAT 400

(2) INFORMATION FOR SEQ ID NO: 4136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4136:

ACCACTGAAT CGTTCATCAT TTTCAAATTT TGAATCTGCT GTCCATTTCG CACTGTATGG 60

TGGGTTCGCA ATAACCGCAT CAAATGTATT GCCTAAAAAG GCTGGATTTT CCAATGTGTC 120

ATCATTACGG ATCTCGAAGT TCTCATAACG CACATCATGT AATAACATAT TCATGCGTGC 180

TAAGTTGTAT GTAGTATTGn TACGTTCTTG TCCGAAATAA CGATACACTT GCGTTTCTTT 240

ACCAACACGT AACAACAATG GAACCGGAnC CACATGTTGG GTCGTACACG TGGACGTAAT 300

TTATCnTTAC CGTGCTGTGA CAATCTTCGC CAGTATCTTA GATACTTG 348

(2) INFORMATION FOR SEQ ID NO: 4137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4137:

TGGACAATAC AAAGGGCAGC GAAACCGCGA GTCAAAGCAA ATCCCATAAA GTTGTTCTCA 120

GTTCGGATTG TAGTCTGCAA CTCGACTACA TGnAAGCTGG nAATCGCTAG TAATCGTAGA 180

TCAGCATGCT ACGGTGAAAT ACGTTCCCGG GTCTTGTACA CACCGCCCGT CACACCACGA 240

GAGTTTGTAA CACCCGAAGC CGGTGGAGTA ACCTTTTAAG GAGCTAGCCG TCGAAAGTGG 300

GGACAAATGA TTGGGGTGAA TCGTAACAAG GTAAGCCGTG ATCGGnAAGG TGCGGCTGGG 360

AT 362

(2) INFORMATION FOR SEQ ID NO: 4138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4138:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT CTCTGGATCA 60

AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120

GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC CATTTTTATA 180

AGTCAAACGC TCACATACGG CTTCGTTTTC ATTATTTTAA ATGCTCATTT ACATAAGTAA 240

ACTCTGCTTT AAAATAATTT AACTGCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT 300

TTAAACGCGT TATTAATCTT GTGAGTGTTC TTTCGAACAC CAGCGATTAn TTCnTGAGGA 360

ATTCAAGCCT AnTTAAAACC CTTA 384

(2) INFORMATION FOR SEQ ID NO: 4139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4139:

CTCATTATGG GACGTGCACA AGATGGTTTT CTTGATCAAG ACAAATATGA CATTATTTTC 60

AAAACAGCTG AAAATTTAGA CGTACCGATT TATCTACATC CCGCGCCAGT TAACAGTGAC 120

ATTTATCAAT CATACTATAA AGGAAATTAT CCTGAAGTAA CTGCGGCAAC ATTTGCTTGT 180

TTTGGTTATG GTTGGCACAT TGATGTCGGC ATTCATACAA TACATCTnGT nTnATCTGGT 240

TCCTTAGAAC GAATGGATGA AGCTTATCCG TGAACATTTG AACCACCCCG GAAGCAATAC 360

TTAAAAATAA ATTTAnTATC ACACCGGGTG GCATGGTACC 400

(2) INFORMATION FOR SEQ ID NO: 4140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4140:

CAACCACATT CGCTCGGCTC ACCTTAGAAT TCTCATCTTG AACTACCTGT GTCGGTTTGC 60

GGTACGGrCA CCTATTTTCT ATCTAGAGGC TTTTCTCGGc AGTGTGAAAT CAACGaCTCG 120

AAGACTCAAT GTCTTCTCCC CATCACAGCT CAGCCTTAAC GAGTACCGGA TTTGCCTAAT 180

ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC CTACTGCGTC 240

CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT 300

AAGCCTGTCG GGCTCAGCTT AAGGACCCGA CTAACCCCAG AACCGGAAGA GCCTTCCTCT 360

GGAAAACCTT AGTCAATCCG TTGGACCGGG ATCTCAACCG 400

(2) INFORMATION FOR SEQ ID NO: 4141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4141:

CATATCGATA ACATGACATA ACTCATGCTG GGTTTCCCCA TTCGGAAATC TCTGGATCAA 60

AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 120

TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTTATAA 180

GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 240

CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT 300

AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACATAG GCGGAGTATT TCTTAAGGAA 360

TnCAAGCnTA TTTAAAACTC TTAATCACnC GGTTTTGCnT 400

(2) INFORMATION FOR SEQ ID NO: 4142:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4142:

GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA GCCATTTTTC 60

TTTGTGTTTA CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA 120

CTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 180

CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 240

TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGGTTCGT CAGATTCAAA CGTTTCACTC 300

GCCAAGCCAT TTTCCTTGGG TTACTTTTAA TTTGACGTTT AAGGCATAAA AAAAAGAGAC 360

TTGCGGGCTC AAATGCGGnT CATCGCATCC ATTTTTGnCn 400

(2) INFORMATION FOR SEQ ID NO: 4143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4143:

TTTAAAATTG ACATTATTAC TGACCAAACA AGTGCACATG ATCCGCTAAA TGGATATGTG 60

CCACAAGGAA GCGAAAGTAT TGCGTGAAAA AGATCCGAAA AAATATGTTG AACTGTCACA 120

AGCTTCAATG GCAAAGCATG TTGAATTAAT GCTTGGAATT CCAAAAACGT GGCGCTGTAG 180

CATTTGATTA TGGTAACAAT ATTCGTCAAG TAGCCTTCAA TAACGGAnGn ATAAATGCTT 240

TTGGACTTCC CAGGTTTTGT ACCAGCTTAC ATTAGACCAT TnATTCTGTG TAGGTTAAAG 300

GGCCATTCCG CTTTGCTGCG TTGGAGTGGT GGATCCAAAA GATATCGAGC GTGCCGGATG 360

GAGGAAATG 369

(2) INFORMATION FOR SEQ ID NO: 4144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGAAAGATAA ATAGCTTCAT CAATGTCATG CGTCACTAAA ATAATAGTTG ATTGCGTTTT 60

ATGTTTTAGT TGCACTAGTT GATCCTGAAG TTTATAACGT GTAAATGCAT CTAATGCACC 120

TAATGGCTCA TCCATCAATA TAACGTTAGG CTTATGCACA TGCGCTCGAC ATAGTGCCAC 180

ACGTTGTTTC ATACCCCCGG ACAGTTGCTC GGGAAAATGC TTTCCCCTGT CTTCTAAATC 240

AACTAATTTA AGCTGTGCnT TAATCTCTTC ATCACTAATT TTCTGTTGTA ATCCAATCCT 300

AATGTTGTCA TTAATCGTTT TCCAGGCAGC AAATTATGGT GTTGAAATAG CATAAACAAn 360

CGGGAGnGGC 370

(2) INFORMATION FOR SEQ ID NO: 4145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4145:

CGAGGTAGCA AAGAACAAAT TGCGAAATAT GTACCTAAAT TACAGTCACA TGAACTGCGT 60

ACATGCTTTG CTTTAACTGA ACCAGAACAC GGTTCGGACG TTGCnGGAGG TCTTGAAACA 120

GTCGCTGAAC GCCAAGGCGA TACTTGGGTT ATCAATGGTG AAAAGAAATG GATTGGTGGT 180

GCACATGTAT CTGATGTCAT TCCAGTATTC GCAGTAAATA AAGAAACTGG GCAAACCCCA 240

TTGCTTTGTA GTCAGACCAG AACAAGATGG GCGTCGATAT TGAAGTCATT GGATAATAAA 300

ATCGCACTTC GGCATTGTTC CTAACGCCCT AATTTnAATT AAnTAATGTT CAAAGTAGGA 360

TTGAAGCGGG 370

(2) INFORMATION FOR SEQ ID NO: 4146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4146:

TGGGGTGTTT TTACCAATAA AGCGTTGCAA GGTGGCGGTA GTTTAATCGA TTATGGTTGC 60

CACTTGTTAG CTACTAGGTA AAGATATGGT GCCGCATGAA GTCTAGGAAA AACATATAAT 120

CAATTGAGCA AACAACCGAA TCAAATTAAT GATTGGGGAA CATTTGATCA TACTAAATTT 180

GAATGTTCGT GGTCTGCAAA TATCAAAGAA GATAAGGTTC ACGTTnTTTT ATCAGGAGGA 300

GGATGGCGGT ATCCAATTTA TTTCCATTTG GAAATATATG GnGCCCCGTT TTGGGAACnC 360

ATTTTTTGGA AAGCCAAGCT 380

(2) INFORMATION FOR SEQ ID NO: 4147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4147:

TACTTATCTA GTTTTCAATG TACAATTTCT TTTTAGTCAA GCGCTCGCAT AAGCAATATC 60

ACTTTAACCA AAAAATATTT GAATGTTAAA TAAACATTCA AAACTGAATA CAATATGTCA 120

CATTATTCCG CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC 180

AGCCGCACCT TCCGATACGG CTACCTTGTT ACGACTTCAC CCCAATCATT TGTCCCACCT 240

TCGACGGCTA GCTCCTAAAA GGTTACTCCA CCGAnTTCGG GTGTTACAAA CTCTCGTGGT 300

GTGACGGGCG GTGTGTACAA GACCCGGGAC GTATTCACCT GGCAGCTTGn CTGGGTTTAC 360

nT 362

(2) INFORMATION FOR SEQ ID NO: 4148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4148:

CACCATACAT GCGAAATGGA CAGCAGATTC AAAATTTGAA AATGATGAAC GATTCAGTGG 60

TTACGGCAAG CTTGCGCCAA AATCCAAAGC AGACTTTGCC TTTATTCAAC ACATGGTACA 120

TTACCTAGAC GATGAAGGTA CCATGGCAGT CGTACTCCCA CATGGTGTAT TATTCCGTGG 180

TGCCGCAGAA GGTGTGATTC GTCGCTATTT AATAGAAGAA AAGAACTACT TAGAAGCCGT 240

GATTGGGTTA CAGCCAATAT TTTCTATGGG nCAAGTATTC CAACATGTAT TTAGTATTAA 300

AAATGTCGCC ACAAGACGCC ACGTACTATT ATCGATGCAT CCAATGATTT GAAAAGGAAA 360

AATCAAACCA TTAAGCGTGC CAAGCGACGA TATnGCnCTA 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: d uble
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4149:

CAGCTATTGA TATCGATTAC CATACTGCTG TGGATAGCGA CAGGTTCACG TTGGAGGATA 60

CACTGAGTCC TCTGAGGAAT CAAATCCAAT TGACTTTGAA GAATCTACAC ATGAAAATTC 120

AAAACATCAC GCTGATGTTG TTGAATATGA AGAAGATACA AACCCAGGTG GTGGTCAGGT 180

TACTACTGAG TCTAACTTAG TTGAATTTGA CGAAGAGTCT ACAAAAGGTA TTGTAACTGG 240

CGCnTGAGCG ATCATACAAC AGTTGAAGAT ACGAAGAATA TACACTGAAG TAATCTGATT 300

GAATAGTGGA TGAATACCTG AAGAGCATGn TCAGCACAAG ACCAGTCGAG GAATnACTAA 360

AACCATCATC ATATTCnCAT CTGGTTAGGA CTGAAATGGC 400

(2) INFORMATION FOR SEQ ID NO: 4150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4150:

AAGGACGACA TTAGACGAAT CATCTGGAAA GATAATCAAA GAAGGTAATA ATCCTGTAGT 60

CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAGCACGTGA AATTCCGTCG 120

GAATCTGGGA GGACCATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCAGT 180

ACCGTGCAGG AGAAGGTGAA AAGCACCCCG GAAGGAGTTG AAATAGAACC TGAAACCGTG 240

TGCTTACAAG TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG 300

GCGAGTTACG ATTTGATGCA AGTTAAGCAT AAATGTGGAG CCGTAGCAGA ACnnGTTnTG 360

AATAGGCGTT A 371

(2) INFORMATION FOR SEQ ID NO: 4151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4151:

TCAGCTTTTT TGATATGTAT TTTATAATGT ACAGCTCGTT GACnnTAATT TTCCTTATAT 60

TAAGTGCCAT CAATACAAAA CCTAGCTCTC GTTTAACTTT ATTTATTCCT CGAACTGACA 120

TTCGAGTGAA CCCAAAATAG CCTTCATAAA TCCAAAAGCA GGCTCTACAT CAATTTTTCT 180

TTGACTATAG ATGTTTTTCG TTTCTGGTTC AGAAAGCTTT TGATTAATTT GGACTTTAAA 240

GTATTCCCAA TTATAATTCT TCATGGATTT TCTTATTGGG ATTTCGAATT TGGTTTCATG 300

CATTGATGTC TCAAAGAACA TGATGGAACA GTCCAnCACA TTCCAGATAG TTTGGAAGTC 360

TCGTTT 366

(2) INFORMATION FOR SEQ ID NO: 4152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4152:

TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 60

CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 120

TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180

TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA 240

GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300

CTAGCGGGAC GTAAGTGGCT ACCATCGACG CTAAGAACCT TTCCTGGACT TGGTGGACAA 360

TCGCnTGCCT CCTTCCTCCT CCTCGGGCTC TCGGCTTACG 400

(2) INFORMATION FOR SEQ ID NO: 4153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4153:

TGATATTCCT GTACCACCTA TAATCGTTTT AATCGATGGG GGGACGCATA GGnATAGGCG 60

ACGTGCGATT GGATTGCACG TCTAAGCAGT AAGGCTGAGT ATTAGGCAAA TCCGGTACTC 120

CCGAGAAAAG CCTCTAGATA GAAAATAGGT GCCCGTACCG CAAACCGACA CAGGTAGTTC 240

AAGATGAGAT TCTAAGGTGG AGCGAGCGAA CTCTCGTTTA AGGACTCGGG CAAATGGACC 300

CCGTTACTTC GGGGAGAnGG GTGCTCTTTA nGGGTTTACG CCCAGAAGAG CCGCATTGAA 360

TAAGGCCCAA GCGnTGTTTT ATCCAAAACA CGGTCTCTGC 400

(2) INFORMATION FOR SEQ ID NO: 4154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4154:

TTTTAGCAAT CATTTTAACA GTCAGTCATA TTAAAGGCTG GCTAACGATT GTTATCTnGT 60

nCAGATTTGT AAGTTAAGAT TTCTTGTAAT GTGTATGCAG CACCATATGC TTCAAGTGCC 120

CATACCTCCA TCTCACCAAA ACGTTGTCCA CCGAATTGCG CTTTACCGCC AAGTGGTTGT 180

TGTGTAACAA GTGAATATGG TCCTGTTGAA CGCGCATGTA ATTTATCATC AACCATGTGC 240

GCAAGTTTCA ACATGTACAT TACACCTACT GAAATACGGT TATCGAATGG TTCACCTGTA 300

CGTCCATCAT AAAGTACAGT TTTACCATCA CGAGCCATAC CAGCTTCTTC AATTGTTGGA 360

CCATACATCG TCATCGTTTG CACCGTCAAA TACTGGTGGA 400

(2) INFORMATION FOR SEQ ID NO: 4155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4155:

GATCCGAAGT TACCAACAGG AGAGAAAGAG GAAGTTCCAG GTAAACCAGG AATTAAGAAT 60

CCAGAAACAG GAGATGTAGT TAGACCACCG GTCGATAGCG TAACAAAATA TGGACCTGTA 120

AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCG AGAAAGAACG TAAATTTAAT 180

CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG TGAGAAGACA 240

ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA AGGTGAATCG 300

AAAGAAGAAA TCACAnAAGT CCAGTTAATG AATTAACAGA TTCGGTGGCG AGAAATACCG 360

(2) INFORMATION FOR SEQ ID NO: 4156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4156:

CAAAGTGACA GGTGGTGCAT GGTTGTCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60

CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATTA AGTTGGGCAC TCTAAGTTGA 120

CTGCCGGTGA CAAACCnGGG GnAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180

TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG CGAGTGCAAG 240

CAAATCCCAT AAAGTTGTTC TCAGTTCGGA TTGTAGTCTG CAACTCGACT ACATGAAGCT 300

GGGAATCGCT AGTAATCGTT AGATCCAGCA TGGCTAACGG TGGAnTACGT TTCCCGGGGT 360

CCTTGTTACA CACCGCCCGT 380

(2) INFORMATION FOR SEQ ID NO: 4157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4157:

TGGAGAAGGA CCCAAAAATG TTGCCGTTTC AAGGTTATGT TTTACAACAT TTCGAACTTA 60

TGGATGATGG ATTCTGCCAA GTTAAAATAA CTGAAGATGT ATTGGAGCAA TTCGGTATTC 120

AGCCAAATGA AGCATCTCAG TTTGTTAATA CAATTGCTGA CATCAAAGGC TTGAAAATAT 180

GGGTATTTGC AGTCGATGGA AGGTAATGAA ATCAGATGTC GATTACGTTC TAAAGGGCAA 240

TTGGATTATT AATGATATTG CGCAGATTTT GGTGGCGGTG GTCATCCGAA TGCGTCAGGA 300

GTTTCAGTGG ACCAGCTGGG GTGGAnTTGA GCCACTTGCT ACCAGCTTTA CGGCACCAAA 360

ACTTnACTTA TAGGAAGGGG CCCATTCCAT CCAGGTGGGC 400

(2) INFORMATION FOR SEQ ID NO: 4158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4158:

AAATCTCTGG GATCAAATCT TACTTACAGC TCCCCAAAGn CATATCGTCG TTAGTAACGT 60

CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT 120

TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 180

AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACACTA GCGATTATTT CTTATGAATT 240

CAAGCTTATT TAAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGn n 351

(2) INFORMATION FOR SEQ ID NO: 4159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4159:

AGTTAAAGGA ACTTTTAAAG TGGTTGGCCG CCGTnATTGC CTTCCTnACC TTTTTGTCCT 60

TCTCTTGtTA CTTTTTCTGT CCCTGGTGCT AAATCmGGAT TAAATTTACG TTCTTTCTTG 120

AATGGAATyT CTTCTTTTTC TACAATCGAG TCTCCTTTTA CAGGTCCATA TTTTGTTACG 180

CTATCGACCG GTGGTCTAAC TACGTCTCCT GTTTCTGGAT TCTTAATTCC TGGTTTACCT 240

GGAACTTCyT CTTTCTCTCC TGTTGGTAAC TTCGGATCAA ATTCGTCTCG ATGACCTGGT 300

GTTATCGTTT CTGGTCCGTA TTCTGTTAAT TCATTAATCG GATCTTTTGT GATTTCTTCT 360

TTTGGTTCAC CnTTnACGAA TAATnACTCC AGTAAAGGAT TTTTTAAGTG TTGGTGTCGT 420

(2) INFORMATION FOR SEQ ID NO: 4160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4160:

ACGATAATGG TGACGGGTTA CAAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGTCCT 60

CCACGTAATC TAGCGCTCAC GTTTCAAAGG CTCCTACCTA TCCTGTACAA GCTGTGCCGA 120

TGCATCTTCA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAnTCGT 240

TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAnT TTCGCTACCT TAGGACCGTT 300

ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAn TAACCACTC 359

(2) INFORMATION FOR SEQ ID NO: 4161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4161:

ATTGACTAAG GTTTCCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA 60

GGCCGGnAAC GGTAGGGCGA TGGATAACAG GTTGATATTC CTGTACCACC TATAATCGTT 120

TTAATCGATG GGGGGACGCA TAGGGATAGG CGAACGTGTC GATTGGATTG CACGTCTAAG 180

CAGTAAGGCT GAGTATTAGG CAAATCCGGT ACTCGTTAAG GCTGGAGCTG TGATGGGGAG 240

AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA GAAAAGCCTC TAGATAGAAA 300

ATAGGTGCCC GTGACCGCAA ACCGACACAG GTAGTnCAAG ATGAGAAnTC T 351

(2) INFORMATION FOR SEQ ID NO: 4162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4162:

AnCGTCCTGC TTTGCACGCC AGAGGTCAGC GGTTCGATCC CGCTAGTCTC CACCATTTAT 60

TTTTTACACG ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT TCCAAAAAAC 120

GTAACTATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT CATAATTTTT 180

ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA CATGCAAGTC 240

GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG AGTAACACGT 300

GGATAACCTA CCTATAAGAC TGGGGATAAC TTCGGGGAAC CGGAGCCAAT ACCGGATAAT 360

AnTTTGAACC GCATnGGTCC AnAAGTGAAA GACCGGCTTG 400

(2) INFORMATION FOR SEQ ID NO: 4163:

(A) LENGTH: 342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4163:

ATTTTATATA TGAAATAATC TGGGACAACA TTCATAAATC TTATTGTCGT CCATTTTTTT 60

AAAATAATAC CAATCTCATT TTTAAATTCT AAACTTGGTT TCGTATAATA CGCTCTTAAA 120

TCTTTAAATT TAGGATTTAT TTCTGTTGGT ACTTGTTTTG TGGTTGGCGA TTGTGGTGTG 180

TCTGATTTAG TAGATTGCAT TGGTTGTGGC GTGTTTGTTG ATGGAGGTGT TGTCACTTTA 240

GTTGnAAGGC GGTGTTGTCG CATTTGCTGT TTGTTGCGGT GCTTCTACTT TnATTGCAGG 300

CGGTGTTGTC GCGTTTGGTT TTGnATGCGG TGCTTCTATT TT 342

(2) INFORMATION FOR SEQ ID NO: 4164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4164:

TCACGACACG AGCTGACGAC AACCATGCAC CACCTGTCAC TTTGTCCCCC GAGGAAGGGC 60

TCTATCTCTA GAGTTGTCAA AGGATGTCAA GATTTGGTAA GGTTCTTCGC GTTGCTTCGA 120

ATTAAACCAC ATGCTCCACC GCTTGTGCGG TTCCCCGTCA ATTCCTTTGA GTTTCAACCT 180

TGCGGTCGTA CTCCCCAGGC GGAGTGCTTA ATGCGTTAnT GCCAGCACTA AAGGGGCGGA 240

AACCCCCTAA ACACTTAGCA CTCCATCGTT TACGGCGTGG AACTACCAGG GTATCTAATC 300

CTGTTTGATC CCCACGCTTT CGCACATCAG GTCATTAACA GACCAGAAAT CGCTTGGCCA 360

nGGGGGTnCC nCCAAAACTT TGGGGATTTA ACGGTAAAAA 400

(2) INFORMATION FOR SEQ ID NO: 4165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4165:

GCATTAATTT CATGTGTACC TTCGTACGTG TAAATCGCTT CTGCATCAGA GAAGAAACGT 120

GCAATATCAT AATCGTCAGC TAGTATGCCA TTACCACCTG TAATACCGCG GCCCATAGCT 180

ACTGTCTCAC GCAAACGTAA GGCATTCATC ATCTTCGCCG TTGAAGTTGC AACCTCGTCA 240

TATTCACCAT GTGCTTGCAT ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGAGCTAAA 300

TTAnCTTGCA TCATTGCTAG CTTTCCTGTA TTAACGGATA TTACTAATnG GTTGCCGAAT 360

GCTTACGCTC AGGGACnTAA CnAAGTGGCA CGTAAGCGGC 400

(2) INFORMATION FOR SEQ ID NO: 4166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4166:

AAAGTTCTTT GGAAATAGTA ACGTTGAAGT TGTACTCACT GGTGATACAT TTGATCACTG 60

TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 120

TAATGTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAGCAAA 180

GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTC 240

AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG GAAAATTATA GGTGTTGGAA 300

CCTTCAGGTG GCAAGTAGTA TGGTATGGAA TCnGGTGGTG GGTAAATAAT CCnGGTnGTC 360

CACATTGGCC CTAATAACCG ATAAAATTTG GGGGGCCGGG 400

(2) INFORMATION FOR SEQ ID NO: 4167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4167:

CTTATAATCC ACACCCTGAG CAAACGCTnC TTATGACAGA GTATTAAAAT AAGCCGATAA 60

AGATACACAC CTTTACCGAC TATTTAAAAT ACACTTCACC AATTCATTTT AATTTAATGG 120

ATTGAAGTAA CTAAATTAAT ATTATGTTGT TCAATTAAAA GCTTCATACA AACCTAATCT 180

ATTTGCACTC CACCGGTAAC ACCGAACACT TGTCCGGTTG TATAACTTGA TTCTTCTGGA 240

GTTTTTTGTA CCAAATGnTT GGGGATTTTA CTTnGTGGGT TGTCCACCAG AAATTTGT 358

(2) INFORMATION FOR SEQ ID NO: 4168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4168:

TTTCTTGACC ATATGGACGT AAAGAGATGT TAGCATCACA ACGTAAAGAT CCCTCTTCCA 60

TCTTAACGTC TGATACACCA GTGTATTGAA TAATTGAACG CAATTTTTCT AAATATGCAT 120

ATGCTTCTTT AGGTGAACGA ATATCTGGTT CAGATACGAT TTCAATTAGC GGTGTACCTT 180

GACGGTTCAA GTCAACTAAT GAATACTCAC CTTTATGTGT TGACTTACCA GCATCTTCTT 240

CCATGTGGAA GACGAGTAAT ACCGATTCGT TTTGTTTCAC CGTCGACTTC GATATCGATA 300

TATCCATTTT CACCAATTGG TTGATCAAAT TGAGAAnTTG AGAGCTTnTG GnTTAGCTGG 360

ATAGAAATAG TTCTTACGGT CAACTTAGAT CCGTTGCGAT 400

(2) INFORMATION FOR SEQ ID NO: 4169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4169:

ACCATGTTTG AATGAATCCA TTGGAATCAT TATTGAAGTA AATTAAGGAA TCTATAATGT 60

TCGTTAAATA AAACTGATCC CGTTGTGCTT CACACCCGAT AGATAGGGAT TTACAGATAA 120

ATTCAGGTCT CTTCCACGTC ATATTTGGAC CCATCGAAAA TTCGGGTTCT CAAATCATCG 180

AACATAACAA AAGAAGCTAA GCAACATGTA GGCCGTTGTC ACTTAACTTC TTGTTTTTCC 240

GATGACAGCT TCTATTTAGA GAATGTCATG ATTATTTTAT ATTCACTTCA ATGTTATCAA 300

TATTAGTGCC ATCTATGACA TCTGCCATGC GATTTTCTTG TAATTTTTTG TGCAATCAAC 360

GTGTACnTCC ACGGTTTTCA TTTAAnAACA ATTTACCGGA 400

(2) INFORMATION FOR SEQ ID NO: 4170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 395 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4170:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA 60

TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTTGGGC ACTGTCTCAA 120

CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG ACAGGACGGA 180

AAGACCCCGT GGAGCTTTAC TGTAGCCTGA TATTGAAATT CGGCACAGCT TGTTACAGGA 240

TAGGTAAGGA GCCTTTGGAA ACGTGAGCGC TAnTTTACGT GGnAGGCGCT GGGTGGGGAT 300

ACTTACCCTA AGCTGTGTTG GCTTTCTAAC CCGCACCAnT TATCGTGGTG GGGAGACCAT 360

GGTCAAGCGG GGCATTTTGA ATGGGGGGCG GTTCG 395

(2) INFORMATION FOR SEQ ID NO: 4171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4171:

TACATTATAG CTTTAATCGT TTGAAGTATA GTTTGAAACC AGTAGTCACA GCTGTTCAAG 60

GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG TACTTTACTC ACCTATTGTT GTCGCTGCAA 120

GTGAAACATA TATCGGTCTT GTTGAAGCAG GTGTTGGCTT ATTACCGAGT GGCGGTGGCC 180

TTGCAGAAAT GGCTGATCGC ATATTACGCA CATCGCATAA GTTTGATGAC AAACAAGCTT 240

CCATGACAAA AGTACTGACG AATATCGCAT TGCGAAnGCT CTACAAATGC CTTTGAGGCA 300

CGTCGTATGG GTATTTACCG TGGATACAGA TACGATnATT TCCAATACAG CACAACGnGT 360

CGAAGTGGCG C 371

(2) INFORMATION FOR SEQ ID NO: 4172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4172:

GCTGAGCTAA GCCCCCATAA TAATTACAGT ATATCGGGAA GACAGGATTC GAACCTGCGA 120

CCCCTTGGTC CCAAACCAAG TGCTCTACCA AGCTGAGCTA CTTCCCGTAT AATTAACGCG 180

CCCGATAGGA GTCGAACCCA TAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG 240

CTACGGGCGC ATATGTTTTT ATTGAAAATn GTGCCGAGGA CCnGAATGAA CCGGTACGTG 300

ATCATTACCG CAGATTTTAA GTCCTGTGCG TCTGCCAGTT CCGCAnCCCG GACTATAAAA 360

T 361

(2) INFORMATION FOR SEQ ID NO: 4173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4173:

GTACAGATGC ATTGTTAAAC AATCAGTTGC AACAGCTGTT GAAACTGGTA GAGTATCTAA 60

TGGTGATTTA ATCATTATTA CTGCTGGTGT ACCAACTGGT GAAACTGGAA CTACTAATAT 120

GATGAAAATC CACCTAGTTG GTGACGAAAT TGCTAATGGT CAAGGTATTG GACGTGGATC 180

AGTTGTTGGT ACTACGTTAG TTGCTGAAAC TGTTAAAGAT TTAGAAGGTA AAGATTTATC 240

TGACAAAGTT ATCGTTACTA ACTCCATCGA TGAAACGTTT GTACCTTATG TAGAAAAAGC 300

TTTAGGCTTA ATTACAGAAG AAATGGTATT nCACACCCAG TGCCATGGTT GGTTAGGAAA 360

AGnAATCCCA CCGTTGTAnG 380

(2) INFORMATION FOR SEQ ID NO: 4174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4174:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAG 60

CTGAGCTGTG ATGGGGAGAA GACATTGAGT CTTCGAAGTC GTTGATTTCA CACTGCCGAG 120

AAAAGCCTCT AGATAGAAAA TAGGTGCCCG TACCGCAAAC CGACACAGGT AGTCAAGATG 180

AGAATTCTAA GGTGGAGCGA GCGAACTCTC GTTTAAGGAA CTCGGGCAAA ATGGACCCCG 240

GCCCAAGCGC TGTTTATCCA AAACACAGTC TCTGCTnAAC CGTAGGGGAT TGTATAGGGG 360

CTTACGCCTG CCCGGTGCCT GGAAGGTTTA AAAGGGTGGT 400

(2) INFORMATION FOR SEQ ID NO: 4175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4175:

AGCCATGGCT CAGCGAGGTA GGACTCGAAC CTACGACCGA TCGGTTAACA GCCGATAGCT 60

CTACCACTGA GCTACTGTGG ATTAATATTA TGCCTGGCAA CGTTCTACTC TAGCGGAACG 120

TAATTCGnAC TACCATCGAC GCTAAGGAGC TTAACTTCTG TGTTCGGCAT GGGAACAGGT 180

GTGACCTCCT TGCTATAGTC ACCAGACATA TGAnTGTAAT TTATACATTC AAAACTAGAT 240

AGTAAGTAAA AGTGATTTTG CTTCGCAAAA CATTTATTTT GGATTAAGTC TTCGATCGAT 300

TAGTATTCGT CAGCTCCACA TGTGCACCAT GCTTnCCACC TCGAACCT 348

(2) INFORMATION FOR SEQ ID NO: 4176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4176:

CATTTTTTTA AAATAATACC AATCTCATTT TTAAATTCTA AACTTGGTTT CGTATAATAC 60

GCTCTTAAAT CTTTAAATTT AGGATTTATT TCTGTTGGTA CTTGTTTTGT GGTTGGCGAT 120

TGTGGTGTGT CTGATTTAGT AGATTGCATT GGTTGTGGCG TGTTTGTTGA TGGAGGTGTT 180

GTCACTTTAG TTGAAGGCGG TGTTGTCGCA TTTGCTGTTT GTTGCGGTGC TTCTACTTTA 240

GTTGAGGGCG GTGTTGTCGC GTTTGGTTTT GATTGCGGTG CTTCTATTTT AGTTGAGGGC 300

GGTGTTGAnT GTGGTGCTTC CACTTTAGGG nAAGATnAGT GGTG 344

(2) INFORMATION FOR SEQ ID NO: 4177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4177:

CAGAACCTTG nAATGAATCG CGATGGAATA TCTCTATCTG nAAACAGATT TCTTTTTGTC 60

CGCCAATGGC CTTGGAATTG TTTAAATAAA TCTATTTGCG CTTCTTTATC AATGTCATAA 120

CCTAATGCTT TTAACTTCTC TGAGAAGCGT GTTTACCAGA TAATTTTCCT AATGGAAGTT 180

CAGTCGTGCT TACACCAACA AGTTGAGGTG TCATAATTTC ATATGTTTCA CGATGTTTTA 240

ATACGCCATC TTGGTGAATA CCTGATTCAT GACTAAATGC ATTTGGCCAA CAATTGCTTT 300

ATTTCTAGGC ACTCGAATAC CTGCATATCT TGAnATTAAA TCCGAGGTTT TAGTTCCTCG 360

AG 362

(2) INFORMATION FOR SEQ ID NO: 4178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4178:

GGAGCTAATA CCGGATAATA TTTTGAACCG CATGGTAAAG nTGGAAAGAC GGTCTTGCTG 60

TCACTTATAG ATGGATCCGC GCTGCATTAG CTAGTTGGTA AGGTAACGGC TTACCAAGGC 120

AACGATGCAT AGCCGACCTG AGAGGGTGAT CGGCCACACT GGAACTGAGA CACGGTCCAG 180

ACTCCTACGG GAGGCAGCAG TAGGGAATCT TCCGCAATGG GCGAAACTTn ACGGAGCAAC 240

GCCGCGTGAG TGATGAAGGT CTTCGGATCG TAAAACTCTG TTATTAGGGG AGGACATATG 300

TGTAAGTAAC TGTGCACATT TTTGACGGTA CCTnATCAGG AAGCCACGGT TTACTAGGGG 360

CCCAGAAGCC CCGGTTAATA CGTGGGTGGG nAAGGGTTTT 400

(2) INFORMATION FOR SEQ ID NO: 4179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4179:

GTTGTTTCAG CAGCGACACA GTGTATTCCA TTCTTAGAAA ATGATGACTC AAACCGTGCA 60

GTTGGTACAG GTATGGAACA CGTTGCAGCA CGTGATTCTG GTGCGGCTAT TACAGCTAAG 180

CACAGAGGTC GTGTTGAACA TGTTGAATCT AATGAAATTC TTGTTCGTCG TCTAGTTGGA 240

AGAGAACGGC GGTTGAACAT GAAAGGTGGA TTAAGATCGC TATCCATTAG CTAAATTTAA 300

ACGTTCAAAC TCAGGTACAT GTTACAACCA ACGTCCAATC GTTGCCAGTT GGGAGATGTT 360

GTTGGnnnTA C 371

(2) INFORMATION FOR SEQ ID NO: 4180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4180:

AAAGGGAATC GAATTTTCTT TCTCTTCCTC CGGGTACTAA GATGTTTCAG TTCTCCGGGT 60

GTGCCTTCTG ATATGCTATG TATTCACATA TCGATAACAT GACATAACTC ATGCTGGGTT 120

TCCCCATTCG GAAATCTCTG GATCAAAGCT TACTTACAAC TCCCCAAAGC ATATCGTCGT 180

TAGTAACGTC CTTCATCGGC TTCTAATGCC AAnGCATCCA CCGTGCGCCC TTAATAACTT 240

AATCTATGTT TCCACCATTT TTATAAGTCA AACGCTCACA TACGGCTTCG TTTTCATTAT 300

nTnAAATGCT CATTTACATA AGTAAACTCT GCTTTAAAAT AATT 344

(2) INFORMATION FOR SEQ ID NO: 4181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4181:

CCGTGATCGG AAGGTGCGGC TGGATCACCT CCTTTCTAAG GATATATTCG GAACATCTTC 60

TTCAGAAGAT CGGGAATAAC GTGACATATT GTATTCAGTT TTGAATGTTT GTTCATTCAA 120

ATTAATGGGC CTATAGCTCA GCTGGTTAGA GCGCACGCCT GATAAGCGTG AGGTCGGTGG 180

TTCGAGTCCA CTTAGGCCCA CCATTAATTT AATACCTATT TGGGGGCTTA GCTCAGCnGG 240

GAGAGCGCCT GCTTTGCACG CnGAGGTCAG CGGTTCGATC CCGCTAGTCT CCACCATTAT 300

TTGTACATTG AAAACTAGAT AAGTGAnGTA AAAATATAGA TTT 343

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4182:

CAGAGCCAAC TCGTATGTGA TTTGTCTGCG CCAATGTATG CATCATCAAA AGTTCTGGAC 60

TACTACACGC AAACGCTGGT ACATTATGAT GTTCCGTAAA CCAAATTCGC TTAAAGCCAA 120

GTCGATCTGC TAATTTTGCA AGTGTCACTG AATCTTGCAA TGCCTTTTGT GCATCCTTAC 180

CTTCATCTAT TAAGGCATAG TCTAATACGC TTAATTTAAC CAATCCGTCA TCTCCAAACT 240

TATCCTGTCA TGTCAAACCG ACATAACATT TTAGCGTCTT AATACCATTC CCTCTTCATA 300

TACCCACGTA TATGATAACG TTTTCAATAA CTTTATATCT TTCGCCTTAT TTnCTTTTCA 360

TATCATATTT CAGACTACAA ATGCATCATA GTTAATTAAA 400

(2) INFORMATION FOR SEQ ID NO: 4183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4183:

AAAGTATGAA AGATGGTAGT GACGCGGTTG GTGATTGGGC TGTATTGAAT GCACTCATTA 60

ACACAGCTGC AGGTGGTTCA TGGATTTCAT TCCATCACGG TGGCGGTGTT GGCATGGGAT 120

ATTCACTTCA TGCGGGTATG GTTGTTGTAG CAGATGGATC AGAGCGTGCT GAAGGAAGAT 180

TGGAACGTGT ATTGACGACT GACCCAGGTA TGGTGTTGCC CGACATGTTG nATGCTGGCT 240

ATGACATCGC TATTCAAACA GCTAAAGAAA AAGGTATTCA nATTCCAATG ATTGGTGAAA 300

GCAGGTGATA AGTAATGAAT GATTTAATAT TAATCAnATA GCAGAnTATT TTTACCGGGT 360

CCAACAGATA AACCTTTGAA GGGTTAGGTA TTAGATGCAT 400

(2) INFORMATION FOR SEQ ID NO: 4184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4184:

TTCCCTGTGC ATCGGCATCA CTATTATTAG CATGACTCAA TTATTGGCAT CACAATATGT 60

CATTGCAGTT ATCATTGGTT TCGTCATATG TGCGATAGGT AATGGTTTAG TCGCAACACC 120

TGGACTTACG ATTGCAATTT TCAGTATGCC TAATGAnAAA GTTGGTTTAG CTACAGGATT 180

ATATAAAATG AGTGGTACAT TAGGTGGCTC CTTTGGTATA GCACTAAGTA CTACAGTTTT 240

CAGTATGTTA CAACTAAACT ATGCACCAAG TGTAGCTGCA ACCGTAACAT TTATAGTCAG 300

CATTGTATTG ATGnTCCTTG GGTnCATTGT CTGCATACAT GA 342

(2) INFORMATION FOR SEQ ID NO: 4185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4185:

AAGCATACTC TGAAGCGGTG AACAAAAATA GAACAGATCA CATTAGACAT TTACTTGAAT 60

TTAAAGCATG TACACCGATT GACATCGACC AAGTTGAACC GGTAAGTGAC ATTGTCAAAC 120

GCTTTAATAC AGGGGCGATG AGTTATGGAT CGATTTCAGC GGAACACATG AAACGTTAGC 180

ACAAGCCATG AACCAATTAG GTGGAAAGAG TAATAGTGGT GAAGGTGGCG AnATGCAAAA 240

CGTTATGAAG TACAAGTTGA TGGAAGCAAC AAAGTAAGTG CGATTnAACA AGTTGCTTCT 300

GGGCGTTTTG GTGTACTAGT GATTATTTAC CACCTGCCAA GGAATTCCAA TTAnACTTGC 360

(2) INFORMATION FOR SEQ ID NO: 4186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4186:

CCCAAGCGGA ATTCTAAAAT GATCGTCGCT CCATTCTTCA TTTTAATAAA TCCAAACGCA 60

GAATCTTCAA CTGTAAATTC ATCTGGATTC CATGAACCCC AAGCGTTTGC CGCATGATGC 120

TGTTTATTTA ATTTATGGAA TGTTGAACCC ATCACTGATT CTGGTTCATA ATTATCCATC 180

ATCCATAACG TTAAATCTAA AGCGTGTGTA CCGATATCGA TTAATGGTCC TCCACCTTGG 240

nCTTTCCGAA GTTAAATGTC TCCTAAGTCG CCACGTTGGC GCTGCCTGGA TGGAAAATTG 360

GACGATCTGC TCGGGAAACG AATTTGGATA AACnGATGGG 400

(2) INFORMATION FOR SEQ ID NO: 4187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4187:

GAATCATCTG GCAACCnCCC CCAAAGAAGG TAATAATCCT GTAGTCGAAA ATGTTGTCTC 60

TCTTGAGTGG ATCCTGAGTA CGACGGAGCA CGTGAAATTC CGTCGGAATC TGGGAGGACC 120

ATCTCCTAAG GCTAAATACT CTCTAGTGAC CGATAGTGAA CCAGTACCGT GAGGGAAAGG 180

TGAAAAGCAC CCCGGAAGGG ATGTGAAATA GAACCTGAAA CCGTGTGCTT ACAAGTAGTC 240

AGAGCCCGTT AATGGGTGAT GGCGTGCCTT TTGTAGAATG AACCGGCGAG TTACGATTTG 300

ATGCAAnGTT AAGCAGTACA TGTGGAGCCG TAGCGAAAGC GAnGTCTGA 349

(2) INFORMATION FOR SEQ ID NO: 4188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4188:

TGGATCCTGA GTACGACGGA GCACGTGAAA TTCCGTCGGA ATCTGGGAGG ACCATCTCCT 60

AAGGCTAAAT ACTCTCTAGT GACCGATAGT GAACCAGTAC CGTGAGGGAA AGGTGAAAAG 120

CACCCCGGAA GGGGAGTGAn ATAGAACCTG AAACCGTGTG CTTACAAGTA GTCAGAGCCC 180

GTTAATGGGT GATGGCGTGC CTTTTGTAGA ATGAACCGGC GAGTTACGAT TTGATGCAAG 240

GTTAAGCAGT AAATGTGGAn CCGTAGCGAA ACGAGTCTGA ATAGGGCGTT TAGTATTTGG 300

TCGTAGACCC GAAACCAGGT GATCTACCCT nGGTCA 336

(2) INFORMATION FOR SEQ ID NO: 4189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4189:

CAAAGGATGT TAAGAAATAC AATTTATTAC CCAGCATTTA ATAATGGTGC TATAGAAGGA 60

ATTAATAATA AGATAAAATT AATCAAGTGA ATTTCTTTTG GTTACAGAAA TTTCAACAAC 120

TTTAAAGCAC GTATAATGAT GATTTTCAGC TTGTACAAAG GAGAAAAAAA GAAGACAACC 180

AAGCCCAATA ATGGACTGGC CGCCTAATAA TAAAAGCTCT AAAAGTTGTA TTTTAAAAAT 240

AGTTCTTTAA ATTATATACC CACCACATTT GGTGGAGGAC CTAAAAAAAA GCACTTCCCC 300

AAAAATGGGA AAGTGCAAGT AGTGAGCCnT AGGAGGGTTC GGACCCTCTn nCCCCTCT 358

(2) INFORMATION FOR SEQ ID NO: 4190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4190:

TCACCAAGTT GAGCAAAGAA GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT 60

AAnGTACCAC CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT 120

GGACCTAACA ATCTTAAGAT GAAGCCATAA ACAAAAGTAC CGATGGCACC TGTTTTCGTT 180

ACAAATCCAC CAACATGATA AATGCCGGCT TGTATGCTTG GCCAAATGAA AAACATCAAT 240

ACACCTAAAA AGATTGCGGC AAATGCTGTG ACAATAGGGA CAnATGTAGA GCCACCAAAG 300

AAACCTAAAT ACGGTGGTAA TACCATTTGT GnTATTTGTT GTGAAGTATT GCGGTCATAA 360

TA 362

(2) INFORMATION FOR SEQ ID NO: 4191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4191:

TGATCACCCA TGTTCTGGAC TCCCAATTGA AATTGAATTG GGCATTCGGA GTTTGTCTGG 60

nATTCGGTAA CCCGnGCAGG GTCCCCTCGT GCCAAACAGT GCTCTACCTC CAATAATCAT 120

nATTTCTCCG CTAACCTCAG TTCATCCGCT CACTTTTCAA CGTAAGTCGG TTCGGTCCTC 240

CATTCAGTGT TACCTGAACT TCAACCTGAC CAAGGTAGAT CACCTGGTTT CGGGTCTACG 300

ACCAAATACT AAACGCCCTA TTCAGACTCG CTTTCGCTAA GGCTCCACAT TTACTGCTTA 360

AC 362

(2) INFORMATION FOR SEQ ID NO: 4192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4192:

CGTGTATTAT GCCTTCTACA TTGGCCATTA TGAAAACTTA TTATCAGGGT GCTGAACGTC 60

AGCGTGCCTT AAGTTATTGG TCTATCGGTT CTTGGGGTGG CAGTGGTATC TGTTCACTCT 120

TCGGTGGTGC AGTTGCGACA ACTATGGGTT GGAGATGGAT TTTCATCTTC TCAATTATCG 180

TTGCCGTACT TTCAATGTTA CTCATCAAAG GGACGCCTGA AACGAAATCA GAAATTACCA 240

ATACACATAA ATTTGACGTT GCAGGGCTAA TTGTTCTAGT AGTATGTTGC TAAGTTAAAC 300

GTTGTCATTA CTAAAGGTGC AGCACTTGGn TACACATCAT TATGGGTCTT GGGTTGAATG 360

CCAATCGGAA ATTGTAGCAT CnTTAATTTC CTAAAAGGTG 400

(2) INFORMATION FOR SEQ ID NO: 4193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4193:

AATCCCATGG ACCCTCAAAT TCTTTATCTA AATAGTACCC TAATGAAGTT TTTCTGTGCA 60

TGTGATTAAT TTCATGTAAA CCGATGACAC CAACTAGCGT TCCTTCATAC CAAATGCCAC 120

ACTGAAATCC ATTACCATCA GCAAATTGCA AAAGTCCTCT TTTAATAAAT GCACGCGTAT 180

CTGATGGTTG CTCAGTTGCA TCTACCCAAG GTAACCATTC CCTAAGTGAA TTTCTTGAAC 240

GATTGACTAA ATTGAAAAGC GCTTCTGTGT CATGAGCTTC TAAAATTTTA ATGTTATTGT 300

TCAATCACTT TCATTCCAAA CATACnATCA CATCCTCATT CATTnTCATA TAATCCGGnA 360

(2) INFORMATION FOR SEQ ID NO: 4194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4194:

ACAAAGGACG ACATTAGACG AATCATCTGG AAAGAGAATC AAAGGTAATA ATCCTGTAGT 60

CGAAAATGTT GTCTCGAGTG GATCCTGAGT ACGACGGAGC ACGTGAAATT CCGTCGGAAT 120

CTnGGAGGAC CATCTCCTAA GGCTAAATAC TCTCTAGTGA CCGATAGTGA ACCAGTACCG 180

TGAGGAAAGG TGAAAAGCAC CCCGGAAGGG AGGTGTAAAT AGAACCTGAA ACCGTGTGCT 240

TACAAGTAGT cAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGAAT GGAACCGGCG 300

AGTTtACGAT TTGgATtGCA AGGTTAAGCA GTAAATGTGG GAGCCGTA 348

(2) INFORMATION FOR SEQ ID NO: 4195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4195:

AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAACTGCCTG GCAACGTTCT 60

ACTCTAGCGG AAnTAAGTnG GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCGG 120

CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180

TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG 240

TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGAACCTAT 300

TAACCTCATC ATCTTTGAGG GATCTTATAA nCGAGTTGGG 340

(2) INFORMATION FOR SEQ ID NO: 4196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAAATTAA TGAAAGATAC AGTAGGTGCT 60

GATGTAGAAG TAAAAGCATC AGGTGGCGTA CGTAATTTAG AAGATTTCAA TAAAATGGTT 120

GAAGCAGGTG CGACACGTAT TGGTGCGAGC GCnGTGTTCA AATTATGCAA GGTTTAGAAG 180

CAGATTCAGA TTACTAATAT ATATnAATnT TGGGAGTGAT AGCTATGACA AGACCATTTA 240

ATCGTGTACA TTTAATCGTA ATGGATTCAG TAGGTATTGG TGAAGCGCCA GACGCAGCTG 300

ATTTTTAAAG ATGGAGGTTC ACATACTTTT A 331

(2) INFORMATION FOR SEQ ID NO: 4197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4197:

GTAGACGTCC CGATAGCCGT TACGCATGGT TACGATGTGT ATTGGTGTCG GCATGGGTGC 60

AGCTGCTATA TTTGAATATG TGCGTTAGAA TGGTTGATTT TGGATGAAGC GGATTCGTTT 120

TGTTATTGAA TGAAGTAGGC TGAAGTTGAA GCCAGTTGAA GTTGAAGCGG GTTGAAGCAA 180

TTTCGTTTTA TTGAATGAAG CTGTGTGAAA TATAGTGATT GAACAAAAAA AGTGGTTTAA 240

TGGGATGGTG GTTATTTCCG TTTTAGAATT TAACATTTAC ACGTCTAATT TTAAATCATT 300

GTTTTAAATT TTATGAATCG AAGCCCTTTG GATTTAATAn TATTGCTAAT GCnAGTAACT 360

nATCTGATTG T 371

(2) INFORMATION FOR SEQ ID NO: 4198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4198:

GCGACCCCAA CCTTGGCAAG GTTGTnATTC TACCGCTGAA CTACTTCTGC ATATGCGGGT 60

GAAGGGAGTC GAACCCCCAC GCCGTAAGCT nAGnATCCTA AGTCTAGTGC GTCTGCCAAT 120

TCCGCCACAC CCGCAAATGG TGAGCCATAG AGGATTCGAA CCTCTGACCC TCTGATTAAA 180

AGTCAGATGC TCTACCAACT GAGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 240

TAAGAATAAA TGGTGGAGAA TGACGGGTTC GnACCGTCGA CCCTGTGCTT GTTAAGGCAG 360

ATGGTTTTCC CACTGGGGTA AATTTTCCGA TTTAAAAATG 400

(2) INFORMATION FOR SEQ ID NO: 4199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4199:

ATCAGTTGCT GTTGCGCCTT GTGGTAATGA ATTTACTAGT CGTACACCAA TAACCTCTGG 60

AATTGGGAAA TAAGAAGGTT GTCCAAGCAT TCCAGCTTCA GCTTCAATAC CACCAACACC 120

CCATCCTAGT ACGCCAATAC CATTTATCAT TGTTGTATGT GAATCAGTAC CAACTAATGT 180

ATCTGGAAAT GCAGTTTTTT CACCATCTAC ATCACGAACA TGTACAACAC TTGCTAAATA 240

TTCTAAGTTA ACTTGGTGAA CTATTCCAGT TGCAGGAGGG AACTGCATTG TAATTATCAA 300

ATGCTTTCGG TTGGCCCAAT TTAAAAAACT GGATAACGTT CATnGTTACG TTCCAATTCC 360

TAATTTCCnA ATTACGGTTC CAnGAGCTTC TGGGATTTTG 400

(2) INFORMATION FOR SEQ ID NO: 4200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4200:

CAACCTTTAT TGGTAAAAAC ACCCCAGCCA GGCACTTTAC GCCTACGCAT CGCTTGTACA 60

CGTGCTACTA nAGGTTTACC AACCACACCT GATTCAATTG CTTTTTTAGC AGTAATTGCC 120

ACATCTGTGT GACGATAATG ATATGCGACA GTTAATAATT TGTGATTTTT ATTAGCCGCT 180

TCAATCATGC GATCACACTC TTCCGTCGTC ATCGCCATTG GCTTTTCACA CAATACATGG 240

CACACCATGG TTCAATGCnT CTATAGAAAG ATCAGCAGGA ATTTATTAGG TGTACAAATG 300

ACCCATCAAC AAGTTTAAAC AGCTCGCTAG GTGnC 335

(2) INFORMATION FOR SEQ ID NO: 4201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4201:

ATGATGTGGC GGTGGTGAAA TCAGACCGAT ACCTGGCGTT GACCCTCTTG TCTTCGCAAT 60

CCACGGATAT ACCTTAGTAC CAGGTAATTG ACCACCTTCA CCAGGCTTTG CACCTTGCGC 120

AACTTTAATT TGAATTTCTT TGGCATGTTG TAAATAATCA CTAGTTACAC CAAAACGCCC 180

AGAAGCAACT TGTTTAATCG CACTTACTTT GTTGCTTCCA TCAACTTGTA CTTCATAACG 240

TTTTGCATCT TCGGCAACTT CACCACTATT ACTCTTTCCA nCTAATTGGG TCATGGGCTG 300

TGCTAACGTT TCATGTGCTT CCGnTGnAAT CGATCCATAA CTCATCGGCC CCGTATTAAA 360

GCGGTTGGAC 370

(2) INFORMATION FOR SEQ ID NO: 4202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4202:

CAGCTAGCGA CTTACCTTGA CGTTTTGnGT ATTCATTCCA GCTTTGTnGG AATGAGtCGG 60

gATATAAGCA TCTTTAGATA ATGCACCATC AACTAATGGA TATTTATGTC CAGTTGGaGC 120

CAGAAATCAT AAACGTCTTC AGTGTAAGCA ACAGCATCTT CaTTTAATGC CAAAATGCTT 180

GGaTTAgTGC AATAACCATC GCAACTGnGC CAnACCTTGT GTTGGCTCGC CGCCTGAATT 240

CAATCCATAA CGTGCTGTAT CTGTAGCAAT AACTAATACT TTTTCATTCG GTCTAGTTGC 300

TAAATAATCT TTAGCTAATT GAATTGCTGG TGTTGCAGCA TAACAAGCTT CTTTCATTTC 360

AAAGCAGCGT GCAAAAGGTT 380

(2) INFORMATION FOR SEQ ID NO: 4203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4203:

GACATGTCAC CAAGAGCATT AGAAGAAGTT ATTTACTTTG CTTCTTATGT TGTTGTAGAT 120

CCAGGTCCAA CTGGTTTAGA AAAGAAAACT TTATTATCTG AAGCTGAATT CAGAGATTAT 180

TATGATAAAT ACCCAGGTCA ATTCGTTGCA AAAATGGGTG CAGAAGGTAT TAAAGATTTA 240

CTTGGAAGAG ATTGATCTTG ACGAGGAACT TAAATTGTTA CGCGATGAGT TGGGAATCAG 300

CTACTGGGTC CAAAGACTTA CTCCGTGGCA ATTAACGGTT TAGAAGTTGT TnGAATCATC 360

CCGTAATCCA GGGTACCACC CTCCnnGGnT GGATTTAGGA 400

(2) INFORMATION FOR SEQ ID NO: 4204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4204:

AAATTCTTCC GCCCTGTAAT TCCTTAACCG CTTCAACGGC ATCGTnAATn TCTTACATTT 60

AGATAAAGAT GCATTGCAAG ATATCGTCAA CTTATTATTA GACGATGTAC AAGTTACATT 120

AGACAAAAAA GGTATTACGA TGGACGTTTC TCAAGATGCG AAAGATTGGT TAATTGAnGA 180

AGGCTATGAT GAAGAATTAG GTGCACGTCC ATTAAGACGT ATTGTTGAAC AGCAAGTACG 240

TGACAAAATT ACAGATTACT ATTTAGATCA TACAGACGTT AAACATGTGG ATATAGATGT 300

TGAGGATAAC GAATTAGTCG TAAAAGGTA 329

(2) INFORMATION FOR SEQ ID NO: 4205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4205:

GGTAAACAAA AAACTTCCCT TTGGAAGCGA ATTATGGAGC GGAAGATAGG ATTTACACCT 60

ATACCTCGTT CCGGGAAGGG CTGTTTCTAA AAGTTGAACT ACTCCCGCAA ATATTAAATT 120

ATGGAGCGGA AGATAGGATT TACACCTATA CCTCATTCCA GGAAGGAATG TATTCTAAGA 180

GTTGAAATAC TCCCGCATTA TTATTAAATT ATGGAGCGGA AGTAGGATTT GCACCTATAC 240

CTCGTTCCGG GAAGGAGCTG TTTCTAAAAG TTGAACTACT ACCGCATAAA CCTGGTGGCG 300

(2) INFORMATION FOR SEQ ID NO: 4206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4206:

TACTTTGTGA ATCCAGAAAA CTTTGAGGAT GTCACTAATA GTGTGAATAT TACATTCCCA 60

AATCCAAATC AATATAAAGT AGAGTTTAAT ACGCCTGATG ATCAAATTAC AACACCGTAT 120

ATAGTAGTTG TTAATGGTCA TATTGATCCG AATAGCAAAG GTGATTTAGC TTTACGTTCA 180

ACTTTATATG GGTATAACTC GAATATAATT TGGCGCTCTA TGTCATGGGA CAACGAnnAG 240

CATTTAATAA CGGATCAGGT TCTGGTGACG GTATCGATAA ACCAGTTGTT CCTGAACACC 300

TGATGAGCCT GGTGAAATTG AACCAATCCA GGGATCAGAT CTGACCCAGG TCAGATCTGG 360

CAGCGATCTA ATCAGnAGCG GTCAGATCGG GnAGGATCAC 400

(2) INFORMATION FOR SEQ ID NO: 4207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 402 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4207:

AAAAAGTTGA GAAAAATGTT TGAATCAGCA AACGTTGTGC AATCGAAATT TCCACACCAT 60

CAAAACCTGC TTTAATCGCG CGTAATGTAG CATCGCnGwk ACTGCTGAAT GATGCTATTG 120

ATTTTCTCAT GAGACATGGC GATAACATCG TGTTtCAATC GGTGAATGCA ATGwCATAGG 180

GCTTGGTCCA TACACCTTTC CAAAATTTAA AATGGCTTGA TTTGAAAAAC GACCAGCATG 240

CGCTACTGGG ATAATAGCGA GGCTACCATG TTGTTTCATC GTAGATCCCA TGTTAGTTAA 300

TCCAGGGATA CAACCATCAT GATCAATATT AAAnCATATC CAACCATTGA CCATAAGGTC 360

AATGTAACAC GCCGGTGACT TCATCCAGCT GAATAGACGC GT 402

(2) INFORMATION FOR SEQ ID NO: 4208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4208:

GAAGAGTTGC AGCAGCAGAT ACAATTTATC CATTCACTCA AGCTGAAAAT GTTTGGTTAC 60

CAAACAAAAA TGACATCATC GAAAAAGCAA AAGAAACTTT AGAATTTTAA TACATTTTAA 120

AAGTTAACGA ATTAGCCGTG ATTTTAGTCT CATTGATTAA AATGAAATnG TTAATTTACG 180

AAATCTTAGG AGGGCAAAAA CGTGGGCATT TGAATTTAGA TTACCCGATA TCGGGGGAAG 240

GTATCCACGA AGGTGAAATT GTAAAATGGT TTGTTAAAGC TGGAGGATAC TATnGGAAGA 300

AGACGATGTT TTAGCTGGAG GTACAAAACC GATAAATCAG TAGTAGAAAT CCCCATCCAC 360

CAGCATCTGG TACnGGTAAG 380

(2) INFORMATION FOR SEQ ID NO: 4209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4209:

AATAAACCTC AGGCTATTCA ATGGCATACA AATTTAACGA ATGAGCGATT CACTACTATC 60

GCACATCGTG GCGCAAGTGG CTATGCACCC GAGCATACGT TTCAAGCATA TGATAAGAGT 120

CATAATGAGT TAAAAGCATC TTATATCGAA ATTGATTTAC AACGTACCAA AGATGGCCAT 180

TTAGTTGCTA TGCATGATGA AACTGTTAAC CGTACAACAA ATGGACACGG TAAAGTTGAG 240

GATTATACCC nTGATGAATT AnAACAGTTA GATGCAGGAA GTTGGTTAAT AAAAAATATC 300

CnAAATACGC CAGAGCAGTA TTAAAATGCT AAAGTACCAC TTAGGTGGAA TTTAGGACGT 360

ATTGGCCCGA TGCCAACnTT TATATTGAAC CAAGCACCTG 400

(2) INFORMATION FOR SEQ ID NO: 4210:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4210:

GCCCACAACC ACAAAGGCTG TAGGCTACAA ATATGGAGAC GGCGGGATTT GAACCCGCGT 60

AAAAGTGATA AACAACCAAC ATGATGCTAG TTTGATTAAG TTTCTTCTAA ACAGACTTCA 180

AACGGCATnG TTAGCATATC CTATTAAGGT TGAATCGCGT TAACAGCACA TAGGAAATGC 240

TGTTAGGCGA TGCAGAGTGC GATTAGGCAG CTACTGCGAA ATTATTGTnT GATTTGCCAG 300

TTATTATnAA CTGTGTGGTG TTGATGACGA 330

(2) INFORMATION FOR SEQ ID NO: 4211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4211:

AAATCATCTT ATGACTGCTT TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC 60

GTTTTCACTT CGCCAAGCCA TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT 120

AAAAAAAGAG ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG 180

TTCTACTCTA GCGGAACGTA AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCnGTG 240

TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC CAGACATATG AATGTAAATT 300

ATACATTCAA AACTAGATAG nAAGTAAAAG TGATTTTGC 339

(2) INFORMATION FOR SEQ ID NO: 4212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4212:

GCGATGGTTG AAACATTGAC TGATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60

TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120

CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180

CGATTTTGGC ATGAAGGTCA CCTnAAATGT ACATTGTTGT AATAAAATTG CCTATAAAAT 240

TTTTAGCACA TAAAATAAGA GGGGCCAnCC ATTTTAGACT ATAACAACGG TTGGCTCTTT 300

GAATTGTAAA AAGAAAACCA TACGCTATGn TATT 334

(2) INFORMATION FOR SEQ ID NO: 4213:

(A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4213:

CTATGATTTC ACCGAGTCTC TCGTTGAGAC AGTGCCCAAA TCGTTACGCC TTTCGTGCGG 60

GTCGTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT ATAGTTACGC CGCCGTTTAC 120

TGGGGCTTCG ATTCGTAGCT TCGCAGAGTA nACCCACTCC TCTTAACCTT CCAGCACCGG 180

GCAGGCGTCA CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT TTGATAAACA 240

GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGGCGTTA ACCCTAAAGA GCACCCCTTC 300

TnCCGAAGTT TACGGGGTCA nTTTGCCGAG TT 332

(2) INFORMATION FOR SEQ ID NO: 4214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4214:

CGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTGGCT ACCATCGTCG CTAAAGACCT 60

TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTACTCATTT 120

AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 180

GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TAnTTTGACG TTTTAGACAT AAAAAAAAGA 240

GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGGCAA CGTTCTACTC 300

TAGCGGAACG TAAGTTGGGT ACCATCGACG CTAAGAACCT TCTTGGAnTG TGGACAACGn 360

TGG 363

(2) INFORMATION FOR SEQ ID NO: 4215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4215:

TTATTTGTAT TGTATAGAGA GAAATAAAAA GAnACCTTGT TTTACAAGGT TTCTAATACG 120

TTATGTTATG TAAATAACAG TTAATTATAC CGGTGGTCGG GGTCGAACCG ACACTCCACA 180

AGTGGAACGG GGATTTTGAG TCCCGCGCGT CTGCCAATTC CGCCACACCG GCTTAATGGT 240

AAACAAAAAA CTTCCCTTTG GAAGCAATTA TGGAGCGGAA GATAGGATTT ACACCTATAC 300

CTCGTTCCGG GAAGGACGTG TTCTAAAAGT TGACTACC 338

(2) INFORMATION FOR SEQ ID NO: 4216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4216:

ACGGTGATCC CATAATGCTT GAACATCAAT TTCATCCATT AATGTTACAT GAGGTGCAGT 60

ATGCTTAGAG TTAACCATTG CTTTCGCAAT TGCTCTACGC ATAGCAGGGA TTTTTTCAGT 120

TGTTTCTGGG AAGTCGCCTT CTAATGTTAC TGCTGCAGGT GCTGCAGGAG TTTCAGCAAC 180

TTCTTCACTT GTAGCTGAAG CAGCTGATTC ATTTGAAGCT GTTGGTGCAC CACCATTTAA 240

GTATGCATCT ACATCTTCTT TTGTAATACG ACCATTTTTA CCAGATCCAG AAACTGCTTT 300

AATGnTAACA CCTnTTTCAC GTGCGTATTA CGACTGAAGG CATGCCTTAA CAGTCnGGTT 360

CACCACTCTC AGTTGAGAGC ACAGGGCTGC nCGCTGGCGC 400

(2) INFORMATION FOR SEQ ID NO: 4217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4217:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60

GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120

CCCATTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180

GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240

TCTATGTTTC CATCCTACAG GAAACGCGTT ATTAATCTTG TGAGTGTnCT TTCGAACATA 300

(2) INFORMATION FOR SEQ ID NO: 4218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4218:

GGCGCCCTCG TGCCAAACAG TGCTCTACCT CCAATAATCA TCACTTGAnG CTAGCCCTAA 60

AGCTATTTCG GAGAGAACCA GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA 120

GTTCATCCGC TCACTTTTCA ACGTAATCGG TTCGGTCCTC CAnTCAGTGT TACCTGAACT 180

TCAACCTGGA CCAAGGGTAG ATCACCTGGn TTCGGGTCTA CGACCAAATA CTAAACGCCC 240

TATTCAGACT CGCTTTCGCT GACGGCTCCA CATTTACTGC TTAACCTTGC ATCAAATCGT 300

AACTCGCCGG TTGCATTCTA CAAAAGGCAC GCCATGCACC CATTA 345

(2) INFORMATION FOR SEQ ID NO: 4219:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4219:

TCTTATGACT GCTTTTTATT ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTC 60

ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA 120

AGAGACCTTG CGGTCTCAAT GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC 180

TCTAGCGGAA CGTAAAGTTC GnACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTCG 240

GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGGAAT GTAAATTATA 300

CATTCAAAAC TAGATAGTAA GTAAAGTGGn TTTGCTTCGC AAACCnTTAT TTTGGTTAGT 360

CTTCGTC 367

(2) INFORMATION FOR SEQ ID NO: 4220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4220:

AAGAGCCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCACTT 60

ACTCATTTAG CTCTACTAAA CTCGTTGCGT TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 120

TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTGCTTTTTA TTTTGACGTT TTAGACATAA 180

nAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT 240

TCACTCTAGC GGAAnTAAGT CGAACTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGTT 300

CGGCATGGGA ACAGGTGTGA CCCCCnTGGC TATAGTCACC AG 342

(2) INFORMATION FOR SEQ ID NO: 4221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4221:

ACCGGATGAC AGCCCCAGGA TGCGATGAGC CGACATCGAG GTGCCAAACC TCCCCGTCGA 60

TGTGAACTCT TGGGGGAGAT AAGCtGTTAT CCCCGGGGTA GCTTTTATCC gTTGAGCGAT 120

GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 180

AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTTC CAACCATTCT 240

GAGGGAACCT TTTGAGCGCC TCCGTTACCT TTTAnGAGGC GACCGCCCCA GTCAAACTGC 300

CCGCCTGACA CTGTCTCnCA CCACGATAAG TGGCGnG 337

(2) INFORMATION FOR SEQ ID NO: 4222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4222:

GGCGCTTGAC TAAAAAGAAA TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT 60

TTACCAAGCA AAACCGAGTG AATAAAGAGT TTTAAATAAG CTTGAATTCA TAAGAAATAA 120

TCGCTAGTGT TCGAAAGACA TCCACCAAGn TTAATAACGC GTTTAAATCT TTTTATAAAA 180

GAAAACGTTT AGCAGACAAT GAGTTAAATT ATTTTAAAGC AGAGTTTACT TATGTAAATG 240

ACATAGATTA AGTTATTAAG GGCGCACGGT GGGTGCCnTG GCACTTAGAA GCCGCTGAAG 360

G 361

(2) INFORMATION FOR SEQ ID NO: 4223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4223:

CGGTAGAATA CAACCTTGCC AAGGTTGGCG TCGCGGGTTC GAATCCCGTC TTCTGCTCCA 60

TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC TTAAAATCCT GCGGTGAGAG 120

ATCACCGTAC CGGTTCGATT CCGGTCCTCG GCACCATTTT AGCGCCCGTA GCTCAATTGG 180

ATAGAGCGTT TGACTACGGA TCAAGAGGTT ATGGGTTCGA CTCCTATCGG GCGCGCCATT 240

TTTAAATTAA TTGAATAACG GGAAGTTAGC TCAGCTTGGT AGAGCACTTG GTTTGGGGAC 300

CAAGGGTCGC AGTTCGAATC CTGTCTTCCC GATTACTCnT AAnTCCATTT AnGGGGGCTA 360

GCTCAGTGGG GAGAGCGCTG CTTGCACGCA GGAGGTCACG 400

(2) INFORMATION FOR SEQ ID NO: 4224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4224:

CATAATATAC TCTTAAGTGT AAAGGGGAAT TTCCTGGGTA ATAATTCGCG TGTGCACCTT 60

GAGTGACTTC TACCATTTTA TAGTCAAATT GCTTTAGTTC GTTTGGTTTA ACGCCGACAC 120

TCGCAAATGT ATAATCAAAG AACTTCACAA TATTGTTGCC TAAGAAGCCT TTGAATTCAA 180

TAGTGTCATT TCCAGCAATT TGTTCGGCAA CAATACTTGC TGCACGGGTG AGCGCCCCCA 240

GnCAAAAGGA CCACTAGCCG GTAGAATCGA CATGTCGATA ATGTGATGGT TGCCAATAAT 300

CGCCTATTGC ATAATGTTTG GACCATTGGT TCCAAATTTA TCGTTACCGG TATGAAACCT 360

TTCGATCCAG TTGGATAATT GAACTTCGnA AATTTGATTG 400

(2) INFORMATION FOR SEQ ID NO: 4225:

(A) LENGTH: 328 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4225:

GGGTTCAATT TCTGCATACC AATCGATGCC AGCTCTATTT CTGACAATAT CCATATATTT 60

TGAAATTTTC TCTAATTCTT TGCCACTAAC CTTTTCACCA TTCAACCAAA ATTGATCCTG 120

TGTTAACTGG TCGTTAAAAG TGACTTTCGT TTCAGTGTAA AATTTTTCTA ATGTAACAGA 180

TATGCTATTA TTCATTGGAA TGATTAGTGC TTCATCTTTT TTACCCCAAT ATTTTATnAG 240

TGCAATATTC GTATGTGCAC GTGCTTTGCC ACTnnTAATC AACGCATTAA CCTCCTAAAT 300

TCTCAATCCA AGTATGTGCT GCACCAGC 328

(2) INFORMATION FOR SEQ ID NO: 4226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4226:

TGACGGGTTC GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA 60

TTCTCCGATT TAAAACTGCC TGGCAACGTT CTACTCTAGC GGAAnGTAAG TTCGnACTAC 120

CATCGACGCT AAGGAGCTTA ACTnCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180

TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 240

GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 300

TCCACATGTC ACCATGCTTC CACCT 325

(2) INFORMATION FOR SEQ ID NO: 4227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4227:

GCGCAACTCA CACAACAAGG TGGCAATCAC TCTGAACAAA GTGCGGCAAn TTnTTCAACA 60

AACCTTACGC AAGAAGCACG TGACGGTTTA TTAGATCCAG TCATTGGTCG TGGATAAAGA 180

AATTCAAGnA ACTGCTGAAG TTTTAAGTAG ACGAACTAAA AACAATCCTA TATTAGTTGG 240

AGAAGCTGGT GTTGGTAAAA CTGCGATTGT TGGAAGGTTT AGCACAGGCA ATCGTTGGAA 300

GGAAATGTAC CAGCAGCAAT CAAAGACAAA G 331

(2) INFORMATION FOR SEQ ID NO: 4228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4228:

AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCATTAATA ATAAGGGCGG CTGAAGGGGA 60

TCGAACCCTC GAATGTCGGA ACCACAATCC GATGTGTTAA CnCTTCACCA CAGCCGCCAT 120

GGCAGGGGCA GTAGGAATCG AACCCACACC AAAGTTTTGG AGACCTCTAT TCTACCGTTG 180

AACTATGCCC CTATTAAAAA TAATAAATGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA 240

AGAGCGGATT TACAGTCCGC CGCGTTTAnC CACTTCGCTA CCCCTCCATA AATGGTGCCG 300

GCCAGAGGAC TTGnAACCCC CAACCTAATG GTT 333

(2) INFORMATION FOR SEQ ID NO: 4229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4229:

CTCTTACTTT GTAAACCAAA TCTTAAATTA AAATATTGAA AATGCAATGn ATCCTTAATA 60

TTTTATTAAA CCTATAATTA CTTATTAAAA ATAACACACA ATATTCATAA AGTTTTAAAA 120

ATATTCTGTT TTATCACCTA CTATTAGTGG AAAAGTACAA TTGCAATTGT ATATAGTTTG 180

CATAACGCTT CAAAAGTAAT TTCTTTTTTG TTTAGTTCAA AAAAATTTAG AGGTGATGTT 240

ATATGAATAA CGGTTTTTTC AATAGCGACT TTGATTCAAT TTTTCGAGGA TGATGAAAGA 300

TATGCAAGGT TCAAATCAAG TCGGAAACAA AAGTACTATA TTnATGGTAA GGAGTTTCAC 360

CTGAGGACTG GCGCAACTnC ACACACCAGG TGGCCATCAC 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4230:

CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTC ACTCCCCTTC 60

CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGTTCACT ATCGGTCACT AGAGAGTATT 120

TAGCCTTAGG AGATGGTCCT CCCAGATTCC GACGGAATTT CACGTGCTCC GTCGTACTCA 180

GGATCCACTC AAGAGAGACA ACATTTTCGA CTACAGGATT ATTACCTTCT TTGATTCATC 240

TTTcCAGATG ATTCGTCTAA TGTCGTCCTT TGTAACTCCG TATAGAGTGT CCTAsAACCC 300

CAACAAGCAA GCTTGTTGGT TTGGGnTCTT GCCGTTTCG 339

(2) INFORMATION FOR SEQ ID NO: 4231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4231:

GAAGTCATAT GCATACACTT GGTTATCATT ATTCATACGT TCAATCGCAT CTGTTAACTG 60

AATTTCGTTA CCTGCGCCTT CTTTTTGCGT TTTTAAATAA TCGAAAATTT CAGGCGTTAA 120

TACATAACGT CCCATAATAG CTAGGnTTGA TGGTGCCGTA CCTTGTGCTG GCTTTTCAAC 180

AAACTTTTTC ACTTCAGACT GACGTCCGTn TTTAGTTAAT GGGTCAATAA TTCCATAACG 240

ATGAGTATCT GCTTCCGGAA CTTCTTGGAC ACCTATAACT GAGTGCCCTG TnTCTTCATA 300

AACGTCAATC AACTGTTTCA CTGCTGGCAC TTCAGAGTCA ACAATATCG 349

(2) INFORMATION FOR SEQ ID NO: 4232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4232:

CCAGGATGCG ATGACCGACA TCGAkGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120

GAGATAAGCC TGTTATCCCC GGGGTAGCTT TTATCCGTTG aGCGATGGCC CTTCCATGCG 180

GAACCACCGG ATCACTAAGT CCGTCTTTCG ACCCTGCTCG ACTTGTAGGT CTCGCAkTCA 240

AGCTCCCTTA TGcCTTTACA CTCTATGAAT GATTTCCAAC CATTCTGAGG GAACTTTGaG 300

CGCCTCCGTT ACCTTTTAGG AGGCGACCGC CCAGTCAAAC TGCCCGCCTG ACACTGTCTC 360

CCACCACGAT AAGGTCG 377

(2) INFORMATION FOR SEQ ID NO: 4233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4233:

GGCTAGCCTC AAGTGATGAT TATTGGAGGT AGAGCACTGT TTGGACGAAG GGCCCCTCTC 60

GGGTTACCGA AGTTCAGACA AACTCCGAAT GCCAATTAAG TTTAACTTGG GAGTCAGAAC 120

ATGGGTGATA AGGTCCGTGT TCGAAAGGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 180

AATATATGTT AAGTGGAAAA GGATGTGGCG TGGCCCAGAC AACTAGGATG TTGGCTTAGG 240

AAGCAGCCGT CATTTAnAGA GTGCGTAATA GCGCACTAGT CGAGTGACAC TGGGGGGAAA 300

GGGTACCGGG GCTGAACATA TTACCGAAGC TGGTGGGTTG TCCTTTGGAC AnTTn 355

(2) INFORMATION FOR SEQ ID NO: 4234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4234:

ATCCGCCTCC CGCAATATTT TATAGGTCTC GTAGTGTAGC GnTTAACACG CCTGCCTGTC 60

ACGCAGAGAT CGCGGGTTCG ATTCCCGTCG AGACCGCCAT CATTACATTT TTATTATGGT 120

TCAGTAGCTC AGTTGGTAGA GCAATGGATT GAAGCTCCAT GTGTCGGCAG TTCGACTCTG 180

TCCTGAACCA TTTCTTAGCC GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCAGT 240

AGGTTGGGGG TTCAAGTCCT CTGGCCGGCA CCATTTATGG AGGGGTAACG AnTGGGCTAA 300

TTAATAATTT TAATAAGGGG CATAnTTCAA CGGTAnAATA 400

(2) INFORMATION FOR SEQ ID NO: 4235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4235:

ATGCCATGTT CACCTTGTTT AAAATCAAGG TTTGTAATGT TTCCTTGTGT CACGATAATA 60

GGCGTAATAT CACTCTTTGC ATGATTGCGG ATGTAGTCTA AATCAAAGTT GATTAATAAA 120

TCACCTTCTT TAACTnnTTG ACCTTCCTCA ACATGTAAAG TAAAGCCTTC TCCGTTTAAT 180

TTAACAGTGT CTAAACCGAT GTGGATTAAT AGTTCTAAAC CACTATCTGA TACAAGACCA 240

ATTGCATGnT TTGTTGGGAA AATCATTTGT ACTTTACCGT TGAATGGTGC ACGAACTTCA 300

CCTTGTGAGG TTTGATAGCG ATACCGTCAC CCATGCATTT T 341

(2) INFORMATION FOR SEQ ID NO: 4236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4236:

GTTGATGCAG CCCGTTGAGC TCTAAACCAA CTGAGCTAAA GGTCCTAAAT ATAATTTTAC 60

AACTAATAAA TAGTGGCGGT GGAGGGGATC GAACCCCCGA CCTCACGGGT ATGAACCGTA 120

CGCTCTAGCC AGCTGAGCTA CACCGCCTTA TATAGTTTGT AAATAATATG GTGGAGACTA 180

GCGGGATCGA ACCGCTGGAC CTCCTGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAG 240

CCCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTCG AACCTGCGAC CCCTTGGTCC 300

CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGnGC CCGTAGGAGT 360

TGAACCCATG AACCTnTTGA TCCnTAGTnC AAACGGTCTA 400

(2) INFORMATION FOR SEQ ID NO: 4237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4237:

nAnTTCTTGA CCTGACATCA CCTGAAATTG AATGGACATG GTCCACCAGG TCATATACTC 60

TAATCCATGG GTCGCCGATA CCTTCAACGn ACAACATCTA CACCACTATT TCTAATACAG 120

AATCTTTCTC CTGCACTACC GTTAATAAAT GCCTTACCAC TTGTCGCACC ATAGAATGAG 180

ACGTTACCAG CAATAATTTC ATTTTGTCGT TCTTCAAAAG GTGCTTTGAC AATGACCGTA 240

CCACCAGATA ATCCTTTACC AACATAGTCA TTCGCATCTC CAGTATGATG AATCATTAAG 300

CCTTTCGGTG CATATGCTGC AAGACTTTGA CCAGCATGAC CATTCGTATA AACATTAATT 360

GTATTTTCAG GAAGTC 376

(2) INFORMATION FOR SEQ ID NO: 4238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4238:

CGATTTAAAG CTAAGCCCAT TTTCGCTCTT TCTCCATAGC CTAACCAAGC AATACGTGAT 60

GGTAGTCCTT GATATGAAAT TTTTTCTTCA GCTAAATCAA GCCATCTTAA TAACTTTTCA 120

TTTTCTGGGA AAAGTTTGCG CATTTCTTCA TCCGCACGCT CGATATCTTT TGGATCACCA 180

CTCAACGCAG CAAAGCGGAA TGGCCCTTTA CCTTCACAGA ATAATGGTCT AATGTAAGCT 240

GGTACAAAAG CTGGGAAGTC AnAAAGCATT TTTCACTCCG TATTGAAGGC TACTTGACGA 300

TATGnTACCA TAATCAATGC TACAGCGCCA CGTTG 335

(2) INFORMATION FOR SEQ ID NO: 4239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4239:

CCACAnTTAC AAGCAACTAC TGAAGGCGCT GTATTTATTA AAGGTGGCGA CGGTTTTGAT 60

TTCGGACACG TAGAAAGATT TATTCAAAAC CCGCCACATG GGGCAACGGT TGCATGGCAT 120

TTACCTAATG GTCAAGGTAC GCGTAATGTT GAAGTTCCAG TCAAAGTTTA TCCAGTTGCT 240

AATGCAAAGG CGCCATCACG TGATGTGAAA GGTCAAAATT TGCTGTTGGA CGGATGCGAT 300

GAACTACATT ACATTTGTCC AnTACAACAC AGATnGTATC ACTGCAGC 348

(2) INFORMATION FOR SEQ ID NO: 4240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4240:

TTGATGTTAA AGATTTAGCA AGGGGCGAGA GAACTGGAGA AGAGGTTGCC AAACGAATGG 60

AACGTGCTTC TGTATTGGCC CAAGTAGATA TTCATCGTGC AGCAACACAT AATAAAGGTG 120

TTATGAATGG CATACATGCT GTTGTTTTAG CAACAGGAAA TGATACGCGT GGTGCAGAAG 180

CAAGTGCGCA TGCATTACGC GAGTTCGTGA CGGACAGTAT CGTGGTATTG CTACATGGCG 240

TTACGATCAA GATCGTTCAA CGATTTGATT GGTACATTGG AAGTGCCTAT GACATTGGCA 300

ATCGTTGGCG GTGGGTACAA AAGTATTACC AATTGCTAAG CCTTCATTAG GAGnTACTAA 360

ATGGTAGAGT CCGCCCCAAG AATTAnGnCC CTGTA 395

(2) INFORMATION FOR SEQ ID NO: 4241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4241:

ACTAATGATT TATTATGTAG TGGTTCTTTG TCATTAGCCA CAGCTATTGT GTACTTAAAA 60

ATAGGAATGC ATGAGTGCAA CTCTAnAnGn AGCATACTAA TTTCTAAAGA AAAAGTATTT 120

CTTTATGTTG GGGCCCCGCC AACTTGCATT GTTTGTAGAA TTTCTTTTCG AAATTCTTTA 180

TGTTGGGGCC CCGCCAACTT GCATTGTTTG TAGAATTTCT TTTCGAAATT CTTTATGTTG 240

GGGCCCCGCC AACTAATTCC AATATATCAT TGTAGAGCTT AGGTCATTGA TTTTTGGCTC 300

GGACTTTTAT GGCGATATGA ACCATGTAAA T 331

(2) INFORMATION FOR SEQ ID NO: 4242:

(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4242:

TGCATTGCAT TATTGTACTG CGTAATTGTA CCTGGCTTTT TACCTTCAGT GCTTACTGGA 60

TCATCTAAAT GATTTTTAGC TGTGATTAAC TCACGTTTAT CCGCTTTTGT GAAAATGGAC 120

TCTTGTACTT CTTCAGTACT ACCATCATTG TAAGTTACTG TCACAGGAAT CGTCGTTGTG 180

CTACCACCAG CTAAATTAGT AGGCATTGCT GTGCCATTTT TAATCGTTGC AGTACGTTTA 240

TTAGCAACTT GAACTGCATT GTTAATTTCA GCTGCTGTTA CATTTGAACC ATAATCTTTC 300

ACAATTnCAG TTGTGTTGAC AGATGAGnGG CGGTGCAGTA AGGACTGGAT ACACTACGAG 360

TGACCGGACT GCTTCGGGnA ATGTGATGA 389

(2) INFORMATION FOR SEQ ID NO: 4243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4243:

ATACGCATGT TAACGATCGA ATGCTTAATG TCCCGGGAAA TAAATCTATC ATAAGTTACT 60

TTAATGAAGT TGTCTCACGA CAAGGTAATC ATGTTGCGCT ATCATGAATG ATTTGACAAT 120

GACGTATGAA CATTACGCAA CTATGTGGAT GCCATTGCGC ACATGCTCCT ATCAAATGGT 180

GTGGGCAATG GTCAACGGGT TGCCTTGTTT ACAGAACGTn TTTTGGAAAT GATTGCGGCG 240

ATGTTGGCGA CAGTTAAAGT AGGTGCATCT TATATACCTA TCGATATTGA TTTTCCGAAT 300

AAACGACAAG GTGCAATTTT GG 322

(2) INFORMATION FOR SEQ ID NO: 4244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4244:

CAGTTCTCCG GGTGTGCCTT CTGTATATGC TATGTATTCA CATATCGATA ACATGACATA 120

ACTCATGCTG GGTTTCCCCA TTCGGAAATC TCTGGATCAA AGCTTACTTA CAGCTCCCCA 180

AAGCATATCG TCGTTAGTAA CGTCCTTCAT TGGCTTCTAG TGCCAAGGCA TCCACCGTGC 240

GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTTATAA GTCAAACGTT AACATGAAGT 300

TACGTTCTTT TATAAAAAGA TTTAAACGCG TTATTAATC 339

(2) INFORMATION FOR SEQ ID NO: 4245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4245:

CCATTAACGG GCTCTGACTA CTTGTAAGCA CACGGTTTCA GGTTCTATTT CACTCCCCTT 60

CCGGGGTGCT TTTCACCTTT CCCTCACGGT ACTGGTTCAC TATCGGTCAC TAGAGAGTAT 120

TTAGCCTTAC GAGATGGTCC TCCCAGATTC CGACGGAATT TCACGTGCTC CGTCGTACTC 180

AGGATCCACT CAAGACAGAC AACATTTTCG ACTACAGGGA TTATTACCTT CTTTGGATTC 240

ATCTTTCCAG ATGATTCGTC TAATGTCGTC CTTTGTAACT CCGTATAGAG TGTCCTACAA 300

CCCCAACAAG CAAGCTTGTT GGTnTTGGGC nACTTCCCGG TTTCGGTTCG GCCGCnAA 358

(2) INFORMATION FOR SEQ ID NO: 4246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4246:

AAAGAGACCT TGCGGTTAGA TGCGGCTCAT CGCATCCATT TTTTGCCTGG CAACGTTCTA 60

CTCTAGCGGA ACGTAAGTnG AnCTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCGG 120

CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180

TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG 240

TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGGAACCTA 300

TTAACCTCAT GCATCTTTGA GGGGnGCTTG ATAACCGA 338

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4247:

CCCCGGGTAG CTTTTATCCG TTGAGCGATG GCCCTTCCAT GCGGAACCAC CGGATCACTA 60

AGTCCGTCTT TCGACCCTGC TCGACTTGTA GGTCTCGCAG TCAAGCTCCC TTATGCCTTT 120

ACACTCTATG AATGATTTCC AACCATTCTG AGGGAACTTT GAGCGCCTCC GTTACCTTTT 180

AGGAGGCGAC CGCCCAGTCA AACTGCCCGC CTGACACTGT CTCCCACCAC GATAAnGGCG 240

GGGGTTAGAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCTCCACG TAACTAnCGC 300

TCACGTTTCA AAGnTCTACC TATCCTGTAC A 331

(2) INFORMATION FOR SEQ ID NO: 4248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4248:

ATAATCATAC AGATGGCAAT ACAACAGCAA CTGAGACAGT GTCAAACGCT AATAATAATG 60

ATGTAGTGTC GAATAATACC GCATTAAATG TACCAACTAA AACAAATGAA AATGGTTCAG 120

GAGGACATCT AACTTTAAAG GAAATTCAAG AAGATGTTCG TCATTCTTCA AATAAACCAG 180

AGCTAGTTGC AATTGCTGAA CCAGCATGCT AATAGACCGA AAAAGAGAAG TAGACGTGCG 240

GCACCGGCAG ATnCCTAAAT GCAACTTCCA GCCAGATCCA GCGGCTGCAG CGGTAnGGAA 300

ACGGTGGTGC CACCAGTTTG CCAATTTACA GCGCCCATAT TACGCCAACA ACTGGTnCCC 360

TAATGCCCAA T 371

(2) INFORMATION FOR SEQ ID NO: 4249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AATTGCATGG CATAACATCG GCGATTAAAA GATGGACGTT TTGATGATGT ACAACAAGAC 60

ATTGAAGCAG TGGTGAAAGC TGCGAAGGTC ACACAGTAAA AGTGATTATT GAGACGGTAT 120

TGTTGGACCA TGACGAAATT GTAAAAGCGA GTGAATTAAC AAAAGCGGCT GGTGCGGACT 180

TCGTTAAAAC TTCAACAGGT TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAATTAAT 240

GAAAGATACA GTAGGTGCTG ATATAGAAGT AAAAGCTCAG GTGGCGTACG TATTnTAGAA 300

GTTTCAATGA AnGGTTGAAG CAGGTGCGAC ACGTAnTGGT GCGAGCGCAG CGTTCAA 357

(2) INFORMATION FOR SEQ ID NO: 4250:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4250:

GAGCCCAAAC CAACAAGCTT GCTTGTTGGG nGTTGTAGGA CACTCTATAC GGAGTTACAA 60

AGGACGACAT TAGACGAATC ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT 120

CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAACACGTGA AATTCCGTCG 180

GAATCTGGGA GGACCATCTC CTAAGGCTGA ATACTCTCTA GTGACCGATA GTGAAGnAGT 240

ACCGTGAGGG AAAGGTGAAA AGCACCCCGG GAAGGGGAAG TGAAATAGAA GCTGGAAACC 300

GGTGTGCTTA CAAGGTAGTC AnAGCCCGTT AATGGGTGAT GGCGTGCCTT TT 352

(2) INFORMATION FOR SEQ ID NO: 4251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4251:

CATTTACTGC TTAACCTTGC ATCAnATCGT AACTCGCCGG TTCATTCTAC AAAAGGCACG 60

CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTCAC 120

TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 180

AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 240

CGTACTCAGG ATCCACTCAA GAGAGACAAC ATnTTCGACT ACAGGATTAT TACCTTCTTT 300

(2) INFORMATION FOR SEQ ID NO: 4252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4252:

TATTTGATAT TTTGTGCATT GCAGTCAAAC CATGGCGGAA ATTGAACCAA TACCATTGCT 60

AATTTTTTCT GTGTATGTAA GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTnGC 120

CTTGTATCTG CAAATGTTTT GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC 180

ACAAATTCAA ATGTATCAGG CGTTTCTTTT ATCCATTTCA ATATATTTCT TTCCGGTTGT 240

ATCGCATAGT ATGTCGCATC TAATTCGCAA CCGGAAAATG TCCAGCATAT GTTTTAAGGT 300

TATCGGTTTG GCGTTCTAAA TCTGCATATA ATGAATAGTG ATCACCCCAA CCTGTTAAAT 360

CCGATGGTTA TCCAnATGAT GATCACCATG TCATCAnACC 400

(2) INFORMATION FOR SEQ ID NO: 4253:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4253:

AAAGGTATCA AAGATGTTAA AGTTACTTTA TTAAATGAAA AAGGCGAAGT AATTGGnACA 60

ACTAAAACAG ATGAAAATGG TAAATACTGC TTTGATAATT TAGATAGCGG TAAATACAAA 120

GTTATTTTTG AnAAGCCTGC TGGCTTAAAC ACAAACAGTT ACAAATACAA CTGAAGATGA 180

TAAAGATGCA GATGGTGGCG AGTTGACGTA ACAATTACGG ATCATGATGA TTTCACACTT 240

GATAACGGAT ACTTCGAGGG GATGACATCA GACAGCGATT CAGACTCCAG ATAGTGACTC 300

AGnCAGCGAC TCAGACTTCA GACAGCG 327

(2) INFORMATION FOR SEQ ID NO: 4254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4254:

AGATGACATT AAATAGCATC TCCTCGTGTT GATTATTTTG GTTGGCTGAC CAATATTTAT 60

TCTAGCACGT AGAGATGCAT TTTTTGTGAC AATGGTAGAA CCTTTTCTGA ACCATACGCA 120

TAGGATTGTn CTnTTTTACA ATTAAAGAGC CAACCGTTGT TATAGTCTAA CAATGGTTGC 180

CCTCTTATTT TATGTGGCTA AAAATTTATA GGCAATTTTA TTACAACAAT GTACATTTAA 240

GGTGACCTTC ATGCCAAAAT CGCATCACTC ATTTAATGGA AGCAGCACGT CTTCATATAA 300

AGTACCGATC CCTAATTCCA ACGCATGTnG 330

(2) INFORMATION FOR SEQ ID NO: 4255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4255:

ATTAGTGATT GTAAAAAAGT AAAACTATTC TTGGGAGTCG GACATAAATC AATGTCTAGA 60

CTCTATAGTG TTGTATTTGG CAGTAGTTGA CGGGGCCCCA ACATAAAGAA ATACTTTTTC 120

TTTAGAAATT AGTATTTCTT ATACATGAGT TTTACTCAGG ATATCCTATT TTTAAATACA 180

CATTAGCTGT GTTTAATGAT AAAGAACCAC TACATCATAA ATCTTTAATG GTTCTTTATC 240

AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTTAAATCAA TATAATTCAA AAAAGGGTCG 300

AAGATATGAn ATCACATCTT CGACCCTTnn TTGTACTAAT TTAA 344

(2) INFORMATION FOR SEQ ID NO: 4256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4256:

CCAGTAATAT CTAAATGAGT TGGATATTTA ACTTTCGCAT TAATTTCAAT ATTAAATTGC 60

GTTACCGCGA CAAGnCATnA CACAACATAC ATAATAAGAT TGGCTAAAAA GATATAGTTA 120

AAGCTAAATT CTGCGACAAA GCCGCCCATT GCAGCACCGA CAGCCACACC AATATTTTGC 180

GCTAAGTATA TCGCATTAAA CGTTTGTCTT CCGCCATTTG GCCACACTGC TCCAGCCATA 240

TACCAAGGCC ACCCGTGGAn AGA 323

(2) INFORMATION FOR SEQ ID NO: 4257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4257:

GCTGACTTTC CACCAGCCTC TGTGTTGGGG CCCCGACTAT TTTTGAAAAG AGCGTGTTAC 60

ACGGTCATTG TTTTACAGTC AACTACTGCT AAAATAAAAT TAACGAGCTT AGGGCTTTGT 120

TTTCTGTCCC AAGCTCGTTA AATCACATAT GATAATTAAT TATGCCCAAC CACGATATCT 180

AGCTGCTTCT GCTGTACGTT TAATACCTAT GGATATATGC TGCAnTCTGC ATATCTATTT 240

TTCGGTTTTG AGACAATTCG TAAATCGTAT CAAATGCCGC TTCTAATTTT TnCACGTGGC 300

TTTTGCATTG AACTTCTTCT nGCAGGACCA ATAATAACCT TGGATTATTT TGTGACCCAT 360

GCGGAGTGA 369

(2) INFORMATION FOR SEQ ID NO: 4258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4258:

CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60

TTTTTAAATA CTAAAATACA TGTTGGAATA CTTGTCCCAT AGAAAATATT GGCTGGTAAC 120

CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGAAT CACACCTTCT 180

GCGGCACCAC GAATAATACA CCATGnGGAG TACGACGCCA nGTACCTTCA TCGTCTAGTA 240

ATGTACCAGT GTTGAATAAA GCAAAGTCTG CTTTGATTTT GGCGCAACTT GCCGTAACCA 300

CTGAATCGTT CATCATTTCA AATTTGAACT GCTGT 335

(2) INFORMATION FOR SEQ ID NO: 4259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4259:

ATTTCGCTAC CTTACGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTCGTA 60

GCTTCGCAGC nACAACCACT CCTCTTAACC TTCCAGCACC GGGCAGGCGT CACCCTATAC 120

ATCACCTTAC GGTTTAGCAG AGACCTGTGT TTTTGATAAA CAGTCGCTTG GGCCTATTCA 180

CTGCGGnTCT TCTGGGCGTT AACCCTAAAG AGCACCCCTT CTCCCGAAGT TACGGGGTCA 240

TTTTGCCGAG TTCCTTAACG AGAGTTCGCT CGCTCACCTT AGAnTTCTCA TCTTGACTAC 300

CTGTGTCGGT TTGCGGTACG GGCA 324

(2) INFORMATION FOR SEQ ID NO: 4260:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4260:

AAGCGGTTGT TAGACAATGC ATTAAGAAAA ATTAAAGCGG AGTTTACTTT TGTAAATGAG 60

CATTTGATTT TTTGAAAATA AAGCAGTATC GGGCGCTTGA CTAAAAAGAA ATTGTACATT 120

GAAAACTAGA TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG 180

TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ACGAGCAAGA 240

TTAATAACGC GTTTAAATCT TTTTATAAAA GAAAACGTTT AGCAGACAAT GAGTTAAnTT 300

ATTTTAAAGC AGAGTTTACT TATGTnAATG GAGCATTGAA AATnATGAAA ACGAGCCCGT 360

ATGTGGAGCG TTTGGACTTA TAAAAATGGT GGGAAACATA 400

(2) INFORMATION FOR SEQ ID NO: 4261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4261:

AATTAATGTG CGAGTTGGGG TGGGACGACG ATAAAGAAAT ACTTTTTCTA TAGAAATTAG 60

TATTTCTTAT GCATGAGTTT TACTCAGTAA TTCCTATTTT TAAGnACACA TTAGCTGTGG 120

CTCCCCTGAG AAGTTTAAAA TTTTATATGT TGGCTTGTTA TGTTAAGGGA ATTAACATGG 240

TTGTCTTGTT TATATTATGT GATTCAAACA TTACTAGTCT TGGTAAATCT AATTCGTAAA 300

ATGCTAAATC TAACCATCTA TTAAATTTAA AACC 334

(2) INFORMATION FOR SEQ ID NO: 4262:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4262:

TTTCGGTCAT ATTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT 60

ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGGCGG TCTCAATGCG GCTCATCGCA 120

TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGnAGTA ATTGGGCTAC CATCGTCGCT 180

AAAGACCTTT CTTGACTTGT GACAATCGCT TGCnTCTTTC CTCTCCTTCG GCTCTCGCTT 240

ACTCATTnAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300

TTCACTTCGC CAAGCCATTT TTCTTTGTGT 330

(2) INFORMATION FOR SEQ ID NO: 4263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4263:

GAGGTATACC CCGGGACGGC TGAAGGGGAT CGAACCCTAC GnAATGTCGG AACCACAATC 60

CGATGTGTTA CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC GAACCCACAC 120

CAAAGGTTTT GGAGACCTCT ATTCTACCGT TGAACTATGC CCCTATTAAA AATAATAAAT 180

GGAGGGGGGC AGATTCGAAC TGCCGAACCC GAAGAGTCGG ATTTACAGTC CGCCGCGTTT 240

AGCCACTTCG CTACCCCTCC ATAAATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 300

TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 339

(2) INFORMATION FOR SEQ ID NO: 4264:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4264:

GTATTTCAAA GTAAAATTAC ATGTTAATAC GTGnTTAATG GGCGAGACTC CTGAGGGAGC 60

AGTGCCAGTC GAAGCCGAGG CTGAGACGGC ACCCTAGGAA AGCGAGCATT CAATACGAGA 120

TnTnATGAAA TAGAGAACAG CAGTAAGATA TTTTCTAATT GAAAATTATC TTACTGCTGT 180

TTTTTAGGGA TTTATGTCCC AGCCTCTTAC TCTAATTATA TTCACTATCA ATTAGACAAA 240

ATGGCCATTT TCAAATATCA CGCGTTGTTT CTGACCTTGA ATATATTTAT TATAATTCTC 300

TTTTTGGAAA ATCAGTTAAC ATTAATTTAG ATGTACCGTA TTTTTAACAC T 351

(2) INFORMATION FOR SEQ ID NO: 4265:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4265:

ATTTTCACTT TAAAACCTGC TTCTTTGGCT TTTTGCATAT AATGTTGCGA TTGTTCTATT 60

GTAAATACAC CTGTTTCACA GAAAATATCC GCAAAGTCTG CATATTGTTT TACTTCCGGA 120

AGTAACGCAA TCATTTCTTC TAAAAATGCC TCATTTGAAC TTGCCTCTTT AGGTACAGCA 180

TGAGGCCCTA GGAAAGTATG TTTCATGTCT AAATCATATT TCTCAGCTAA ACGnTTAGAC 240

ACTTTCAATT GCTTCAGTTC ATTTTCTCTA TCTAATCCAT AAACCACTCT TGACTTTCAA 300

CTGCAGTCAC GCCGTGTTTn AATCCATAGT AAGACAAAnC ATGACT 346

(2) INFORMATION FOR SEQ ID NO: 4266:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4266:

TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT TTATTGAAAA TGGTGCCGAG 60

GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGGAT TTTAAGTCCT GTGCGTCTGC 120

CCAACCTTGG CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA 240

GTCGAACCCC CACGCCGTAA GGnTGAGATC CTAAGTCTAG TGCGTCTGCC AATTCCGCCA 300

CACCCGCCAA TGGTGAGnCA TAGAGGnTTC GAACCTCTGA CCCTCTG 347

(2) INFORMATION FOR SEQ ID NO: 4267:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4267:

GACTTGTTCT CTTGGACCTA TATCATGTTC TTTATTTTCT AATGCAGGAT CTTTAATTGC 60

ATCTTTAAGT GATTCATCCG CTGCAGGATA GTTTTTCGCA GTGTTTGCTG GTTGCGTGAG 120

GTnTGTGTTT GATTTGTATC CTTAGGTGGC TGAGTTGTAG TTGCATTATT ATTTTGATTT 180

TCCGAGATTT TATCTGAAGT ATTTGTATTT TCTGCTGCTT GTGCTTGATG TTGAGAAGTA 240

ATTAAAAATA GTGTACTGAC AATGACCGAT GCAACGCCTA GAGTTGATTT TCTAATAGAA 300

TAGGAAAGAC CnTnAATTTT GGGTGGATGT TTGTTCA 337

(2) INFORMATION FOR SEQ ID NO: 4268:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4268:

ATACATGTTG GAATACTTGT CCCATAGAnA ATATTGGCTG GTAACCCAAT CACGGCTTCT 60

AAGTAGTTCT TTTCTTCTAT TAAATAGCGA CGAATCACAC CTTCTGCGGC ACCACGGAAT 120

AATACACCAT GTGGGAGTAC GACTGCCATG GTACCTTCAT CGTCTAGGTA ATGTACCATG 180

TGTTGAATAA AGGGCAAAGT CTGCTTTGGG ATTTTGGCGC AACTTGGCCG TTAACCACTG 240

GAATCGTTCA TCATTTTTCA nATTTTGGAA TCTGGCTGGT TCCATTTTCG GCACTGGTAT 300

GGTGGGGGTT TCGGCAATAA ACGGCATTCA AATGGTATTT GGCCTAAACA AGGCCGGGAT 360

TTTTCCAATG GGGGTCATCA TTAAnGGGAT CnTCGAAGTT 400

(2) INFORMATION FOR SEQ ID NO: 4269:

(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4269:

GGCTCATCGC ATCCTGGGGC TGTAGTCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAAG 60

CGGTACGGAG CTGGGTTCAG AACGTCGTGA GACAGTTCGG TCCCTATCCG TCGTGGGCGT 120

AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 180

TACCAGTTGT CGTGCCAACG GCATAGCTGG GTAGCTATGT GTGGACGnGA TAAGTGCTGA 240

nAGCATCTAA GCATGAnGCC CCCTCAAGAT GAGATTCCCA ACTTCGGTTA TAAGATCCCT 300

CAAAGATGAT GAGGATATAG GTCGAGGTTG GAGCATGGTA CATGT 345

(2) INFORMATION FOR SEQ ID NO: 4270:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4270:

AAGAATTAAT TATACATTTT ATTAACATTT AAGTCAATAA CTTTTTTTAT CTTGTCCATT 60

TTATTTTTTA ACCAAAATTT GATTAAAAAA CTGCCTGGCA ACGTTCTACT CTAGCGGAAn 120

TAAGTCGaCT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 180

TGACCTCCtT GCTATAGTCA CCAGACATAT GaATGTAATT TATACATTCA AAACTAGATA 240

GTAAGTAAAA GTGGATTTTG CTTCGCAAAc ATTTATTTTG ATTAAGTCTT CGATCGATTA 300

GTATTCGTCA GCTCCaCATG GTCACCAGCT TCCACCTCGA ACCTATTGGn CGCATCATCT 360

CGCAGGGAnC 370

(2) INFORMATION FOR SEQ ID NO: 4271:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4271:

ATTAACAAAA GGCATTGATT TAGAAGGGCG GACATTTTTA CACAATTATG ATTGGCGTAA 120

AGATAAAGAT GGCACATTAT TAAATACCAT CATTTCTGGT CCGGCACTTG TGGCACAATG 180

GaTTAATTTA CAATATTATG CGTCGACAGT TGCGCCGCAT TTTTaCGGtA ATGGGAATAA 240

AGCGACACAA ACCGTCACGT CAGTGTTGGT GTCATGCAAG GTAATGCGAG TGCATCTGAT 300

GTAGGGCTTA TCATGGCCAA TCTGTTA 327

(2) INFORMATION FOR SEQ ID NO: 4272:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4272:

CATTCTTTAA ACTCTGTAAG TACTTCTTCA ATCTCAGGGG CATCTACTAA CATATCATCA 60

GTAATATGCG TCAAATTGAT AATCGTTTCC GATAATCGTT CATGCGGATT ACTAAACCTT 120

TCAAACTTAT CGATGATTTC ACCGTTATGA ACTTTCACAG CTGCAAnTCG ATGATTTTAT 180

CATACTGATT TGATAAACCA GTTGTCTCAA CGTCGAACAC AACATAAGTA GCATCTTTTA 240

ATACGACATC TTGTGGGTTG TATGCAATCG GGAACACCAT CATCAACTAA CATACCTTCC 300

ATACCGGnAT ATCATTTTAA nGCCA 325

(2) INFORMATION FOR SEQ ID NO: 4273:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4273:

TCCGGCCTTG ACCTGAAGAA CACTTGTCTT GTCGTTAAGA TGACTCTAGA CTCTTATGTT 60

TATTATCAAC CGTTAATAAA CTTACCATCA AGAGTGCACC TACCCATACT GACAGTGCAG 120

TATAGAATGG TGTCATACCT GAACCATAAT CCTTAACTGG GAAAACATCA ACAGTCTTCT 180

TATTAATAGG ATTTGCAATA ATACCCGCTT GCTTTTTCAA ATCATTCTTA AGTGTGTCGA 240

TnAATTTGTC GACTGCATCA TCTnTGTCTA ATTTCTTGAA AATTTTGATT CGCTTTTTTC 300

CAAATCCTTn TCCAACATCA GGCAATTTTA TTTTGAGAAA AATCAGCCAA ATCCGGA 357

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4274:

ACGTTAGCAC AAGCCATGAA CCAATTAGGT GGAAAGAGTA ATAGTGGTGA AGGTGGCGAA 60

GATGCAAAAC GTTATGAAGT ACAAGTTGAT GGAAGCAACA AAGTAAGTGC GATTAAACAA 120

GTTGCTTCTG GGCGTTTTGG TGTAACTAGT GATTATTTAC AACATGCCAA AGAAATTCAA 180

ATTAAAGTTG CGCAAGGTGC AAAGCCTGGT GAAGGTGGTC AATTACCTGG TACTAAGGTA 240

TATCCGTGGA TTGCGAnGAC AAGAGGGTCA ACGCCAGGTA TCGGTCTGAT TTCACCACCG 300

CCACATCATG ATATTTnATT CCATAnGAGG ATTTAGCCGC CACCTGATAC CTGGATTTTG 360

GAAAAATGGC GAATTAAGGT TGCnGATTTT CCCCGGGTAA 400

(2) INFORMATION FOR SEQ ID NO: 4275:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4275:

AACGTCGTTA ATTGAATAAC GCTTATGTTA TAAGAGCACT CATACCAAAC CATAATCATC 60

TATAGATATA ACAATTCACG ATATAAGGGC TGTGTTTGGC ATAGCCTTTA GATATACACT 120

TAATTCCTAT TAAAATAGTA GGGATTAAAA GGGGGCTTGT CATGGATTAA AATTCAACAA 180

TTACAACATC ACTTTGGATC ACATAAAGTA ATTCATAACT TTAATTTGGA CATTAGCAAG 240

GGAGAAATAG TCACTTTCAT AGGGGAAAAG TGGTTGCGGA AAGTCTACTT TACTCAATAT 300

TATCGGTGGA TTTnTTCCAT CCATCGnCTG GTCGTGTCCA n 341

(2) INFORMATION FOR SEQ ID NO: 4276:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TAGTGATATA CGACATCACA GCATAATATT GCTTTAGAAA GTCGTGCCGA ACTGGAACTT 60

ACAAGTCTAG TTCGAACACA CACTGATGTG AGTGGTTTTC TTTATTTTAA ACATGAACAA 120

TCAGATAAGT TACTAGCATT AGCAAATATT ATTAAATCAA AGGGCTTCGA TTCATAAAAT 180

TTAAAACAAT GATTAAAATT AGACGTGTAA ATTGTTAAAT TCTAAAACGG AAATAACCAC 240

CATTCCATTA AACCACTTTT TTGTTCATCA CTATATTTCA CACnGCTTCA TTAATAAACG 300

GAATGCTTCA nCCGCTTCAA CTTCAACTGG CTTCAACTTC nGCCTACTTC ATCATACCAA 360

ACGGTCCG 368

(2) INFORMATION FOR SEQ ID NO: 4277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4277:

ATGGAAGTAC GTGACGTTCA CTACTCTCAC TATGGCCGTA TGTGTCCAAT TGAAACACCT 60

GAGGGACCAA ACATTGGATT GATTAACTCA TTATCAAGTT ATGCACGTGT AAATGAATTC 120

GGCTTTATTG AAACACCATA TCGTAAAGTT GATTTAGATA CACATGCTAT CACTGATCAA 180

ATTGACTATT TAACAGCTGA CGAAGAAGAT AGCTATGTTG TAGCACAAGC AAACTCTAAA 240

TTAGATGAnA ATGGTCGTTT CATGGGATGA TGAAGTTGTA TGTCGTTTCC GTGGTAACAA 300

TACAGTnATG GCTAAAGn 318

(2) INFORMATION FOR SEQ ID NO: 4278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4278:

CACTTGTACT TTCTGATGTT GAGCCAGACT CTGATGTACT TACCGATGTA GATAAACTTG 60

CAATGGTCGA CATGCGGTTT GAAGTTGATG TACTTAGCGA ATCACTTAAT GATGCTGATG 120

TGCTTTGTGA ATCGGATTCG CTCGTGCTTG TACTTGTTGA GTTTGAGGCA CTTTGGCTTG 180

CTGAGTTTGA GTCTACTCCG CTTTGATTCA TTGAGGCACT TAGTGACAAT GATGTACTCG 240

TACTTATGCT CATTGGATGT TGAATCGGAT TTACTTTCAC TTGAATGATG TTGAGTCGGA 360

TTCACTTTCA CTTGTAGAAC CACTTAATGA TGTGGGATGT 400

(2) INFORMATION FOR SEQ ID NO: 4279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4279:

TTTGTACTTC GATTTAAAAG ATATTAGACA TAAAATCTAA AAnCAGCAGT AAGATGATTT 60

ATGATTAAAA ACTATCTTAC TGCTGTTCAC TTTTTATAAT ACTTCTGAAT GTCTTCACTT 120

ATACTTCTAG TCACAGATTT AAATAATCAA AAGTGCACAT TATTAAAATA TCAATTTCAC 180

ACTCAATGCG GCTCATCGCA TTCATTTCTT GTCTAGCAAC GTTCTACTCT AGCGGAAGTA 240

AGTTAGCTAC CATCCTCGCT AAGAACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC 300

CTCTCCTTCG GCTCTCGCTT ACTC 324

(2) INFORMATION FOR SEQ ID NO: 4280:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4280:

CTCACTAGTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60

GTGGATTGTC CTTTGGCATG TGnTTAGGAG AGCGTTCTAA GGGCGTTGAA GCATGATCGT 120

AAGGACATGT GGAGCGCTTA GAAGTGAGAA TGCCGGTGTG AGTAGCGAAA GACGGGTGAG 180

AATCCCGTCC ACCGATTGAC TAAGGTTTCC TGnGGAAGGC TCGTCCGCTC TGGGTTAGTC 240

GnGTCCTAAG CTGAGGCCGA CAGTAGGGCG ATGGGATAAC AGGTTGATAT TCCTGTACCA 300

CCTATAATCG TTTAATCGAT GGGGGG 326

(2) INFORMATION FOR SEQ ID NO: 4281:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4281:

TCGAACATGA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACTCG 60

GTTTTGCTTG GTAAAATCTA TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG 120

GTGGGCCTAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGCGTGCG CTCTAACCAG 180

CTGAGCTATA GGCCCATTTT TTTGAATGTT AAATAAACAT TCAAAACTGG AATACAATAT 240

GTCACGTTAT TCCGCATCTT CTGAAGAAGA TGTTCCGAAT ATATCCTTAG AAAGGnAGGT 300

GATCCAGCCG CACCTTCCGA TACGGGCTGA CCTTGTTGAC GACTTGCACC CCAAGCATTT 360

GTGCCCAnCn 370

(2) INFORMATION FOR SEQ ID NO: 4282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4282:

GAGAGATGAC ACGGnACTGA ATTGGTTTGA CACCACGTGA TGAATGTGAT CGTCGGCCTT 60

CTTCACGATT GnAATACTTT TACATCAAGA ACGATACCGC CAGCGCCGTG AGGTACACGT 120

AATGAAGTAT CTCTAACTTC ACGTGCTTTT TCACCAAAGA TTGCATGTAA CAATCTTTCT 180

TCGGCAGTTA ACTCAGTTAC ACCTTTAGGC GTTACTTTAC CAACTAAAAT ATCTCCATCT 240

TTTACTTCTG CACCAATATA AACGATACCA CGATCGTCTA AGTTCTTAAG TGCACTTTCA 300

GAAACATTAG GnATATCTCT TGTGATTTCC TCAGGGCCTA ACTTAGTATC ACGTGCCTCT 360

GAATCCATAC TCCTTCAATA TGAATAGAAG TATACACGGn 400

(2) INFORMATION FOR SEQ ID NO: 4283:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4283:

AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAACA AAGAGAAATT GGATTCCCAA 60

TCTGTCCCAC TCCCGATTAT CTCGTCGCAA TATTTTTTTC AAAGCGATTT AAATCATTAT 180

CATGTCCAAT CATGATTAAA ATATCACCTA TTTCTAAATT AATATTTGGA TTTGGTGAAA 240

TGATGGACTC TTTGCCTCGT TTAATTGCCA TAATGTTAAT nCCATATTGT GCTCTTATAT 300

CTnAATCCAT GATAGACTGn CCCG 324

(2) INFORMATION FOR SEQ ID NO: 4284:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4284:

AAATCGTAAC GAGTGAACTT TCTTATTTAG GTGGCGAAGT AACTTACTAG CACCTGACGA 60

AACGGTTTTA GATCGTATTC AATTGAAAAG GCCGGTATTG AATGAATCAC ACTTAGCAGC 120

GATTGATCAG GAACATTTTA AATTAACTTA TTTATCAACG GTATATGAAG GGGATTTGGC 180

AAGATGCGTT ATAAGCATTA GGCCGTAGAA GCAGTGAAAT GCTGTnAAAC AAGGGCGCTC 240

AAATTCTAGT GTTAGATGAT AGTGGATTAG TTGGATAGCA ATGGCTTTGC AATGCCGATG 300

TTTACTCGCA ATGAAGTGCA TGTGCCATGC AATTGACTTC TTTAAAGCCA GATTTACGTG 360

ATGTCTAACA AGTTTTnTnC GCTAAAATCn GGGTGGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 4285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 560 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4285:

CATTTTTCTT TGTGTTTACT TTTTATTTTG ACGTTTTAGA CATAAAAAAA GAGACTCACG 60

GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC 120

TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCATCTTT CCTCAnCATC GGnTnTAGCT 180

TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT 240

TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA 300

AAAAAAAGAG ACCTTGnCGG TCTCAATGCG GGCTCATCGC ATCCATTTTT TGCCTGGCAA 360

TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA 480

ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATT 540

TTTCTTTGTG TTTACTTTTT 560

(2) INFORMATION FOR SEQ ID NO: 4286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4286:

GTAACACTCG GnATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GTAGCTAATA 60

CCGGATAATA TTTTGAACCG CATGGTTAAA AGTGGAAAGA CGGTCTTGCT GTCACTTATA 120

GATGGATCCG CGCTGCATTA GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA 180

TAGCCGACCT GAGAnGGTGA TCGGCCACAC TGGAACTGAG ACACGGTCCA GACTCCTACG 240

GGAGGCAGCA GTAGGGAATC TTCCGCAATG GGCGAAACTG GACGGAGCAA CGCCGCGTGA 300

TGnATGGAAG GTCTTCGGAT CGTAAAACTC TGTTATT 337

(2) INFORMATION FOR SEQ ID NO: 4287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4287:

CAATCGTGCT CAnTGCGCAT CGTnACTCAT CTGTATGTGT TCCAGCATAT ACAATTTTGC 60

CATCTTTAAT GACAACTGTA CCATTTTTCA CAACATTTAA TTCATCTAAT TCCTTACCCT 120

TCAAAGGTTT ATCTGTTGAT CTCGGTAAAA TTAATTCTGG CTATATGATT AATTATTAAA 180

TCATCATTAC TTATCACCTG CTTTATCAAT CATGGAATAT GAATACCTTT TTCTTTAGCT 240

GTTTGAATAG CGATGTCATA GCCAGCATCA ACATGTCGGG CAACACCCAT ACCTGGGTCA 300

GTCGTCAATA CACGTTCCAA TCTTCTTTCA GCACGCTCTG AATCCATCTG G 351

(2) INFORMATION FOR SEQ ID NO: 4288:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4288:

CTATTCACTG CGGCTCTTCT GGGCGTTAAC CCTAAAGAGC ACCCCTTCTC CCGAAGTTAC 60

GGGGTCATTT TGCCGAGTTC CTTAACGAGA GTTCGCTCGC TCACCTTAGA ATTCTCATCT 120

TGACTACCTG TGTCGGTTTG CGGTACGGGC ACCTATTTTC TATCTAGAGG CTTTTCTCGG 180

CAGTGTGAAA TCAACGACTC GAAGACACAA TGTCTTCTCC CCATCACAGC TCAGCCTTAA 240

CGAGTACCGG ATTTGCCTAA TACTCAGCCT TACTGCTTAG GACGTGCAAT CCAATCGCAC 300

GGTTTnGCCT ATCCTA 316

(2) INFORMATION FOR SEQ ID NO: 4289:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4289:

TTnTTTATGT CTAAAACGTC AAAATAAAAG CAAACACAAA GAAAGATGGC TTGGCGAAGT 60

GAAAACGnTT GAATCTGACG AAACGAGAAA TGTAAAGTAT AATAAAAAGC AGTCATAAGA 120

TGATTTCAAT TAGAAATCAA TTTATGACTG TTTTTCTTAC TATGTGTTAA ATTAACAATG 180

AATATAACAT CTTATTTTCA TTAATATAAA TATTGGAAGG ATCGAnATGA TTTACACGTT 240

GTTTGAGTTG TATTAAATCA TCATGATCTT TAAGTTGAAT ACCAATAATG ACAGTACCTG 300

TATTTTGAGA GATTTTTTAA GT 322

(2) INFORMATION FOR SEQ ID NO: 4290:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4290:

TCATTTAGCT CTACTAAACT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT 60

CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT AGGCATAAAA 120

CTCTAGCGGA AnTAATTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC 240

GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCnACT AAACTCGTTG 300

CGCTCTTnTC TCGTTTCGTC AGATTTCAAA CGTTTTCA 338

(2) INFORMATION FOR SEQ ID NO: 4291:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4291:

AATTGGTTTA CACCAGGTGA TAATGTATCG TCGCCTTCTT CACGATTGAA TACTTTTACA 60

TCAAGAACGA TACCGCCAGC GCCGTGAGGT ACACGTAATG AAGTATCTCT AACTTCACGT 120

GCTTTTTCAC CAAAGATTGC ATGTAACAAT CTTTCTTCGG CAGTTAACTC AGTTACACCT 180

TTAAGGCGTT ACTTTACCAA CTAAAATATC TCCATCTTTT ACTTCTGCAC CAATATAAAC 240

GATACCACGA TCGTCTAAAG TTCTTGAAGT GCACTTTnCA GAAACATTGA GGGAATGATC 300

TCTTGTGATT TCTTCCAGGT CCTAACTTGA GTGATCACGT GGCTTCTGGA TTGCAGACGC 360

TTGCAAGATG GAATGAGAAG TGAnACACGT GCATCCTTGC 400

(2) INFORMATION FOR SEQ ID NO: 4292:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4292:

AAACGTTTTC ACTTCGCCAA GCCATTTTTC TTTGTGTTTA CTTTTTATTT TGACGTTTTA 60

GGCATAAAAA AAAGAGACCT TGCGGTCTCA AATGCGGCTC ATCGCATCCA TTTTTTGCCT 120

GGCAACGTTC TACTCTAGCG GAACGTAATT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 180

GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 240

TACTAAACTC GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA 300

GCCATTTTTC TTTGTGTnnA CTTTnT 326

(2) INFORMATION FOR SEQ ID NO: 4293:

(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4293:

GGGGACAATT CCCTGGGGGT TCAAGTCCTC TCGGGCCGGC ATCAAAATTC TTAATTTAAA 60

TAAGCGGGTG TAGTTTAATG GCAAAACCTC AGCCTTCCAA GCTGATGTTG TGGGTTCGAT 120

TCCCATCACC CGCTCCATAG ATAATTTTAA TGAACATTGA AAACTGAATG ACAATATGTC 180

AACGTTAATT CCAAAAACGT AACTATAAGT TACAAACATT ATTTAGTATT TATGAGCnAA 240

TCAAACATCA TAATTTTTAT GGAGAGTTTG ATCCTGGCTC AGGATGAACG CTGGCGGCGT 300

GCCTAATACA TGCCAGTCGA GCGAACGGAC GAGAAGCCTG CCTCnCnGAT GTTAGC 356

(2) INFORMATION FOR SEQ ID NO: 4294:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4294:

TTATCACCCA TGTTCTGACT CCCAAGTTAA ATTAATTGGC ATTCGGAGTT TGTCTGAATT 60

CGGTAACCCG AGAGGnCCCC TCGTCCAAAC AGTGCTCTAC CTCCAATAAT CATCACTTGA 120

GGCAGCCCTA AAGCTATTTC GGAGAGAACC AGCTATTTCC AGGTTCGATT GGAATTTCTC 180

CGCTACCCTC AGTTCATCCG CTCACTTTTC AACGTAATCG GTTCGGTCCT CCATTCAGTG 240

TTACCTGAAC TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT 300

AAACGCCCTA TTCA 314

(2) INFORMATION FOR SEQ ID NO: 4295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4295:

AAGTGAAAGA ACTCGGCGTG ACACCTATTG CACGATTCGT TGGTTTTAAG GCAGTAGGCG 60

GCAATCTATC TGTTGAAGAC ATTGATTTGA TCGAATTGAA CGAAGCATTT GCTTCTCAAA 180

CGATTGCATC TATTAAAGAA GTAGGTCTAG ATATATCACG TACGAATGTG AATGGTGGCG 240

CTATTGCTTT AGGTCATCCA TTAGGTGCTA CAGGCGCCAA TGTTAACCCG CGCGTTTACC 300

TAATGAAATG GGGTAAACCG nCCCGATAGn CCGTAnCGCA AGGGT 345

(2) INFORMATION FOR SEQ ID NO: 4296:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4296:

TAAATTGATT TCTAATTGAA ATCATCTTAT GACTGCTTTT TATTATACTT TACATTTCTC 60

GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATC TTTCTTTGTG TTTGCTTTTA 120

TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 180

ACTTTTTGCC TGGCAACGTT CTACTCTAGC GGAAnTAATT CGnACTACCA TCGACGCTAA 240

GGAGCTTAAC TTCTGTGTTC GGCATGGGAA CAGGTGTGAC CTCCTTGGCT ATAGTCACCA 300

GACATATGAA TGTnAATTGA TACATTGCAA AACTAGGATA GTGAAGTAAA AGTGATTTTG 360

C 361

(2) INFORMATION FOR SEQ ID NO: 4297:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4297:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACT GTTTTCACTT CGCCAAGCCA 60

TTTTTCTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAAGA GACCTCACGG 120

TCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 180

AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 240

ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300

TTCACTTCGC CAAGCCATTT TnCTTTGTGT nTACTnT 337

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4298:

GTATTCCTCC ATTATTATAG GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA 60

CGGGAATCCT GCGTGACAGn CAGGCGTGTT ACCGCTACAC TACGAGACCA TTAGTAAAAC 120

GGAGGAAGAG GGATTCGAAC CCCCGCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA 180

TCCCTTCAGC CGGACTTGGG TATTCCTnCA AAATTATATG GACCTnGCAG GACTCGAACC 240

TGCGACCGAA CGTTATGAGC CTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT 300

TTTTACAACT AATAAAATAG TGG 323

(2) INFORMATION FOR SEQ ID NO: 4299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4299:

CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT CCATTAAATG 60

AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT AAAATTGCCT 120

ATAAATTTTT AGCACATAAA ATAAGAGGnG CCAACCATTG TTAGACTATA ACAACGGTTG 180

GCTCTTTAAT TGTAAAAAGA AAACCATACG CTATGnTGTT ACAAnGAAAA AGGTTCTACC 240

ATTGTCACAA AAAATGCATC TCTACGTGCT AGAATAAATA TTGGTCAGCC AACCAAAATA 300

ATCAACACGA GGAGATGCTA TTT 323

(2) INFORMATION FOR SEQ ID NO: 4300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4300:

TGAATCCAGA TAAAATTGGA ATGATTAACG CGAATCACTT TTACTACCAA TGTTCCAAAG 120

CTGCTCTGCA AACGCATTGT ACTCTGAGCT TTTTGGATTA AATGAATTTG CTCCAAATAA 180

AAATACAATT GCCATTAAAA TACCACCAGA TATTACAAGT GGCAACATGT TAGAAACACC 240

GTTnCATTGA AGTGTTTGAT AGAATGCTTT ACCTGGGGCT TGAATTTTTC TTGGACTGTG 300

CATTTGAGTT ACCTTTTCTT TGGACCATCA CGGGGCAACA AAAGGTTTGA CGACTTGTGA 360

GCTGAATGGC TTnGnTGAAT GAATT 385

(2) INFORMATION FOR SEQ ID NO: 4301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4301:

TCCTGTACCA CCTATAATCG TTTTAATCGA TGGGGGGACG CATAGGAATA GGCGACGTGA 60

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 120

GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA 180

GAAAAGCCTC TAGATAGAAA ATAGGTGCCC GTACCGCAAA CCGACACAGG TAGTCAAGAT 240

GAGAATTCTA AAGTGAACGA ACGAACTCTC GTTAAGGGAC TCGGCAAAAT GAnCCCGTAA 300

CTTCGGGGAA AAGGGTnCTC TTTAnGGTTA ACGCCCCAAA AAACCGCT 348

(2) INFORMATION FOR SEQ ID NO: 4302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4302:

AATGGAACGT GCTTCTGTAT TGGCCCAAGT AGATATTCAT CGTGCAGCAA CACATAATAA 60

AGGTGTTATG AATGGCATAC ATGCTGTTGT TTTAGCAACA GGGAAATGAT ACGCGTGGTG 120

CAGAAGCAAG TGCGCATGCA TnACGCGAGT CGTGACGGGA CAGTATCGTG GTATTGCTAC 180

ATGGCGTTAC GATCAAGATC GTTCAACGAT TGATTGGTAC AATTGCAAGT GCCTATGGAC 240

ATTGGGCAAT CGTTGGCGGT GGTACAAAAG TATTACCAAT TGCTAAAGCT TCCATTAGGn 300

TTTTGAGCGG CAAAAACTTT GnCAG 385

(2) INFORMATION FOR SEQ ID NO: 4303:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4303:

AGTGCGACGA TTGGTATTTT ACAAGAATTT TATCAACAAG ATTTAATTAG CTTAAACGCA 60

GCAATCCCTG TGTTACTAGG CGATAACATT GGTACCACGA TTACAGCTAT CTTAGCTAGT 120

TTAGCCGGCT CAATCGCTGC AAAACGTGCG GCGCTTGTAC ACGTCATCTT TAACTTAATC 180

GGGGTAATTA TCTTCACAAT TTTCTTGCCA GTTGTGATTC ATTTGATTAG TTTGTTACAA 240

GATTTATGGG CACTTAAAAC CAGCGATGAC GATTGCAGTA TCACATGGnA TCCTTCAACA 300

TAACCAATAC CTTGGATTCC ATTTACCAAT TTGTAGCCnG GTTTAGCATn GGATTGGTTA 360

CCAAGCCTTG TCCC 374

(2) INFORMATION FOR SEQ ID NO: 4304:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4304:

AAAACAGGAT ACTTCGATAA GTTAATGATT TCTGTTGTGA ATCGCGCACC ACGTTTCTTA 60

ATTTTACCGA CTATTATATT AATTGGTATT TTAGGTAGTA CAGCCGGCGA TGCTGCGACA 120

ATTTCTTGCC GCCGCTTGCA GCAATGCTTT TTATTAAAAT TGGCTATCAC CCTATCGCTG 180

GACTAACGAT GGCATATGCT TCCGCTGTTG GAGGATTTGC AGCAAATATA GTTGTTGGTA 240

TGCAAGATGC TTTGGTCTAT TCATTTACAG AACCGGCAAC ACGTATCGTT TCAGATTCTA 300

TTAAAACAAA CGTT 314

(2) INFORMATION FOR SEQ ID NO: 4305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4305:

CGTTGCAGAA TGTGTTGAAA TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG 60

CCATTAATTT ACGGTTACCA ACCAATATAT GGTGATGATC AATCGTTGCT TCAATACCAT 120

GGCCAGGTAC TGCTTTAAAT GTTGTTGTCT CAGTTAATAT TAATTGCTTT TCTTTTGCAT 180

AATTGACAAT GGCTTCTGCC AATGGGTGTT CAGAATCTTT TTCAGCAGTA GCAAGTAGTT 240

GTAGCGTTTG ATTGTCACCA TGATAATCTG TCACGACTGG GACGACCATT TGTAATGGnA 300

nCCGTCCTTA TCTAAAACGA TGGGTATCAA TTTGATGnGG GCGG 344

(2) INFORMATION FOR SEQ ID NO: 4306:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4306:

AGTTTCCCTG AAAATTAATC AAGGACTTAA CATTGCGAGT CAAGGTATTG ATCAAGCTAA 60

TGGACAGTTA AATGATGCCA AAGCTTCGTC ACACAAGTTA GAAGTAGAGT CGGTGATTAT 120

CAAGATGCAA TTCGACGCGC GCAAGATTTA AATCGAAGAA ACCAGCAACA GATTCCTCAA 180

AATAGCGCGG CGAACAACGA AACATCAAAT AGTGCACCTG CAGCTGGTAA TGGTGTAGCA 240

TCAACGCCAC CAAGTGCACC AAGTGGCGAT ACTGCACCAA ATAATAATGT TACGCAAAAT 300

ACCGCACCAG ATGAGTGAAT AATGCGCCTG TATCGACTAC ACCACAAATG ACAnnCCGGG 360

GAAnAGATGG TCAAATTT 378

(2) INFORMATION FOR SEQ ID NO: 4307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4307:

GGACTTGGGT ATTCCTCCAA AATTATATGG ACCTTGCAGG ACTCGAACCT GCGACCGAAC 60

GGTTATGAGC CGTTAGCTCT AACCAACTGA GCTAAAGGTC CTAnATATAA TTTTACAACT 120

CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG 240

GATCGAACCG CTGGACCTCC TGCGTGGCAA AGCAGnCGCT CTCCCAGCTG nGCTAAGCCC 300

CCATAATAAT TACAGTAT 318

(2) INFORMATION FOR SEQ ID NO: 4308:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4308:

TGTACGTTTA ATACCTATGA TATATGCTGC AAGTCTCATA TCTATTTTTC GGTTTTGAGA 60

CAATTCGTAA ATCGTATCAA ATGCCGCTTC TAATTTTTCA CGTAGCTTTT CATTAACTTC 120

TTCTTCAGAC CAATAATAAC CTTGATTATT TTGTACCCAT TCGAAGTAAG AAACCGTTAC 180

ACCACCAGCA CTTGCTAATA CGTCTGGAAC TAATAATATA CCACGTTCAG TTAAAATACG 240

TGTTGCTTCT GGTGTTGTAG GTCCATTAGC AGCTTCAACA ACGATACTAG CTTTAATATC 300

ATGTGCATTG TCCTCnGTAA TTGGGTTGAA TAGCGnGGGA CTAAATGCAC ATCnAATCAA 360

CAATCCTATT GGATGTCCCA AnAATTGTAC GACCAACACC 400

(2) INFORMATION FOR SEQ ID NO: 4309:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4309:

CAAATAAACC AGAGCTAGTT GCAATTGCTG AACCACATCC TAATAGACCG AAAAAGAGAA 60

GTAGACGTGC GGCACCGGCA GATCCTAATG CAACTCCAGC AGATCCAGCG GCTGCAGCGG 120

GTAGGAAACG GTGGTGCACC AGTTGCAATT ACAGCGCCAT ATACGCCAAC AACTGATCCT 180

AATGCCAATA ATGCAGGACA AAATGCACCT AACGAATnGT TGTTCATTTG ATGACAATGG 240

TATTAGACCA AGTACCAACC GTTCTGTGCC ACnTnAAACG TTGTTAATAA CTTGCCGGGC 300

TTCACACTAA TCAATGGTGG CAAAGT 326

(2) INFORMATION FOR SEQ ID NO: 4310:

(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4310:

TCAAAGCGCC AATAACATCT TCTACTGAAG TTTCTTTAGA TTTAGCATTC AGTGATAATG 60

TTATTGTTGC TTTTTCTTCC ATTGGAATAC TTTGATGAAT CGTTAATACA GATAGTTCTA 120

ACTTTGATAT AACATCTAGT ACACGTGCCA ACATACCAAC AATATCAGTT ACATATAAAA 180

TTAATGTAAA TTCTCGATGG TCAAGCATTT TATCGGCTAC TGGAAATATC GTTTCTCTAT 240

ATnTATAAnA AGCACTTCTA GATAGATCAA ACTGTTTAAC GGCATCATAA ATGGnCAATG 300

TCGGATCACT TTT 313

(2) INFORMATION FOR SEQ ID NO: 4311:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4311:

GGTTCGAATC CAGCTAGCCC AGCCATTAGA GCCATTAGCT CAGTTGGTAG AGCATCTGAC 60

TTTTAATCAG AGGGTCAGAG GTTCGAATCC TCTATGGCTC ACTACTTGCA CTTTCCATTT 120

TTGGGAAGTG CTTTTTTTTA GGTTCTCCAC CAAATGTGGT GGGTATATAA TTTAAAGAAC 180

TATTTTTAAA ATACAACTTT TAGAGCTTTT ATTATTAGGC GGCCAGTCCA TTATTGGGGC 240

TGGTTGTCTT CnTTTTTTCT CCTTTGTACA AGCTGAAAAT CATCATTATA CGTGCTTAAA 300

GTGGTGAATT CTGAACCAAA GAATCACTTG ATAATTTATC TATATAATCC TCnATAGACC 360

ATATAATGCT GGAATAATGG ATCTACAnCC TGAGTTCCAn 400

(2) INFORMATION FOR SEQ ID NO: 4312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4312:

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 120

AGGCATCCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 180

ACGCTCACAT ACGGCTTCGT TTTCATTATT TTAAATGCTC ATTTACATAA GTAAACTCTG 240

CTTTAAAATA ATTAACTCAT TGTCTGCnAA ACGTTTTCnT TTATAAAAAG ATTAAACGCG 300

TTATTAAnCT GTGGAGTG 318

(2) INFORMATION FOR SEQ ID NO: 4313:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4313:

ACGGTGATCA CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GCCAGTTCCG CCACCCCGGC 60

ACTATAAAAA TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG 120

TATTCTACCG CTGAACTACT TCTGCATATG CGGGTGAAnG GAGTCGAACC CCCACGCCGT 180

AAGGCATAGA TCCTAAGTCT AGTGCGTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC 240

CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCn 300

AATGGnTCTT CCATGG 316

(2) INFORMATION FOR SEQ ID NO: 4314:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4314:

AGGAAAAGTC GTTGTGATAC ATCAACCAGC TGAAGAAGTA CCACCAGGTG GTGCTAAAAC 60

AATGATTGAA AATGGTGTAT TAGACGGTGT TGATCATGTA TTAGGTGTAC ACGTCATGAG 120

CACAATGAAA ACAGGTAAAA GTGTATTACC AGACCTGGTT ATGTTCAAAC AGGACGCGCA 180

TnCTTCAAAT TGAAAGTCAA GGTAAAGTGG TCATGGTTCA TCACCACATA TGGCCAATGA 240

TGCCATTGTT GCAGGTAGCT ACTTCGTCAC AGCGTTACAA ACAGTGTATC TAGACGACTA 300

GGCCATTTGA ACCGGTGGTT TCACATCGGT CATTTnCCGT AAAAGnCCAT TCCATG 356

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4315:

TATCAGCATT TGTAACTGTT ATTGTTTATA ACTTCTGTGT GAAGCGCAAT ATTACAATTA 60

AAATGCCGAA AGAAGTACCG CCGAATATTT CACAAGTATT TAAGGACTTA ATTCCATTTT 120

CAGCGGTAAT CATCATTCTT TATGCATTAG ATTTAGTCAT CGCAACAGCT TTAAATCAAA 180

TGTAGCGGAA GGnATTTTAA AATTATTCGA ACCATTATTT ACAGCAGCAG ATGGGATGGA 240

TTGGTGTCAC AATTATCCTT GGnGGCCTTT GCATATTCnG GGTTGTAGGG AATCAGGTCC 300

GTCAATGTAG AGCCAGCAAT TGCAGCCATT ACATATGCGA TATCGGAGCG GACTTCAAGT 360

TGCCTCAGCG GAGGACACGC 380

(2) INFORMATION FOR SEQ ID NO: 4316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4316:

GCTCTAGGAT GACTGATTGA ATGTCCATGA ATGAACAACC CCTTTGTTTA ATATCGAGTT 60

TGGCAAATTT ACGTTTATCA GCGTTTCTAT GATCAGTACT TCTACGGGTA GCGTTTCTAT 120

GTAATTTACA TCATCTTAAC ATATAAATAC TTCGCTATTT AATTGAAAAC ATATCCTATT 180

ATTCTTTGTC CGTTCTGACG TTTAATATCT AGCCTTAGGC ATTTCACTTG TTAATGAATT 240

TAACTTTCTT CCACTAACCG TCCCTAAACC CAATCCCGCA ACAGTTTTTA ACTTTTTCGT 300

TGTTGTCCTG ACATCTCATT AAGAAAGTTT ATTCTGCTTA AAACTTATAA TCCACACCCT 360

GAGCAAACGn TnCTTATGAC AGAGTATTAA AATAAGCCGn 400

(2) INFORMATION FOR SEQ ID NO: 4317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4317:

CCTTATTGAT AATGGTATGA GAATATTTGT TCGAGATGGA TGAAGGTAAT GAGTGAGAAA 60

CTGGATTTTT AAAGTATGAG ACAATATTTT AAAAAGTTCA ATTATTAACT TATAAGCAAA 120

TAATTGCTAT AAAAAAGTTT GGACGTGTAC AATTGCAATA TGAAGATTTT AAATTAATTG 180

TAAAGTATCG TGGAGTGGGT AACGTGTCAG AACATGTATA TAATCTTGTG AAAAAGCATC 240

ATTCTGTTAG AAAATTTAAG AATAAACCTT TAAGTGAAGA CGTTGTTAGG AAATTGGTAG 300

GAGCTGGGCA AAGCGCTTCG ACGTCAAGTT TCCTGCCAGC ATACTCCATT ATTGGTTCGG 360

CGGTGGGAGG TTAAnGGAAT TTACGGGGAG GTTCTGGGCA 400

(2) INFORMATION FOR SEQ ID NO: 4318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4318:

TAACTACGTC TCCTGTTTCT GGATTCTTAA TTCCTGGTTT ACCTGGAACT TCCTCTTTCT 60

CTCCTGTTGG TAACTTCGGA TCAAATTCGT CTCGATGACC TGGTGTTATC GTTTCTGGTC 120

CGTATTCTGT TAATTCATTA ATCGGATCTn TTGTGATTTC TTCTTTCGAT TCACCTGTAC 180

TAATAATTTC TCCAGTTAAT GGATTTTTTA GTGTTGGCGT CGTTATTGTC TTCTCACCTn 240

TTTGTCCTTC TCTTGTAACT TTTTCTGTCC CGGTGCTAAA TnCGGATTAA ATTACGGTCT 300

TTCTTGAAGG AATCTCTTC 319

(2) INFORMATION FOR SEQ ID NO: 4319:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4319:

AGGTGCATTG AGAGAATTTG TAAATGACGT ATTAGGACCT CAAGACGATA TTACTAAATT 60

TGAATACTTA AAAAAATCTT CTCAAAATAC AGGTACTGTC AATTATTGGT ATTCAACTTA 120

AAGATCATGA TGATTTAATA CAACTCAAAC AACGTGTnAA ATCATTTCGA TCCTTCCAAT 180

ACAGTCATAA ATTGATTTCT AATTGAAATC ATCTTATGAC TGCTTTTTAT TATACTTTAC 300

ATTTGCTCGT TTCGTCAGAT TGCAAACGTT TTCACTTCGC CAAGCCCATC TTTCnTTGGn 360

GTTTGCCT 368

(2) INFORMATION FOR SEQ ID NO: 4320:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4320:

TAAGTTAGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60

TCCTCTCCTT CGGCTCTCGC TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120

CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180

TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT CTCAACTTGC CTGGCAACGT 240

TCTACTCTAG CGGAAnTAAA GTTGGnCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 300

GACAATCGCT TGCTTCTTTT CCTCTCCTnC GGCTCTCGGT TAACTCA 347

(2) INFORMATION FOR SEQ ID NO: 4321:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4321:

GGGCAAGTTA CAGTGGTGCA TGGTTGTCGT CACTCGTGTC GTGAGATGTT GGGTTAAGTC 60

CCnCAACGAG CGGCAACCCT TAAGCTTAGT TGCCATCATT AAGTTGGGCA CTCTAAGTTG 120

ACTGCCGGTG ACAAACCGTA GGAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180

TTTGGcTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGC GAGTCaAGCA 240

AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGaCTaC ATGaAGCTGG 300

aATCGCTaGT aATCgTGGTC CAGCATGCTA CGGT 334

(2) INFORMATION FOR SEQ ID NO: 4322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4322:

CTGTTAAACG ACTACAGGAA GTATTTACAA TCAAACTAAG CAAAAGTATT CAGATGCCTC 60

AGATAAAGCT TGGGCGCATT CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA 120

CGATATAAAA GTGCAAAGGG TTGGCTAATA GATATGGCTA ATAAATCGCG CTCGAAATGG 180

GATAATATTT CTAGTACAGC ATGGTCGAAT GCAAAATCCG TTTGGAAnGG AGCATCGAAA 240

TGGTTTAGTA nCTCATTACA AnTCTTTAAA GGGTTGGACT GGGGATATGT ATTCAGAGCC 300

CACGATCGTT TTGATGCATT TCAGTTCGGC 330

(2) INFORMATION FOR SEQ ID NO: 4323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4323:

CAATGATGCC ATGAGCAGTG CCTCCTTTAA TAGCATTTTA GCACTGTTTT GTCGTATTTT 60

TAAATATAAA TTTGGAATGA ATAATAAAGT AGTGATTAAA TTAAGTTGTG TGATAGGAAA 120

CTTGGACATC AATCAAAGTA ATAGGCACTA CAACGCTTAT TGGCGGGGCC CCAACAAAGA 180

AGCTGACGAA AAGTCACTTG CAATAATGTG CAAGTCnGGG ATGGGCCCCA ACATAGAGAA 240

ATTGGGTCCG nAATTTCTAC AGACAATGCC AGTTGGCGGG GCCCCCACAT AGAGAATTTC 300

GAAAAGGAAT TCTACCAGCA ATGCCAGTTG GGGGAnG 337

(2) INFORMATION FOR SEQ ID NO: 4324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4324:

TTACTTACTA TCTAGTTTTG AATGTATAAA TTACATTCAT ATGTCTGGTG ACTATAGCAA 60

GGAGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG TCGATGGTAG 120

GCATTGAGAC CGCAAGnTCT TTTTTTTATG TCTAAAACGT CAAAATAAAA AGCAAACACA 240

AAGAAAAATG GCTTGGCGAA GTGAAAACGT TTGAATCTGC CGAACGAGAA AGAGCGnACC 300

GAGTTTAGTA GAnTAAATGA GTAAGCGAGA 330

(2) INFORMATION FOR SEQ ID NO: 4325:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4325:

TTCATCCGCT CACTTTTCAA CGTAATCGGT TCGGTCCTCC ATTCAGTGTT ACCTGAACTT 60

CAACCTGACC AAGGGTAGAT CACCTGGTTT CnGGTCTACG ACAAATACTA AACGCCCTAT 120

TCAGACTCGC TTTCGCTACG GCTCCACATT TACTGCTTAA CCTTGACATC AAATCGTAAC 180

TCGCCGGTTC ATTCTACAAA AGGCACGCCA TCACCCATTA ACGGGCTCTG ACTACTTGTA 240

AGCACACGGT TTCAGGTTCG ATTTCACTCC CCTTCCGGGG TGGCTTTTCA nCTTTCCCTC 300

ACGGnACTGG TTCAC 315

(2) INFORMATION FOR SEQ ID NO: 4326:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4326:

TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT TAnATGCGGC TCATCGCATC 60

CACTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGAACTAC CATCGACGCT 120

AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC TATAGTCACC 180

AGACATATGA ATGTAAATTA TACATTCAAA ACTAGATAGT AAGTAAAAGT GTTTTGCTTC 240

GCAAAACCAT TTATTTTGAT TAAGTCTTCG ATCGnTTAGT ATTCGTCAAC TCCACATGTC 300

ACCATGCTT 309

(2) INFORMATION FOR SEQ ID NO: 4327:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4327:

AAAGCTTATA AACGCTCATC TGACATTGTA GAATTCATGC TTTCAAAAGA CGATATACTA 60

CGACACTCCT ACGAACTTGT CCAAGGATTA CGAAAAGACC TAAGGTTATG TAATTnGCCT 120

AAATTTATTA ATCGTTTAAA TTCAGTTAGT AAAAAGTCTG TGAGTAAGGG TGTATGGAAA 180

GTGGTTAAAT ATTATAGAAA ACATCAAAGG ATGTTAAGAA ATACAATTTA TTACCCAGCA 240

TTTAATAATG GTGCTATAGA AGGAATTAAT AATAAGATnA AATTAATCAA GTGAATTTCT 300

TTTGGTTnCA G 311

(2) INFORMATION FOR SEQ ID NO: 4328:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4328:

TAGCTTCTGC GAGCTAGCGG AATCGAAGCC CCAGTAAACG GCGGCCGTAA CTATAACGGT 60

CCTAAGGTAG CGAAATTCCT TGTCGGGTAA GTTCCGACCC GCACGAAAGG CGTAACGATT 120

TGGGCACTGT CTCAACGAGA GACTCGGTGA AATCATAGTA CCTGTGAAGA TGCAGGTTAC 180

CCGCGACAGG ACGGAAAGAC CCCGTGGAGC TTTACTGTAG CCTGATATTG AAATTCGGCA 240

CAGCTTGTAC AGGATAGTAG GAGCTTTGAA ACGTGAGCGC TACTTACGTG GAGGCGCTGG 300

TGGGATACTA CCCTAGCTGT TTTGGTnTCT nACCCGACCA 340

(2) INFORMATION FOR SEQ ID NO: 4329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4329:

AATCCATAGC GAAATGTATA CCATCACCCA TGCGTCCTTC TAAAGGTAAA TCTCTACCTT 60

TTTGTGCACC AGTACATAAT ATAATGGCAT CATACTCAGA TTCTAACGTT GCTTTATCAA 120

TACGACGTCG AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC 240

CGCCTGATTC TCTAGCACGT TCATAAATAG TTACTTGnTA TCCTnGTAGA TTAAGTTCTT 300

CAGCAGCAGT AATCCTGnTG GACCG 325

(2) INFORMATION FOR SEQ ID NO: 4330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4330:

CACTTCACCA CAGCCGCCAT GGCAGGnGCA GTAGGAATCG AACCCACACC AAAGGTTTTG 60

GAGACCTCTA TTCTACCGTT GAACTATGCC CCTATTAAAA ATAATAAATG GAGGGGGGCA 120

GATTCGAACT GCCGAACCCG AAGAGCGGAT TTACAGTCCG CCGCGTTTAA CCACTTCGCT 180

ACCCCTCCAT AAATGGTGCG GGCGnGnAGG ACTTGAAACC CCCAACCTAC TGATTACAAG 240

TCAGTTGCTC TGACCAATTG AGCTAAGGCC GGCTAAGAAA TGGTTCCAGG ACAGAGTCGA 300

AACTGCCGAC ACATGGGAGC TTTCAAT 327

(2) INFORMATION FOR SEQ ID NO: 4331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4331:

GCATCATTTT CAGCTTCCCA CTTCCACATT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 60

CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 120

ATAATGACCA TTTCCCAAAT GCCTAAGAAA ATAATAAATG TGATAATAGG TAATATAAAT 180

TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCAACAA 240

AGTCATCATA TGCAGGTGGA TTAAACAAAT GATGTTGTTT TACCAATGTC GTAATTTCTT 300

GGATAGCCGG ATGGnTTAAA TTGTTAAAAT CACCATAGGG TGTCCCnGCC GTGGACTGTG 360

GTTAAAAACG TCACGGACTT TGTTTAAAAn GGTGCGTCAT 400

(2) INFORMATION FOR SEQ ID NO: 4332:

(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4332:

CTGGTATGCA GATTTACCAC CTGCCTCTCC ACAAnTnnGG GGAGAGCAAA CAGATGTGCC 60

TGAATCAAGT GACTGGTATA ACGCATCATA CATTATTATG TGGGGCTCTA ATGTACCTTT 120

AACACGTACT CCGGATGCAC ATTTTATGAC TGAAGTCCGC TATAAAGGTA CAAAAGTCAT 180

TTCAGTAGCA CCAGATTACG CAGAAAATGT GAAATTTGCA GATAACTGGC TAGCACCGAA 240

TCCTGGTTCA GATGCTGCAA TTGCACAAGC AATGACGGCA TGTTATTTTA CAAGGAACAT 300

TATGTTAAAT CCAACCTGAA TGAACGGTTT TTATTAAATT ACGGTTAAAA CCATTATTAC 360

CAGGAT 366

(2) INFORMATION FOR SEQ ID NO: 4333:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4333:

TATTATTTCA TTGAGCAGAA AGAAAATTAT GGCACCAAAC TTTAATATTT TTTTCAATGT 60

CATTCTTTTG AnGGGAGTGG GACAGAAATG ATATTTTCGC AAAATTTATT TCGTCGTCCC 120

ACCCCAACTT GCATTGTCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCATC 180

CCCAACTTGG CACATTATTG TGAAGCTGAC TTTTCGTCAC TTGCTGTGTT GGGGCCCTCA 240

CCCCAACTCG CATTGCCTGT AGAATTTCTT TTCGAAATTC TCTGTGTTGG GGCCCCTGGA 300

CTGAGAATTG GAAAAAAGCT TGTTGACAAG CGCnATTTTC GTTCCATGCA ACTGACTGCC 360

AAGAGAACnT CGTGAGAGCn ATGAAGAAGA TTGGATTTGA 400

(2) INFORMATION FOR SEQ ID NO: 4334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA ACGCGTTATT AATCTTGTGA 60

GTGTTCTTTC GAACnTATGC GATTATTTCT TATGAATTCA AGCTTATTTA AAACTCTTTA 120

TTCACTCGGT TTTGCTTGGT AAAATCTATA TnTTACTTAC TTATCTAGTT TTCAATGTAC 180

AATTTCTTTT TAGTCAAGCG CTCGCATAAG CAATATCACT TTAACCAAAA AATATTTGAA 240

TGTTAAATAA ACATTCAAAA CTGAATACAA TATGTCACAT TATTCCGCCA TCTTCTGnAA 300

GAAGATGTT 309

(2) INFORMATION FOR SEQ ID NO: 4335:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4335:

nAGGACTTTT CTCGGTCAGT GTGAAAATCA ACGCACTCGT AnACACAATG TCTTCTCCCC 60

ATCACAGCTC AGCCTTAACG AGTACCGGTA TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA 120

CGTGCAATCC AATCGCACGC TTCGCCTATC CTACTGCGTC CCCCCATCGA TTAAAACGAT 180

TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCG GnCTCAGCTT 240

AGGACCCGAC TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA 300

CGGGATTCTC ACCCGTCTTT CGCTACTCA 329

(2) INFORMATION FOR SEQ ID NO: 4336:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4336:

CAAAGTGACA GGTGGTGCAT GGTTGTCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60

CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATTA AGTTGGGCAC TCTAAGTTGA 120

CTGCCGGTGA CAAACCGnnn GAAGGTGGGG ATGACGTCAA ATCATCATGC CCCTTATGCA 180

TTTGGGCTAC ACACGTGCTA CAATGGGACA ATACAAAGGG CAGCGAAACC GTGAGTGCAA 240

GCAAATCCCA TTAAAGTTGT TCTCAGTTCG GATTGTAGTC TGCAACTCGG ACTACATGAA 300

(2) INFORMATION FOR SEQ ID NO: 4337:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4337:

CCAGCACCGG GGCAGGCGTC ACCCTCATAC ATCACCTTAC GGTTTAGCAG AGACCTGTGT 60

TTTTGATAAA CAGTCGCTTG GGCCTATTCA CTGCGGCTCT TCTGGGCGTT AACCCTAAAG 120

AGCACCCCTT CTCCCGAAGT TACGGGGTCA TTTTGCCGAG TTCCTTAACG AGAGTTCGCT 180

CGCTCACCTT AGAATTCTCA TCTTGACTAC CTGTGTCGGT TTGCGGTACG GGCACTATTT 240

TCTATCTAGA nGGCTTTCTC GGCAGTGTGA AATCAACGAC TCGAAGACAC AnTGGCTnCT 300

CCCATCAGAG CTCAGCCTTA ACGA 324

(2) INFORMATION FOR SEQ ID NO: 4338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4338:

CGGACATCAA ACGGATGCTG CTCGATTGGC AAATGCATAT AACTAGTAAC ATGATCATCG 60

ACATCAAATT TAGATGATCA AATGTcCCCA ATcATTAATT TGATTCGGTT GTTTGCTCAA 120

TTGATTATAT GTTTTTCCTA GCACTTCATG CGGCACCATA TCTTTACCTA GTAGCCACAA 180

AGATAAGTCT AACAAGTGGC AACCATAATC GATTAAACTA CCGCCACCTT GCAACGCTTT 240

ATTGGTAAAA ACACCCCAGC CAGGCACTTT ACGCCTACGC ATCGCTTGTA CACGTGCTAC 300

TAAAGGTTTA CCAACCACAC CTGATTCAAT TGCTTTTTTA GCAGTAATTG CCACATCTGT 360

GTGACGATAA TGATATGCGC CAGTAATAnT TTGTGnTTT 399

(2) INFORMATION FOR SEQ ID NO: 4339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4339:

TGAGGCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG 60

CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120

CTAAGTGGAC TCGAACCACC GACCTCACGC nTATCAGGCG TGCGCTCTAA CCAGCTGAGC 180

TATAGGCCCA TTTnTTTGAA TGTTAAATAA ACATTCAAAA CTGGAATACA ATATGTGCAC 240

GTTATTCCGC ATCTTCTGAA GAAGATGTTn CCGAATATAT CCTTAGAAAG GAGGTGATCC 300

AGCCGCACCT TCCGGATACG GCT 323

(2) INFORMATION FOR SEQ ID NO: 4340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4340:

GGCTAGCCCT AAAGCTATTT CGGAGAGAAC CAGCTATTTC CAGGTTCGAT TGGAATTTCT 60

CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCGGTC CTCCATTCAG 120

TGTTACCTGA ACTTCAACCT GACCAAGGGT AGATCACCTG GTTTCGGGTC TACGACCAAA 180

TACTAAACGC CCTATTCAGA CTCGCTTTCG CTACGGCTCC ACATTTACTG CTTAACCTTG 240

CATCAAATCG TAACTCGCCG GTTCATTCTT ACAAAAGGCA CGCCATCACC CATTAACGGG 300

CTCTGAACTA ACTTGGTAAA GCnCCGGTTT nCnGGTCCAA TTTT 344

(2) INFORMATION FOR SEQ ID NO: 4341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4341:

TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGnGATAGGC GAACGTGCGA 60

TTGGATTGCA CGTCTAAGCA GTAAGGCTGA GTATTAGGCA AATCCGGTAC TCGTTAAGGC 120

TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTCACA CTGCCGAGAA 180

AAGCCTCTAG ATAGAAAATA GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240

TTCnGGGAAA AAGGGnTCCC CTTTAAGGGT TAACCGCCCC AAAAAACCCC C 351

(2) INFORMATION FOR SEQ ID NO: 4342:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4342:

AATAATGACT CCTACGGGAC TCGAACCCGn GTTACCGCCG TGAAAGGGCG TGTACTTAAC 60

CGTATGACCA AGGAGCCATG GCTCACCAGG TAGGACTCGA ACCTACGACC GATCGGTTAA 120

CAGCCGATAG CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC 180

TCTAGCGGAA nTAAATTCGA ACTACCATCG ACGCTAAnGA GCTTAACTTC TGTGTTCGGC 240

ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT 300

TCAAAACTAG ATAGTAAGTA AAAGTGA 327

(2) INFORMATION FOR SEQ ID NO: 4343:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4343:

ACCGCTTGGG CTGACATTTT TGGCTTGTTA AGCAGCTTGC CTACTTTTTT GGCAATAGCA 60

CCATACGTTG TTAGAGTCCC ATAAGGAACC TGTCTTAATT CATTCCAAAC ACACTGTTGA 120

AAATGACTAC CTGTTGGCTT TAAAGGTATT GTGATTTCAG GATTGTCACC TTTAAAATAC 180

GCGTCTAACC ACTGTGTCGC CTCTCTAAAT ATCGCTAAAG ACGTATTTTC TTCCCTAGTA 240

CCATCACCTT GTTGATTTTC AAACAAAACA GCGGTCAGAC TTACCCCATC ACTCAAAAGT 300

TCCAAnCGTC CTGACAGGCG AAnCAGAGTG AACGCTGAGA CTCCAGAAAA ATCCCCCTnT 360

(2) INFORMATION FOR SEQ ID NO: 4344:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4344:

ATTCCGACAT CTTCTGAAGA AGATGTTnCC GAATATATCC TTAGAAAGGA GGTGATCCAG 60

CCGCACCTTC CGATACGnCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 120

GACGGCTAGC TCCTAAAAGG TTACTCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT 180

GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT AGCATGCTGA TCTACGATTA 240

CTAGCGATTC CAGCTTCATG TAGTCGAGTT GCAGACTACA ATCCGAACTG AGAACAACTT 300

TATGGGATTT GCT 313

(2) INFORMATION FOR SEQ ID NO: 4345:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4345:

ATTTTATCGT AAGATTTTTT CGCAATGAGA TTTGGATCGT TTTTGTCCAC TACAATATCT 60

AATAGTTTTA CTTTAAGTCC AGCATTCACA AAAAGTGCTG CCAGTTGAGC GCCCATTGTG 120

CCTGCGCCAA GAACGGTTAC TTTATTAATT GTCATAGTGA TTCCTCCAAT TTAGTTGAGG 180

ATAAGATAAC CATTAAGATA ATTGGAATAA CGTTGCTATT TTATAAAATT AATTAAGTAT 240

CTTTGACAGT CATCTTAGCC TCTTATTTAA GGnAAAAGCn TTATGCTTAA nATAAGTCTT 300

TTTTA 305

(2) INFORMATION FOR SEQ ID NO: 4346:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4346:

GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGCA AGTCTTACGG CATCTTCTAT 60

TTTTAAGCTT GAATTTAACA AATCATAAGC CGTATGAATA TTTAAATATG CCACCATGAT 120

TGAATGGnCC CTTTCTATTA GTTAAGTTTG TGCGTAAAGC TGTAGCAAGT TGCTCAAATT 180

CATCCCCAGC TGTCCACTGA AACTCCTGGA CGCATTCGGA TGAnCAACGC CAACCAAAAT 240

AnTACCTTCA TCGACTGCAA ATACCCATAA TTTCCAGCCT TGATGTCAGC AATGTAATAA 360

CCAACTGAGA TGCTCATTGG CTGATACGAT GnTCCATACA 400

(2) INFORMATION FOR SEQ ID NO: 4347:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4347:

TCTGGGTTGA GTCGGGTCCT AAGCTGAGGC CGACACGTAG GCGATGGATA ACAGGTTGAT 60

ATTCCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT 120

GGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT 180

AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA GTCGTTGATT TCACACTGGC 240

CGAGAAAAGC CTCTAGATAG AAATAnGTGC CCGTACCGCA ACCGACACAG GTAGTCCAAG 300

ATGAGATTCn TAAGGTGGAG CGACGAATCT CCGTTAA 337

(2) INFORMATION FOR SEQ ID NO: 4348:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4348:

GTTAAGACAC CGCCCTTTCA CGGCGTAACA CGGGTTCGAG TCCCGTAGAG GTCACCATTT 60

TTTAGGTCTC GTAGTGTAGC GATTAACACG CCTGCCTGTC ACGCAGAGAT CGsGGGTTCG 120

ATTCCCGTCG AGACCGTACA AATGCCTATC CAAGAGGATA GnATTTTTTT TGCGTTTAAT 180

ATTATATTAA TAAAAGATAT ATGGACGAAT GATAATCATA TTGATTTATC TGTTCGTCCA 240

TTTTCTTTAA AATGTATGAA CCTCAAGTAA CTTAGTGGTT GGATATGAAA GATAAACGTn 300

GACAATAAAA TCTTTATT 318

(2) INFORMATION FOR SEQ ID NO: 4349:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4349:

CTTTAAAGCA CGTATAATGA TGATTTTCAG CTTGTACAAA GGAGAAAAAA AGAAGACAAC 60

CAAGCCCAAT AATGGACTGG CCGCCTAATA ATAAAAGCTC TAAAAGTTGT ATTTTAAAAA 120

TAGTTCTTTA AATTATATAC CCACCACATT TGGTGnAGnA ACCTAAAAAA AnGCACTTCC 180

CAAAAATGGA AAGTGCAAGT AGTGAGCCAT AGAGGATTCG AACCTCTGAC CCTCTGATTA 240

AAAGTCAGAT GCTCTACCAA CTGAGCTAAA TGGCTCTAAA TGGCTGGGCT AGCTGGGATT 300

CGAACCAACG AGTGACGGA 319

(2) INFORMATION FOR SEQ ID NO: 4350:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4350:

ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 60

GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC 120

CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 180

AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACCGATCGGT 240

TAACAGCCGA TAGCTCTACC ACTGnAGCTA CTGTGGATTG AATCATTATG CCTGGCAACG 300

TTCTTACTAT AGCGGAAnGT CAAGTTCCGC ATnACCATAC GAAGCT 346

(2) INFORMATION FOR SEQ ID NO: 4351:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4351:

ACGTCCTTCA TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT 60

ATGTTTCCAC CATTTTTATA AGTnAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG 120

ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG 180

ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGA GACTAGCGGG ATCGAACCGC 300

TGACC 305

(2) INFORMATION FOR SEQ ID NO: 4352:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4352:

GTTCATCAAT TGCTAATTCC AGTCCGCCTA ACGGATCAAT TTCATCCGCA TGTATTTTCA 60

CTTTAAAACC TGGCTTCTTT GGCTTTTTGC ATATAATGTT GCGATTGTTC TATTGTAAAT 120

ACACCTGTTT CACAGAAAAT ATCCGCAAAG TCTGCATATT GTTTTACTTC CGGAAGTAAC 180

GCAATCATTT CTTCTAAAAA TGCCTCATTT GAACTTGCCT CTTTAGGTAC AGCATGAGGC 240

CCTAGGAAAG TATGTTTCAT GTCTAAATCA TATTTCTCAG CTAAACGATT AGnCACTTTC 300

AA 302

(2) INFORMATION FOR SEQ ID NO: 4353:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4353:

TCTACCGCTG AACTACTTCT GCGGGTGAAG GGAGTCGAAC CCCCACGCCG TAnnTGAGGA 60

TCCTAAGTCT AGTGCGTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC CATAGAGGAT 120

TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AAtGGCTCTT 180

CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA 240

CCAATTGAGC TAGGCCGGCA ATATGTAAGA ATAAATGGTG GAGAATGACG GGTTCGAACC 300

GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC CGnTTTAAAA 360

CTGCTGGCnA CGGTCTAnTC TAAGGGGACG TAAGGTCGAC TACCATCGAC G 411

(2) INFORMATION FOR SEQ ID NO: 4354:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4354:

TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTGGa 60

CGACAACTGG TACACCAGAG GTATGTCCAT CCCGGTCCTC TCGTACTAAG GACAGCTCCT 120

CTCAAATTTC CTACGACCAC GACGGATAGG GACCGAACTG TCTCACGACG TTCTGAACCC 180

AGCTCGCGTa CCGCTTTAAT GGGCGAACAG ACAAGCCCTT GGGGACCGAC TACAGCCCCA 240

GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTnCCCGT CGATGTGAAc TCTTGGGGGA 300

GATAAGnCTG TTATCCCCGG GGTAACTTTT ATCCGTTGAG CGATGGGCCC TTACCATGCG 360

GAAACCA 367

(2) INFORMATION FOR SEQ ID NO: 4355:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4355:

GTATTTTAAA TCATAGTGGT TTATGCGTCT TTTTCAAATT CTATAAAAAA TCGGATGACG 60

TGTAATCTGC CATAGATTAA CACATTCATC CGATTTATAA TAATAAGATA GACTAACATT 120

TATTGAGAGC GGGACGGAAA TGATAAAGAA CGACTAATGA TTGATTATGT AGCGATTCTT 180

TATCATTAGT CACAGCTAAT GTGTACTTAA AAATATGAAT GCATGAGTTA CACTCAnATT 240

AGAGGAAATA CTAATTTCTA AAGAAAAAGT ATTTCTTTAT GTTGGGGnCC ACCCCAACTT 300

GnCATTGTCT GTT 313

(2) INFORMATION FOR SEQ ID NO: 4356:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4356:

GGGCTGGGTT CAGAACGTCG AGGCAGTTCG yTCCCTATCC GTCGTGGGCG TAGGAAATTT 60

TCGTGCCAnG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AGATCCTGAA 180

GCATGAAGCC CCCCTCAAGA TGAGATTTCC CAACTTCGGT TATAAGATCC CTCAAAGATG 240

ATGAGGTTAA TAGGTTCGAG GTGnGAAGCA TGGTGACAGT GGnAGCTGAC GAATACTAAT 300

CGATCGAGGA CTTAATCAAA ATAAATGTTT TGCGA 335

(2) INFORMATION FOR SEQ ID NO: 4357:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4357:

GCTCTAAAAG TTGTATTTTA AAAATAGTTC TTTAAATTAT ATACCCACCA CATTTGGTGn 60

nGAACCTAAA AAAAAGCACT TCCCAAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT 120

TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA 180

ATGGCTGGGC TAGCTGGATT CGAACCAACG AGTGACGGAT nAAAGTCCGT TGCCTTACCG 240

CTTGGCTATA GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA 300

AGAG 304

(2) INFORMATION FOR SEQ ID NO: 4358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4358:

ATAATGGTGA CGTTGATGAT GCATTAACAC AAGGTAAAGC AGCAATTGAT GCTATTCAAG 60

TAGATGCTAC TGTTAAACCT AAAGCGAACC AAGCTATTGA AGTTAAAGCA GAAGATACGA 120

AAGAATCTAT TGATCAAAGT GACCAGTTAA CTGCTGAAGA AAAAACTGAA GCATTAGCAA 180

TGATTAAACA AATTACAGAT CAAGCTAAAC AAGGTATTAC TGATGCAACA ACAACTGCTG 240

AAGTTGAAAA AGCGAAACTC AAGGACTTGA AGCATTTGAT AACATTCAnn TCGACTCAnC 300

AG 302

(2) INFORMATION FOR SEQ ID NO: 4359:

(A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4359:

GGTTGGGAAA TCATTGCATG AGAGTGTGAA AGGGCATAAG GGGAGCTTGG ACTGCGAGAC 60

CTACAAGTCG AGCAGGGTCG AAAGAGGACT TAGTGATCCG GTGGTTCCGC ATGGAAGGGC 120

CATCGCTCAA CGGATAAAAG CTACCCCGGG GATAACAGGC TTATCTCCCC CAAGAGTTCA 180

CATCGACGGG GAAGTTTGGC ACCTCGATGT CGGCTCATCG CATCCTGGGG CTGTAGTCGG 240

TCCCAAGGGT TGGGCTGTTC GCCCATTAAA GCGGTACAnG GCTGGGTTCA GAACGTCGTn 300

AGAAAGTTCG GTCCCTATCC GTCCTGGGGC GTAGGAAATT TnGAGAGGAG 350

(2) INFORMATION FOR SEQ ID NO: 4360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4360:

AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC 60

GGTGTGTACA AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA TTACTAGCGA 120

TTCCAGCTTC ATGTAGTCGA GTTGCAGACT CACAATCCGA ACTGAGAACA ACTTTATGGG 180

ATTTGCTTGC ACCTCGnGGT TTCGCTGTCC CTTTGTATTG TCCATTGTCA GCACGTGTGT 240

AGCCCAAATC ATAAGGGGCA TGATGATTTG GACGTTCATC CCCAnCTTCC TCCGGnTTGT 300

ACACCGGCAG TTCAACTTAG AGTGCCCAA 329

(2) INFORMATION FOR SEQ ID NO: 4361:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 424 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4361:

AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA CTCTAGCGGA 60

CTnTCCTCTC CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCGCTCTTT 180

TCTCGTTTCG TCAGATTCAA ACGTTTTCAC TnCGnCAAGC CATTTTTCTT TGTGTTTACT 240

TTTTATTTTG ACGTTTTAGG CATAAAAAAA wGAGAcCTTG CGGTCTCAAT GCGGCTCATC 300

GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG GCTAACAACG 360

TCGCCAAAGA CCTTTCTTGA CTTGTGACAA TCGGCTTGCT TCTTTCCTCT CCTTCGGCTC 420

TCGC 424

(2) INFORMATION FOR SEQ ID NO: 4362:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4362:

CACAACAAGT ATCTAAGATA CTGGCCGAAG ATTGTCACAG ACGGTAGGGG AAGGGGGTCA 60

CGTGTACGAC CCAACATGTG GTTCCGGTTC ATnGTTGTTA CGTGTTGGTA AAGAAACGCA 120

ATTnAnTCGT TATTTCGGAC AAGAACGTAA CAATACTACA TACAACTTAG CACCATGAAT 180

ATGTTATTAC ATGATGTGCG TTATGAGAAC TTCGAGATCC GTAATGATGA CACATTGGAA 240

AATCCAGCCT TTTTAGGCAA TACATTTGAT GCGGTTATTG CGAACCATAC AGTGCGAAAT 300

TGGACAGCAG ATTCCA 316

(2) INFORMATION FOR SEQ ID NO: 4363:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4363:

GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60

CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCGG AAATCTCTGG ATCAAAGCTT 120

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 180

AGGCATCCAC CGTGCGCCCT TGAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG 240

TTGATTAATC TTGTGGAGTG TTCTTTCGAA CATAGCGATT ATnTCTTATG GAATTCAAGC 300

(2) INFORMATION FOR SEQ ID NO: 4364:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4364:

nTGCACTTAA GAACTTAGAC GATCGTGGTA TCGTTTATAT TGGTGCAGAA GTAAAAGATG 60

GAGATATTTT AGTTGGTAAA GTAACGCCTA AAGGTGTACT GCAGTTAACT GCCGAAGAnA 120

GATTGTCACA TGCAATCTTT GGGTGAAAAA GCACGTGAAG TTAGAGnATA CTTCATTACG 180

TGTACCTCAC GGCGCTGGCG GGTATCGTTC TTGCATGTTA AAAGTATTCC AATCGTGCAA 240

GAAGGGCGAC GATACATTAT CCACCTGGTG TTAAACCAAT TTTAGTACGT GGTATATATC 300

GTTCCAAAAA CGT 313

(2) INFORMATION FOR SEQ ID NO: 4365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4365:

AACCATTCGA TGCAATAGCG TCATTCTTGG ATATTAATCC CTAAATTGCC GTGATATCCC 60

GCGTCTATCT TGGCCTGTTT CAATCACTAA ATGCGTTTTA CTACTTACAC CACTACGGGC 120

TAGTTAATAG TCCGACATAG CCCTCTGGTA TGCTTACAGC TACATCTGTn TTAATCACTG 180

CCTTTTCTTG TGGCTCAAGT ACGACAGTTC AGCTGAGAAT ATGTCATAAC CTGCATCCGn 240

CTTATGATTT CGTTCGGGCA TTCTAGCATT TTCTGATAAT AGCCTTACTT GTAATGTGTn 300

AGTCATTTTC 310

(2) INFORMATION FOR SEQ ID NO: 4366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AGTGGTACTT CTGTTAATTG GTGAATTTGG ATACTGGTTA TATTCAGCTG CACCGCAAGC 60

AACTTCTATT GATGGCCTAA CTGCCTTTTT ACCTCAAGCA ATGGGTATGG TAATTGTTGC 120

AGTCATTTAT GGCTTTATGA ATATGAAAGC AGAGAATCCA TTCCGTAATA AAATTACGTG 180

GTTACAAATT ATTTCAGGTT TCTTCTTTGC ATTTGGTGCT TTAACATATC TTATTTCAGC 240

ACAACCTAAT ATGAATGGTT TAGCACTGGA TTTATCCTTC TCAACATCCG TGGTGCTGCT 300

ACATTAAnGG TATTAATTCT TAAACCACAT AAACGTCAAA GAATGGTAAT ACAATCACGG 360

CTAGTACCAT TTAGTAGCCG CTCCGTACCG nAATTATAAA 400

(2) INFORMATION FOR SEQ ID NO: 4367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4367:

CACCTGGACG AAACGGTTTT AGATCGTATT CAATTGAAAA GGCCGGTATT GAATGAATCA 60

CACTTAGCAG CGATTGATCA GGAACATTTT AAATTAACTT ATTTATCAAC GGTATATGAA 120

GGGGATTTGG AAGATGCGTT AGAAGCATTA TGCCGAGAAG CAGTGAATGC TGTAAACAAG 180

GCGCTCAAAT TCTAGTGTTA GATGATAGTG GATTAGTTGA TAGCAATGGC TTTGCAATGC 240

CGATGTTACT CGCnATAAGT CATGTGCATC AATTACTTAT TAAAGCAGAT TACGnATGnC 300

TACAAATTTA ATCGCTAAAT CTGGTG 326

(2) INFORMATION FOR SEQ ID NO: 4368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4368:

ATTATAGCCG AAATGCCCAA AATAGATTTT GACGAATATT ACGAATGGTT GCTTTACTTG 60

CATAAATGGC TTTAGGAATA AGCATCAAGT CGCCACCAAG AATAGTAATA TCAGCTGCTT 120

CAATGGCAAC TTCTGTACCT GTAnCAATGG CGATACCGAT ATCAGCTTTA ACTAATGCAG 180

GTGCATCATT TACACCGTCA CCAnCCATCG CAACCTTCTT ACCTTGTTGC TGTAGTTTCG 240

GTTTTGC 307

(2) INFORMATION FOR SEQ ID NO: 4369:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4369:

TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCAC CGGGTGTGCC TTCTGATATG 60

CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT 120

CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 180

TCGGCTTCTA GTGCCAAGgC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT 240

CCTACAGGAA ACGCGTTATT AATCTTGTGA GTGTTCTTTC GAACAyTAGC GATTATTTCT 300

TATGAATTCA AGCTTATTTA AAACTCCTTA TTCAATCGGT TTTGCTTGGG TAAAATCCTA 360

TATTTTACnT ACCnTATCGA GTTTTCAATG TAACAA 396

(2) INFORMATION FOR SEQ ID NO: 4370:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4370:

CAGTAAGATA ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT 60

CGTATTGAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT 120

GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACA TGTAATTTTA CTTTTACATA 180

CTTTTAAAAA ATAAGACACT TTGCCAAACT TGCACATAAA TGTTTAATTC AATAATTTGA 240

ATTTTCTGTG TTGGGTCCCT TCGTATAATT TAATAAATAC CACTAAACTA AaTTArTGAA 300

GTGCCTTATG TATAA 315

(2) INFORMATION FOR SEQ ID NO: 4371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4371:

GTCGTCAAAT GTACCTTCAC CAAGTAGTGA TGTACATATT TACCGCCTTG TTCAACAGCA 60

CGTGTCGGCG CACCTGTAAT CGCAATGACA GGTATGCGTT CAnATATGAA CCTGCGATAC 120

CGTTGACGGC ACTTAATTCG CCAACACCAA ATGTAGTAAC TAATGCAGCG AGTCCATTAA 180

GACGGGCATA ACCGTCCGCT GCGTAACTTG CGTTTAATTC ATTTGTATTT CCTACCCAAT 240

CTACAATGGG GTTGCTGATA ATATCGTCTA GAAAAGCGAG ATTAAAATCA CCAGGGnCAC 300

CAAAATTTTT ATCGACGGCn TG 322

(2) INFORMATION FOR SEQ ID NO: 4372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4372:

CCTAAGTCTA GTGCGTCTGC CAATTCCGCC ACACCCGCAA ATGGTGAGCC ATAGAGGATT 60

CGAACCTCTG ACCCTCTGAT TAAnAGTCAG ATGCTCTACC AACTGAGCnA ATGGCTCTTC 120

CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA GTTTGCTCTA 180

CCAATTGAGC TAGGCCGGCA ATATGTAAAG AATAAATGGT GGGAGAATGA CGGGTTCGnA 240

ACGGCGGAAC CCTCTGCTTG TAAAGCAGAT GCTCTCCAGC TTGAGCTAAA TCTCCGATTT 300

AAAACTGCTG GGCAAGTTCT ACTCTAG 327

(2) INFORMATION FOR SEQ ID NO: 4373:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4373:

CATTTTAATT TATTGTACAG AACGAAATGT GATGTTAGTA GATCATAGGG TTGATGATAA 60

TATTAAAGCT GAAAACGTTA TATTTATTGG CCTTTTGTGT AAACATGGAC ATTGGCATGC 120

AGTCATTTAT GACATTGCTC AAGACAAAAC TGCCGAACTC GAAATTGAAA ATATTATAGA 180

TCAATTTTTA AACCCCATCG ATTCCTAAAA AACAGCAGTA AGATGATTTT CAATTAGAAA 300

ATATCTTGCT GCTGTTCTCT ATTTATACAA TACTTCGTAT TGAATGGCTC GCTTTCCCAG 360

GGnGCCGCTC AGCCTGGGCC TCGACTGGCA ATGCTCCCTC 400

(2) INFORMATION FOR SEQ ID NO: 4374:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4374:

TAATGGATTT TTTAGTGTTG GTGTCGTTAT TGTCTTCTCA CCTTTTTGTC CTTCTCTTGT 60

TACTTTTTCT GTCCCTGGTG CTAAATCAGG ATTAAATTTA CGTTCTTTCT CGAATGGAAT 120

CTCTTCTTTT TCTACAATCG AGTCTCCTTT TACAGGTCCA TATTTTGTTA CGCTATCGAC 180

CGGTGGTCTA ACTACATCTC CTGTTTCTGG ATTCTTAATT CCTGGTTTAC CTGGGAACTT 240

CCTCTTTCTC TCCTGTTGGT AACTTCGGGA TCAAATTCGT CTCGATGGAC CTGGTGTTGA 300

nCGTTTCTGG GTCCGnAAGT CTGTnGAATT GCAG 334

(2) INFORMATION FOR SEQ ID NO: 4375:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4375:

ATACATGCAA GTCGAGCGAA CGGACGAGAA GCTTGCTTnG TGAATGTTAG CGGCGGACGG 60

GTGAGTAACA CTGGATAACC TACCTATAAG ACTGGGATAA CTTCGGGAAA CCGnAGCTAA 120

TACCGGATAA TATTTTGAAC CGCATGGTnA AAGCTTGCAA AGACGGTCTT GCTGTCACTT 180

ATAGATGGAT CCGCGCTGCA TTAGCTAGTT GGTAAGGTAA CGGCTTACCA AGGCAACGAT 240

GCATAGCCGA CCTGAGAGGG TGATCGGCCA CACTGGAACT GAGACACGGT CCAGACTCCT 300

ACGGG 305

(2) INFORMATION FOR SEQ ID NO: 4376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4376:

GATAAAGTGA AAGAACTCGG ACGTGACACC TATTGCACGA TTCGTTGGTT TTAAGGCAGT 60

AGGCGTTGAC CCGAAAATTA TGGGTATTGG GCCTGGCATA TGCGATTCCT GAAGTATTGT 120

CACTCAGCAA TCTATCTGTT GAAGACATTG ATTTGATCGA ATTGAACGAn CATTTGCTCT 180

CAAACGATTG CATCTATTAA AGAAGTAGGT CTAGATATAT CACGTACGAA TGTGAATGnT 240

GGCGCTATTG CTTTAGGTCA TCCATTAGGT GCTACAGGCG CAATGTTAAC CGCGCGTTTA 300

CTTAA 305

(2) INFORMATION FOR SEQ ID NO: 4377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4377:

AATGTCTTCT ACCCCATCAC AGCTCAGCCT TGAACGAGTA CCGGGTTTGn CCTAATACTC 60

AGACCTTGAC TGCTTAGACG TGACAATCCA ATACGACACG CTTCGCCTAT CCTACTGCGT 120

CCCCCCATCG ATTAAAACGA TTATAGGTGG TACAGGAAAT ATCAACCTGT TATCCATCGC 180

CTACGCCTGT CGGCCTCAGC TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG 240

GAAACCTTAG TCAATCGGTG GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT 300

TCTCACTTCT AAGCGCTCCA CATG 324

(2) INFORMATION FOR SEQ ID NO: 4378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4378:

CATCATGCTT AGAAAACGCT TAATTTAGGT TTTGACTTTT TAATCAGAGT ATATAAGCAA 60

AACTTATCAT ACAGGTAAGG TGTAATAAGT ATTTTTTATT AATTGAGAAT AATTATCAAT 120

TGGCACCAAA CTTTAATATT TTTTTCAATG TCATTCTTTT GATGGGAGTG GGACAGAAAT 240

GATATTTTCG CAAAATTTAT TTCGTCGTCC CACCCCAACT TGCATTGTCT GTAGAAATTG 300

GGGAATCCCA ATTCCTCCTT GGTGGGGGCC CATCCCCACC TTGCACATAA TGGnAGCnGG 360

ACCTTTCCGC CGCTCCGGGG TGGGGGCCTC nACCCCAnTC 400

(2) INFORMATION FOR SEQ ID NO: 4379:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4379:

ATAAAATATA TCACTTGAAA AATTTCATGT AGAAAAGATG ATGGATAGGC TATAAAGTAA 60

TTGTGACTGA GATGAACTTT TATGTCTTAG ACACTACAAC ACTATATTGG CAGTAGTTGA 120

CTGCGGGGCC CCAACATAGA GCAAATTGGA TTCCCAATTT CTACAGACAA TGCAAGTTGG 180

GGTGGGCCCC AACATGAAAG AAATACTTTT TCTTTAGAAA TTAGTATTTC TTATGCATGA 240

GTGTACTCAT GTTGCGATTA TTTTTnAGTA CACATTAGCT GTGGACTAAT GATAAAGGnn 300

TCGCTACATA ATCCATCCAT TAGGTCGTTC CTTGATTCAT TCCCT 345

(2) INFORMATION FOR SEQ ID NO: 4380:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4380:

CTAAAGCTGn CATATGCGGC TTGCCGATGA AGCCAACCCT GCTGCTGTTG GTACAAAATT 60

GTCGCTTTCA ATTTCTGCAT ACCAATCGAT GCCAGCTCTA TTTCTGACAA TATCCATATA 120

TTTTGAAATT TTCTCTAATT CTTTGCCACT AACCTTTTCA CCATTCAACC AAAATTGATC 180

CTGTGTTAAC TGGTCGTTAA AAGTGACTTT CGTTTCAGTG TAAAATTTTT CTAATGTAAC 240

AGATATGCTA TTATTCATGG AAGATTAGTG CTTCATCTTT TTTACCCCAA TATTTTATAA 300

GTGCAATATC GTAGTGCAGG CTTGCCACTT TAACACGCAT AACTCCTAAA TCTCAACCAG 360

ATn 363

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4381:

ACCTGAATGA CTCAAACTTG ACTTTnCGAC AATTGACTGT nCATTTTGCA TAGTTGTATG 60

nCTCCATTnC GTAATTATTA GATTTGTTCG CTTACGTCTA TTGAATCATA CAGCTTTATT 120

ATAGTTAGCG TATTTGCACC TTTGCACATT AAACCATGTT TAATAATCAT TGAATCATTA 180

TTAAGTAAAT TAAGGAATCT ATAATGTTCG TTAAATAAAA CTGATCCCGT TGTGGCTTCA 240

CACCCGATAG ATAGGGATTT ACAGATAAAT TCAGGTCTCT TCCACGTCCA TATTTGGGAC 300

CCATCGAAAA TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACAGTAGG 360

GCCGTTGTCA CTTAACTTCT GTTTTTCCGA TGACAGCTTC 400

(2) INFORMATION FOR SEQ ID NO: 4382:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4382:

GnACTACAAA GCAATGGGGT TTGCCAGTTT CTTTATTTAC TGACGAATAC TGGCAATGAC 60

ATCAGATACA TGTGGCAnCA CCAATCCATT TCTTTTCACC ATTGATAACC CAAGTATCGC 120

CTTGGGTTGC AGGGACTGTT TCAAGACCTC CCGCAACGTC CGAACCGTGT TCTGGTTCAG 180

TTAAAGCAAA GCATGTTACG CnTTCATGTG AACTGTAATT TAGGTACATA TTTCGCAATT 240

TGTTCTTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG AACACCGAGT 300

AGGG 304

(2) INFORMATION FOR SEQ ID NO: 4383:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GTGCATTATT TTGGAGAATT AGCTCAGCTG GGAGAGCATC TGCCTTACAA GCAGAGGGTC 60

GGCGGTTCGA ACCCGTCATT CTCCACCATT TTGATTATTA AATTATATGA ATAAGCTGGA 120

GGGGTAGCGA ATGGCTAAAC GCGGCGGACT GTAAATCCGC TCCTTCGGGT TCGGCAGTTC 180

GAATCTGCCC CCCTCCACCA TCTATATATT GGGCTATAnC CAAGCGGTAA GGCAACGGAC 240

TTTGACTCCG TCACTCGTTG GTTCGAATCC AnCTAGCCCA GCCATTAGAG nCATTAACTC 300

AGTTGGTA 308

(2) INFORMATION FOR SEQ ID NO: 4384:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4384:

AATTTTGGCC AAAACACCCA TCCGCTGTAA CTTCAGAGTG TCATTGGCAT TTATTACACT 60

ATCTCCAACT CCTAGTGGAA CAACCACATC TCGTCCTTGG GGTGCATGGA ATGTTCCGTC 120

AGCCCTGTGA ATTATTTCTT GAACTCCACC ACCTGGGGCG TTTCCAGAAC CTCTATCATT 180

TAATACAGCA AATGTCGGTT GCGTTAATGC TCCTGAATTA TCGGkAGCTA CACCCTTTCC 240

TGCTAAAGTA CCAGTAGACA ATGTAGGTAT TGGCTTGATG AGATTTTtTAT CAGTAATGGC 300

TTTAGAnAT 309

(2) INFORMATION FOR SEQ ID NO: 4385:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4385:

AAAGGTGAAA AGCACCCCGG AAGGnAGGTG AAATAGAACC TGAAACCGTG TGCTTACAAG 60

TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG GCGAGTTACG 120

ATTTGATGCA AGGTTAAGCA GTAAATGTGG AGCCGTAGCA nAACAGGTCT GAATAGGGCG 180

TTTAGTATTT GGTCGTAGCC GAnAACCAGG TGATCTACCC TTGGTCAGGT TGAATTCAGT 240

AACACTGAAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA ACTGAAGGTA 300

(2) INFORMATION FOR SEQ ID NO: 4386:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4386:

TAGAATCTTC ATCAATATGA TCTAACCAAT ATTGATAAAA CCTTGATGTG TTTCGTGTCA 60

ATGACATACC ATATCGACTA GGTACCTTTT TAGAATGTTG ATTAATCAnG GCAAATATCA 120

TGGCAAGGTC ATCTTCAAAA TGATTCGATT CAAGTGGAAG GCATATGACG TCTCATCACT 180

ATACCCTTTT TCCCATTCTG CAAATCCACC ATAAATACTA CGCGACGCGG AACCCGGACC 240

CATTCGCGGC AATCTCGGTn AATCCTTATC TGGACAGCTG GCATGTCTAG CGGCTGGATT 300

TACAAGCTGG CTGGCTAAAG CTGGCATATG CGCTTGCCGG TTGAAGCCCA ACCTGGCTGG 360

CTGGTGGGGn ACAAATTGGT CGCTTTTCAA TTTCnGGCAT 400

(2) INFORMATION FOR SEQ ID NO: 4387:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4387:

TCAATTTATG GGGCATTATG ACTTTATATA CCTAAAATAC TATTAAGAAG TCCTGAAAAA 60

TTCACATTAG CAGTTGGATT GTTCAACTTT ATTAATGATA AGTATGCAAA TAATTTCACA 120

GTGTTTGCAG CAGGGGCAAT TATGATTGCA GTACCTATAG CAATCGTATT CTTGTTCTTG 180

CAACGCTATT TAGTATCAGG TTTAACAACA GGTGCGACAA AAGGTTAGTT TGAAATTCnC 240

GnGTGGGGCA GAATTGATAA AGAACCACnA ATGACGATAA AGATTAAAAG GAGGACGTTA 300

TGGATGACGA 310

(2) INFORMATION FOR SEQ ID NO: 4388:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4388:

AACATCATGC TGATGTTGTT GAATATGAAG AAGATACAAA CCCAGGTGGT GGTCAGGTTA 60

CTACTGAGTC TAACCTAGTT GAATTTGACG AGATTCTACA AAAGGTATTG TAACTGGTGC 120

TGTTAGCGAT nCATACAACA ATTGAAGATA CGAAAGAATA TACGACTGAA GTAATCTGAT 180

TGAACTAGTA GATGAACTAC CTGAGGAACA TGGTCAAGCG CAAGGACCCA TTCGAGGAAA 240

TTACTGGAAA ACATCATCAT ATTTCTCATC nGGTTTAGGn ACTGAAATGG TCACGGTAAT 300

TTTGGCGTGG 310

(2) INFORMATION FOR SEQ ID NO: 4389:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4389:

TTTACCATAT CATCCACTAT TTATTAAACC TAATAAAGAT GAATTAGAAG TGATGTTTAA 60

TACAACAGTG AACTCAGACA CAGATGTTAT TAAATATGGT CGTTTGTTAG TTGATAAAGG 120

TGCGCAATCT GTTATTGTCT CGCTTGGCnG TGGATGGTGC TATTTATATT GATAAnGAAA 180

TCAGTATTAA AGCAGTTAAT CCACAAGGGA AAGTGGTTAA TACAGTTGGC TCTGGTGATA 240

GTACAGTTGC AGGCATGGTG GCTGGGAATT GCTTCAGGTT TAACGnTTGA AAAGGCATTC 300

CA 302

(2) INFORMATION FOR SEQ ID NO: 4390:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4390:

AAAGAGTGCG TAATAGCTCA CTAGTCGAGT GACACTGCGC CGAAAATGTA CCGGGGCTAA 60

ACATATTACC GAAGCTGTGG ATTGTCCTTT GGACAATGGT AGGAGAGCGT TCTAAGGGCG 120

TTGAAGCATG ATCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG 180

CGAAAGACGG GTGAGAATCC CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC 240

TnCCTTACCA CCTATAATCG nTTAATCGTG GGG 333

(2) INFORMATION FOR SEQ ID NO: 4391:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4391:

AGTGCGTTTG TGCACAnACT TGACTGnAAC TTAGTGCCAT TGCAGCACCA GCAACCCATG 60

GCGCAATAAG CCCAATGCAG CTATAGGGAT ACCGnCAATA TTATAGCCGA ATGCCCAAAA 120

TAGATTTTGA CGAATATTAC GAATGGTTGC TTTACTTGCA TAAATGGCTT TAGGAATAAG 180

CATCAAGTCG CCACCAAGAA TAGTAATATC AGCTGCTTCA ATGGCAACTT CTGTACCTGT 240

ACCAATGGCG ATACCGATAT CAGCTTTAAC TAATGCAGGT GCATCATTTA CACCGTCACC 300

AACCAT 306

(2) INFORMATION FOR SEQ ID NO: 4392:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4392:

TACGGTATGC ATATCTTTTA AAACCTATTC TTTTGTTATT AGGACATATA AATTCATCAT 60

TAAGTTCGTC ATATTTCCAA TTTTAAGTGT TGAAAATGTC ACTTTTAAAC TTTCTAGTTT 120

TATCTTTAAT AAACATGCCA TACGTAATAA GTGGCGTTTT ATTAAAATCA TCTATAATAG 180

CCATATAGTT TTGCTCACTA CCATAACCTG CATCAGCTAC AATATACTCC GGTAAATAAC 240

CGAAGGGATT TTGAATCATT GTTAAAAATG GAATTAAAGT TCTAGTATCT GTTGGGTTTT 300

GAATAGGGTC ATGGGATAAA CCAAATGnGG AATTTGCCnC AATTnGTAAA TGGAA 355

(2) INFORMATION FOR SEQ ID NO: 4393:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4393:

CATTCCGTAA TAAAATTACG TGGTTACAAA TTATTTCAGG TTTCTTCTTT GCATTTGGTG 60

CTTTAACATA TCTTATTTCA GCACAACCTA ATATGAATGG TTTAGCAACT GGATTTATTC 120

TTTCTCAAAC ATCCGTTGTG CTTGCTACAT TAACTGGTAT TTATTTCTTA AAACAACATA 180

AAACGTCAAA AGAAATGGTT ATTACAATCA TCGGCTTAGT ACTCATTTTA GTAGCCGCTT 240

CTGTTACAGT ATTTATAAAA TAAGGAGTGT AGATGTCATG AAAAAATCAG CGGTTTAAAT 300

GGAACCTATT CCAAAGCCAT CGCGACCAAT GGGTCATTTG GATTAnTAAC GATAATGGCG 360

nnGG 364

(2) INFORMATION FOR SEQ ID NO: 4394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4394:

GATTAAAACG ATTATAGGTG GTACAGGAAT ATCAACCTGT TATCCATCGC CTACGCCTGT 60

CGGCCTCAGC TTAGGACCCG ACTAACCCAG GAnCGGACGA GCCTTCCTCT GGAAACCTTA 120

GTCAATCGGT GGACGGGATT CTCACCCGTC TTTCGCTACT CACACCGGCA TTCTCACTTC 180

TAAGCGCTCC ACATGTCCTT ACGATCATGC TTCAACGCCC TTAGAACGCT CTCCTAnCAT 240

TGTGCCAAAG GACATGCCAC AGCTTCGGTG AATATGTTTA GCCCCGGTAC ATTTTCGGCG 300

CATGTnCACT CGACT 315

(2) INFORMATION FOR SEQ ID NO: 4395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4395:

AGCCCCCAAA TGGGTATTGA AATTGAATGG TGGGnCCTGA AnTGGACTCG AACCACCGAC 60

CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT AGGCCCATTA ATTTGAATGA 120

ACAAACATTC AAAACTGAAT ACAATATGTC ACGTTATTCC GCATCTTCTG AAGAAGATGT 180

TACGACTTCA CCCCAATCAT TTGTCCCACC TTCGACGGCT AGCTCCTAAA AGGTTACTCC 300

ACCGGCTTCG GGTGTTACAA AC 322

(2) INFORMATION FOR SEQ ID NO: 4396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4396:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC 60

AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTTCTTTG TGTTTACTTT TTATTTTGAC 120

GTTTTAGACA TAAAAAAAGA nACCTCACGG TCCAAACTTG CCTGGCAACG TTCTACTCTA 180

GCGGAAnTGA ATTGGCTACC ATCGnCGCTA AAGACCTTTC TTGACTTGTG ACAATCGCTT 240

GCTTCTTTCC TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT 300

CTT 303

(2) INFORMATION FOR SEQ ID NO: 4397:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4397:

TAAGAATATA AATGATTTTG AAAGCATTTG AAAGCTACAA CATTTCTATA AAATTTTTCA 60

ATAACAATTG CGCCACTAAA ACTCAAAATT TCCACCACCA ACATCCAAAT TATCAACATC 120

GCAACATAAC CAAATGTTAT AATAAATCTA TTACACAAAG AGATAAATTA CTTATGCAAA 180

GGCGGAGGAA TCACATGTCT ATTACTGAAA AACAACGTCA GCAACAAGCT GAATTACATA 240

AAAAATTATG GTCGATTGCG AATGATTTAA GAGGGACATG GATGCGAGTG AATTCCGTAA 300

TTACATTTTA GGCTTGATTT TCCTATCGCn TCCTTATCTG GAAAAAnCCG ACCAGGATnT 360

GCAGATGCCT GGCCAGG 377

(2) INFORMATION FOR SEQ ID NO: 4398:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4398:

TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT TGAGCAGTGT TTTTATTATC 60

GCCAGTTAAC ATGGGCAACT TCAATGCCCA TATCATGGCA ATTGTTTTAT AGCATCTTTG 120

GGCATGATnT TTGACAGTAT CTGCCACTGC GATGATACCA GTTAATGAAT AATTAACAGC 180

AATGAGCATA nCAGTTTTAC CATCTCGTTC ATAATGTGTT AAATCATCAG AAATATGCTT 240

AAGCAACTAA TATCATTGTC AACCATTAAT TTACCGTTAC CAACCAATAT ATGGTGATGA 300

TCnATCCTTC CTC 313

(2) INFORMATION FOR SEQ ID NO: 4399:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4399:

TGGCTATGAT CATCCAAAAT ATGGTGAATC AATTGCTGCA GCCATTATAC TTCGCGAAGA 60

TGAACCTCAT TACGCTGAAA TTTTAAATCA ACATATGCGA AGTCGTTTAG CAGGTTATAA 120

AGTCCCAAGA ATGTATGTAC CAGTGACACA TATGCCGTTA AACAGTACGC AGAAACCAGA 180

TAAACTTGCG ATTCGACAAA TGATGAATGA CAAAGTCTCG CAAACACTTT AAAGGTGATA 240

AAAATTTTTG ACATTTAGTG TAAGCGTTTA CAAATAAAGC GTGTTGTTTT TGAATTAAAT 300

GCATTTCACA TTAGTATTCA TATTATnTTT AGGAGGAATT TATATGACAT TTGAAAAAGA 360

ACGGGCTTAA AACATTATTC CTGAGATGTA CTAGTATGCT 400

(2) INFORMATION FOR SEQ ID NO: 4400:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 409 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4400:

CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTTCTCGT TTCGTCAGAT TCAAACGTTT 60

AAAAGAGACC TCgtCTCAAC TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTGGC 180

TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 240

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC 300

ArATTCAAAC GtTTTCAcTT CGGCCAAGGC ATTTTTCTTT GTGGTTACTT TTTAATTTGG 360

ACGGTTTTAG GCATAAAAAA AAAGGGGACC CTGCGGGCTC nAAAGGGGG 409

(2) INFORMATION FOR SEQ ID NO: 4401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4401:

TCATGTAGAC TTTCAAGAAT CGACACATGA AAATTCAAAA CATCATGCTG ATGTTGTTGA 60

ATATGAAGAA GATACAAACC CAGGTGGTGG TCAGGTTACT ACTGAGTCTA ACCTAGTTGA 120

ATTTGACGAA GATTCTACAA AAGGTATTGT AACTGGTGCT GTTAGCGATC ATACAACAAT 180

TGAAGATACG AAAGAATATA CGACTGACAT nnATCTGATT GAACTAGTAG ATGAACTACC 240

TGGAAGAACA TGGTCCAAGC GCAAGGnCCA ATCCGAGGAA ATTGACTGGA AAACAATCCA 300

TCCATATTTC C 311

(2) INFORMATION FOR SEQ ID NO: 4402:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4402:

TTAACGGATT ATTTGGCAAT TCGGTTAGTT GTCGAACAAT TGCTAGTTGG TGATGAGTTT 60

AAGTCAGTCG CTAAAGATTG TGAAAGTAGA TCGGAAAATT GGTTTAAGCA AACTGTTGCA 120

TCATGGTGTT ACTACAGTGA TATGCCTAGC GATGTATTAC TACAACATGG ACGTCAATGT 180

AAATTnCAAA CGTTTATTCA TTTTGGCAGC AACTATGGAA TAAAAATGTA TTTAAAAATT 240

TATGGCTAAT TGCCTGGGGA AATGACATAC GAATCTCAGG TTAAAACAGA AAATTAAAGC 300

AGGTCCATGT nAAGTGTGGG CGGGnCGCAT 330

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4403:

TGnTCACACA TAATTTGCGG CCATATGTTG TTGGCACTGG CCGTTTTGAT TATCTGGCAC 60

TTTGGGCCCA TATGTTGnCA AAATACGCGC CAATTGCTTC TTTATAAGTT GTTATTTTTT 120

TACTTTTTCC ATCGATAAGC CATACCTCTG GATGATACAT ATGATGCCCC ATCGCAGACC 180

AATAGCGAAA TTCACCCGTT AAAGTTTCGA GCTCTGATAA TTGTATAGAC CATTGATGAT 240

TTTGAGGTGG TACTTGATAT AAATTTTCTT CTCTAAAATA TTCATTTAAA ATGCGTTCGA 300

TAGCCGCATA CGCTGCCATG TTGTATTAAT CnTTAATTTG 340

(2) INFORMATION FOR SEQ ID NO: 4404:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4404:

TTAACATATA TTTTGGGACC TTAGCTGGTG GTCTGGGCTG TTTCCCTnnA CGAACACGGA 60

CCTTATCACC CATGTTCTGA CTCCCAAGTT AAATTAATTG GCATTCGGAG TTTGTCTGAA 120

TTCGGTAACC CGAGAGGGGC CCCTCGTGCC AAACAGTGCT CTACCTCCAA TAATCATCAC 180

TTGAGGCTAG CCCTGAAAGC TATTTCGGGA GAGAACCAGC TGATTTCCAG GTTCGATTGG 240

AATTTCTCCG CTACCCTCAG TTCATCCGCT CACTTTTCCA ACGTnAATCG GTTCGGTGCC 300

TGCCATT 307

(2) INFORMATION FOR SEQ ID NO: 4405:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4405:

AnACTTGAGT GCAGAAGAGG AAAGTGGAAT TCCATGTGTA GCGGTGAAAT GCGCAGAGAT 120

ATGGAGGAAC ACCAGTGGGC GAAGGCGACT TTCTGGTCTG TAACTGACGC TGATGTGCGA 180

AACGTGnGGG ATCAAACAGG ATTAGATACC CTGGTAGTCC ACGCCGTAAA CGATGAGTGC 240

TAAGTGTTAG GGGGTTTCCG CCCCTTGAGT GCTGnCAGCT AAACGCATTA AGCACTCCGC 300

CTGGGGGAGT GACGGACCGC AAG 323

(2) INFORMATION FOR SEQ ID NO: 4406:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4406:

AATTATGGGA TGCAATGGGA TACGAACGTG TTAAAACACG TATGGAAGAC GAACTTGGAG 60

ACTTACCACA ATGGATTAGT GATTTAGATG GTGGCTTTTA TAAACAAGAT GAGACCATTG 120

AATATGCAAC ACCTATTTCT CACTTCGTAA AAGATGAACT TTGGGATAAA GGTGATGCCA 180

AACTTTCCGT AACTCATGAT GATCAACTGT TACTGAAATT ACAAAGTAAA AATAATGTCA 240

TTACCGATGA ATTCAACGGT GCGTTAGTTG ATGCGATTGA TTTACTGGGA AATGACCCTT 300

ACnCnAGnAT GGGTA 315

(2) INFORMATION FOR SEQ ID NO: 4407:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4407:

CACCACCTCC CTACCTACTC GCCCCCCATC ATAAAATAGG TGGACAGGAA TATCAACCTG 60

TTATCCATCG CCTACCCTGT CGCCTCAGCT TAGGACCCGA CTAACCCAGA GCGGACGAGC 120

CTTCCTCTGG AAACCTTAnT CAATCGGTGG ACGGGATTCT CACCCGTCTT TCGCTACTCA 180

CACCGGCATT CTCACTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT 240

AGAACGCTCT CCTACCATTG TCCAAAGGAA TCnCACAGCT TCGGTAATAT GTTTAGCCCC 300

GGTACATTTT CGGCGCATGT CACTCGACTA nTG 333

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4408:

ATTTAATGAA GTGCTTGTTA ATGAACCAAG CGCTAAAGAT ACTGTTGAAA TTTTAAAAGG 60

TATTCGCGAA AAATTCGAAG AACACCATCA AGTAAAATTA CCAGATGACG TATTAAAAGC 120

ATGTGTTGAC TTATCAATTC AATATATTCC ACAACGATTA TTACCAGATA AAGCAATCGA 180

TGTGTTAGAT ATTACAGCAG CACATTTATC TGCGCAAAGT CCCAGCTGTC GATAAAGGTT 240

GAAACTGAAA AACGGATTTC TGGATTTnGA AAATGATAAA CGTAAAGCAG TAAGTGCTTG 300

AAGGGATTTT AAAAAAGCTG ACGGACCATT CCAAAATTGG AATCCAAATC nnTTACCAGG 360

TTAAATTTGG GAAAATGGTT AATTGGTGGG ACC 393

(2) INFORMATION FOR SEQ ID NO: 4409:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4409:

GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 60

TACTAAACTC GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA 120

GCCATTTTTC TTTGTGTTTA CTTTTTATTT TGACGTTTTA GGCATAAAAA AAAGAGACCT 180

TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTTGCCTG GCAACGTTCT ACTCTAGCGG 240

AAGTnAATTG GGCTACCATC GTCGCTAAAG ACCTTTCTTG ACTTGTGGAC AATCGCTTGG 300

CnTCTnTCCT CTCCTTCGG 319

(2) INFORMATION FOR SEQ ID NO: 4410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AATTAAACAT TTCATTTTAA TCAATGAGAC TAAnATACGC CTAACTTCGT TAACTTTTAA 60

AATGTATTAA AATTCTAAAG TTTCTTTTGC TTTTTCnATG ATGTCATTTT TGTTTGGTAA 120

CCAAACATTT TCAGCTTGAG TGAATGGATA AATTGTATCT GCCTGCCTGA ACTCTTCCAA 180

TAGGTGCTTC TAATGAAAGG ATTGCACGTC ACTTAATTCA GCTAACAACT GCTGCACCAA 240

CACCAGCTTG CnGTTGTGCT TCTTGACTAC AAACTGACGA CCAGTTTTTC AACTGAGCAC 300

AATTGTGCAC ATCGATTGGT GACAG 325

(2) INFORMATION FOR SEQ ID NO: 4411:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4411:

GAGTTGGACA ATGCCGAAGC GTGAGCAAAG TTTTTACCAT GCATGGTTGC ATTTAGCGCA 60

ACATGACCAT AGTTTTACTA AAGCACAGCG CCAAGTGATT AAAGGCTTAC CCAATGATCC 120

TGAAATGACG ATAGAGTCAG TATTAACTCA TTTTTCAATA GATCAGGAAG ACTAnCAAGC 180

TTATGTTGAA GGACATCTTT TGGCGTTACC GGGTTnGGCA nGTATGTTGT ATTACCGTTC 240

ACCACAGCAT CACTTTGAAC CACCTTTGTT AACGGGTTAA TTGGCCATTC GGGTAAGTTG 300

TCCGACCATT GCCAAGTGGG TGATGAGTTn AGGCCAGTCC GCAAAAGATT GGGAAAGTAG 360

TCCGGAAAAT GGGTTAAGCC AACCTGTTGC CATCCAGGGG 400

(2) INFORMATION FOR SEQ ID NO: 4412:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4412:

GATATATGGC AGCTCAAAGG AATGGGTTTC AGTTGAAGTG AAATTATCAC AGTCACTAGA 60

CCCGAGCACA TTATTTCATC TCACTGACAA TGAGGCAGGA GATCGCTTTT ATATGCGTTT 120

GAATGATAAT CGAACGTCAT ATTTTGGCTA CAAAGCAATT CAATTATTCA AAAATAATTC 180

TAAAAATAAA CAATCTATTT TAAAAGACTG GGGAAAATTA AACATAACCA TCACCATTTA 240

CCATAAATCA GATGATGAAT GGCGnGAGTT TGGCCTAAAn CATTTGGAAT ACCCGGAGTT 360

TTAATTCCA 369

(2) INFORMATION FOR SEQ ID NO: 4413:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4413:

TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 60

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC 120

AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTTCTTTG TGTTTACTTT TTATTTTGAC 180

GTTTTAGACA TAAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCnACTCTA 240

GCGGAAGTAA GTGGGCTACC ATCGTCGCTA AAGACCTTTC TTGGACTTGT GGACAAnCGC 300

TTGCGTCCTT nCCTC 315

(2) INFORMATION FOR SEQ ID NO: 4414:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4414:

GACCATCTCC TAAGGCTAAA TACTCTCTAG TGACCGATAG TGAACCAGTA CCGTGAGGAA 60

AGGTGAAAAG CACCCCGGAA GGAGGTGAAA TAGAACCTGC AAACCGTGTG CTTACAAGTA 120

GTCAGAGCCC GTTAATGGGT GATGGCGTGC CTTTTGTAGA ATGAACCGGC GAGTTACGAT 180

TTGATGCAAG GTTAAGCAGT AAATGTGGAG CCGTAGCAGA ACAGGGTCTG GAATAGGGCG 240

TTTAGTATTT GGTCGTAnCC GnAAACCAGG TGATCTACCC TTGGTCCAGT TGAAGTTCAG 300

GTTnACACT 309

(2) INFORMATION FOR SEQ ID NO: 4415:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4415:

TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 60

TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT 120

CTCAAATGCG GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAAnTA 180

AGTTCGGACT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 240

TGACCTCCTT GGCTATAGTC ACCAGnACAT ATGAATGTGA AATTTATACA TTCAAAACTn 300

(2) INFORMATION FOR SEQ ID NO: 4416:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4416:

AGAAAAATAA GCGAACTGnA ATAAATAAAG ATTCAATTAA CGCATCAGTA TTAGGATTCA 60

CTCTAAAACG ATTAATAGTT TTATAAGAAG GTGTTTGATC TTGAGCTAAC CACATCATTC 120

GAATACTGTC ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT TGAGTATATG 180

CATATAAGAT GATTTTTAAC ATCATCTTTG GATGATAGGA TGTTGCGCCA CGATGATGTC 240

TGAATTCATC GAATTTGCTA TCAGGTATCG TTTCAACAAT TTCATT 286

(2) INFORMATION FOR SEQ ID NO: 4417:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4417:

TTTGATAAAA ATGGGCCATC GTCACGAGCT TCAACAATTC GTTTCGCAAC GTTTTCGCCA 60

AGCCCAGCCT GATATATTAC ATGAGGAGCG GTGCAAATGT TGTTAGAAAT TAAAGATTTA 120

GTGTATAAAG CGAGCGATAG AATCATACTA GATCATATCA GTCTAAAAGT AGATAAAGGC 180

GAGAGTATTG CCATTATAGG TCCATCAGGT AGTGGTAAAA GTACATTTCA AAAGCAAATA 240

TGTAATTTGT TTAGTCCAAC TAGTGGAGAA CTTTATTTTA AAGGTAAACC CTATAATGAT 300

GTTTGGTGGA ACGnATTGGA nGATAACCAT GGATAATTCC 400

(2) INFORMATION FOR SEQ ID NO: 4418:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4418:

GTATTTACAA TCAAACTAAG CAAAAGTATT CAGATGCCTC AGATAAAGCT TGGGCGCATT 60

CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA CGCATATAAA AGTGCAAAGG 120

GTTGGCTAAT AGATATGGCT AATAAATCGC GCTCGAAATG GGATAATATT TCTAGTACAG 180

CATGGTCGAA TGCAAAATCC GTTTGGnAAA GGAnCATCGA AATGGTTTAG TAACTCATAC 240

AAATCTTTAA AAGGTTGGAC TGGGGATATG TATTCAAGAG CCCACG 286

(2) INFORMATION FOR SEQ ID NO: 4419:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4419:

CTCACTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT AGAACGCTCT 60

CCTACCATTG TCCAAAGGnA TGCnCACAGC TTCGGTAATA TGTTTAGCCC CGGTACATTT 120

TCGGCGCATG TCACTCGACT AGTGAGCTAT TACGCACTCT TTAAATGATG GCTGCTTCTA 180

AGCCAACATC CTAGTTGTCT GGGCAACGCC ACATCCTTnT CCACTTAACA TATATTTTGG 240

GACCTTAGCT GGGTGGTCTG GGCTGTTTCC CTTTCGAACA CGGACCTTGA TCACCCCATG 300

(2) INFORMATION FOR SEQ ID NO: 4420:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4420:

GGTGAGCGGA GCGAACTCnC GTTAAGGAAC TCGGCAAAAT GACCCCGTAA CTTCGGGAGA 120

AGGGGTGCTC TTTAGGTTAA CGCCCAGAAG AGCCGCAGTG AATAGGCCCA AGCGACTGTT 180

TATCAAAAAC ACAGGTCTCT GCTAAACCGT AAGTGATGTA TAGGGGCTGA CGCCTGCCCG 240

GTGCTGGAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAAcT ACGAATCGAA GCCCCAGTAA 300

ACGGcGGCCG TAACTATAAC GGTCTAGACG ATCTGC 336

(2) INFORMATION FOR SEQ ID NO: 4421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4421:

GGnCACCCTC GTGCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG GCTAGCCCTA 60

AAGCTATTTC GGAGAGAACC AGCTATCTCC AGGTTCGATT GGAATTTCTC CGCTACCCTC 120

AGTTCATCCG CTCACTTTTC AACGTAATCG GTTCGGTCCT CCATTCAGTG TTACCTGAAC 180

TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT AAACGCCCTA 240

TTCAGACTCG CTTTCGCTAC GGCTCCACAT TTACTGCTTA ACCTTGCATC AAATCGT 297

(2) INFORMATION FOR SEQ ID NO: 4422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4422:

GTACATCGTC TAATAATAAG TTGACGATAT CTTGCAATGC ATCTTTATCT AAATGTAAGA 60

ATTCAACGAT GCCGTTGAAG CGGTTAAGGA ATTCAGGGCG GAAGAATTTT TTCATTTCGT 120

GCATAATATC TTTTTCTTCA GCGTCATTGC CATTGCCAAA GCCAGCATTT GATGTACAAA 180

TAATAATTGT ATTTTTAAAG TTGATGACAT TACCTTGACC ATCAGTCAAA TTACCATCAT 240

CCATTACTTG TAATAACAAT GTTAAAATTG TGGATTGCTT TTCGATTCAn CAATAGAATG 300

ACTGAGAnGG GATACGGCGA CTTTTCAGTA AACGGATTGA ATGGCATCAT AnCCACATAC 360

CAGCGTGGAC CATCATTTTG GAACAGCGTG GGCACATATC 400

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4423:

AAGTTGAGTC GCATAGCTAG TATGAAACGT GGTGTGCGCA TGGGAACTAT CAAGCTTTGA 60

AGATGTGGTA CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT 120

CCATTAAATG AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT 180

AAAATTGCCT ATAAATTTTT AGCACATAAA ATAAGAnGnG CCAACCATTG TTAGACTATA 240

ACAACGGTTG GCTCTTTAAT TGTAAAAAGA AAACCATACG CTATGGTAGT T 291

(2) INFORMATION FOR SEQ ID NO: 4424:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4424:

AACTGCCACC ACCTGGGGnC GTTTCCAGAA CCTCTATGCA TTTCAATCAC AGnCAAATGT 60

GCGGTTGACG TTCAATGACT ACCTGCAATT CATCGGTCAG CTCACACCCT TTACCTGnCT 120

AAAGTACCAG TAGACAATGT AGGTATTGGA CTTGCATGAG CATTTTTATn CAGTAATGGG 180

CTTTAGATAT TTTATTAATA CCGGCCAATC ATGCTATTCA AACCGCCAAT AGCTTTATTA 240

GCAACATTTT TACCTAAATC AGCCGCAGCT CTTCCCATGT CTTTACCAAT ATCTCTAATC 300

CAATCATATG TTTTTGCATA GCCATTTTCT AAAACCATTA AATACTGATT TAGCGTTAGA 360

CCATGCCGAA CTTGAAATTG CATCAAAACG ATCGTGGGCT 400

(2) INFORMATION FOR SEQ ID NO: 4425:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4425:

AGATGATAAA AGCAACAGGT GGTTTTGCGA AAAGTGAAGT ATGGCGTCAA ATGATGTCAG 120

ATATATTTGA CACAGAGTTA GTGGTTCCTG AAAGTTATGA AAGTTCATGC TTAGGTGCCT 180

GCGTGCTCGG ACTTAAAGCT GTAGGTGACA TTGAAGATTT TTCAATCGTT TCATCGATGG 240

TCGGTGCCAC AAACAATCAT ACGCCGATTG AAGAAAATGC ACTGTTACCA AGAnTCGAAT 300

CCATTnTTAT CATTAAGCGT CTTAnCAGAG ATATGACAAT 340

(2) INFORMATION FOR SEQ ID NO: 4426:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4426:

CTGAAGATGA TAAAGATGCA GATGGTGGCG AGTTGCACGT AACAATTACG GATCATGATG 60

ATTTCACACT TGATAACGGA TACTTCGAnG AATTATCATC AGACAGCGAT TCAGACTCAG 120

ATAGTGACTC AGACAGCGAC TCAGACTCAG ACAGCGACTC AGACTCAGAC AGTGATTCAG 180

ATTCAGACAG CGACTCAGAT TCAGATAGCG ACTCAGATTC GGACAGCGAT TCAGACTCAG 240

ATAGCGACTC AGATTCAGAT AGCGATTCAG ACTCAGACAG CGACTCAGAT TC 292

(2) INFORMATION FOR SEQ ID NO: 4427:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4427:

AACAGTGCTC TACCTCCAAT AATCATCACT TGAGGCTAGC CCTAAAGCTA TTTCGGAGAG 60

AACCAGCTAT TTCCAGGTTC GATTGGAATT TCTCCGCTAC CCTCAGTTCA TCCGCTCACT 120

TTTCAACGTA ATCGGTTCGG TCCTCCATTC AGTGTTACCT GAACTTCAAC CTGACCAGGG 180

TAGATCACCT GGTTTCGGGT CTACGACAAA TACTAAACGG CCCTATTCAG ACTCGGCTTT 240

CGCTACGGTT CCCACATTTA CTGGCTAAAC CTTGCATCAA AATCGGTAAC TCGnCGGGTC 300

ATTCTAn 307

(2) INFORMATION FOR SEQ ID NO: 4428:

(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4428:

GACCATACAT CGTCATCGTT TGCACCGTCA AATACTGGTG ATGCAACGTG AATACCAAGA 60

TTTTTAGCAG CCATACCTAA GTGTAGCTCT AATACTTGTC CGATGTTCAT ACGAGATGGT 120

ACACCAAGAG GATTTAACAT GGATATCGAT CGGGACGTCC ATCTGGTGAA GTGAAGGCAT 180

ATCTTCTTCA GGGAACAATC TTGAGGAAAT GGACACCTTT GTTGACCATG TCGGACCACA 240

CATGCTTATG CACCAACATG GAATTTTACG TTTTTGGAAn GATGATTATT ACACGTnACT 300

AATTGGTTTA CACCAGGTGG AnAATGTTAT CGTCGGCCTT GCTTCACGAT TGGA 354

(2) INFORMATION FOR SEQ ID NO: 4429:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4429:

GTGnACTATC nGCTTGTCTA TGATAATATT ATTCTTTGTA CTTGTTTAAA AGATATTAGA 60

CTAAAACTAA AAACAGCAGT AAGATGATTT ATGATTAAAA CTATCTTACT GCTGTTCACT 120

TTTTATAATA CTTCTGAATG TCTCACTTAT ACTTCTAGTC ACAGATTTAA ATAATCAAAA 180

GTGCACATTA TTAAAATATC AATTTCACAC TCAATGCGGC TCATCGCATT CATTTCTTGT 240

CTAGCAACGT TCTACTCTAG CGGAACGTAA GTAGCTACCA TCTCGCTAAG GAACTTTCTT 300

GACCTGGTGA CAACCGCTGC GnCTnTCTCT CTTCGGCTCT CGCTTACTCC ATTTAGCTCC 360

ACTAAACTCG TGCGGCCCTT CCCGTTCGGC AGATCCAACG 400

(2) INFORMATION FOR SEQ ID NO: 4430:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4430:

ACCATTCACA CCTTGACAGC CACATAACAT AACTAAGTTT AAGATnGGGG GATAAATCGT 120

ATCTGAGTTA AACCAATGGT TAATACCCGC ACCCATGATA ATCATTGAAC GCCCTTCAGT 180

ATCGATAGCG TTTTGCGCAA ATTCTTTCGC TACTTGAATG ACAACACTTT GTTTTACGCC 240

TGAAATGGCT TCTTGCCAAG CAGGTGTATA TTTTGATTCT GCATCGTCGT AA 292

(2) INFORMATION FOR SEQ ID NO: 4431:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4431:

TGAGCCGnAC ATCGAGGTGC CAAACCTCCC CGTTCGATGT GAACTCTTGG GGGAGATAAG 60

CCTGTTATCC CCGGGGTAGC TTTTATCCGT TGAGCGATGG CCCTTCCATG CGGAACCACC 120

GGATCACTAA GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCATC AAGCTCCCTT 180

ATGCCTTTAC ACTCTATGAA TGATTTCCAA CCATTCTGAG GGAACTTTGA GCGCCTCCGT 240

TACCTTTTAG GAGGCGACCG CCCAGTCAAA CTGCCCGCCT GACA 284

(2) INFORMATION FOR SEQ ID NO: 4432:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4432:

TATCATTGTG GTACGATAAG GCATATGTTG TACCTATGnA TGGTGGAAGA GCCTTCAGTT 60

GTCGCTGCAG CTAGTTATGG TGCAAAGCTA GTGAATCAGA CTGGCGGATT TAAAACGGTA 120

TCTTCTGAAC GTATTATGAT AGGTCAAATC GTCTTTGATG GCGTTGACGn TACTGGAAAA 180

TTATCAGCAG ACATTAAAGC TTTAGAAAAG CAAATTCATA AAATTGCGGn TGAGGCATAT 240

CCTTCTATTA AGCGCGTGTG GTGGTTACCA CGTATAGCGA TTGATACATT CCTGGCCACC 300

AGTTCTATCT TT 312

(2) INFORMATION FOR SEQ ID NO: 4433:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4433:

CGGTACTCGT TAAGGCTGAG CTGTGATGGG GAGAAGACAT TGAGTCTTCG AGTCGTTGAT 60

TTCACACTGC CGAGAAAAGC CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC 120

AGGTAGTCAA GATGAGAATT CTAAGGTGAG CGAGCGAACT CTCGTTAAnG AACTCGGCAA 180

AATGACCCCG TAACTTCGGG AnAAAGGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC 240

AGTGAATAAG CCCAAGCGAC TGTTTTATCC AAAACACAGG TCTCTGCT 288

(2) INFORMATION FOR SEQ ID NO: 4434:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4434:

GGACCGAACC GACTTACGTT GAAAAGTGAG CGGATGAACT GAGGGTAGCG GAGAAATTCC 60

AATCGAACCT GGAGATAGCT GGTTCTCTCn nAAATAGCTT TAGGGCTAGC CTCAAGTGAT 120

GATTATTGGA GGTAGAGCAC TGTTTGGACG AGGGGCCCCT CTCGGGTTAC CAATTTCAGA 180

CAAACTCCGA ATGCCAATTA AATTTAACTT GGGAATTCAG AACATGGGTG ATnAAGTCCG 240

TGTTTCGAAA GGAAACAGCC CAGACCACCA GCCAAGTCCC AAAATATATG TTTAATGGGA 300

AAAGGTGTGG CCTTTGCCCA GGACAACCAA GAAGTT 336

(2) INFORMATION FOR SEQ ID NO: 4435:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4435:

ATTGACGCCG CATTTTTACG GAATGGGAAT AAAGCGACAC AAACCGTCAC GTCnGTGTTG 60

GTGTCATGAC AAGGTAATGC GAGTGATCTG ATGTATGGCT TATCATGGCA ATCTGTTATG 120

GnCTGACTGA TCGGACGATG TATCATTCGC CAATTCGTTT ACTTGTCGTT ATTCAGGCAC 180

AATCATTGGC TGCGTTTTAA TGAGCGTAAT GAGGAAGGGG CGTTTAAAAA GTTGGATTTA 300

ACGA 304

(2) INFORMATION FOR SEQ ID NO: 4436:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4436:

AATATACTCC GGTAAATAAC CGAAGAGTTT TGAATCATTG TTAAAAATGG AATTAnAGTT 60

CTAGTATCTG TTGGGTTTTG AAATAGGTCA TAGGATAAAA CAAATnGAGA ATTTGTCGCT 120

ATTTGTAAAT TGTATCCTGG CTTAAGTTGG CCATTTTTCA TATGGTCTTC CTTCATTCTC 180

ATAAAAGTTG CATCATGGAT CAGTTTTAGA AAAGCTATTT CTATCTTTAA GAATCGATTT 240

TTGTTCTTCA TATTTATTTT TTCTTTCGGA ATAATCATCA AATTTATnTT TGGAACTTCT 300

TAATC 305

(2) INFORMATION FOR SEQ ID NO: 4437:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4437:

ATCGTTTAAA TCAGTTAGTA AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAAATA 60

TTATAGAAAA CATCAAAGGA TGTTAAGAAA TACAATTTAT TACCCAGCAT TTAATAATGG 120

TGCTATAGAA GGAATTAATA ATAAGATAAA ATTAATCAAG TGAATTTCTT TTGGTTACAG 180

AAATTTCAAC AACTTTAAAG CACGTATAAT GATGATTTTC AGCTTGTACA AGGGGGAnAA 240

AAGGAnGnCA ACCAAGCCCA ATAATGGACT GGCCGCCTAA TATTAAAAAC TCTAAAGGTT 300

GTATTTTAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA CCCGTTAAC 359

(2) INFORMATION FOR SEQ ID NO: 4438:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4438:

ACTTACAGTT ATTTTAACTT GGnCAGAATC CATCATCCAT AAGTTCGAAA TGTTGTAAAA 60

CATAAACCTT GnAAACGGCA ACATTTTTGG GTCCTTCTCC ATCATTTTAT TTAAAAGCGC 120

ATTATGATCA ATATCATGCC CAATTAACTT TCCAGCAATT TCCATAGTAT GTTCTGAGGT 180

ATTGTTAAAA AGGAATCGCC CAGTATCACC GACGATACCA AGATATAAAA CGCTCGCGAT 240

ATCTTTATTA ACAATTGCTT CATCATTAAA ATGTGAGATT AAATCG 286

(2) INFORMATION FOR SEQ ID NO: 4439:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4439:

TCGCTTGACT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAnCTCT ACTAAACTCG 60

TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT 120

TTGTGTTTAC TTTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180

TGCGGCTCAT CGCATCCATT TTTTGCCTGG CAAcGTTCTA CTCTAGCGGA ACGTAAGTTG 240

GCTACCATCG ACGCTAAGAA CCTtTCTTGA CTTGTGACAA aTCGCTTGCT TCTTTCCTCn 300

TCTTCGGTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCGCTCTTT TCTCGTTTCG 360

TCAGATTCAA CAGTTTTCAT TCGCCAAGCC ATTT 394

(2) INFORMATION FOR SEQ ID NO: 4440:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4440:

TAATAGGTTC GAGGTGGAAG CATGGTGACA TTGGCAGCTG ACGAATACTA ATCGATCGAA 60

GACTTAATCA AAATAAATGT TTTGCGACAA TGCAACTTTT ACTTACTATC TAGTTTTGAA 120

TGTATAAATT ACATTCATAT GTCTGGTGAC TATAGCAAGG AGGTCACACC TGTTCCCATG 180

TAGAACGTTG CCAGGCAAAA AATGGATGCG ATGACCGCAT TGAGACCGCA GCnTn 295

(2) INFORMATION FOR SEQ ID NO: 4441:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4441:

TTTCATAAAA AGATTTCAAA CGCGTTCATC AAnCCTCGTC GCAGGTCTTT CGAACACTAG 60

CGATTATTTC tTATGAATTC AAGCTTATTT AAAACTCTTT ATTCaCTCGG TTTTGCTTGG 120

TAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA CAATTTCTTT TTAGTCAAGC 180

GCTCGCATAC TGCTTTATTT TCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 240

TAAATAAACA TTCAAAACTG AATACAATAT GTCACGTTAT TCCgCATCTT CTGAAGAAGA 300

TGTTCCGAAT ATATCCTTAG AAAGGAGGTG ATCCnGCCGn ACCTT 345

(2) INFORMATION FOR SEQ ID NO: 4442:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4442:

AATCATTGTC AAAACTACGT TCTGGTAAAC AAGGACAACC CGTTTGAACC ATTGGCCCAC 60

ACCATTTGAT AGGCAGnCAT GTGCGCAATG GACATCCACA TAGTTGCGTA ATGTTTCATA 120

CGTCATTGCT CAAATCATTC ATGACTAGCG CAACATGATT ACCTTGTCGT GnGCACCTTC 180

ATTAAAGnAA CTTATGATAG ATTTATTTCC CGGGACATTA AGCATTCGCA TCGTTAACAT 240

GCGTATTGCA CCCAATTTAG AAGTTCCTCC GTGCCGTTTG GTATATCACA AATTTGTAGT 300

GTATCTTGGA TGC 313

(2) INFORMATION FOR SEQ ID NO: 4443:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4443:

AGCATGGTGT TTCTCAGATT GTCGGATGTA TAAATGTGTA TGTTATGTTT TAATTTTTCC 60

CAGTCTTTAA AAATAGATTG TTTATTTTTA GAATTATTTT TGAATAATTG AATTGCTTTG 120

TAGCCAAAAT ATGACGTTCG ATTATCATTC AAACGCATAT AAAGCGTATC TnCTGCCTCA 180

TTGTCAGTGA GATGAAATAA TGTGCTCGGG GTCTAGTGAC TGTGGATAAT TTCACTTCAA 240

CTGAAACCCC ATTCCCTTTG AGCTGCCCAT ATATCTCTTT GGACAATATC GGTCCCTCTA 300

ATACGGnCCG TAGnCCATTC CATTTCAATT CTTTTC 336

(2) INFORMATION FOR SEQ ID NO: 4444:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4444:

CAGACTGGGA TATTTATAAA ACGTTGGCAA AAGCATTTTC AGAAATGGCA AAAGACTATT 60

TACCTGGAAC GTTTAAAGAT GTTGTGACAA CTCCACTTAG TCATGATACA AAGCAAGAAA 120

TTTCAACACC ATACGGCGTA GTGAAAGATT GGTCGAAGGG TGAAATTGAA GCGGTACCTG 180

GACGTACAAT GCCTAACTTT GCAATTGTAG AACGCGACTA CACTAAAATT TACGACAAAT 240

ATGTCACGCT TGGGCCTGTA CTTGAAAAAA GGGGAAATTT GGAGCACCTG GGGGTAAGTT 300

TCCGTGTCCA GTTGAACCAT TATGGAGGAn TTnAAAAAGT ATGTTAAGGG ACCTGGGAGT 360

TGAATACCCA ATGGATnGAT TCCCGTGAAG AGCCGAATCC 400

(2) INFORMATION FOR SEQ ID NO: 4445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4445:

TACGCCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA GCTCGCGTAC 60

CGCTTGTAAT GGGCGAACAG CnATCGCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA 120

GCCGACATCG AGGTGCCAAA CCTCCCCGTC GATGTGAACT CTTGGGGGAG ATAAGCCTGT 180

CACTAAGTCC GTGCTTTCGA CCCTGACTAC GGACTTGTnA GGTCTGCGGC ATTCAAGCTT 300

CCCTTGATGG CCTTTGACAC TGCTTATGGA ATGnATTTG 339

(2) INFORMATION FOR SEQ ID NO: 4446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4446:

CAATTTTAAG TGTTGAAAAT GTCACTTTTA AACTTTCTAG TTTTATCTTT AATAAACATG 60

CCATnCGTAA TAAGTGGCGT TTTATTAAAA TCATCTATAA TAGCCATATA GTTTTGCTCA 120

CTACCATAAC CTGCATCAGC TACAATATAC TCCGGTAAAT AACCGAAGGA TnTTTGGAAT 180

CATTGTTAAA AATGGAATTG AAAGTTCTAG TATCTGTTGG GTTTTGAAAT AGGTCATAGG 240

ATAAAACAGG GTGAGAATTT GTCGCTATTT GTAAATTGTA TCCTGGCTTA AGTTGGCCAT 300

TTTTnCATAG GTCTTCCT 318

(2) INFORMATION FOR SEQ ID NO: 4447:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4447:

TTTTGAAATT CTCTATGTTG GGGCCCGGAC TATAATTGAA AAATGCTTGT TACAAGTGCA 60

TTTTATTTCA GTCAACTACT AACAATATAA CATTGTGGAG CCCAGAnCTT TGATTAATGT 120

ATATGAAAAT CAAAGTAATG CTTATGTATG ATTATTTCAA ATATTTTACA TACATGAACT 180

TTTCCAATGT ACGATACTAT TATTATAAAG CGCTCGCTAA GATTTTACGA TGATTAGAGG 240

GTAAAAAATG AACGATCAAT GGTnTAACCA TTTAATTGG 279

(2) INFORMATION FOR SEQ ID NO: 4448:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4448:

GACACCGGCA TTCTCACTTT CTAAGCGCTC CACATGTCCT TACGATCATG CTTCAACGCC 60

CTTAGAACGC TCTCCTACCA TTGTCCAAAG GACAATCCAC AGCTTCGGTA ATATGTTTAG 120

CCCCGGTACA TTTTCGGCGC AGTGTCACTC GACTAGTGAG CTATTACGCA CTCTTTAAAT 180

GATGGCTGCT TCTAAGCCAA CATCCTAGTT GTCTGGGGCA ACGnCACATC CTTTTCCACT 240

TAACATATAT TTTGGGACCT TTAGCTGGTG GTCTnGGGCT GTTTTCTGnA TTGAACACGG 300

GA 302

(2) INFORMATION FOR SEQ ID NO: 4449:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4449:

CGTTGGTATA TAGAGGGCAA CCGTCACCTG ATAAAATGTG GACACAGTTT TTACAAGAGG 60

TTAAGGAAAT GAGTTTGGAG GCATACGAGC ATCAAGAATA CCCATTCGAA TGTTTAGTAA 120

ATGACTTAGA TCAATCACAT GATGCCTCAC GGAATCCATT ATTTGATGTC ATGTTAGTAC 180

TACAAAACAA TGAnACGAAA TCATGCTCAT TTTGGGCATA GTAAATTTAA CACACATTCA 240

ACCCCAAATC AGTGACGGGC GGAAATTTGG ATTTnTCCTT TTCCATCATT GGAAGAAGGA 300

TCGCGGATGA CCTAATAnCA ATCCAATTAT CGGGGTATAA ATACCGGATT TTATAACCA 359

(2) INFORMATION FOR SEQ ID NO: 4450:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4450:

GATGACAAAA TTTGCTTGAA AACCGAAATG GATGGTCATC ATTGACTGnA TCAAGGTACA 60

TCATTCTTTG GTGCTTATGC ATTTAGACAT TATACAAAAA CAATACTTTT ATAGGGCAAC 120

CTTATGGGGT TCTATCGGCT ATACATTACC TGCAACATTA GGTTCACAAT TAGCAGACAA 180

AGATCGTCGn TAACTTATTA TTAATTGGTG ATGGCTCATT GCCAACTAAC TGTTCAAGCT 240

GCTATACGGT AGAACGACTT ATTCCC 326

(2) INFORMATION FOR SEQ ID NO: 4451:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4451:

GAAAACATCA AAGGATGTTA AGAAATACAA TTTATTACCC AGCATTTAAT AATGGTGCTA 60

TAGAAGGAAT TAATAATAAG ATAAAATTAA TCAAGTGAAT TTCTTTTGGT TACAGAAATT 120

TCAACAACTT TAAAGCACGT ATAATGATGA TTTTCAGCTT GTACAAAGGA GAnAAAAAGA 180

AGACAACCAA GCCCAATAAT GGACTGGCCG CCTAATAATA AAAACTCTAA AAGTTGTATT 240

TTAAAAATAG GTCTTTAAAT TATATACCCC CCCCATTTGG GTGGAGAACC GGTAAACCAT 300

GCCTAGGTGC CTAACCTCCn ATAATGGnAC CCCTCCTTAC CATTTGGGCC ATGGGGCCAA 360

TAAAGCGGGG GGCAATTGGG G 381

(2) INFORMATION FOR SEQ ID NO: 4452:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4452:

TTAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG TTATTAATCT TGTGAGTGTT 60

CTTTCGAACA CTAGCGATTA TTTCTTATGA ATTCAAGCTT ATTTAAAACT CTTTATTCAC 120

TCGGTTTTGC TTGGTAAAAT CTATATTTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 180

CTTTTTAGTC AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAAATAT TTGAATGTTA 240

AATAAACATT CAAAACTGAA TACAATATGT CACATn 276

(2) INFORMATION FOR SEQ ID NO: 4453:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4453:

GGCGAAACCG CGTAGCGTTT TTTAAGTCTG ATGTGAAAGC CCACGGTCAA CCGGGAGGGT 60

CATTGGAAAC TGGAAAACTT GAGTGCAGAA GAGGAAAGTG GAATTCCATG TGTAGCGGTG 120

AAATGCGCAG AGATATGGAG GAACACCAGT GAGCGAAGCG ACTTTCTGGT CTGTAACTGA 180

CGCTGATGTG CGAAACGTGG GGGATCAAAC AGGATTAGAT ACCCTGGTGA GTCCACGCCG 240

TAAACGATGA nTGCTAAATG TTAGGGGGTT TCCGCCCCTT AGTGGCTGCC AGCTAnACGC 300

ATTGAAGCAC TGCCGCCTGG GGAGTGACGA CCGCAAnTTG A 341

(2) INFORMATION FOR SEQ ID NO: 4454:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4454:

ACnCTCCCCA AAGTCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA GTGnCCAAGG 60

CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTTAT AAGTCAAACG 120

CTCACATACG GCTTCGTTTT CATTATTTTA AATGCTCATT TACATAAGTA AACTCTGCTT 180

TAAAATAATT TAACTCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT TTAAACGCGT 240

TATTAATCTT GTGAGTGTTC TTTCGAACAC TAGCGATTAT G 281

(2) INFORMATION FOR SEQ ID NO: 4455:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4455:

ATGTCTTCAC TTATACTTCT AGTCACAGAT TTAAATAATC AAAAGTGCAC ATTATTAAAA 60

TATCAATTTC ACACTCAATG CGGCTCATCG CATTCATTTC TTGTCTAGCA ACGTTCTACT 120

CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 180

GCTTGCnTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG 240

CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCnGT 279

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4456:

ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT 60

CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 120

AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 180

ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TnTCGTCAGA TTCAAACGTT 240

nTCACTTCGC CAAGCCATTT TTCTTGTGTT TACTT 275

(2) INFORMATION FOR SEQ ID NO: 4457:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4457:

ATCCGATTCA CAAAGCACAT CATCATATAC AAGTCAGTCA ACAAGCCAAA GTGAATCCAC 60

ATCGACATCA ACGTCACTAA GCGATTCAAC AAGTATATCT AAAAGTACGA GTCAATCAGG 120

TTCGGTAAGC ACATCAGCGT CATTAAGTGG TTCAGAGAGT GAATCTGATT CACAAAGTAT 180

CTCAACAAGT GCAAGTGAGT CAACATCAGA AAGTGCGTCA ACATCACTCA GTGACTCAAC 240

AAGTACAAGT AACTCAGGAT CAGCAAGTAC GTCAACATCG CTCAGTAACT CAGCAAGCGC 300

AnTGGAATCC GATTTGTCGT CAACATCTTT AAGTGGATTC AACATCTGCG TCnATGCCAA 360

AGnnGTGAAT CCGATTCACA AAGCACATCA GCATCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4458:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4458:

AGTCGCTGTC TGAATCTGAA TCACTGTCTG AATCCGAATC GCTATCTGAT TCTGAGTCGC 120

TATCTGAACC TGAGTCGCTG TCTGAGCCTG AGTCACTGTC TGAATCCGAA TCCGGATCCG 180

GGTCTGGGGn TGGTTCCGGT TCTGGGTCTG GGACTTGGTT CTGGATCTGG CGTTGGTTCT 240

GGGTCTGGGG TCTGGACTGG TTCTGGGGTC AAACGGCGGC CCTGGAGTGG GGTCTTTCGG 300

AATnAACGGC GGAATCACCA TCAAGCAACT TnCAACAACC ATAACGAAAA A 351

(2) INFORMATION FOR SEQ ID NO: 4459:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4459:

ATCCTGCAGT TGATCAGTAT GGTGATATTA ATTTAGTTAA TACGAACGCG TCATCTACAA 60

GTGAAATCAT TTACGATTTA ATCTCACATT TTAATGATGA AGCAATTGTT AATAAAGATA 120

TCGCGAGCGT TTTATATCTT GGTATCGTCG GTGATACTGG GCGATTCCTT TTTnACAATA 180

CCTCAGAACA TACTATGGAA ATTGCTGGAA AGTTAATTGG GCATGATATT GATCATAATG 240

CGCTTTTAAA TAAAATGATG GAGAAGGnCC C 271

(2) INFORMATION FOR SEQ ID NO: 4460:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4460:

ACTGTGGATT AATATTATGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTCGACTAC 60

CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 120

TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 180

GATTTTGCTT CGCAnAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 240

GCCACATGTC ACCATGCTTC CACCTCGAAC CTATnAACCT CAG 283

(2) INFORMATION FOR SEQ ID NO: 4461:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4461:

CTTCTACAAG TCCTGAATAT ACTTATGAAT CTCTTCTTTC GTGTATGCAA ACTGACGTTG 60

TAATTTAAAT AACGTCTCAT CTTTCCATTG CGAATCTTGA TATTGTATAT TTTCAAAATC 120

AAAGTCAACT TTATGGTTAT CAATCCACGC TTTATATGGT AATTCTCCAG CAATCGCACC 180

TTTTAAATCA TTATTTTCAA TGACTTTATT CTGTTAAAAT CAACAAnCAT AACTTTCCnG 240

GATTCAATTG ACCTTTAAAA GCAACATTAC TTCC 274

(2) INFORMATION FOR SEQ ID NO: 4462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4462:

GGCTGCTAAA AATCTTGGTA TTCACGTTGC ATCACCAGTA TTTGACGGTG CAAACGATGA 60

CGATGTATGG TCAACAATTG AAGAAGCTGG TATGGCTCGT GATGGTAAAA CTGTACTTTA 120

TGATGGACGT ACAGGTGAAC CATTCGATAA CCGTATTTCA GTAGGTGTAA TGTACATGTT 180

GAAACTTGCG CACATGGTTG ATGATAAATT ACATGCGCGT TCAACAGGAC CATATTCACT 240

TGnTACACAA CAACCACTTG GCGGTnAAGC G 271

(2) INFORMATION FOR SEQ ID NO: 4463:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4463:

GCGGCTCATC GCATTCATTT CTTGTCTAGC AACGTTCTAC TCTAGCGGAA CGTAATTAGC 60

TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 120

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC 180

AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTTCTTTG TGTTTACTTT TTAnTTTGAC 240

(2) INFORMATION FOR SEQ ID NO: 4464:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4464:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA 60

TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTTGGGC ACTGTCTCAA 120

CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG GACAGGACGG 180

GAAAGACCCC GTGGGAGCTT TTACTGGTTA GCCTGGATAT TGGAAATTCG GGCACACTTG 240

GTTACAGGAT AGGTAAGGAG CCTTTTGGAA ACGTTGAGCG CTACTTTAnG TTGGGAGGCG 300

CTGGTnGGGA TACTTACCCT AACTGTGTTT GGCTTTTCTn AACCGGCACC ACTTATCCTG 360

G 361

(2) INFORMATION FOR SEQ ID NO: 4465:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4465:

CTGTATGTAC ACCACCAATC GGTTTAGGTT TAGCAACGTT TGTTCAAAAG TATAAATTCA 60

ATCATTCCGA AAGAGAAATG GGTAAGGCTT CCTTCACTAT GGGACTATTT GGTATTACTG 120

AAGGTGCTAT TCCTTTCGCA GCCCAAGATC CATTGCGCAT TATACCTGCA AACATCATTG 180

GTGCAATGAT TGCATCAGTC ATTGCAGCCA TTGGTGGTGT CGGCGATAGA GTCGCACATG 240

GnGGTCCCAA TCGTGGCTGT ATTAGGTGGG TTTTTGTTTT TTTTTnTTTT TT 292

(2) INFORMATION FOR SEQ ID NO: 4466:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GCAAACAAAA CAGTATTAGT AGATTATGAA AAATATGGTA AGTTTTATAA CTTATCTATT 60

AAAGGTACAA TTGACCAAAT CGATAAAACA AATAATACGT ATCGTCAGAC AATTTATGTC 120

AATCCAAGTG GAGATAACGT TATTGCGCCG GTTTTAACAG GTAATTTAAA ACCAAATACG 180

GATAGTAATG CATTAAnAGA TCAGCAAAAT ACAAGTATTA AAGTATATAA AAGTAGATAA 240

TGCCnCTGAT TTATCTGAAA GTTACTTTGT GGAATCCCGG AAACCTTGAG GGTGGCCCCT 300

AATAnTGG 308

(2) INFORMATION FOR SEQ ID NO: 4467:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4467:

AAGCAGGCGC TCTCCCAGCT GAGCTAAGCC CCCATAATAA TTACAGTATA TCGGGAAGAC 60

AGGATTCGAA CCTGnGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120

CCCGTATAAT TAAnGCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180

CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATAGTG CCGAGGACCG 240

GAATCGAACC GGTACGTGAT CACTCACCGC A 271

(2) INFORMATION FOR SEQ ID NO: 4468:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4468:

TGTGTTAGGT ATTACATCAT CACATTTATC TGCGTCAAAG TCCAGCTGTC GATAAAGTTG 60

TAAACTGTAA AAACGCAATT TCTGAATTAG AAAATGATAA ACGTAAAGCA GTAAGTGCTG 120

AAGAnTATAA AAAAGCTGAC GACATTCAAA ATGAAATCAA ATCATTACAA GATAAATTAG 180

AAAATAGTAA TGGTGAACAT ACTGCTGTTG CTACAGTTCA TGATATTTCA GATACTATTC 240

AACGATTAAC TGGTATTCCA GTTTCTCAAA TnGATGATAA CGnTATTGAA CGTTTAAAAA 300

ATATTT 306

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4469:

GGTTTATTAA CAGCATTCTT ATCAGCATTT GTAACTGTTA TTGTTTATAA CTTCTGTGTG 60

AAGCGCAATA TTACAATTAA AATGCCGAAA GAAGTACCGC CGAATATTTC ACAAGTATTT 120

AAGGACTTAA TTCCATTTTC AGCGGTAATC ATCATTCTTT ATGCATTAGA TTTAGTCATT 180

CGCAACAGCT TTAAATCAAA TGTAGCGGAA GGTATTTTAA AATTATTCGA ACCATTATTT 240

ACAGCAGCAG ATGGATGGGT TGGTGGTCAC CATTTAACnT TGGGnGCnTT TGCATTAATC 300

CTGGGTTTGT AGGGTAATCC ATGGGTCCG 329

(2) INFORMATION FOR SEQ ID NO: 4470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4470:

AACTGGGTGA TAAGGTCCTG TTCGAAAGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 60

AATATATGTT AAGTGGAAAA GGATGTGGCG TTGCCCAGAC AACTAGGATG TTGGCTTAGA 120

AGCAGCCATC ATTTAAAGAG TGCGTAATAG CTCACTAGTC GAGTGACACT GCGCCGAAAA 180

TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTGGACAAT GGTAGGAGAG 240

CTTCTAAGGA CTTGAAGCTG ATCGTAAGAC TGTGGAGCGn TAGAATGAGA TGCCGTGTGA 300

TAGnAAAGAC GGTGAGATCC CTCCACCGTT GACTAAGTTC CAGAGGAAGC TCTCCGTCGG 360

GTTATCCGGT CCTAAGnGAG GCCGACAGCT AGGCATGGnT 400

(2) INFORMATION FOR SEQ ID NO: 4471:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TCATTTTTAG AAATATTATC TTTTCCACAA ATCATTTGAT ATAAAGTGCG ATCATTTGCC 60

GCGAGTGCTG CCATTGACAC TAGCTGTTGC GTATCATTTT TGGCTAGCAC TTCGGGATAC 120

TTTCTTAGCT GAACAGTTAG ATGACCTAAT TGATCTTTGA AAATATCATT ATCTTGACCC 180

ATATATGACC ACCAAGCTGT TTCATCACAA ACCATGACAT ACTTAGCTAG TGCTTCATCT 240

TTTTCTATAA GCTGACGTAA TAATTGTCTG CTTGTCCTCC GTTTTnCATG TACCGCGAGG 300

CGTAAnCTTA AAGGGCCCAA GGnCG 325

(2) INFORMATION FOR SEQ ID NO: 4472:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4472:

CCCGTCTTTC GCTACTCACA CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA 60

TCATGCTTCA ACGCCCTTAG AACGCTCTCC TACCATTGTC CAAAGGACAA TCCACAGCTT 120

CGGTAATATG TTTAGCCCGG TACATTTTCG GGGGCAGTGT CACTCGACTA GTGAGCTATT 180

ACGCACTCTT TAAATGATGG GCTGCTTCTA AGnCAACATC CTAGTTGGTC TGGGGCAACG 240

CCACATCCTT TTTCCACTTT AACAnATATT TTGGGA 276

(2) INFORMATION FOR SEQ ID NO: 4473:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4473:

AATTTnCCAA AAAATTCAAA TGGCTCATTT ACCAAAAGGT AAACCTCCGC CTTTAAnTTT 60

CTTaATGCAT kGTCTAACAA cCGCTTTCTT TAAAAgAATA GATTGTCAAG CGCTCGCATA 120

AGCAATATCA CTTTAACCAA AAAATATTTG AATGTTAAAT AAACATTCAA AACTGAATAC 180

AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTC CGAATATATC CTTAGAAAGG 240

AGGTGATCCA GCCGCACCTT CCGATACGGC TACCTtGTTA CGACTTCACC CCAATnCATT 300

TGTCCCACCT TCGACGGGCT AGCTCCGAAA AGG 333

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4474:

TATAAAATAG CAACGTTATT CCAATTATCT TAATGGTTAT CTTATCCTCA ACTAAATTGG 60

AGGAATCACT ATGACAATTA ATAAAGTAAC CGTTCTTGGC GCAGGCACAA TGGGCGCTCA 120

ACTGGCAGCA CTTTTTGTGA ATGCTGGACT TAAAGTAAnA CTATTAGATA TTGTAGTGGA 180

CAAAAACGAT CCnAATCTCA TTGCGAAAAA ATCTTACGGT TAAATTACAG GTAAGAAACG 240

GCCGCTACTA TTCGnCTTAA ATCTAGCGGT CATTTACCAT ATGGTATTTT GATGTGCTTG 300

GTAAATGTGT GCTGTTTGAT ATCGA 325

(2) INFORMATION FOR SEQ ID NO: 4475:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4475:

TAACTGCGGC AACATTTGCT TGTTTTGGTT ATGGTTGGCA CATTGATGTC GGCATTCATA 60

CAATACATCT AGTATTATCT GGTATTTTTG ATCGTTATCC AAAGTTAAAT AATGATTATT 120

GGACATTGGG GTGAGTTTAT CCCATTCTTC TTAGAAACGT ATGGATGAAG CTTATTCGCT 180

GACATTTnAC CACCCTGTAA GCTATACTTT AAAAATAATT TTTAATCACA CCGAGTGGCA 240

TGTTAACGAG CCACAGTTTG ATTTAGTCAA GAAGnAGAGG TATTGTAGAn TCTTATGCGC 300

TGATATCC 308

(2) INFORMATION FOR SEQ ID NO: 4476:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4476:

CCTACCTATC CTGTACAAGC TGTGCCGAAT TnCAATATCA GGCTACAGTA AAGCTCCACG 120

GGGTCTTTCC GTTCCTGTCG CGGGTAACCT GCATCTTCAC AGGTACTATG ATTTCACCGA 180

GTCTCTCGTT GAGACAGTGC CCAAATCGTT ACGCCTTTCG TGCGGGTCGG AACTTACnCG 240

ACAAGGAATT TCGCTACCTT TAGGACCGTT ATAGTTACGG 280

(2) INFORMATION FOR SEQ ID NO: 4477:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4477:

GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG 60

CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 120

GTTTTCACTT CGCCAAGCCA TTTTTCTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA 180

TAAAAAAAGA GACCTCACGG nCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA 240

ATTGGGCTAC CATCGnCGCT AAAGACCTTT CTTGACTTG 279

(2) INFORMATION FOR SEQ ID NO: 4478:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4478:

GAGGATCCCG GAATGTTGAA CCCATCACTG ATTCTGGTTC ATAATTATCC ATCATCCATA 60

ACGTTAAATC TAAAGCGTGT GTACCGATAT CGATTAATGG TCCTCCACCT TGAGCTTCTT 120

CGTCTAGAAA GACACCCCAT GTTGGnACTG CTCGACGACG AATGGCATGT GCCTTTCCGA 180

AGTAAATGTC TCCTAAGTCG CCACGTTGCG CTGCTTGATG TAAAAATTGA CTATCTGCTC 240

GGAnACGATT TTGATAACCT ATTGTTAATT TT 272

(2) INFORMATION FOR SEQ ID NO: 4479:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4479:

GAAATTGGGA ATCCAATTTT nCTTTGTTGG GGCCCATCCC CAACTTGCAC ATTATTGTAA 60

GCTGACTTTT CGTCnCTTAC TGTGTTGGGG CCCTCACCCC AACTCGCATT GCCTGGTAGA 120

ATTTCTTTTC GAAATTCTCT GTGTTGGGGC CCCTGACTAG AATTGAAAAA AGCTTGTTAC 180

AAGCGCATTT TCGTTCAGTC AACTACTGCC AATATAACTT CGTAGAGCAT AGAATATTGA 240

TTTATGTCCC AGCCTGAGTT AATTT 265

(2) INFORMATION FOR SEQ ID NO: 4480:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4480:

ACATAGAAAT GCCACTTTTA CAAACAAATG AATATTCGTC TTTTTACATC ATTACGCATA 60

ATAAAAGAAG CTAAGCAACA TGTAAACCGT TGTCACTTAA CTTCTTGTTT TTCCGATGAC 120

AGCTTCTATT TAGAGAATGT CATGATTATT TTATATTCAC TTCAATGTTA TCAATATTAG 180

TGCCATCTAT GACGTCTGCC ATACGATGCT CTGGCAGTTT TTTGGTGGTA ATTCAAACGT 240

ATATTCCCAC CGTTTTCATT TAATAACGTT GTCCnGGACC CATGTACCGT AAGATATGTT 300

TTCATAGTGG TTCCAATTAA ACCAnTCTTC AGGAACCTCn TAG 343

(2) INFORMATION FOR SEQ ID NO: 4481:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4481:

ACTGCGGCAA TAGCAGCAGC ACCACAAACG GCCTGTGTCC GGACACCTAG GTAATAATGC 60

GCATGTTTTT GTCACCATGC CAACAGTTTG TTGACAAAGA GCATCATTAC AATACTGGAA 120

AATAACGACA CCTACATCGA TGGCTAATAG TTTACTACCT TGACCGATAA TATCGAATAT 180

ATTGAGTTTA AGTCCATATA GGATGATTGC AAATCTTAAT AAATATTTAG ATGAAAACGT 240

(2) INFORMATION FOR SEQ ID NO: 4482:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4482:

GAGGCATCCC CGGGCCTTCC TTCCCAACAG TCGCTTCAAA GTTTGGTGGT AAACCTGnTA 60

CATCAAATTA TCGGTGCTAC TGTnAGGTAC GTGTAATCTT CGCTATTTTA TTAGCCGTAT 120

CACATCAAGT GGCTTCCCTA CTGGAACCAA TTTGCTATTC GCCTTATTAT CAGGTGCAGG 180

ATGGGGATTC GGACAAATCA TTACATTTAA AGCGTTCGAA TTAGTCGGCT CATCTCGTGG 240

CCATGCCAGT CACAACAGCA TTCCAATTAT TAGGCGCATC TTTATGGGG 289

(2) INFORMATION FOR SEQ ID NO: 4483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4483:

AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC ATCGCATTCA 60

TTTCTTGTCT AGCAACGTTC TACTCTAGCG GAACGTAAGT TAGCTACCAT CCTCGCTAAG 120

AACCTTTCTT GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT 180

CATTTAGCTC TACTAAACTC GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTnC 240

ACTTCGCCAA GnCATTTTTC TTTG 264

(2) INFORMATION FOR SEQ ID NO: 4484:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4484:

CTGTACCACC TATAATCGTT TTAATCGATT GGGGGACGCA TAGGATAGGC GAnGTGGCGA 60

TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTCACA CTGCCGAGAA 180

nAAGCCTCTA GATAGAAAAA GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240

AATTCTAAGG TGAGCGAGCG A 261

(2) INFORMATION FOR SEQ ID NO: 4485:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4485:

ATGCAGCTAT TATTTTTGAC AGATTCCATA TCGTTCAACA TTTAAATAGA GAACTTAATA 60

AGTATCGTGT ACAAGTTATG AATGAATACC GTAATAAAAA AGGACCTGAT TATACAATTT 120

TTAAGAATAA CTGGAAAGTC CTATTGATGG ATACTAGTAA AACCATATTT AGTAAATACA 180

GATGGAnTAA ATCTTTTAAG GCTTATAAAC GCTCATCTGA CATTGTAGAn GTCATGCTTT 240

CAAAAGACGA TATACTACGA C 261

(2) INFORMATION FOR SEQ ID NO: 4486:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4486:

AGCAACATGA TGCACTTCTC GTGTCTCACC AGATTTAGCG ACTAAACTTG TAGACATACG 60

TAAATCTGCT TTAATAAGTA ATTnATGCAC ATGACTTATT GCGAGTAACA TCGGCATTGC 120

AAAGCCATTG CTATCAACTA ATCCACTATC ATCTAACACT AGAnTTTGAG CGCCTTGCTT 180

TACAGCATTC ACTGCTTCTC GGCCTAATGC TTCTAACGCA TCTTCCAAAT CCCCTTCATA 240

TACCGTTGAT AAATAAGTTA 260

(2) INFORMATION FOR SEQ ID NO: 4487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4487:

ATGAGGTGCA TAGGGATAAA ACAGnnAGCA GCAATTTGTC GCTATTTGTA AATTGTATCC 60

TGGCTTAAGT TGGCCATTTT TCATATGGTC TTCCTTCATT CTCATAAAAG TTGCATCATG 120

ATCAGTTTTA GAAAAGCTAT TTCTATCTTT AAGAATCGAT TTTTGTTCTT CATATTTATT 180

TTTTCTTTCG GAATAATCAT CAAATTTATT TTTGAACTTC TTAATCTTAG TTCTTTTTTA 240

CGGGTCTGTT TTCCAATTTG AGTACTATCC TCGTTCCCCA ATAGAATGAA TTTAAACCTT 300

CCGATTTCCT TTAAnC 316

(2) INFORMATION FOR SEQ ID NO: 4488:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4488:

CACTTTTACT GCTAAAACGT CAATTGTTGA TGAGTCGTGT TTTATCTCAA GATGTGTTAC 60

TCAAAAAGTT ATAGAAGAAG CTACTAAAGT TAAAACAGAG ATTGATACTG CCAGAAGATA 120

ACTGTATCTC TCCATCTACT GTAAGTCCGT ATTAGAACTA AAGCGGCTAA TTCATTACGA 180

ATTAAACCCT TTAATTGTTT GCCAGACACA TCGCTATGGA TGAATTTAAA GCGTnAAAAT 240

GTACTGGATC ATGAGTTCAT TTTTATAGnT ATGTACnCAT GTGTATAGTA TTTAGAAATA 300

GACTCAA 307

(2) INFORMATION FOR SEQ ID NO: 4489:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4489:

TTGGCAAATG TCATATAACT AGTAACATGA TCATCGACAT CAAATTTAGT ATGATCAAAT 60

GTTCCCCAAT CATTAATTTG ATTCGGTTGT TTGCTCAATT GATTATATGT TTTTCCTAGC 120

ACTTCATGCG GCACCATATC TTTACCTAGT AGCCCCACAA AGATAAGTCT AACAAGTGGC 180

ACCATAATCG ATAAACTACC GCCACCTGCA CGCTTATGGT AAAACACCCA GCCAGCACTT 240

TAGCAGTATG CCACnCCGGn GACGATATGG TAGCGACGTA AnAA 344

(2) INFORMATION FOR SEQ ID NO: 4490:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4490:

CCCAACCGGC ACATTGTTGT AAGCTGACTA TATGTCACTT CnTGTGTTGG GGCCCCTGTC 60

TTCGACTGGC ACTGCTCCCT CAGGAGTCTC GCCATTAATA CTACGTATTA ACATGTAATT 120

TTACTTTTAA ATACTTTAAA AAAATAAGAC ACTTTGGTCC AACTTAAGCC AGGGATACAA 180

TTTACAAATA GCGACAAATT CTCAATTTGT nTTATCCTAT GGACCTATTT CAAAACCCAA 240

CAGGTACTnA GTAACTTTGA ATTCCATTTT TTAACAATGG ATTGCAAAAT GACCTTACGG 300

TTCATTTGAC CGG 313

(2) INFORMATION FOR SEQ ID NO: 4491:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4491:

AGGTCTGACT CTAGAGGATC CCCGATGAGT TTAAAGAAAA ATATCAAACA CCTGAATTAT 60

ATTTTAAAGC TTGGCAAGGT TTTTACCACG AGGTTCACAA TGAGCCAGAA CGTGATGAAG 120

TAATGCGTTA TATTCTGACT TTCTTAAATA ACAGCGTCAA TACAATGGGC TTTATTGTTG 180

AAGATGACGA AATTGTAGAA ATTTAATATT CTAAAAAGGT TGGGACATAA ATCCCTAAAA 240

AACAGCAGTA AGATAATTTT CCATTAGAAA ATATCTTACT GCTGTGCnCn A 291

(2) INFORMATION FOR SEQ ID NO: 4492:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GCCGTCTCAG CCTTGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAATACT 60

ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACTTAAAAAA ATAAAACACT TTGCCCAACT 120

TACACTACCA ATAGAAACTG CTGTTAGAAT TCCTCAAAAT GATATTTCGC GATATGTTAA 180

TGAAATTGTT AAAAAGATAG CTGATAGCGA GATTCGATGG AATTCAGACA TCATCGTGGG 240

CGCAACATCC TATCATCTAA AAATGATGTT AAAAATCACC TGCATATTGC ATATACTGCA 300

ATCTGGAATT TTCTGGGCCG TGAGAATGAG AAAAATnGAC nTCATGAACA GTGATTGCGA 360

ATGGATGTGG GTTAAGCTnC AAGATTCAAA CACCTTGCnT 400

(2) INFORMATION FOR SEQ ID NO: 4493:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4493:

TGATCCAGAG ATTTCCGAAT GGGGAAACCC AGCATGAGTT ATGTCATGTT ATCGATATGT 60

GAATACATAG CATATCAGAA GGCACACCCG GTAGAACTGA AACATCTTAG TACCCGGAGG 120

AAGAGAAAGA AAATTCGnTT CCCTTAGTAG CGGCGAGCGA AACGGGAAGA GCCCAAACCA 180

ACAAGCTTGC TTGTTGGGGT TGTAGGACAC TCTATACGGA GTTACAAAGG AnGACATTAG 240

ACGAATCATC TGGAAAGGTG AATCA 265

(2) INFORMATION FOR SEQ ID NO: 4494:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4494:

CATTACTAAA AAAGATAATC AAGGTATGAT TTCACGCGAT GTTTCAGAAT ACATGATTAC 60

TAAGGAAGAG ATTTCCTTGA AAGAGCTTGA TTTTAAATTG AGAAAACAAC TTATTGAAAA 120

ACATAATCTT TACGGTAACA TGGGTTCAGG AACAATCGTT ATTAAAATGA AAAACGGTGG 180

GAAATATACG TTTGAATTAC ACAAAAAACT GCAnGAGCAT CGTATGGGCA GACGTCATAG 240

ATGGGCCCTA TATTGATACC ATTGGAGGTG AATnTAAATA ACCATGCACT CTC 293

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4495:

ACTTACAAAG TTCTGTGAAC CAAGTACCAT CAACTGCTGG TATGACGCAA CAAAGTATTG 60

ATAACTATAA TGCGAAGAAG CGTGAAGCAG AAACTGAAAT AACTGCAGCT CAACGTGTTA 120

TTGACAATGG CGATGCAACT GCACAACAAA TTTCAGATGA AAAACATCGT GTGCGATAAC 180

GCATTTAACA GCATTnAAAC CAAGCGAAAC ATGAnTTTAA CTGCAGATTA CACATGCCTT 240

AGGAGCAAGC AGTGCA 256

(2) INFORMATION FOR SEQ ID NO: 4496:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4496:

GTCATCAGAA ACCCTTGTCA CACAAGGCTT GTATTTTTTA TACTTATTTT TTAAATTAAA 60

TTCATCATTA TCTAATTTAA AACAATATAC TAAACGTTTC ATAATTATCG CCTGTACAAT 120

ACGCACAAAA ACATGTCTTG AAACGCCTTT CATTACTCTA AnATACCCAA TATACTTTTT 180

ATATCGTTCG GATTCTGAGT ATTTCAGACG ATTTTCTGCA TAnAAATAAA CGTGTTTCAA 240

GGCAATATAT TGCA 254

(2) INFORMATION FOR SEQ ID NO: 4497:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4497:

AATCGGCTGT CTGATTCTGA ATCGCTATCT GAGTCCGAAT CGnTATCTGA ATCCGAGTCG 60

CTATCCGAGT CTGAGTCGCT ATCTGAATCC GAGTCACTGT CGGAGTCGGA ATCACTATCT 120

GAGTCACTGT CGGAATCTGA ATCGCTATCT GAATCCGAAG TCACTGGTCG GGAATCTGAG 240

TCACTGTnGG AATCTGAATC GCTATCTGA 269

(2) INFORMATION FOR SEQ ID NO: 4498:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4498:

CACCCCGGCA CTATAAAAAT GGAGCAGAAG ACGGGATTCG AACCCGCGAC CCCAACCTTG 60

GCAAGGTTGT ATTCTACCGC TGAACTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC 120

CCACGCCGTA AGCTTAGnAT ACCTCAAGTC TAGTGCGTCT GCCAATTCCG CCACACCCGC 180

AAATGGTGAG CCATAGAGGA TTCGAACCTC TGACCCTCTG ATTAAAAGTC AGATGCTCTA 240

CCAACTGAGC TAAATGGCTC TTnCAGGTGC CGG 273

(2) INFORMATION FOR SEQ ID NO: 4499:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4499:

GTAGTAAAAC GCATTTAGTG ATTGAAACAG GCAAGATAGA CGCGGGATAT CACGGCAATT 60

TAGGGATTAA TATCAAGAAT GACGCTATTG CATCGAATGG TTATATCACA CCAGGTGTTT 120

TTGAATATTA AAAGGAGAAT CGATTTGAAG TGCnnCATAA GACAATACGG ACTTATCAAA 180

TCAACGAAGG AGACAAACTA GCTCAATTGG TTATCGTGCC TATATGGACA CCTGAACTAA 240

AGCAAGTGGA GGAATTCGAA GTTGTTCAnA CGTGGAGAAA AGGCTCGGAG AGCGGGTGAA 300

AGCATCTTAG TCGA 314

(2) INFORMATION FOR SEQ ID NO: 4500:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4500:

ATTGTAAGGC TATCATGTCA AAGATTATAA CAATAAATCT GGTTGAGATT TGGTGGCGGG 60

GCGATGGAAG CTATCTATTT GACCATCCAT TTGGCAAAGG TTTGGGAGTT ACACAGGTGG 120

ACTTAACTTT AATGGCGGTC GTCACTATGG TATCGACTTT GGTATGCCTA CAGGAACGAA 180

CCATTTATGC TGTTAAAAGG CGGTATAGCT GATAAAGTAT GGnCTGATTA CGGTGGCGGT 240

AATTCTATAC AAATTAGGAC CGGTGCTAAC GAATGGAnCT GGTATATGCA TTTATCTAnG 300

CATT 304

(2) INFORMATION FOR SEQ ID NO: 4501:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4501:

TTCCTTCATT CTCATAAAAG TTGCATCATG ATCAGATCAG TTTTAGAAAA ACTATTTCTA 60

TCTTTAAGAA TCGATTTTTG TTCTTCATAT TTATTTTTTC TTTCGGnATA ATCATCAAAT 120

TTCTTTTTGA ACTTCTTAAT CTCAGTTATT TTTTTACGGG TCTGTTTTCT AATTTGAGCA 180

CAATCTTCGT TCTCAATAAG AATGATTTAA ATCTnCGATT TCTTTATCTA AATGGACTAC 240

CAATTAAATC TAT 253

(2) INFORMATION FOR SEQ ID NO: 4502:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4502:

AGTTCGGTCC CTATCCGTCG TGGGCGTAGG AAATTTTnGA GGAGCTGTCC TTAGTACGAG 60

AGGACCGGGA TGGACATACC TCTGGTGTAC CAGTTGTCGT GCCAAnGCAT AGCTGGGTAG 120

CTATGTGTGG ACGGGATAAG TGCTGAAGAT GCTTAAGCAT GAAGCCCCCC CAAGATGAGA 180

TTTCCCAACT TCGGTTATAA GATCCCTCAA AGATGATGAG GTTAATAGGT TCGAGGTGGA 240

AGCATGGTGA CATGTGG 257

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: d uble
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4503:

ATACGTTTAA TACACAAAAA ACTGCAAAGC ATCGATGGCA GACGTCATAG ATGGCACTAA 60

TATTGATAAC ATTGAAGTGA ATATAnAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA 120

TCGGAAAAAC AAGAAGTTAA GTGACAAGnT TTACATGTTG CTTAGCTTCT TTTATTATGC 180

GTAATGATGT AAAAAGACGA ATATTCATTT GTTTGTAAAA GTGGCATTTC TATGTCTTAA 240

AAGTGACGAA ACTTCAAATG TGCCAAGTGT 270

(2) INFORMATION FOR SEQ ID NO: 4504:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4504:

TACCTTGACC GAAGTTCTTA CCTACATCAC CTAAATTAAT GACATGTCCA CCAGTCATAT 60

ACTCTAATCC ATGGTCGCCG ATACCTTCAA CGACAACATC TACACCACTA TTTCTAATAC 120

AGAATCTTTC TCCTGCACTA CCGTTAATAA ATGCCTTACC ACTTGTCGCA CCATAGAATG 180

AGACGTTACC AGCAATAATT TCATTTTGTC GTTCTTCAAA AGGTGCTTTG ACAATGACCG 240

TACCACCnGn T 251

(2) INFORMATION FOR SEQ ID NO: 4505:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4505:

AGAAGTTAAG CTCCTTAGCG TCGATGGTAG TCGAACTTAC GTTCCCGCTA GAGTAGAACG 60

TTGCCAGGCA AATGACAAAT CGGAGAATTA GCTCAGCTGG GAGAGCATCT GCCTTACAAG 120

TAGCTCAATT GGTAGAnCAC TGACTTGTAA TCAGTAGGTT GGGGGGTCAG TCCTCTGGCC 240

GGCACCATCT TTTGnCCATA 260

(2) INFORMATION FOR SEQ ID NO: 4506:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4506:

TTCTTTAGTA GATACTAAGG CGTTATTAGA CGCATTAGAC AATGGTGTGA TTAAAGGTGC 60

AGCACTTGAT ACGTATGAAT TTGAACGCAA ACTTTTCCCA AGTGATCAAA GGGGCAAAAC 120

ACTGAACGAT CCATTGTTAG AATCGTTGAT TGACAGGGAA GATGTCATAT TAACACCACA 180

TATTGCGTTT TATACTGAAG CTGCAGTTAA AAATCTATTG TCGTGCATTA GGTGCAACAT 240

TAGGTGTATT GCAGCTTGGG GAACTTnGnT ACGGGTAAAT TTAAAATCGG CTGTGGGTAT 300

TTTGGnTTTT GGG 313

(2) INFORMATION FOR SEQ ID NO: 4507:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4507:

GnCAATACGG CCAATTCCTA AGATTGCTAC TTCTGGGTGG ATTGATAACT GGAGTGAACC 60

ATTGTCCACC AGCTGnAACC GATATTACTG ATTGTGCATG TAGCACCTTT CATTTCATCG 120

GCTGTTAATT TACCATCACG TGGCTTTAAC AGCTAATTCA TTAATTTCAT CTGAAATTTG 180

GGAAAATAGA CTTACGGATC AGCATGTTTA ACAACAGGTA CTAATAATCC TCTATCAGTG 240

TCTGCTGCAA TT 252

(2) INFORMATION FOR SEQ ID NO: 4508:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4508:

CATCGAACCA GATGTACTCG CACTTGTTGA GTCTGATGTT GAATCACTAA CACTATCAGA 60

TAATGACGTT GAATCACTCA TACTTGTTGA TGTACTTGTC GAAAGCGACA TACTTTGTGA 120

ATCACTAGTA CTTGTACGCA TCGAAGTACT AGTTGAAGCT GATGTACTAC GAGAGTCACT 180

TGTTGATGTT GATGTACTTG CTGATCCTGA TGCACTTGTA CTTCTTGATG TGCTTTGTGA 240

ATCGGATTTC GCTCGTGCnT GGTACTnG 268

(2) INFORMATION FOR SEQ ID NO: 4509:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4509:

CGAGAGTGCG TTAATTCGGT TACTGCTATC ACgTAAGGGG CGGAAACCCC CTAACACTTA 60

GCACTCATCG TTTACGGCGT rGACTACCAG GGTATCTAAT CCTGTTTGAT CCCCACGCTT 120

TCGCACATCA GCGTCAGTTA CAGACCAGAA AGTCGCCTTC GCCACTGGTG TTCCTCCATA 180

TCTCTGCGCA TkTCACCGCT ACACATGGAA TTCCACTTTC CTCTGCTGGC ACTCAAGTTT 240

TCCAGTGTCC AATGACCCTC CACGGTTGAG CCGTGGGCTT nCACATCACA CTTAnA 296

(2) INFORMATION FOR SEQ ID NO: 4510:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4510:

TTACTACTTA CTGAGTGACC TGTACCTGCT TTCGGAGTAA TTGTGATTGA TGAATTTGGT 60

TTTATAGTAT TGGCATTGAA CGTCACTTTA CCAGTTTGTG CATCTAACGT TACATAGTCA 120

GGCTTATTCG CAATTGTCCA TTGnTTATTT TGACCACGAA CAACATTAAT TGTCTTACTA 180

TGTTGCTGCA CCATTACCCA CTTnTTCAGT GTAAGCAATA TCCATTGCTT GAGTTGGGAT 240

TAATTAAATG GTCCTGA 257

(2) INFORMATION FOR SEQ ID NO: 4511:

(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4511:

AAAATCACAT CAGCCTGCAT TAACGACGTC GTTAATTTAT ATACATCTCC TGTAGTATCT 60

AGATAATTCT TTCCAACGCT AAATTCTAAT TCAAGTTCTC GTAAATCCAT CAACTCTATT 120

TGATGTCCCT CATTGATGAC TTCTAGTTCA TTTTTTAAAT CATCCATAGC AATTCTCGTT 180

TTAGAACCTA CTGTGGAACC TGACAATAAT ACAATATTCA nGAnGACGCC CCTCCTATTT 240

TGATAAATGC 250

(2) INFORMATION FOR SEQ ID NO: 4512:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4512:

AGCTGGnTTC GAACCAACGA GTGACGGAGT nAAAGTCCGT TGCCTTACCG CTTGGCTATA 60

GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGATT 120

TACAGTCCGC CGCGTTTAGC CACTTCGCTA CCCCTCCAGC TTATTCATAT AATTTAATAA 180

TCAAAATGGT GGAAGAATGA CGGGTTCGAA ACCGCCGACC CTCTGCTTGT AAGGCAGATG 240

CTCTCCCCAG CTG 253

(2) INFORMATION FOR SEQ ID NO: 4513:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4513:

GnCGACCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA CGTTAACATG 60

nAAGTTACGT TCTTTTATAA AAAGATTTAA ACGCGTTATT AATCTTGTGC AGTGTTCTTT 120

CGAACACTAG CGATTATTTC TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG 180

GTGGAGACTA GC 252

(2) INFORMATION FOR SEQ ID NO: 4514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4514:

GTCATTGAAT ATGGAAACTT TAGAATTACA AGGCGCTAAA TTACGATACC ACCAAGTCGG 60

ACAAGGACCC GTGCTCATCT TTATTCCTGG TGCAAACGGT ACCGGAGACA TTTTTCTGCC 120

TCTTGCAGAA CAGTTAAAAG ACCATTTTAC TGTTGTAGCC GTTGATCGTC GTGATTATGG 180

AGAAAGCGAG TTAACTGAAC CACTCCCTGA TTCCGCTTCA AACCCTGACA GTGATTATCG 240

TGTC 244

(2) INFORMATION FOR SEQ ID NO: 4515:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4515:

TATTAGGCAA ATCCGGTACT CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT 60

TCGAGTCGTT GATTTCACAC TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCGTAC 120

CGCAAACCGA CACAGGTAGT CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA 180

AGGAACTCGG CAAAATGACC CCGTAACTTC GGGAGAAGGG GTGCTCTTTA GGGTTAACGC 240

CCA 243

(2) INFORMATION FOR SEQ ID NO: 4516:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4516:

GATTGTCCTT TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG 120

ACATGTGGAG CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC 180

CCGTCCACCG ATTGACTAAG GTTTCCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT 240

CCCTAAACCT GAGGCCGCAA nnGTAGG 267

(2) INFORMATION FOR SEQ ID NO: 4517:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4517:

TTGAATCTGA CGAAACGAGA AAAGAGCGCA ACGAGTTTAG TAGAGCTAAA TGAGTAAGCG 60

AGAGCCGAAG AGAGGAAAGA AGCAAGCGAT TGTCACAAGT CAAGAAAGGT CTTTAGCGAC 120

GATGGTAGCC AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAAAAA ATGGGATGCG 180

ATGAGCCGCA TTGGAGACCG CAGTCCTnTn TnTTTTTTTA TGGCCTTAAA ACGTCAAAAT 240

TAAAAAGTTA AACACAAAGA AAATGGGCTT TGGCGAGTGG AAACGTTTTG AATCTGGACG 300

GAACGAGAAA GAGCGCACG 319

(2) INFORMATION FOR SEQ ID NO: 4518:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4518:

GGTATAATAG ATGACTATGT ACTATTTCCG GTACATCCTT GGCAATATCA GCATATTCTG 60

CCGAACGTCT TTGCGAAAGA GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT 120

GGAGATTATC TGTCGTCTTC AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC 180

CATGTCAAnG TACCATTTGC AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GnCTACGGTT 240

ACATGAAAAA CGGGGAACA 259

(2) INFORMATION FOR SEQ ID NO: 4519:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4519:

ATAGGGTGTT GCTGAATAGG GCGTTTAGTA TTTGGTCGTA CCGnnAACCA GGTGATCTAC 60

CCTTGGTCAG GTTGAAGTTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA 120

AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGG AGATAGCTGG 180

TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGA TTATTGGAGG TAGAGCACTG 240

TTTGGACGAG GGG 253

(2) INFORMATION FOR SEQ ID NO: 4520:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4520:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT 60

TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT 120

CTCAACTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCnACC ATCGTCGCTA 180

AAGACCTTTC TTGACTnGTG ACAATCGCTT GCTTCTGTCC TCTCCTTCGG CTCTCGCTTA 240

CTCAT 245

(2) INFORMATION FOR SEQ ID NO: 4521:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4521:

GGGCCTAAGT GGACTCGAAC CACCGACCTC ACGCTTATCA GGCGTGCGCT CTAACCAGCT 60

GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAAA ACTGAATACA ATATGTCACG 120

TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG 180

CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TnCCCACCTT 240

(2) INFORMATION FOR SEQ ID NO: 4522:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4522:

nATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGT TGATGGCGTG 60

CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTTAAGCAG TAAATGTGGA 120

GCCGTAGCGA AACGATGTCT GAATAGGGCG TTTAGTATTT GGTCGTAGAC CGAAACCTGG 180

TGATCTACCC TTGGTCAnGT TGAAGTTCAG GTAACACTGA ATGGAGGACC GAACCGACTT 240

ACGTTTGAA 249

(2) INFORMATION FOR SEQ ID NO: 4523:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4523:

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG 60

GGATGGACAT ACCTCTGGTG TACCAATTGT CGTGCCAAnG CATAGCTGGG TAGCTATGTG 120

TGGACGGGAT AAGTGCTGAA GATCTnAAGC ATGAAGCCCC CCTCAAGATG AGATTTCCCA 180

CTTCGGTTAT AAGATCCCTC AAAGATGATG AGGTTAATAG GTTCGAGGTG GAAGCATGGT 240

GACAGTGG 248

(2) INFORMATION FOR SEQ ID NO: 4524:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4524:

AACGTTAAGA TCCCTATTAA ATTATCTTAG GAATCATCAT GGGCATTTAT GATGTCTTAA 60

AAATTAGTAA TCTGAATCTG CTTCTAAACC TTGTCATAAT TTGAnCGGCT GTGGCTCGnA 180

CCAATACGGG TCGGACCTGC TTnAACCATT TTATTGGAAA TCTTCTAAAT TACGGACGGC 240

ACCCGGATGC TTTTACTTCT ATATCAGCAC CTACTGTATC TTTCATTAAT TTAACGGCTT 300

CTGCAGTCGG ACCGGCAACT GCAAAA 326

(2) INFORMATION FOR SEQ ID NO: 4525:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4525:

AAGAGCACCC TTCTCCGAGT TACGGGGTCA TTTGCCGGTT CCTTAACGAG AGTCGCTCGT 60

CACCTTAGAT TCTCATCTTG ACTACCTTGT CGGTTTGCGG TAnGGCACCT ATTTTCTATC 120

TAGAGGTTTT CTCGGCATGT GAAATCAACG ACTCGAGACA CAATGTCTTC TCCCATCACA 180

GTCAGCCTTA ACGAGTACCG GATTTGCCTA ATACTCAGCC TACTGCTTAG nGGCATCCAT 240

CGCAGTTnGC TATCCACTGG TCCCCCTCGA TTAAACGATT ATAGGTGGTA CAGATATCAA 300

C 301

(2) INFORMATION FOR SEQ ID NO: 4526:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4526:

TGATATTATG AGCTGTGTTT TTAGCTTTAG AACCGAAGTC CCCTGCTTTT TTACCAAGAT 60

TTTCAGTAAC TTGTnCCATC CATTTTTTCT TTTTCGTACC ACCATGGAAT TTTGGCAAAA 120

CACCCATCCG CTGTAACTTC AGAGTGTCAT TGGCATTTAT TACACTATCT CCAACTCCTA 180

GTGGAACAAC CACATCTCGT CCTTGGGGTG CATGGAATGT nCCGTCAGCC CTGTGAATTA 240

T 241

(2) INFORMATION FOR SEQ ID NO: 4527:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4527:

CGATCACACT CTTCCGTCGT CATCGCCATT GGCTTTTCAC ACAATACATG GACACCATGG 60

TGTCAATGCT TCTATAGAAA GATCAGCATG GAATTTATTA GGTGTACAAA TGACCACCGC 120

ATCAACAAGT TTAAACAGCT CGCTAGGTGT CTCAACTGCA TGAGGTATAT TGAAAGCGCT 180

TCGCAACCAT nCAATCATCT GGCACTGTTA TTGAATATCT TGTGACTGGC AACTTAATGA 240

GnACTGTGTC TTTTGGAGTT TCCAGnCAAT GCCGGGAATT ATGGACGGGT CTTGGTGGCA 300

ATACCACCCA ACACCT 316

(2) INFORMATION FOR SEQ ID NO: 4528:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4528:

GTCCCAAGGG TTGGGCTGTT CGCCCATTAA AGCGGTACCG ACGACTGGGT TCAGAACGTC 60

GTGAGACAGT TCGGTCCCTA TCCGTCGTGG GCGTAGAAAT TTGAGAGGAG CTGTCCTTAG 120

TACGAGGAGG AnCGGGATGG ACATACCTCT GGTGnACCAG TTGTCGTGCC AACGGCATAG 180

CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAAGCAT CTAAGCATGA AGCCCCCCTC 240

AAGATGAGAT T 251

(2) INFORMATION FOR SEQ ID NO: 4529:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4529:

AGTACGTGAC GTTCACTACT CTCACTATGG CCGTATGTGT CCAATTGAAA CACCTGAGGG 60

ACCAAACATT GGATTGATTA ACTCATTATC AAGTTATGCA CGTGTAAATG AATTCGGCTT 120

TATTGAAACA CCATATCGTA AAGTTGATTT AGGATACACA TGCTATCACT GATCAAATGA 180

ATGGTCGTTC AGGTGATGAG TGTATGCGTT CGGGnACnAT CAGTATGCAA GAAAAGGTTT 300

GTGACGCGAC AGTGTCnA 318

(2) INFORMATION FOR SEQ ID NO: 4530:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4530:

TAGCTGTGTG ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC 60

GGCCTGACAT ACAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGA TCACCAAGTT 120

GAGCAAAGAn GATGTTCTnC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC 180

CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA 240

(2) INFORMATION FOR SEQ ID NO: 4531:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4531:

CGGCTCTTCT GGGACGTTAA CCCTAAAGTG CACCCCTTCT CCCGAATTAC GGGGTCATTT 60

TGCCGAGTTC CTTAACGAGA TTCGACTCGn TCACCTTAGA ATTCTCATCT TGACTACCTG 120

TGATCGGTTT GCGGTTAGGG GCACCTATTT TCTATCTAGA GGCTTTTCTC GGCAGTGTGA 180

AATCAACGAC TCGAAGACAC AATGTCTTCT CCCCATCACA GCnCAGCCTT AACGAGTACC 240

GGATTTGCCT AATA 254

(2) INFORMATION FOR SEQ ID NO: 4532:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4532:

TGAATAAACC GAATGTGGCT AAAGTCGTTA ACGCAAAATA TGACGTCATC TATAACGGAC 120

ATACTTTTGC AACATCTTTA CCAGCGnAAT TTGTAGTAAA AGATGTGCAA CCAGCGAnAC 180

CAACTGTGAC TGAAACAGCG GCAGGAGCGA TTACAATTGC ACCTGGAGCA AACCAAAC 238

(2) INFORMATION FOR SEQ ID NO: 4533:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4533:

GGTCATTAAT AAAATATCTA AAGCCATTAC TGCATAAAAA TCTCATCAAG CCAATACCTA 60

CATTGTACTA CTGGnCACTT TAGACAGGnC AAGGGTGTAG CTACCGATAA TTCAGGAGCA 120

TTAACGCAAC CGACATTTGA CTGTATTAAA TGATAGAGGT TCTGGAAAAC GCCCCAGGTG 180

GTGGAGTTCA AGAAATAATT CACAGGGCTG ACGGAACATT CCTGCACCCC AAGGACGAGA 240

TGTGGTTGTT CCACTAGGAG TTGGAA 266

(2) INFORMATION FOR SEQ ID NO: 4534:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4534:

TACTCAGAGG ATACCCCGAC GTAATGCATT CAATTCAATT TTTAAACGTA TTATTTCATT 60

GAGCAGAAAG AAAATTATGG CACCAAACTT TAATATTTTT TTCAATGTCA TTCTTTTGAn 120

GGGAGTGGGA CAGAAATGAT ATTTTCGCAA AATTTATTTC GTCGTCCCAC CCCAACTTGG 180

CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTTTGTnG GGGCCCATCC CCAACTTGCA 240

CATTATTGTA AGCTGACTTT TCGT 264

(2) INFORMATION FOR SEQ ID NO: 4535:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4535:

GCGAATGGAT AACAGTTGAT ATTCCTGTAC CACCTGATAA ATCGTTTTAA TCGATGGGGG 60

GACGCATAGG nATAGGCGAC TGCCGATTGG ATTGCACTCT AAGCAGTAAG GCTGAGTATT 120

AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA 180

GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AAATAGGTGC CCCGTACnGC 240

AAACCGACAC 250

(2) INFORMATION FOR SEQ ID NO: 4536:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4536:

AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 60

AATTCTCCGA TTTAAAACTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA TTCGAACTAC 120

CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180

TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAnATAGT AAGTA 235

(2) INFORMATION FOR SEQ ID NO: 4537:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4537:

TGCATCTTCA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60

TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120

ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAG CTAACCACTC 180

CTCTTAACCT TCCAGCACCG GGCAGGCGTC AGCCCTATAC ATCACCTTAC GGTT 234

(2) INFORMATION FOR SEQ ID NO: 4538:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4538:

ACCCTCTGCT TGTnAGGCAG ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC 60

CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGACTACC ATCGACGCTA AGGAGCTTAA 120

CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 180

TGTAATTTAT ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACCATT 240

TA 242

(2) INFORMATION FOR SEQ ID NO: 4539:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4539:

TCATTAACAC CATCACCATA AATAAAACCT TCCATATCTG TTCCTGTGCC AATAAAGCCA 60

TATTGCGTTT GGnCTGTCGT GCCAGTGCAA GATTTCCAAC GATAATTTCT AGGCGTCACT 120

GCTGGCGAAC CATCTAATGG ATAATCATAA TCCATCGTGC GTCCAAGAAG TACTTGnTTT 180

ATTTAAAGTT TGTATTGTGG AATCCTGTGC ACATGTTCTC ACTCCTCTGT ACCT 234

(2) INFORMATION FOR SEQ ID NO: 4540:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4540:

ACACAAAGAA AAATGGCTTG GCGAAGTGAA AACnGTTGAA TCTGACGAAA CGAGAAAAGA 60

GCGCAACGAG TTTAGTAGAG CTAAATGAGT AAGCGAGACC GAAGAGAGGA AAGAAGCnAG 120

CGATTGTCAC AAGTCAAGAA AGGTTCTTAG CGAGGATGGT AGCTAACTTA CGTTCCGCTA 180

GAGTAGAACG TTGCTAGACA AGAAATGAAT GCGATGAGCC GCATTGAGTG TGAAATTGAT 240

AT 242

(2) INFORMATION FOR SEQ ID NO: 4541:

(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4541:

GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTTATAA GTCAAACGCT CACATACGGC 60

TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120

ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180

GnAGTGTTCT TTCGAACATA GGCGATTATn TCTTATGAAT TCAAGCTTAT TTAAAACTCT 240

(2) INFORMATION FOR SEQ ID NO: 4542:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4542:

AAGCTAGCAA TGATGTCAAG CAATGGCAAC ATGTGCTCAn TTAGCTAATA TGCAAGCACA 60

TGGTGAATAT GACGAGGTTG CAACTTCAAC GGCGAGGnTG ATGAATGCCT TACGTTTGCG 120

TGAGACAGTA GCTATGGGCC GCGGTATTAC AGGTGGTAAT GGCATACTGA GCTGACGATT 180

ATGATATTGT CACGTTTTCT TCTCTGTATG CAGAAGCGAT TTACACGTAC GAGGTACACA 240

TG 242

(2) INFORMATION FOR SEQ ID NO: 4543:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4543:

TGGTGAGCCA TAGAGGATTC GAACCTCTGA CCCTCTGATT AAAAGTCAGA TGCTCTACCA 60

ACTGAGCTAA TGGCTCTTCC ATGGTGCCGG CCAGAGGACT TGAACCCCCA ACCTACTGAT 120

TACAAGTCAG TTGCTCTACC AATTGAGCTA GGCCGGCAAT ATGTAAGATT AAATGGTGGA 180

GAnTGACGGG TTCGAACCGC CGACCCTCTG CTTGTAAGGC AGATGCTCTn CCAGCTGAG 239

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

ATAGAGGATT CGAACCTCTG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC AACTGAGCTA 60

ATGGCTCTTC CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA 120

GTTGCTCTAC CAATTGAGCT AGGCCGGCAA TATGTAAGAA TAAATGGTGG AGAATGACGG 180

GTTCGAACCG nCGACCCTCT GCTTGTAAGG CAGATGCTCT nCCAGCTGAG CTAAATTCT 239

(2) INFORMATION FOR SEQ ID NO: 4545:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4545:

AATTCATGCT TTCAAAAGAC GATATACTAC GACACTCCTA CGAACTTGTC CAAGGATTAC 60

GAAAAGACCT AAGGTTATGT AATTGGCCTA AATTTATTAA TCGTTTAAAT TCAGTTAGTA 120

AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAnATA TTATAGAAAA CATCAAAGGA 180

TGTTAAGAAA TACnATTTAT TACCCAGCAT TTAATAATGG TGCTATAGAA GGA 233

(2) INFORMATION FOR SEQ ID NO: 4546:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4546:

ACTTTGTTGT CTTCCATCAA CTTGAGACTT CATAACGTTT TGCATCTTCG CCACCTTCAC 60

CACTATTACT CTTTCCACCT AATTGGTTCA TGGCTTGTGC TAnTTTTTCA TGTGCTTCCG 120

CTGAAATCGA TCCATAACTC ATCGCCCCTG TATTAAAGCG TTTGACAATG TCACTTACCG 180

GTTCAACTTG GnCGATGTCA ATCGGTGTAC ATGCTTTAAA TTCAAGTAAA TGTCTAATGT 240

(2) INFORMATION FOR SEQ ID NO: 4547:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4547:

GAGGAAATTA CTGAAAACAA TCATCATATT TCTCATTCTG GTTTAGGAAC TGAAAATGGT 60

CACGGTAATT ATGGCGTGAT TGAAGAAATC GAAGAAAATA GCCACGTGGA TATTAAGAGT 120

GAATTAGGTT ACGAAGGTGG CCAAAATAGC GGTAATCCAG TGCATTTGAG GAAGACACAG 180

AAGAAGTTTA AACCGAAATA TGnAACCAAG GTGGGCATTA TCGTTGGTTA TCGATTTTCG 240

ATAGTGTACC TCAAATTTCA TGGGTCCAAA TTAATGGTTA ACCCATCCAT TCGAnGnAGG 300

(2) INFORMATION FOR SEQ ID NO: 4548:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4548:

TTGCTATAGT CACCAGACAT ATGAATGTAA ATTATACATT CAAAACTAGA TAGTAAGTCA 60

AAGTGATTTT GCTTCGCAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 120

AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGGA 180

TCTTGATAAA CCGnAAGTTG GGGAAATCTC ATCTTTACGG GGGGGCTTCA TGCTTAGGAT 240

GGCTTTnCAG CACTTTATGC CCGGTnCCAC ACATTAGGCT TACCCAGCCT ATGCCCGTTT 300

GGCACG 306

(2) INFORMATION FOR SEQ ID NO: 4549:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4549:

CTTCTACTTT TGTACCATCA ATAAGATTTT GCTTTAAACA TTGACTATGA AACTGGATAA 120

ATAAAGATTC AATTAACGCA TCAGTATTAG GATTCACTCT AATACGATTA ATAGTTTTAT 180

AAGAAGGTGn TTGATTTTGA GCTAACCACA TCATTCGAAT ACTGTCATGn AG 232

(2) INFORMATION FOR SEQ ID NO: 4550:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4550:

CTGGGTTCAG AACGTCGTAT GnAGTTCGGA TCCCTATCCG TCGTGGGCGT AGGAAATTTG 60

AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG TACCAGTTGT 120

CGTGCCAAnG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AACATTCTTA 180

AGCATGAAGC CCCCCTCAAG ATGAGATTTC CCAACTTCGG TTATAAGATC CCTCAAAGAT 240

GATGAAGTTA ATAAGTTC 258

(2) INFORMATION FOR SEQ ID NO: 4551:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4551:

TTACAGGCAT GCGAGTTGGG GTGAGGGCCC ACACAGAAGC TGACGAAAAG TCATGACAAT 60

AATGTGCAAG TTGGGGATGG GCCCACAAAG AGAAATTGGA TTCCCAATTT TACAGACAAT 120

GCAAGTTGGG TGGGACGACG AAATAAATTT GCGAAAATAT CATTTCTGTn CCCTCCCTCA 180

AAAGATGACA TTGAAAAAAT ATTAAAGTTG GTGCCATATT TTCTTCTGCT CATGAATATA 240

CGTTAAAATT GATTGATCAT CGCGAATTGA TATTATTCTC ATTATAAAAA TACTTATTAC 300

ACTTACCGTA TGATAGTTTG nTATATACTC TGATAAAGTC AAACCTAATA GCGTTTCTAG 360

CTGTGnGTGT TTCATAATTA TATACATTAT CAGGCTTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4552:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4552:

ATAGGAAACT GCCAATTGGA CGGTTGCCGC ATTCAAACCC AGCACGATTA CGGCGAATTG 60

CACGTGAAnC ATTTCTACAG CTTGATCTTG ACCTATGATT TTACTTCTTA AACGATTAGA 120

AATATTTTTT AAACGTTCAA TATCGTTATC ATCCATTTGG AGAAACTGGG AATACCATTG 180

AATCGTTGnA ATAGTATCTG GAAATATCAT GGAACTGTAG CAACAGCAGT GTGTTGCACC 240

ATTnACTGAT TTTGCTAATT TATCTTGGTG AATGGATTTG GATTTGCATT TTGGAATGTG 300

CGTGCAGCTT TT 312

(2) INFORMATION FOR SEQ ID NO: 4553:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4553:

AGCAGCGATC AAAAATAATC CGCAATACGC TGGCAAACTA CCAATACCAA ACCATAGAAC 60

AACAAATGGT GCCCATGCTA TCGGAGATAT CGGCCTAATC AATTGAAATA GCGGTTCGAT 120

AGCGTTGTAT AGCCAACGAT TCCTTCCAAG CAAGAAGCCC AATGGAATAG CAACCAACAA 180

TGCGACAACA AAGnCCGCTA CAAATCTCCA TGAACTAATT GCTAAATGTG GnGAATTTCT 240

CCAGTAACAA TGGA 254

(2) INFORMATION FOR SEQ ID NO: 4554:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4554:

GGTCTGAATC GCTATCTGAG TCTGAATCGC TATCTGAGTC TGAATCACTG TCTGAGTCCn 60

AGTCACTGTC TGAATCTGAC TCACTATCTG ATTCTGAGTC GCTATCTGAT TCTGAGTCGC 120

TGTCTGGAAT CTGAATCACT GTCTGGAATC CGAATCGCTA TCTGGATCTG AGTCGCTATC 180

CTGGGGCTTG G 251

(2) INFORMATION FOR SEQ ID NO: 4555:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4555:

TACACAAAGA GATAAATTAC TTATGCAAAG GCGGAGGAAT CACATGTCTA TTACTGAAAA 60

ACAACGTCAG CAACAAGCTG AATTACATAA AAAATTATGG TCGATTGCGA ATGATTTAAG 120

AGGGAACATG GATGCGAGTG AATTCCGTAA TTACATTTTA GGCTTGATTT CTATCGCTTC 180

CTATCTGAAA AAGCCCnACC AGAATATGCA GTGCCCTGTC AAGnGAAGAC ATCACGTTCC 240

AGAAGCATGG C 251

(2) INFORMATION FOR SEQ ID NO: 4556:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4556:

AGCTACCCCG GGGATAACAG GCTTATCTCC CCCAAGAnTT CGCATCGACG GGGAGGTTTG 60

GCACCTCGAT GTCGGCTCAT CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT 120

TCGCCCATTA AAGCGGTACG GAGGCTGGGT TCCGAACGTC GTGAGnCCGT TCGGTCCCTA 180

TCCGTCGTGG GCGTAGGAAT TTGAGAGGAG CTGTCCTTAG TACGAGAGGA CCGGGTGGAC 240

ATA 243

(2) INFORMATION FOR SEQ ID NO: 4557:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4557:

TCATTATTTT AAATGCTCAT TTACATAAGT AAACTCTGCT TTAAAATAAT TTAACTCATT 120

GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTTAAACGCG TTATTAATCT TGTGAGTGTT 180

CTTTCGAACA CTAGnCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTG 235

(2) INFORMATION FOR SEQ ID NO: 4558:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4558:

CCGTTAAGCA CTAAATCCGC TTAATAACGG CTTTCTATCG CGCGCAACAT CTCGTTTGAC 60

TGCTTTTTCT TTCAAAGCTT GACGTTATCA TATTTTTTCT TACCTCGTGC ACACCAAGTA 120

ATACTTTACA ATGTCCATGC TTCAAATAAA GCTTTAACGG ACAATCGAAT AACCAAnCTC 180

ACGTGTTTGA TCACCCAATT TAATGATTTC ACGCTTGTGC AATAATnATT TTCGAGACGA 240

GAGGATCGGA TTAAAACGAT CCCCTCCTCG TATGG 275

(2) INFORMATION FOR SEQ ID NO: 4559:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4559:

TTATATGGAT GTATCGCCGA AGCAAGTTGT TTCAGCAGCG ACAnATGTAT TCCGATGACT 60

CAAACCGTGC ATTGATGGGT GCGAACATGC AACGTCAAGC AGTGCCTTTG GATGAATCCA 120

GAAGCACCAT TTGTTGGTAC AGGTATGGAA CACGTTGCAG CACGTGTATT CTGnGTGCGG 180

CTATTACAGC TAAAGCACAG AGGTCGTGTT GAACATGTTG GAATCTAATG AAAT 234

(2) INFORMATION FOR SEQ ID NO: 4560:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTATTTTGAC GTTTTAGACA TAAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60

TTCTACTCTA GCGGAAnTAA nTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTGA 120

CAATCGCTTG CTTCTTTCCT CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAAACT 180

CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AG 232

(2) INFORMATION FOR SEQ ID NO: 4561:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4561:

TCAAAGGACG CATACCATTA CGGGTCTGCT ACTTGTAAGC ACACGGTTTC AGGTTCTATT 60

TCACTCCCCT TCCGGGGTGC TTTTnACCTT TCCCTCACGG TACTGGTTCA CTATCGGTCA 120

CTAGAGAGTA TTTAGCCTTA GGAGATGGTC CTCCCAGATT CCGACGGAAT TTCACGTGCT 180

CCGTCGTACT CAGGATCCAn TCAAGAGAGA CAACATTTTC GACTACAGGA TTATTACCTT 240

CTTTGATTCA TCTTGTC 257

(2) INFORMATION FOR SEQ ID NO: 4562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4562:

TACCTAATAA GTTGTGAATT TGAACAGCGG CTGCTTTACA nTGGAACTGC TGATTCAGTT 60

GCCACAATTA CCATACCAAT TTTCTTTTTG TCTTCGTCTG TnATAATGTC CTTAGCAGCG 120

TTAGCTCCGA TTGAAACGAT GTCTTGGTTT ACAGGACTAA CAGCCATTTC AGTTTGACCA 180

ATTCCAATTA AAAATTTGTT TGGGTCTACT TGGCGTGGCT TCCTGCTGAA TTTAGCCATG 240

(2) INFORMATION FOR SEQ ID NO: 4563:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4563:

CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 60

TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACTTAAT CTATGTTTCC ACCATTTTTA 120

TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTATTTT AnATGCTCAT TTACATAAGT 180

nGACTCTGCT TTAAAATAAT TTAACTCATT GTCTGCTAAA CGTTT 225

(2) INFORMATION FOR SEQ ID NO: 4564:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4564:

TGTTAATTGG nGAATTTGGA TACTGGTTAT ATTCAGCTGC ACCGCAAGCA ACTTCTATTG 60

ATGGCCTAAC TGCCTTTTTA CCTCAAGCAA TGGGTATGGT AATTGTTGCA GTCATTTATG 120

GCTTTATGAA TATGAAAGCA GAGGAATCCC ATTCCCGTAA TAAAATTACG GTGGTTACAA 180

AATTATTTCA GGTTTCTTTC TTTTGCATTT GGGTGCTTTA ACCATATCTT nTT 233

(2) INFORMATION FOR SEQ ID NO: 4565:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4565:

AGCTCAGATA GCGCTCAGAC TCAGACAGCG ACTCAGATTC AGATAGCGAT TCAGACTCAG 60

ACAGCGACTC AGACTCAGAC AGCGACTCAG ACTCAGATAG CGACTCAGAT TCAGATAGCG 120

ATTCAGACTC AGACAGCGAC TCAGATTCAG ATnGCGATTC GGAnTCAGAC AGCGATTCAG 180

ATTCAGACAG CGACTCAGAC TCGGATAGCG ATTCAGATTC AGATA 225

(2) INFORMATION FOR SEQ ID NO: 4566:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4566:

CCAACTGGAG CTAATGGCTC TTCCATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 60

TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 120

TGGAGAnTGA CGGGTTCGAA CCGCCGAnCC TCTGCTTGTG AAGGCAGATG CTCTCCCAGC 180

TGAGCTAATT CTCCGATTTA AAACTGGCCT GGGCAACGTT CTACTCTAGC GGGAACT 237

(2) INFORMATION FOR SEQ ID NO: 4567:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4567:

GTTGGAGATA GTGTAATAAT GCCAATGAGC CACTCTGAAG TTACAGCGGA TGGGTGTTTT 60

GCCAAAATTC CATGGTGGTA CGAAAAAGAA AAAATGGATG GAAACAAGTT ACTGAAAATC 120

TTGGTAAAAA AGCAGGGGAC TTCGGTTCTA AAGCTAAAAC ACAGCTCATA ATATCAAAAA 180

GGTGCAGAGG AAATGGTTGA nnGGCAGCGG ATAAATCAAG ATGGTGCACT TGGTTAGCGT 240

TAAATCGCGA TGTGTGGGTT AnTACACATC CGGGAACTAG TAATAAGTAT GTCAGTTTAA 300

(2) INFORMATION FOR SEQ ID NO: 4568:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4568:

ATCCCGTGGA GGTTCAAGTC CTCTCGGCCG CATCAAAATT CTTAATTTAA ATAAGCGGGT 60

GTAGTTTAAT GGCAAAACCT CAGCCTTCCA AGCTGATGTT GTGGGTTCGA TTCCCATCAC 120

CCGCTCCATA GATAATTTTA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 180

TCCAAAAACG TAACTATAAG TTACAAACAT TnATTTTAGT ATTTGATGGA GCCTnAATCC 240

AAACATTCCA 250

(2) INFORMATION FOR SEQ ID NO: 4569:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4569:

GATCCCCTAG CTTTACGTTC AACTTTATAT GGGTATAACT CGAATATAAT TTGGCGCTCT 60

ATGTCATGGG ACAACGAGTA GACATTTAAT AACGGATCAG GTTCTGGTGA CGGTATCGAT 120

AAACCAGTTG TTCCTGAACA ACCTGGTGAG CCTGGTGAAA TTGAACCAAT TCCAGAGGnT 180

TCAGATTCTG ACCCAGGTTC AGATTCTGGG CAGCGnTTCT AATTCAGATA GCGGT 235

(2) INFORMATION FOR SEQ ID NO: 4570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4570:

AATCTATTTC TTCTATTGTT AAATCGCTAT CTCCATCTTC TTTTATCTCT GGTATTATTT 60

TTTCTTCAAC TAAGTCACGA TATAATGTTT TTGAATTTTC GTTCAATTTC GATTCGTGAT 120

TTTGAATACT TTTCTTCCAC ACAAATGTAT ACCTATTGGC ATTAGCnTCT ACTTTTGTAC 180

CAnCAATAAG ATTTTGCTTT AAACATTGAC TATGAAACTG GGA 223

(2) INFORMATION FOR SEQ ID NO: 4571:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4571:

CATGATATTT TGAACCGCAT GGTTAAAGTT GCAAAGACGG TCTTGCTGTC ACTTATAGAT 60

GGATCCGCGC TGCATTAGCT AGTTCGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG 120

CCGACCTTAG AGGGTGATCG GCCACACTGG nACTAAGACA CGGTCCAGAC TCCTACGGGA 180

GGCAGCAGTA GGGAATTTTC CGCAATGGGC GAAAGCTGTA CGGCGCAACG TCGTGTGnAG 240

TGCTGCAGGT TCTTCGGATC GTAAAAT 267

(2) INFORMATION FOR SEQ ID NO: 4572:

(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4572:

AATnCAACTT TTACTTACTA TCTAGTTTTG AATGTATAAA TTACATTCAT ATGTCTGGTG 60

ACTATAGCAA GGnGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG 120

TCGATGGTAG TCGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAT AATATTAATC 180

CACAGTAGCT CAGTGGTAGA GCTATCGGCT GTTAACCGAT C 221

(2) INFORMATION FOR SEQ ID NO: 4573:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4573:

GCAGAAATGC CAGCCGCATT GAGTGAACAC AGAGTTACAG GGTATTCTGT AGCCGAACCA 60

TTCGGTGCAn TGGGGGAAAA GTTAGGCAAA GGTAAGACTT TGAAACATGG TGATGACGTT 120

ATACCTGATG CGTATTGCTG TGTGCTAGTA CTnAGAGGGG AATTGCTTGA TCAACACAAG 180

GATGTAGCGC AAGATTTGTA CAAGGTTATA AAAAGTCTGG CTTTAAAATG 230

(2) INFORMATION FOR SEQ ID NO: 4574:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4574:

TCACATATCG ATAACATGAC ATAACTCATG CTGGGTTTCC CCATTCGGAA ATCTCTGGAT 60

CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 120

TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACTTAAT CnATGTTTCC ACCATTTTTA 180

TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTAnTTT AAATGGCTCA 230

(2) INFORMATION FOR SEQ ID NO: 4575:

(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4575:

CTTACAATAG TGTGCAAGTT GGGGTGGAGC CCCGACACAG AGAAATTAGC TCCTCAATTT 60

CTACAGACAA TGCAAGTTGG CGGGGCCCCA ACACAGAAGC TGGCGAAAAG TCAGCTTACA 120

ATAGTGTGCA AGTTGGGGTG GGACGACGAA ATAAATTTTG CGAAAATATC ATTTCTGTCC 180

CACTCCCAAA AAGACCGCAG TAGGATAATT CCATTTGGAA ATACCTTACT GCCnGTTTTT 240

AAAGTAATAG CnAATATTTT GGAATTAnGT TTCCTAGTTA ACCATACCAA CTAATGGCCT 300

CCTTAAATT 309

(2) INFORMATION FOR SEQ ID NO: 4576:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4576:

TGATTCTAGG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGGTAAA 60

ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAA TAATGGTGGG CCTAAGTGGA 120

CTCGAACCAC CGACCTCACG CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC 180

ATTTTTTTGA ATGTTAAATA AACATCnAAA CTGGnATACC ATATGTCACG GTAATCCGCA 240

(2) INFORMATION FOR SEQ ID NO: 4577:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4577:

CTTCGTGTTA AAATTTGATG CACAATGGTC ATCATTTTTA TCTTTCCAAT AAGTACTGTC 60

TGGGTAAAAA TnTATTAATT GGGTGGTTCG TGAAATGCAA TCTTTTTAAC GACTTCAGGG 120

TAATCTTTTA ACACATGCAT CGCAACGATT GAACCTnAAC TTGAACCTAA TATATAGACA 180

(2) INFORMATION FOR SEQ ID NO: 4578:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4578:

TAGGCATACC AAAGTCGATA CCATAGTGAC GACCGCCATT AAAGTTAAGT CCACCTGTGT 60

AACTCCCAAA CCTTTGCCAA ATTGGATGGT CAAATAGATA GCTTCCATCG CCTCCGCCAC 120

CAAAATCTTC AAACCACGAT TTACTTTGnC TACTAATTTC TTTTTGAGCA ATGAGTACGC 180

GCCTTAGCAA TTTTAnGTAG CGTAGTCCGC TCCAAAATAA TATTAAACTG ACATACTTAT 240

TACnAGTTCC CTGGATGTGT ACATAATCCA CACATCGCGA TTTATCGCTA ACAGAGCACA 300

CTTGATTACG CGCGCTCAAC ATTC 324

(2) INFORMATION FOR SEQ ID NO: 4579:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4579:

AATGTAAAAA CTGATTTCTA TTAATTATTT GATAGAAATC ACTTTTTTGT ATTTTATAAT 60

GTACAGCTCG TTGCATTCAT ATAGCTTGAA GTCACGTTTA AAACCATATC TATCATTATG 120

GTATGCATAT CGTTTAAAAC CTATTCTTTT GTTAnTAGGA CATATAAATT CATCATTAAT 180

TCGTCATATT TCCAATTTTG AGTGTnAAAA ATGTCACTTT TAAACTTTC 229

(2) INFORMATION FOR SEQ ID NO: 4580:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4580:

CGGGGACTCn AACCCGTGTT GACCGCCGTG GAAAGGGCGG TGTCTTAACC GCTTGnACCA 60

CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA 180

CGTAAGTTCG ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCGGC ATGGGAACA 239

(2) INFORMATION FOR SEQ ID NO: 4581:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4581:

CCGnACGAAT TTACACGTGT TCCGTCGTAC TCAGGATCCA CTCAAGAGAG ACAACATTTT 60

CGACTACAGG ATTATTACCT TCTTTGATTC ATCTTTCCAG ATGATTCGTC TAATGTCGTC 120

CTTTGTAACT CCGTATAGAG TGTCCTACAA CCCCAACAAG CAAGCTTGTT GTnTTGGGCT 180

CTTCCCGTTT CGCTCGCCGC TACTAAGGGA ATCGAATTTT CTTTCTCTTC CTC 233

(2) INFORMATION FOR SEQ ID NO: 4582:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4582:

TTAGTAAAAA GTCTGTGAGT AAGGGTGTAT GGAAAGTGGT TAAATATTAT AGAAAACATC 60

AAAGGATGTT AAGAAATACA ATTTATTACC CAGCATTTAA TAATGGTGCT ATAGAAGGAA 120

TTAATAATAA GATAAAATTA ATCAAGTGAA TTTCTTTTGG TTACAGAAAT TTCAnCAnCT 180

TTAAAGCACG TATAATGATG GATTTTCAGC TTGTACAA 218

(2) INFORMATION FOR SEQ ID NO: 4583:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4583:

TAATAAACAT GCCATACGTA ATAAGTGGCG TTGTATTAAA ATCATCTATA ATAGCCATAT 60

ATTTTGGAAT CATTGTTAAA AATGGAATTA AAGTTCTAGT GATCTGTTGG GTTTTGGAAA 180

TAGGTCATAG GGTnAAAACn TTTTTGAGAA TTTGTCGCTA TTTGTTAAAT TGTATCCCGG 240

CTTGAAGTTG G 251

(2) INFORMATION FOR SEQ ID NO: 4584:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4584:

TTTAGGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTCGTA GCTTCGCAGA 60

nTAACCCACT CCTCTTAACC TTCCAGCACC GGGGCAGGCG TCACCCCTAT ACATCACCTT 120

ACGGTTAGCA GAGACTGTGT TTTTGATAAA CAGTCGCTnG GCCTATTCAA TGGGGGCTCT 180

TCTGGGGGTT AAACCTAAAG AGCAACCCTT CTCCCGAAGT TACGGGGTC 229

(2) INFORMATION FOR SEQ ID NO: 4585:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4585:

TTATAAAAAG ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ATAGCGATTA 60

TTTCTTATGA ATTCAAGCTT ATTTAAAACT CTTTATTCAC TCGGTTTTGC TTGGTAAAAT 120

CTATATTTAC TTACTTATCT AGTTTTCAAT GTACAATTnC TTTTTAGTCA AGCGCTCGCA 180

TACTGCTnTA TTTTCAAAAA ATCAAATGCT CATTTACA 218

(2) INFORMATION FOR SEQ ID NO: 4586:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4586:

GGAATTCCAC TTTCCTCTTC TGCACTCAAG TTTTCCAGTT TCCAATGACC CTCCACGGTT 120

GAnCCGGGGC TTTTCACATC AGACTTAAAA AACCGCCTAC GCGCGCTTGT ACGCCCAATA 180

ATTCCGGATA ACGCTTGCCA CCTACGTATT TACCGCGGGC TGCTGGCACG TATTnAGCCG 240

T 241

(2) INFORMATION FOR SEQ ID NO: 4587:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4587:

CAGCCACCTG TTGCCACCAG CTACACTTGC ATTGTTTGCT ACGACACGCC CAAACAATGC 60

TGAAGTGAAT AAGAAATCAA TCATTTGCTC TTCTGTTAAA TCATGTGTTT TTTCTAATTT 120

AAAAAGTGCA CCGGGAATGG TACCCGAGGA ACCAGCTGTT GGCGTTGCAC AAATAATACC 180

CATCGCAGCA TTGACTTCAT TGTTGCAAGG CACCnTTGAC TGCGGCAATC ATTCATATCC 240

GACnAAGCAG ATG 253

(2) INFORMATION FOR SEQ ID NO: 4588:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4588:

ATGAACGGGT GGTAGCGAGT GGACGAAAAA CATCAATGAA AAGCTAGCTG TAGTTGCAAG 60

AGAAACTGGC TTACGATGGC ATTGGATCAA CACATGCGGC ATTGAGAAAT CCACGCATGG 120

CTGAGACGTT TACGATTGCG CGAAAAATGA ATCCTGAAGG CATTTTAGCA ATGTTGGTGC 180

GGACGTACCA GTAGAAAAGG CTTTGGAAGC AGTTGAAT 218

(2) INFORMATION FOR SEQ ID NO: 4589:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4589:

GCCATGGCTC CACAGGTAGG ACTCGAACCT ACGACCGATC GGTTAACAGC CGATAGCTCT 60

ACCACTGAGC TACTGTGGAT TAATATTATG CCTGGCAACG TTCTACTCTA nCGGAACGTA 120

AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT 180

GACCTCCTTG CTATAGTCAC CAGACATATG nATGTA 216

(2) INFORMATION FOR SEQ ID NO: 4590:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4590:

AGATTTAAAT AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC 60

ATCnCATTCA TTTCTTGTCT AGCAACGTTC TACTCTAGCG GAACGTAAGT TAGCTACCAT 120

CCTCGGCTAA GAACCTTTCT TGACTTGTGA CAATCGGCTT GCTTCTTTCC TCTCCTTCGG 180

CTCTCGCTAC TCAATTTAGC TCTACTAAAC TCGGTTGCGG CTCTTTTCTn GTTT 234

(2) INFORMATION FOR SEQ ID NO: 4591:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4591:

AATTGACTGA CTTCGTTTTA CCGCGTGTTT AATATTGTTA TACATATATT CTAATTGCAC 60

ATTTAAACTT CGTAAATGCC AATGTGnGTG GGACAGAAAT GATATTTTCG CAAAATTTAT 120

TTCGTCGTCC CACCCCAACT TGnCACATTA TTGTAACCTG ACTTTCCGCC AGCTTCTATG 180

TTGGGGCCCC GCCAACTTGC ACATTATTGT AAGCTG 216

(2) INFORMATION FOR SEQ ID NO: 4592:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4592:

ATTCCGGATA ACGCTTGCCA CCTACGTATT ACCGCGGCTG CTGGCACGTn TTAGCCGTGG 60

CTTTCTGATT AGGTACCGTC AAGATGTGCA CAGTTACTTA CACATATGTT CTTCCCTAAT 120

AACAGAGTTT TACGATCCGA AGACCTTCAT CACTCACGCG GCGnTGCTCC GTCAGGCTTT 180

CGCCATTGCG GAAGATTCCC TACTGCTGCC TCCCCG 216

(2) INFORMATION FOR SEQ ID NO: 4593:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4593:

TTGGACTAGA ACCAATGAAG GACGTTACTA ACGACGATAT GCTTAAAGGA GCTGTAAGTA 60

AGCTTTGATC CAGAGATTTC CGAATGGGGA AACCCAGCAT GAGTTATGTC ATGTTATCGA 120

TATGTGAATA CATAGCATAT CAGAnGGCAC ACCCGGAGAA CTGAAACATC TTAGTACCCn 180

GTGGAAGAGA AAGAAAATTC GATTCCCTTA GTAGCGGCGA GCAGAACG 228

(2) INFORMATION FOR SEQ ID NO: 4594:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4594:

CAATCGTTGA AGGAAATGTA CCAGCAGCAA TCAAAGACAA AGAAATTATT TCTGTAGACA 60

TTTCATCATT AGAAGCTGGA ACGCAATATC GTGGTGCTTT TGAAGAAAAT ATTCAAAAAT 120

TAATCGAAGG TGTTAAATCT TCACAAAATG CCGTACTATT CTTTGATGAA ATCCATCAAA 180

TTATCGGTTC AGGTGCCACA GnAAGTGGAT TCCAGGTTAG CCAAAGGGGT TAATCTGGAT 240

TAATTTTTTT Tn 252

(2) INFORMATION FOR SEQ ID NO: 4595:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4595:

ACTCTCTAGT GACCGATAGT GAACCAGTAC CGTGAGGAGA AGGTGAAAAG CACCCCGGAA 60

GGAGnTGAAA TAGAACCTGA AACCGTGTGC TTACAAGTAG TCAGAGCCCG TTAATGGGTG 120

ATGGCGTGCC TTTTGTAGAA TGAACCGGCG AGTTACGATT TGATGCAAGG TTAAGCAGTA 180

AATGTGGAGC CGTAGCAGAA GCACGGTTCT GGAATAGGGG CGTTTTAGTT ATTTTGGGTC 240

GTTACCCGGG AGnAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4596:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4596:

CCTACCGCTG CAGCCGCTGG ATCTGCTGGA GTTGCATTAG GATCTGCCGG TGCCGCACGT 60

CTACTTCTCT TTTTCGGTCT ATTAGATGCT GGTTCAGCAA TTGCAACTAG CTCTGGTTTA 120

TTTGAAGAAT GACGAACATC TTCTTGAATT TCCTTTAAAG TAGATGTCCT CCTGAACCAT 180

TnCATTGTTT AGTTGGGTAC ATTAATGCnG TATTATCGAC ACTACATCA 229

(2) INFORMATION FOR SEQ ID NO: 4597:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4597:

GCTCACCTTA GAATTCTCAT CTTGCACTCA CCTGGTGGTC GGTTTGGCGG GTAGGGTCAC 60

CTATTTTCTA TCTAGCAGGC TTTTCTCGGC AGTGTGAAAT CAACGACTCG AAGnCACAAT 120

GGTCTTCTCC CCATCACAGC TCAGCCTTAA CGAGTACCGG ATTTGCCTAA TACTCAGCCT 180

TACTGCTTAG ACGTGCAATC CAATCGCACG CTTCGCCTAT CCTACTGnGG TCCCCCCATC 240

GATTAA 246

(2) INFORMATION FOR SEQ ID NO: 4598:

(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4598:

AAGAAAATAA AGAATGCTAC AATTACGATT GCAATCAAAC CAAAGAACCA TAATGATGTG 60

TACCAAGTGC TGCACCTTTA GTAATGACAA CGTTTAAACT TAGCAACATA ACTACTAGAA 120

CAATTAGCCC TGCAACGTCA AATTTATGTG TATTGGTAAT TTCTGATTTC GTTTCAGGCG 180

TCCCTTTGAT GAGTAGCATT GAAAGTACGG nAACGATGnG TTG 223

(2) INFORMATION FOR SEQ ID NO: 4599:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4599:

nTnTCACTGT TTGACCCGGT ACCGTGTCAG ATAATCCCGC ACGCAATGCA ATCGTTCGTG 60

CAATGTTTTG GCCTTGTAAT CCTTCTGGAA AAGCCGTACC AACAATGACA TCTTCAATCA 120

TATTCTTATT GAATTTTCCG TCAATACGTT TCAATACGCC TTGTAATACT TTGGCTGCGA 180

CATCATCAGG TCTTTCGTGG AATAATGCGC CTGCTTTGC 219

(2) INFORMATION FOR SEQ ID NO: 4600:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4600:

AAGGTTAAGA GGAGTGGTTA GCTTCTGCGA ATACCGAATC GAAkCCCCAG TAAACGGCGG 60

CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC CGACCCGCAC 120

GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACGAGAGACT CGGTGAAAAT CATAGTACCT 180

GTGAAGATGC AGGTTACCCG CGGACAGG 208

(2) INFORMATION FOR SEQ ID NO: 4601:

(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4601:

AGTGCCAGTG ATTAACTGCA TTTTTCAATA GATCAGGGAA GACTACCAAG CTTATGTTGA 60

AGGACATCTT TTGGCGTTAC CGGTTGGGCA GGTATGTTGT ATTACCGTTC ACAACAGCAT 120

CACTTGAACA ACATTTGTTA ACGGATTATT TGGCAATTCG TTATTGTCGA ACAnTGCnAG 180

TTGGTGAGAT TTAATCATCG CTAAAGATGT GAAATAGATC GAAAATGGTT TAAGCAAACG 240

TTGCTCAGGT GTTACTACGT GATATGCCTA GCGAGTATAC TACAAC 286

(2) INFORMATION FOR SEQ ID NO: 4602:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4602:

ATATGGCTAT GGTATTCACA TATCGATnAA CATGGACATA ACTCATGCTG GGTTTCCCCA 60

TTCGGGAAAT CTCTGGGATC AAAGCTTACT TACAGCTCCC CAAAGCATAT CGTCGTTAGT 120

AACGTCCTTC ATGGCTTCTA GTGCCAGGCA TCCACCGTGC GGCCTTAATA ACTTAATCTA 180

TGGTTCCACC CATTTTTATA GGTCAAACGG TAACATGAGG TAGGGTCTTT TATAAAAAGG 240

nTTAAACGGG GTATTAATCT TGTG 264

(2) INFORMATION FOR SEQ ID NO: 4603:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4603:

GAAACGTTAG CACAAGCCAT GAACCAATTA GGTGGAAAGA GTAATAGTGG TGAAGGTGGC 60

GAAGATGCAA AACCGTTATG AAGTACAAGT TGATGGAAGC AACAAAGTAA GTGCGATTAA 120

ACAAGTTGCT TCTGGGCGTT TTGGTGTAnC TAGTGATTAT TTACAACATG CCAAAGAATT 180

TATCCn 246

(2) INFORMATION FOR SEQ ID NO: 4604:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4604:

ATTAACTAAC ATGGGCATCT ACGATGGAAA CAGACGTGGT ATCCTCGCTA TTATCCAGCT 60

AnCGCCATGC TGGCTCGTTT TTCAAATCAA GCCATTTTAA ATTTTGGAAA GGTGTATGGA 120

CCAAGCCCTA TGACATTGCA TTCACCGATT GAACACGATG TTATCGCCAT GTCTCATGGA 180

GAAAATCAAG AGCATCATTC AGCAGTATCG CGATGCTACA TTACGCGCGA TTAAAGCAGn 240

TTTGATGG 248

(2) INFORMATION FOR SEQ ID NO: 4605:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4605:

CAAGTTTTCC AGTTTCCAAT GACCCTCCAC GGTTGAGCCG GGACTTnTCA CATCAGACTT 60

AAAAAACCGC CTACGCGCGC TTTACGCCCA ATAATTCCGG ATAACGCTTG CCACCTACGT 120

ATTACCGCGG CTGCTGGCAC GTATTAGCCG TGGCTTTCTG ATTAGGTACC GTCAAGATGT 180

GCACAGTTAC TTAACACATG ATGTTCTTCC CCTAAATGAA CAGAGTTTTG TTTTGTTTTn 240

TGGGTT 246

(2) INFORMATION FOR SEQ ID NO: 4606:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4606:

TGTATCTGCA GTTAAATCAT GTnTCGCTTG GTTTAATGCT GTTAATGCGT TATCGACACG 120

ATGTTTTTCA TCTGAAATTT GTTGTGCAGT TGCATCGCCA TTGTCAATAA CACGTTGAGC 180

TGCAGTTATT TCAGTTTCTG CTTCACGCTn CT 212

(2) INFORMATION FOR SEQ ID NO: 4607:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4607:

TAGTCAAGAT GAGAATTCTA AGGTGAGCGA GCGAACTCTC GTTAAGGAAC TCGGCAAAAT 60

GACCCCGTAA CTTCGGGAGA GGGGTGCTCT TTAGGGTTAA CGCCCAGAAG AGCCGCATGA 120

ATAGGCCCAA GCGACTGTTT ATCAAAAACA CAGGTCTCTG CTAAACCGTA AGGAnTGTAT 180

AGGGGCTGAC GCCTGCCCGG TGCTGGAAGG TTAAGAGGAG TGGTTAGCTT CTGCGAGTAC 240

GGAATCGAAG CCCCAGTAAA CGGCGG 266

(2) INFORMATION FOR SEQ ID NO: 4608:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4608:

TTCAGTACGT AAATACGCAC GTGAAAAAGG TGTTAnATTA AAGCAGTTTC TGGATCTGGT 60

AAAAATGGTC GTATTACAAA AGAAGATGTA GATGCATACT TAAATGGTGG TGCACCAACA 120

GCTTCAAATG AATCAGCTGC TTCACTGACA AGTGAAGAAG TTGCTGAAAC TCCTGCAGCA 180

CCTGCAnCAG TGAACATTAG AAGGCGACTT CCCAG 215

(2) INFORMATION FOR SEQ ID NO: 4609:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGGTTCATAC ATGTCAATAG TAACCGTCTT AACTTGTTGT CGATTTTTTA AATCGAATCG 60

CTCGAAATAG GCACGCAAGA ATCTTGTAGT TCTATTTTCT AAAATATCTA TAACATCATG 120

GTATCATTAT CTATAAAAAT GAAACTCATT GATCCAGTTA CATTTTTAAC GCTTTTAAAT 180

TCATCCATAG CGATGTGGTT CCTGCCAACC ATTAAAGGGG TTAATTCnGA ATnGATTAGC 240

C 241

(2) INFORMATION FOR SEQ ID NO: 4610:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4610:

ATTCATTTCT TGTCTAGCAA CGTTCTACTC TAGCGGAACG TAAGTTAGCT ACCATCCTCG 60

CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 120

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 180

TTTCAnTTCG CCAAGCCATT TTTCTTTGGT GnTTA 215

(2) INFORMATION FOR SEQ ID NO: 4611:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4611:

GTGCCATCTT TCTTCATCAA TTCATTAATA ATTGCTGGGA CGCCACCAGC TTCATGCACA 60

TCATGCATTG AATACGATGA ACTAGGTGCT ATTTTTGATA AATATGGCGT GCGTTTGGCA 120

ATAGCATTAA TGCGCTCTAA GTCATAATCA ATACCAGCTT CATTGGCAAT GGCTAACGTA 180

TGCAGTACCG TGTTTGTTGA ACCACGGCAC ATCTTCGCCA ATTTCTTCTT TAAACAAGTT 240

TAAATTATCT TGTGATTCAG GTAAATCCAT CTTGTTAGCT ACTACGATTT GAGGTCTATC 300

TTCTAAACGT TGCTCGTACG GCGGCTAATT CTGGATTAAT GACTTTATAA TCTTCAATAG 360

GGTCTCTACC TTCAGAACCG CTCCATATCC ATCCTGTGGA 400

(2) INFORMATION FOR SEQ ID NO: 4612:

(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4612:

AATACTATTA AGAAGTCCTG AAAAATTCAC ATTAGCAGTT GGATTGTTCA ACTTTATTAA 60

TGATAAGTAT GCAAATAATT TCACAGTGTT TGCAGCAGGG GCAATTATGA TTGCAGTACC 120

TATAGCAATC GTATTCTTGT TCTTGCAACG CTATTTAGTA TCAGGTTTAA CAACAGGTGC 180

CGACCAAAGG GTTAGTTTGA ATTTAGGAGT GGGGCCAGAT TGGTTAAGGA CCnCCTAATG 240

ACCGTTAAGG TTnAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4613:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4613:

GACTTCGTTT CAGTGTAAAA TTTTTCTAAT GTAACAGATA TGCTATTATT CATTGGAATG 60

ATTAGTGCTT CATCTTTTTT ACCCCAATAT TTTATAAGTG CAATTCGTAT GTGCACGTGC 120

TTTGCCACTT TTAATCAACG CTTAACCTCC TAAATTCTCA ATCCAAGTAT GTGCTGCACC 180

AGCTTTTTTC TACAGCTTTT ACAATATTnn 210

(2) INFORMATION FOR SEQ ID NO: 4614:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4614:

TAGCGTATTA ATCGGCGGAT CGGCTGAGCG TATCTGAGTC TGAATCGCTG TCTGAGTCTG 60

AGTCGTATCC GAGTCTGAGT CGCTGTCTGA nTCTGAATCA CTGTCTGAAT CCGnATCGCT 120

ATCTGAATCT GAATCGCTAT CCGAGTCTGA GTCGCTGTCT GAATCTGAAT CGCTGTCTGA 180

GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAA 235

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucl ic acid
(C) STRANDEDNESS: doubl
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4615:

ATGTGCGTGG TTTATTTTAA TAGGTTAGTA ATATATTAGG TCATGTTATG TTTAAnTTTA 60

TAATGAATAA ATAATTTAGA AATATGCTTC CGATTGTTCG ATGCTTTAAT TCAGTTAGAA 120

GCATCATAGA ATGCATGATT ACTGTTGTAA AGATACGTAA TGTTTTGTAT TGACTGTATG 180

TCnTTGGATA GAGTTACAAA CTTATTTTG 209

(2) INFORMATION FOR SEQ ID NO: 4616:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4616:

ATGCGCAAGA TATGGAGAAC ACCATCGCGA AGCGACTTTC TGGTCTGTAA CTGACGCTGA 60

TGTGCGAnAC nTGGGGATCA AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT 120

GAGTGCTAAG TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGCTAACGCA TTAAGCACTC 180

CGCCTGGGGA GTACGACCGC AAGTTGGAAA CTCAAAGGAA TT 222

(2) INFORMATION FOR SEQ ID NO: 4617:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4617:

CAGTTTGCAA CACCCCAATT CTTGCCAGTC AGCATGATTC TGTTCATTTC TGCGATTTCT 60

TTGTCGATAT TTTCAAATCT TGTTGGACTT GATCTAAATC AATTGGTGCT TCTTCTTCGA 120

ATGTATCAAC ATATCGCGGT ATGTTTAAGT TGTAATCGTT ATCGGnGATC TCTTGTAATG 180

TCGCGCTGTG GCTATATTTA TCAATCGTGG CTTTACGCTT ATATGGGGCT ATAATACGTT 240

(2) INFORMATION FOR SEQ ID NO: 4618:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4618:

TCTAATTGAT AGTGAATATA ATTAGAGTTn GAGGCTGGGA CATAAATCCC TAAATTTCAn 60

CAGTAAGATA ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT 120

CATTGGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG ACTGGGCACT 180

GCTCCCTCAG GGGTCTCGCC ATTTAATACT ACGTAT 216

(2) INFORMATION FOR SEQ ID NO: 4619:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4619:

ATGTATCGCG CCGAGCAACA CAAGATAAGC ATTGTAGATG TGGATGCCTT AACTGGGCAA 60

GCGATTnGTC GTCCTAAAAC AGGTACATAT GCGCTATCTG ACCTAGTCGG TTTAGATATT 120

GCAGTGTCTG TAATTAAAGG CATGCAACAA GTACCTGAAG AAACACCCnT ATTTTCATGA 180

TGGTCAAAAT TTGTAAATAC GTTGTTTTGA CAATGGGCGC ACCTCGGACC GTAAAACG 238

(2) INFORMATION FOR SEQ ID NO: 4620:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4620:

AACCATTGAA GCACCCCATT ACGTTTTGGC TGACACGnAC GTATATCGCC TGCCCAAGCA 60

GATGCAGCCT TATTAACACC TGAACCACTT CGAACGCCAC TACCTTTAAG TGACTTCAAC 120

CATTTTTCCT GGATCTTTAG CTGTATGCAT TGCCCTGGAT GCGACCCTTG nCATCAATTG 180

TTGACCAGC 249

(2) INFORMATION FOR SEQ ID NO: 4621:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4621:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCA AGAAAGAACG 60

TAAATTTAAT CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG 120

TGAGAAGACA ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA 180

AGGTGAATCG AAGAGAAATC ACAAAGTCCG TTnTGGnTTA CAGGTACGGC AGAACGATAC 240

ACAGTCTCGG GCGATTGTCG AGTCCAC 267

(2) INFORMATION FOR SEQ ID NO: 4622:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4622:

CAAAAGGTAG TTTAAATTAG GAGTGGGGAA ATTGATAAGA CCACTAATGA CGATAAAGAT 60

TAAAAGGAnG ACGTTATGAT GACGATTAAA GTTGGATCAT TGGGTGTGGT GGTATTCCAA 120

TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAATGTTG AAATGAnCGC ATTTTGTGAC 180

GTAGACATTT CGAAGCAGCG AGTGCGGCAG AAGCATACGG ACTGACAATG C 231

(2) INFORMATION FOR SEQ ID NO: 4623:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4623:

CGAAACCGGC CCGACCCGGA CCnACCCGAG GAAAGGTACC CnAAAGnTGA AGCCCGGGAA 60

CCCAACACCC ACCCGGACAC CAGAAGTGCC GGAGTGAGCC AGAAACTCCA ACACCGCCAA 180

CACCAGAGGT ACCAGCTGAA CCTGGTAAAC CAGTACCACC TGCCAAAGAA GAACCTAAAA 240

AGCCTTCTAA ACCAGTGGAA CAAGGTAAAG TAGTAACACC TGTTATTGAA ATCAATGAAA 300

A 301

(2) INFORMATION FOR SEQ ID NO: 4624:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4624:

CGAGGTGCTG CAGAAGGTGT CATTCGTCGT TATTTAATTG AAGAAAAGAA CTACTTAGAA 60

GCTGTGATTG GTTTGCCAGC GAATATTTTC TATGGGACAA GTATTCCAAC ATGTATTTTA 120

GTATTTAAAA AATGTCGCCA ACAAGACGAC AACGTACTAT TTATCGATGC ATCCAATGGT 180

TTTGAAAAAG GGGnAAATCA TAATCATTnG GCGATGCCCA AG 222

(2) INFORMATION FOR SEQ ID NO: 4625:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4625:

TGGAAAGTGA ATCAAAGAGG TAATATCCGT AGTCGAAATG TTGTCTCTCT TGAGTGGATC 60

CTGAGTACGA CGGAGCACGT GAAATTCCGT CGGAATCTGG GAGGACCATC TCCTAAGGCT 120

AAATACTCTC TAGTGACCGA TAGTGAACCC AGTACCGTGA GGGAAAGGTG AAAAGCACCC 180

CCGGAAGGGG AAGTGAAATT AGGAACCCTG AAAACCCGTG TGCTTTACCA AAGTTAnGTT 240

CAAGAGGCCC CGTTTAAATT GGGGTnnAAT TGGCGGTGCC CTTTTTTGGT AGGAATTGAA 300

A 301

(2) INFORMATION FOR SEQ ID NO: 4626:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4626:

GAATGAAGGA AGACCATATG AAAAATGGCC AACTTAAGCC AGGATACAAT TTACAAATAG 60

CGACAAATTC TCAATTTGTT TTATCCTATG ACCTATTTCA AAACCCAACA GATACTAGAA 120

CATTAATCCC ATTTTTAnCA ATGATTCAAA ATACCTTCGG TTATTTACCA GAGTATATTG 180

TAGCTGATGC AGGTTATGGT AGTGAGCAAA ACTATATGGC nAT 223

(2) INFORMATION FOR SEQ ID NO: 4627:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4627:

TTGTTGGGGC CCCGCCnGCG nCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG 60

GGGCCCCTGA CTAGAATTGA AAAAAGCTTA TTACAAGCGC ATTTTCGTTC AGTCAATTAC 120

TGCCAATATA ACTTCGTAGA TCATAGAACA TTGATTTATT TCCCAGCCTA TTCTTTTCAT 180

AAAAAAAAGA CGGATTAATT ATCCGCTTTT TCCTTATATC T 221

(2) INFORMATION FOR SEQ ID NO: 4628:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4628:

ATATATTCGT ATTTATAGTA AAATTAAATA AAGAGnATTA TATAACACGA GGTGTAGTAA 60

GTATGAAATT TGAGnAAATA TATAGATCAC ACTTTATTGG AAGCCTGAGT CAACACGTAC 120

GCAAATCGAT CAAATCATCG ATGAAGCGAA GCATACCAAT TTTAAATCTG TATGTGTGAA 180

TCCACCACAT GTTAAATATG CAGCAGAG 208

(2) INFORMATION FOR SEQ ID NO: 4629:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4629:

ACAATAATGC ATCATAATGC GCAACAACAA TCAATACTGC GAAAACAGAA GCACAACAAG 60

TGATTAATAA TGAGCGTGCA CACCACAACA AGTTTCTGAC GCACTAACTA AAGTTCGTGC 120

ACACAACTAA GATTGATCAG CTAAAGCTTA CTTCAAAATA AAGAGATATA GCCATTAGTA 180

ACGTTAAAAT AACTTACAAG nTCTGTGACC AGTACCTCAC TGTGGTATGA CGCACAAGTA 240

TTGATACTnT ATCGAGAGCG TGAGnGAACT GAATACTGCG CTCACGGTAT TACATGCGTG 300

CACTG 305

(2) INFORMATION FOR SEQ ID NO: 4630:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4630:

TCGACTACCA TCGACGCTAA GGAGCTTAAC TTCTGTGTTC GGCATGGGAA CAGTGTGACT 60

CCTTGCTATA GTCACCAGAC ATATGAATGT AATTATACAT TCCAAACTAG ATAGTAAGTA 120

AAAGTGATTT GCTTCGCCAA ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT 180

CAGCTCCACA TGTCACCATG CTTCCAnCTn GAA 213

(2) INFORMATION FOR SEQ ID NO: 4631:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4631:

GAnGTGAAAT AGAACCTGAA ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA 60

TGGCGTGCCT TTTGTAGAAT GAACCGGCGA GTTACGATTT GATGCAAGGT TAAGCAGTAA 120

ATGTGGAGCC GTAGCAAAAA CnAAGTTCTG AATAGGGCGT TTAGTATTTG GTCGTAGCCG 180

GAAACCAGGT GATCTACCCT TGGTCAAGTT GAA 213

(2) INFORMATION FOR SEQ ID NO: 4632:

(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4632:

GCTTTTAAAT CAAATGATAG CGGAAGGGnA TTTTAAAATT ATTCGAACCA TTATTTACAG 60

CAGCAGATGG ATGGATTGGT GTCACAATTA TCTTTGGTGC CTTTGCATTA TTCTGGTTTG 120

TAGGTATTCA TGGTCCGTCA ATTGTAGAGC CAGCAATTGC AGCCATTACA TATGCGAATA 180

TCGAAGCGAA CTTCAAGTTG CTTCA 205

(2) INFORMATION FOR SEQ ID NO: 4633:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4633:

AGTTATATTG ACAGTAGTTG ATGGGGCCCC AACATAGAGA AATTGGAACA CCAATTTCTA 60

CAGACAATGC AAGTTGGGGT GGGCTCTAAC ATAAAGAAnT ACTTTTTCTn TAGAAATTAG 120

TATTTCTTAT ACATGGGTTT TACTCAGTAT TTCCTATTCT TAAGTGCACA TTAGCAGCGG 180

CTAATGTGTT AAGAACTACT ACAT 204

(2) INFORMATION FOR SEQ ID NO: 4634:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4634:

GCCGATGGAT TAGAGTATAT GACGTGGTGG CATGTCATTA ATTTAGGTGA TGTAGGTAAG 60

AACGTTnGGG CAAGGTATGA GTGGTGGTAT TGCGTTACGT TAGCCCGTCT GATGTAGAAG 120

CTTTTGTTGA AAATAATCAA CTAGATACGC TTTCGTTTAC AAAGATTAAA CACCAAGAAG 180

AAAAAGCATT CATTAAGCAA ATGCTGGAAG AnCCATGTGT CACACA 226

(2) INFORMATION FOR SEQ ID NO: 4635:

(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4635:

CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA ATATACTCTG GTAAATAACC 60

GAAGAGTTGT TGAATCATTG TTAAAAATGG GATTAATGTT CTAGTATCTG TTGGGTTTTG 120

AAATAGGTCA TAGGATAnAA CnGTACGGAG AATTTGTCGC TATTTGTAAA TTGTATCCTG 180

GCTTAAGTTG GCCATTTTTC ATATGGTC 208

(2) INFORMATION FOR SEQ ID NO: 4636:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4636:

TTTTTCTTTG TGTTTATTTT TATTTTGAAC GTTTTAGGAC ATAAAAAAAA GTAGACCTTG 60

CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 120

CGTAAGTTGG CTACCATCGA CGCTAAGAAC CTTTCTTGAC TTGTGACAAT CGCTTGCTTC 180

TTTCCGCTTC TTCTGCTCGn GCTTACTCAT TGAGCnCTAC TAAACTCG 228

(2) INFORMATION FOR SEQ ID NO: 4637:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4637:

CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACTTATA GATGGATCCG CGCTGCATTA 60

GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA TAGCCGnCCT GAGAGGGTGA 120

TCGGCCACAC TGGAGCTGAG ACACGGTCCA GACTGCTACG GGAGGCAGCA GTAGGGnATC 180

TTCCGCAATT GGCGAAAGCT GTACGGGCAA CG 212

(2) INFORMATION FOR SEQ ID NO: 4638:

(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4638:

ATnTnATTAA ATAGAGAACA GCAGTAAGAT ATTTTCTAAT TGAAAATTAT CTTACTGCTG 60

TTTTTTAGGG ATTTATGTCC CAGCCATTTT TGTATTCATA TTTAAATTTC GATAATTTTT 120

CAGGAAGCAT TTTAATTTTA CTAATGAAGC CATATTTTTA GATTAACCAA AATTAATATT 180

TACATTTCCT AACCATTTTT ATGTAACATT TACAGTTCCA AAAATGGGGG TAATAATCCA 240

GGTTAGGATA AAGAGG 256

(2) INFORMATION FOR SEQ ID NO: 4639:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4639:

AnAGnAACCA CTACATAATA AATCATTAGT GGCTCTTTAT CATTTCTGTC CCACTCCCCT 60

GAGAAGTTTA AAATTTTATA TGTTGGCTTG TTATGTTAAG GGAATTAACA TGGTTGTCTT 120

GTTTATATTA TGTGATTCCA ACATTACTAG TCCTGGTAAA TCTAATTCCG TAAAATGCTA 180

AATCTAACCA TCTATTAAAT TTTAAAACC 209

(2) INFORMATION FOR SEQ ID NO: 4640:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4640:

nGnAAAGGTG AAAAGCACCC CGGAAGGGAG GTGAAATAGA ACCTGAAACC GTGTGCTTAC 60

AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA CCGGCGAGTT 120

ACGATTTGAT GCAAGTTAAG CAGTAAATGT GGAGCCGTAG CAGAAGCATG GTCTGAATAG 180

GTGCGTTTAG TATTTGGTCG TAGCCCGCAG AACCAGGGTG ATCT 224

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4641:

CACTCACnCA GATTTTTAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA 60

AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TTTATTCTAC 120

CGCTGAACTA CTTCTGCATA TGCGGGTGAA GGGAGTCGAA CCCCCACGCC GTAAGCTAnG 180

ATCCTAAGTC TAGTGCGTCT GCCAA 205

(2) INFORMATION FOR SEQ ID NO: 4642:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4642:

AGCTGACATG ATCAGTCAGC TTACAACAAT GTGCCGGTTG GGGTGGCTGG ACACGGCACC 60

CTGAGGGAAG GGCACCCGTC ATCAAAAATT CTATTTATAG AATTTTACAG TAATGTGACA 120

GACGGGCAAA GCGAACCATT CAATACGAAG TATTGTATAA ATAGAGAACA GCAGTAAGAT 180

ATTTTCTAAT TGAAAATTAT CTTACTGCTG TnTTTTTAGG GATTTATGTn CCCAG 235

(2) INFORMATION FOR SEQ ID NO: 4643:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4643:

AGnAAGGTGG GGATGACGTC AAATCATCAT GCCCCTTATG ATTTGGCTAC ACACGTGCTA 60

CAATGGACAA TACAAAGGCA GCGAAACCGC TAGTCAAGCA AATCCCATAA ATTGTTCTCA 120

GTTCGATTGT AGTCTGCGAC TCGACTACAT GAAGCTGGAA TCGCTATAAT CTAGATCAGC 180

ATGCTACGTG ATAGTTCCGG GTCTnTACAC ACGCCCGTCA CACCACGGAG GGTTTTACAC 240

(2) INFORMATION FOR SEQ ID NO: 4644:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4644:

CAGCAGGCCA CCAAAATTGT GGTCCGAGAT GTTCATATAA AACTTTATAT AATTCATCAG 60

TTCCTAACAT TTACACCCTC CATTTTAGAG GGAGTGGGAC AGAAATGATA TTATCGTAAA 120

ATTTATTTCG TCGTCCCACC CCAACTTGCA TGTCTGTAGA AATGGGGATC CAATTCnCTT 180

GTTGGGGGCC CGCGGGCAAG GTnACTAGAA TGAAAAAAGC CTGTTACAAG CGATTTTCGG 240

TTCAGTCCAC TACTGGCAAT ATAACTTGTA GAGCTAGGAC ATTGG 285

(2) INFORMATION FOR SEQ ID NO: 4645:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4645:

GCTATTACTC TGCTATCAAT GTACCTAAAG CTACCGATGA TTTCCGAGAC ATAGACCGTG 60

CGCTTGTnTG GGGGTTCAAC TGGAAACTTG GTCCATTCCA ATTATGGGAT GCAATGGGGn 120

TACGAACGTG TTAAAACAGT ATGGAAGACG AACTTGGAGA CTTACCACAA TGGGTTAGTG 180

ATTTAGATGG TGGCTTTTGA TAAACA 206

(2) INFORMATION FOR SEQ ID NO: 4646:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4646:

ACAGTTACCG ATACAACTGA AGATGATAAC GATGCAGATG GTGGCGACGT TGACGTCACA 60

CTTACGGATC ATGATGATTT CACACTTGAT AACGGATACT TCGAGATGAT ACATCAGACA 120

CnGACAGTGA TTCAGATTCA GACAGCGACT CAGATTCnGA TA 222

(2) INFORMATION FOR SEQ ID NO: 4647:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4647:

GTACTATTCG TGTGTGACAA TGTTCTTCCA GCATTTGCTT AATGAATGCT TTTTCTTCGT 60

TTAATCTTTG TAAACGAAAG CGTATCTAGT TGATTATTTT CAACAAAAGC nTCTACATCA 120

GnCGGGATAA CGTAAGCAAT ACCACCACTC ATACCTTGAC CGAAGTTCTT ACCTACATCA 180

CCGAAATTAA TGACAGTCCA 200

(2) INFORMATION FOR SEQ ID NO: 4648:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4648:

CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC TGGGAGAGCG CCTGCTTTGC 60

ACGCAGGAnG TCAGCGGTTC GATCCCGCTA GTCTCCACCA TTATTTGTAC ATTGAAAACT 120

AGATAAGTAA GTAAAATATA GATTTTACCA AGCAAAACCG AGTGAATAnA GAGTTTTAAA 180

TAAGCTTGGA ATTCATTAAG A 201

(2) INFORMATION FOR SEQ ID NO: 4649:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4649:

AGTAAATACA GATGGAATAA ATCTTTTAAG GCTTATAAAC GCTCATCTGn CATTGTAGCA 60

ATTCATGCTT TCAAAAGACG ATATACTACG ACACTCCTAC GAACTTGTCC AAGGATTACG 120

AAAGTCTGTG AGTAAGGGTG TATGGAAAGT GGTnAAAT 218

(2) INFORMATION FOR SEQ ID NO: 4650:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4650:

GTGGCGGTGC GACTGTCAGA AGCACGTTAA ATTAATGAAA GATACAGTAG GTGCTGATGT 60

AGAAGTAAAA GCCATCAGGT GGCGTACGTA ATTTAGAAGA TTTCAATAAA ATGGTTGAAG 120

CAAGTGCGAC ACGTATTGGT GCGAGCGCAG GTGTTCAAAT TATGCAAGGT TTAGAAGCAG 180

ATTCnGATTA CTAATATnTA TG 202

(2) INFORMATION FOR SEQ ID NO: 4651:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4651:

AGCGGCGGAC GGGTGAGTAA CACGTGGATA ACCTACCTAT AAAACTGGnA TAACTTCnGG 60

AAACCGGAGC TAATACCGGA TAATATTTTA AACCGCATGG TTCAAAAGTA AAAGACGGTC 120

TTGCTGTCAC TTATAGATGG ATCCGCGCTG CATTAGCTAG TTGGTAAGGT AACGGCTTAC 180

CAAGGCAACG ATGCATAGCC GACCTGAGA 209

(2) INFORMATION FOR SEQ ID NO: 4652:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4652:

TGAAGATGCA GGTTACCCGC GACAGGACGG AAAGACCCCG TGGAGCTTTA CTGTAGCCTG 60

ATATTGAAAT TCGGCACAGC TTGTACAGGn TAGGTAGGAG CCTTTGAAAC GTGGAGCGCT 120

CCACTTATCG TGGTTGGAGA CA 202

(2) INFORMATION FOR SEQ ID NO: 4653:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4653:

CCGTGCGACC CCTTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC GTTCCCGGTA 60

TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGCTCT 120

ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG 180

AACCGGTACG TGATCACTCA ACnGn 205

(2) INFORMATION FOR SEQ ID NO: 4654:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4654:

AGACGAAACG TTGTTGTTGC GAAGATAAAT CGCACAGCGA TTGAGCCTAT CTGCTGCACC 60

ATTAACTGGT GAAGTAACAC CATTATCAGA AGTGCCTGAT CAAGTGTTCA GCGAAAAAAT 120

GATGGTGACG GTATCGCTAT CAAACCTTCA CAAGGTGAAG TTCGTGCACC ATTCAACGGT 180

AAAGTACCAA TGATTTCCCA ACCAAACATG CCATTGGTCC TGTATCAGAT AGTGGTTAGn 240

CTATTAATCC ACACGGGTTA GAnG 264

(2) INFORMATION FOR SEQ ID NO: 4655:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4655:

GACGATTACA TATCATCGCT AATAACTTAG CATTAAAACC GCTTGATGCG CCACCACAAG 60

AACACAACGA ACTGGGnACA TGCTTCGGTT AAATCCATCA ATTTCAACGC TTGTnACGCG 180

AAATCAGTTT GCTCTTGGCT GCAGTAAATC G 211

(2) INFORMATION FOR SEQ ID NO: 4656:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4656:

TTTACATTTA TCGGTTTAGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC ATCTTTCTTT 60

GTGTTTGCTT TTATTTTGAC GTTTTAGACA TAAAAAAAGA GACCTTGCGG TCTCAATGCG 120

GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTCGACT 180

ACCATCGACG CTAAGGnGCT TAACTGnTGG GT 212

(2) INFORMATION FOR SEQ ID NO: 4657:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4657:

TGGGTTCGAA nTCCACTTAG GACCCACCAT TAACTTAATA CCTATTTGGG GGCTTAGCTC 60

AGCTGGGnAG AGCGCCTGCT TTGCACGCAG AGGTCAGCGG TTCGATCCCG CTATCTCCAC 120

CATTATTTGT ACATTGAAAA CTAGATAAGT AAGTAAAATA TAGATTTTAC CAAGCAAAAC 180

CGAGTGAATA AAGAGTTTTA 200

(2) INFORMATION FOR SEQ ID NO: 4658:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4658:

TACAGTATAT CGGGAAGACA GGATTCGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT 60

CTCTTGATCC GTAGTCAAAC GCTCTATCCA ATTGAGCTAC GGGCGCATAT GTTTTTATTG 180

AAAAn 185

(2) INFORMATION FOR SEQ ID NO: 4659:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4659:

AAGTGTTAGG GGGTTTCCGC CCCTTAGTGC TGCCAGCTAA CGCATTAAGC ACTCCGCCTG 60

GGGAGTACGA CCGCAAGTGT ATAACTCAAA GGAATTGACG GGGACCCnCA CAAGGTTGGA 120

GCATGTGGTT TAATTCGAAn CAACGCGCAG TAACCTTACC AAATCTTGAC ATCCTTTGAC 180

AACTCTAGAG ATAGAGCCTT CCCCTTCG 208

(2) INFORMATION FOR SEQ ID NO: 4660:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4660:

ACGTCGCGAG AACGCAATTA GCTGAAAAAG ATTACAACAT TAGAACAAGA TTTAAAGTCA 60

CATTTAGTGA ACATCAAAGG CCGAATAACA TCATAAATTA CGATTAGATA TAACAAAAGA 120

GCTTGGGACA TAAGTCCTAA AGTCTTAGGC AAGTAAAAAA GTGATTTCTA TTATTTATTT 180

GATAGAAATC ACTTTTTGAT ATGTATTTnT ATGTACAGCT CGTTGAGCnC TATTTTCCTT 240

ATATTAGTGC CATAATACAA ACCTAGCTCT TGTTTAACTT TATTATTCCG AACTGACATC 300

GGTGAACCCA ATAGCCTCAT AAGCAAACAG CTTACATCAT TTTCTTGAnT GGTTTTCGTT 360

CTGTC 365

(2) INFORMATION FOR SEQ ID NO: 4661:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4661:

AAAGTATTTC TTTATGTTGG GGGGCACCCC ACTTTGnCAT TGTCTGTAGA AATTGGGAAT 60

CCAATTCTCC TnATGTTGGG GCCCCGCAGT TCAACTACTG CCAATATAGT GTTGTAGTGT 120

CTAAGACATA AAAGTTCATC TCAGTCACAA TTACTTTATA GCCTATCCAT CATCTTTTCT 180

ACATGAAATT TTTCCAAGTG ATATATTTT 209

(2) INFORMATION FOR SEQ ID NO: 4662:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4662:

TTATGGCACT TAAAACCAGC GATGACGATT GCAGTATCAC ATGGTATCTT CAACATAACA 60

AATACTTTGA TTCAATTACC ATTTGTAGCA GGTTTAGCAT GGATTGTTAC AAAGCTTGTC 120

CCAGGTAAAG ATATTGCTGA TGACTATAAA CCTCAGCACT TAAACCAAGG TCTGTTATCA 180

CGCACCTGGT GTTTGCATAC CAGGAACTCC AAAAGGATTA CCAAATGTnG GGGCAGAnTG 240

GCCTAA 246

(2) INFORMATION FOR SEQ ID NO: 4663:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4663:

AATGGTGTAT TATGAGTAGT AATAATTAGC AAAGAGGTAA ATTAAGTGAT GTCGCGTCAT 60

TTAAGGAAGC GATTCACAAT CGAGAATCAC AAAGTACAAC TGGTATCGGC GAAGGTATnG 120

CCATTCCACA TGCCAAAGTG GCCGCAGTTA AGTCACCAGC TATTGCGTTT GGTAAATCTA 180

AAGCAGGCGT AGATTATCAA AGnTTTTGGT ATGCAACCAG CACACT 226

(2) INFORMATION FOR SEQ ID NO: 4664:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4664:

TTCCGTCTCG GCACCATTTT AGCGCCGTAG CTCAATTGGA TAGAGCGTTT GACTACGGAT 60

CAAGAGGTAT GGGTTCGACT CCTATCGGGC GCGCATTTTT AAATTAATTG AATAACGGGA 120

GTAGCTCAGC TTGGTAGAGC ACTTGGTTTG GGACAAGGGC GCAGGTTCGA ATCCTGTCTC 180

CCGATTACTT CTAAATCCAT TTATGGGGCT ACTCACTGGG nACGCCTCTT nCAC 234

(2) INFORMATION FOR SEQ ID NO: 4665:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4665:

GTACATCTAA AATCATCCAT GAAGGTTTGT TACCTGAATT ACGGAATGAT TCAACAACTT 60

CTAAACGTTT AATTnACCAG TAAGTCTTTG CCAAGTAGCT GATTCCAACT CATCGCGTAC 120

AATTTAAGTC TTCGTCAAGA TCAATCCTCT TCAAGTAAAT CTTTAATAAC CTTCTGCACC 180

CATTTTTGCA CGAATT 196

(2) INFORMATION FOR SEQ ID NO: 4666:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4666:

CCGCCGAACA ACTACTTTGT TTGTTGATTC TCTCCACCTG TTTCAGTAGT TCAGATTTCT 60

TAGATTGTGG TTTTTTAGTT GGTGCCATGC TTTAACCTTT TCATTGATTT CAATAACAGG 120

TGTTACTACT TACCTGTTCC ACGGTTTAGA AGGCTTTTAG GTTCTTCTTG GCAGTGGTAn 180

GGTTTACCAG TTCAGCGGTA CCGCGGTGTT GGnCGTGTTG GATTTC 226

(2) INFORMATION FOR SEQ ID NO: 4667:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4667:

GTTCTGAATA GGGCGTTTAG TATTTGGTCG TAGCCGAnAA CCGGTGATCT ACCCTTGGTC 60

AGGTTGAAGT TCAGGTAACA CTGGAATGGG AGGACCGAAC CGACTTACGT TGAAAAGTGA 120

GCGGATGAAC TGAGGGTAGC GGAGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTC 180

CGAAATA 187

(2) INFORMATION FOR SEQ ID NO: 4668:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4668:

CTAAGTGGAG TTGTCACAAC ATCTTTAAAC GTTCCAGGTA AATAGTCTTT TGCCATTTCT 60

GAAAATGCTT TTGCCAACGT TTTATAAATA TCCCAGTCTG AACGCGATTC CCATAACGGA 120

TCAATGGCAG GATTGAAAGG ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGn 180

TT 182

(2) INFORMATION FOR SEQ ID NO: 4669:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4669:

AGTTACGTTA AAAGATGAAA ACGACAAAGT TTTAAAAACA GTTACAACAG ATGAnAATGG 60

TAAATATCAA TTCACTGATT TAAACAATGG AACTTATAAA GTTGAATTCG AGACACCATC 120

AGGTTATACA CCAACTTCAG TAACTTCTGG GAAATGATAC TGCAAAAAGA TTCTAATGGT 180

TT 182

(2) INFORMATION FOR SEQ ID NO: 4670:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4670:

GGGGCAAAGT CATTnCATAG ATTAATGGTT CTCCGATACC TAGGAAACCA ACTGGCAATG 60

CACCTTTTAA AGTATTACGT AATGTTGTGT TGCGTTTACA TCTTACCCAA AGTGCTAATG 120

CGGCACCTAC TTGTCCAGCA CCAGCCATCG CTGCAATTGG CAATAAGTAA GTAGCACCTG 180

ATTGG 185

(2) INFORMATION FOR SEQ ID NO: 4671:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4671:

CTGACGAACG AGAAAAGAGC GCAACGATTT AGTAGAGTAA ATGAGTTAAG CGAGACCGAA 60

GAAGAGGAAA GAAGCAAGCG ATTGTCACAA GTCAAGAAAG GTTCTTAGCG TTCGATGGTA 120

GCCAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAA AAAAATGGAT GCGATGACCG 180

CATTGAGACC GCAAGGnTnT 200

(2) INFORMATION FOR SEQ ID NO: 4672:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4672:

CCCGGGGTAC AGTTATTCCC CAGAGTCAAC GCGGGGGTTG GACTCGATGT CGGTCATCGC 60

ATCCTGGGCT GTAGTCGGTC CCAAGGGTTG GGCTGTTCGC CATTAAAGCG nACGnTGCTG 120

GGTTCAGACG CGTGAGCAGT CGGTCCCTAT CCGTCGTGGG CGTAGGAAAT TTGAGAGGGC 180

TGTCCTTAGT ACGAGAGGCC GGGATGGCAT ACCTTGGTGT ACCATTGTCG TGCCACGCAT 240

AGTGGGTAGT ATGTGTGGAC G 261

(2) INFORMATION FOR SEQ ID NO: 4673:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4673:

ATAGGGCGTT TAGTATTTGG TCGTAnCCAG AAACCAGGTG ATCTACCCTT GGTCAGGTTG 60

AAGTTCAGGT AACACTGGAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA 120

ACTGAGGGTA GCGGAGAAAT TCCAATCAAA CCTGGAGATA GCTGGTTCTC TCCGAAATAG 180

CGTT 184

(2) INFORMATION FOR SEQ ID NO: 4674:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4674:

CCCAGTCAAA CTGCCCGCCT GACACTGTCT CCCACCACGA TAAGGTCGTG GGTTGAGAAA 60

GCCAACACAG CTAGGGTAGT ATCCCACCAG CGTnCTCCAC GTAAGCTAGC GCTCACGTTT 120

CAAAGGCTCC TACCTATCCT GTGACAAGnT GTGCCGAATT TCAATATCAG GCTACAGTGA 180

AAGCTCCACG GGGTTCTTTC CGT 203

(2) INFORMATION FOR SEQ ID NO: 4675:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4675:

nnGTTTGTAA ATAATATGGT GGAGACTAGC GGGATCGAAC CGCTGACCTC CTGCGTGCAA 60

AGCAGGCGCT CTCCCAGCTG AGCTAAGCCC CCATAATAAT TACAGTATAT CGGGAAGACA 120

GGATTCGAAC CTGCGACCCC TTGGGTCCCA AACCAAGTGC TCTACCCAGC TGGAGCTTAC 180

TTTCCCGGTA TTATTTAACG CGGCCCGATA GGGAGTCGGA ACCCATTAA 229

(2) INFORMATION FOR SEQ ID NO: 4676:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4676:

TCTAAAAATC GCGCACTTAA ACCGCTTATG ACAATCATTA TTACCTCAAT ATGCTTGTCA 60

TCACTTGCCT TTATCGTCGT TCATTGGCTA TATAGTTAAT ATGAAAAGAC GCTCAAACAC 120

TTACAAATTT AGTGTGCnGA GCGTCTTATT TTTATACTTT AAAAGTCGTA TTGGTTGT 178

(2) INFORMATION FOR SEQ ID NO: 4677:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4677:

GCAAGTAAGC ATAATGTGGA GCCGTAGCGA AACAGTCTGA ATAGGGCGTT TAGTATTTGG 60

TCGTAGACCG GAAACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG TAACACTGAA 120

TGGAAGGACC GAACCGACTT ACGTTGAAAA ATGAGCGGAT GAACTGAAGG TAACCGGAGA 180

AAATCCCAAT CGAACCCTGG GAGATAAGCT TGGGnTCTCC TCCCGAAAAT AAGCCTTTTA 240

GGGGCTTAAG CCTCCAAAGT GGATGATTTA ATTTGGAAGG TAAAAn 286

(2) INFORMATION FOR SEQ ID NO: 4678:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4678:

CACACGGCTT ATGGTAACAA AAAATTCCTT TGGAGCATTA TGGAGCGGAA GATAGGTTTA 60

CACCTATACC TCGTTCCGGA AGGAnTGTTC TAAAAGTGAA CTACTCCCGC AATATTAAAT 120

ATGGAGCGGA GATAGGATTT ACACCTATAC CTCATTCCAG AGGATGTATT CTAAGAGTGA 180

AATACTCCCC ATATATTAAA TATGGAGCGG AGATAGGATT GACCATACn 229

(2) INFORMATION FOR SEQ ID NO: 4679:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4679:

ATGACTGCTT TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT 60

CGCCAAGCCA TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG 120

ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG TTC 173

(2) INFORMATION FOR SEQ ID NO: 4680:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

AAAAGTAACA AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACGCCAA CAAAAATCCA 60

TTAACTGGAG AAATTATTAG TAAAGGTGAA TCGAAAGAAG AAATCACAAA AGATCCCATT 120

AATGnATTAA CAGAATACGG ACCAGAAACG ATAACACCAG GTCATCGAGA CGAGTTTGAT 180

CCC 183

(2) INFORMATION FOR SEQ ID NO: 4681:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4681:

CGGTGCTTTC ACTTTCCTAC AGACTGGTTA CTATCGGTCA GAGAGAGATT TAGCnTTAGG 60

AGATGGTCCT CCCAGATTCC GACGAATTTC ACGTGTTCCG TCGTACTCAG GATCCACTCA 120

AGAGAGACAA CATTTTCGAC TACAGGATTA nTACCTTCTT TGATTCATCT TTCCAGATGA 180

TTCGTCTAAT GTCGTCCTTT GTA 203

(2) INFORMATION FOR SEQ ID NO: 4682:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4682:

GGGTCACACC TGTTCCCATG CCGAACACAG AAGTTAAGCT CCTTAGCGTG CGATGGTAGT 60

CGAACTTACG TTCCGCTAGA GTAGAACGTT GCCAGGCAAA AAGTGGGATG CGATGGAGCC 120

GCATTGGAGA CCGCAAGCCT CTGTTCTTTG ATGTCTAAAA CGTnCAAAAT AAAAGCGAAC 180

ACAAAGA 187

(2) INFORMATION FOR SEQ ID NO: 4683:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4683:

GGCTACACTG GTCATGATGC TGCTAAACTA CGTGATTATn ATGAAACACA TCATGCTTTG 60

TCTGGATATG AAATGATTGA CGCAGCAAAG GTGCCATTGC AACAAATGAA GTCAATGCTG 120

CGATGGGTAT ATTTGTGCAA CGCCAACAAC TGGTTCCTCC GGTACCATCC CGGTGCAGTT 180

TTAAATT 187

(2) INFORMATION FOR SEQ ID NO: 4684:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4684:

AGTGCCAAGG CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA 60

AACCGTTATT AATCTTGTGA GTGTTCTTTC GAACACTAGC GATTATnTCT TATGAATTCA 120

AGCTTATTTA AAACTCTTTA TTCACTCGGT TTTGTAAAAT CTATATTT 168

(2) INFORMATION FOR SEQ ID NO: 4685:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4685:

ACGGGAAGTA GCTCAGCTTG GTAGAGCACT TGGTTTGGGA CCAAGGGGTC GCAGGTTCGA 60

ATCCTGTCTT CCCGATTACT TCTTAAATTC CATTTTATGG GGGCTTAGCT CAGCTGGGAG 120

AGCGCCTGCT TTnCACGCAG GAGGTCAGCG GTTCGATCCC GCTAGTCT 168

(2) INFORMATION FOR SEQ ID NO: 4686:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4686:

ATGATTCAAG CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT 60

TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTTA GTCAAGCGCT CGCATACTGC 120

nTTATTTTCA AAAAATCAAA TGCTCATTTA CAAAAGTAAA CTCCGCTTTT AATT 174

(2) INFORMATION FOR SEQ ID NO: 4687:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4687:

TGTTGTTGAA TATGAAGAAG ATACAAACCC AGGTGGTGGT CAGGTTACTA CTGAGTCTAA 60

CTTAGTTGAA TTTGACGAAG AGTCTACAAA AnGTATTGTA ACTGGCGCAG TGAGCGATCA 120

TACCACAGTT GAAGGTACGA AAGAATATAC AACTGAAGTA ATCTGA 166

(2) INFORMATION FOR SEQ ID NO: 4688:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4688:

AGAACCTTAC CAAATCTTGA CATCCTTTGA CAACTCTAGA GATAGAGCCT TCCCCTTCGG 60

GCAACGAGCG CAACCCTTAA GCTATTGCCA TCATTAAGTT GGGCATCTAA TTGACTGCCG 180

GTGACAAAC 189

(2) INFORMATION FOR SEQ ID NO: 4689:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4689:

TAACCACTCC TCTTAACCTT CCAGCACCGG GCAGGCGTCA CCCCTATACA TCACCTTACG 60

GTTTAGCAGA GACCTGTGTT TTTTGATAAC AGTCGCTTnG GGCTATTCAC TGCGGCTCTT 120

CTGGGCGTTA ACCCTAAGAn ACCCTTCTCC CGAAGTACGG GGGCATTTTG CGAGTCCTAA 180

CGAGGTCGTC GTCACTTAGA TTCTCATCTT GATACTGTGT GGTTGCG 227

(2) INFORMATION FOR SEQ ID NO: 4690:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4690:

AGATAATGCA CCATCAACTA ATGGATATTT ATGTCCAGTT GGGGGCCAGA AATCATAAAC 60

GTCTTCAGTG TAAGCAACAG CATCTTCATT TnGCAGCCAA AATGCTTGGA TTATGTGCAA 120

TAACCATCGC AACTGCGCCA CACCTTGTGT TGGCTCGCCG CCTGAAGTGG GGTG 174

(2) INFORMATION FOR SEQ ID NO: 4691:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4691:

TTTTTTTTTA AAAAAAGGGA AGGGAAAAnA AAAAGGGAAA AAAATTTAAC CCAAGGGTTT 60

TTAAAGGGGG CCCAATTTTT CCCAAAAAAA AAACCCTTTG GGTTAAATTT TTTTTAAAAA 120

GTTAAATTTT TTTAAAAAGG GTTCCCTTTT AAATTTTGGG AAAAACCCCC TTTTTTTTTT 240

TTAAGGGAAT TTAAAAAATT TAAGGCCCTC CCCTAAATTA AAATTAAAGG TGGGAAAAAA 300

AAAATTAATT AAAnAACCCA TTTTTTTTTT TTAATTTTTT AACCCAAAGG GGGTAATTTG 360

GCC 363

(2) INFORMATION FOR SEQ ID NO: 4692:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4692:

TAGTGTCAAT TTTATTGATA TTTGCAATTA AACTGAAATT TAATTTTTCG GATGTATTTT 60

nTTTACTTAA AGTAAAATAG AACACGATTT TGATGTCTGG GAATAGTGGA AATGATAAAA 120

ACTACTAATG ATTGATTAAG TAGTGGTTCT TAACATTAGC CTCAGCTAAT TGTTACTTAA 180

AAATAGGAAT ACATGAGTAA AACTCAnTGG 210

(2) INFORMATION FOR SEQ ID NO: 4693:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4693:

ATAGTAGTAA AGTATTTTCT TCCAAACATT TATTTTGATT AAGTCTTCAT CATTAGTATT 60

CTCAGCTCCA CATGCACCAT CTTCCACCTC AACCTATTAA CCTCATCATC TTTAGGATCT 120

TATAACCAAT TGGAAATCTC ATCTTGAGGn nGCTTCATCT TAGATGCTTT CACACTTATC 180

CCTCCACACA TAGCTACCCA GCTATCCGT 209

(2) INFORMATION FOR SEQ ID NO: 4694:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GCACATTAAC CnAAGCACCA GGCCATATAG CAATTGTTGA TACAGTATTT AAATATTTAG 60

CATGTGACGG AATAGTTACA TATGTATTCA CTAAGGCCAT AATGACAAAT CCATTAAAAA 120

GTTGGATGCT TATTCGACCC TGCTAGATGA TCTGATGAAC GGAACGCATA TTAAATAAGT 180

ACGTGGTTAT GGATCAGTAA GATACTCTAC CAGTTACCAG nG 222

(2) INFORMATION FOR SEQ ID NO: 4695:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4695:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60

TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120

TCTTCAACTA AGTCACGATA TAATGTTTTT GAATTTTCG 159

(2) INFORMATION FOR SEQ ID NO: 4696:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4696:

AATATGGTAG TTTTTAACTT ATCTATTAAG GTACAATTGA CCAAATCGAT AAAACAAATA 60

ATACGTATCG TCAGACAATT TATGTCAATC CAAGTGGAGA TAACGTTATT GCGCCGGTTT 120

TAACAGGTAA TTTAAAACCA AATACGGATA GTAnTGCATT A 161

(2) INFORMATION FOR SEQ ID NO: 4697:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4697:

CCAAACTCAA TATGGCTTTA TTGGCACAGG GAACAGATAT GGAAGGTTTT ATTTATGGnT 60

ATATGGGATC AACACACAAA GCCGGACGCA GTGAATATTA CGCAAAATGA 170

(2) INFORMATION FOR SEQ ID NO: 4698:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4698:

CCACGGCTAA CTACTGCCAG CAGCCGCGTA ATACGTAGTG GCAAGCGTTA TCCGGAATTA 60

TTGGGCGTAA ACGCGCGTAG GnGTTTTTTA AGTCTGATGT GAAACCCACG GTCAACCGGA 120

GGGTCATTGG AAACTGGAAA CTTGAGTCAG AAGAGGAAGT G 161

(2) INFORMATION FOR SEQ ID NO: 4699:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4699:

TAAATCTTCA TCAATATGAT CTAACCAATA TTGATAAAAC CTTGATGTGT TTCGTGTCAA 60

TGACATACCA TATCGACTAG GTACCTTTTT AGAATGTTGA TTAATCACAA CAAATATCAT 120

GGGCAAGGTC ATCTTGCAAA ATGGATTCGA TTCAAGTGGG AGGGnCGATG ATGGACGTGC 180

TGCATGCACT GATGACCCTT TTTGCCCATT CTGGCAAATC CCACCATGAA ATGACTGACG 240

CGGACGCn 248

(2) INFORMATION FOR SEQ ID NO: 4700:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4700:

CCCGACGAAG CGAACGTTTG GCACTGTCTC AACGAGAGAC TCGGTGAAAT CATAGTACCT 60

GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 120

(2) INFORMATION FOR SEQ ID NO: 4701:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4701:

TACAGGGTAG TGAGATTTCG AAACAATATG GAGAAGCAGG ACTTCCTGGA AAATACAATT 60

AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTCTTGCA GGCATATGCA CCGAAAGCTT 120

AATGATTCAT CATACTGGAG ATGCGAATGA CTATGTTGGG TAAAGGATTT ATCTGGT 177

(2) INFORMATION FOR SEQ ID NO: 4702:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4702:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 60

GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA 120

GAAAAGnCTC TAGATAGAAA ATAGGTGCCC GTACCG 156

(2) INFORMATION FOR SEQ ID NO: 4703:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4703:

CTTGAAAAAG ATGGTTATTC TGTTGAAGTA ATTGACTTAC GTACTGTTCA ACCAATCGAT 60

GTTGACACAA TTGTAGCTTC AGTTGAAAAA ACTGGTCGTG CAGTnGTCAG CAAGACGCAC 120

AACGTCAAGC TGGTGTTGGT GCAGCAGTTG TAGCTGAATT AAGTGA 166

(2) INFORMATION FOR SEQ ID NO: 4704:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4704:

GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGnCT CGAACCTACG 60

ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGATTAA TATTATGCCT 120

GGCAACGTTC TACTCTAGCG GAACGTAAGT TCG 153

(2) INFORMATION FOR SEQ ID NO: 4705:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4705:

AGGTAGAGCA CTGTTTGGAC GAGGGGCCCC TCTCGGGTTA CCGAATTCAA ACAAACTCCG 60

AATGCCAATT AATTTAACTT GGGAAGTCAG ACACATGGGT GATAAGGTCC GTATTCGAAA 120

nGGAAACAGC CCAGACCACC AGCTAAGGTC CCAAAATATA TGT 163

(2) INFORMATION FOR SEQ ID NO: 4706:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4706:

TAAGGTTGGG ATTGTTTGTG GGCTCGTTGC CACCCATTGT ACGGCACTCA TCAnTTCAAG 60

CCACCAGCTA CAGTATATCT CCTTGACCAG CCATAATTTG ATTGGCTGCA GTCGCGATGG 120

TTTGTAATCC TGATGAGCAG TAGCGATTCA TGTTTGACCn GTACCCGTCA GATATCCGCA 180

GCAATGCAAT GTTGTGCAAG TTT 203

(2) INFORMATION FOR SEQ ID NO: 4707:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4707:

CGGGTGAGAA TCCGTCCACC GATTGACTAA GGTTTCCAGA GGAGGCTCGT CCGCTCTGGG 60

TTAGTCGGGT CCTAAGCTGA GGCGCAGnGT AGGCGATGGA ATAACAGGTT GATATTCCTG 120

TACCACCTAT AATCGTTTTA ATCGATGGGG GGC 153

(2) INFORMATION FOR SEQ ID NO: 4708:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4708:

nCTATAATGA ATAAATAATT TAGAAATATG CTTCCGATTG TTCGATGCTT TAATTCAGTT 60

AGAAGCATCA TAGAATGCAT GATTACTGTT GTAAAGATAC GTAATGTTTT GTATTGACTG 120

TATGTCTTTG GATAGAGTTA CAAACTTATT 150

(2) INFORMATION FOR SEQ ID NO: 4709:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4709:

AAAATTCGGG TTCTCAAATC ATCGGAACAT AACAAAACAA CCTAAGCAAC ATGTAGGCCG 60

TTGTCACTTA ACTTCTTGTT TTTCCGATGA CAGCTTCTAT TnAGAGAATG TCATGATTAT 120

TTTATATTCA CTTCAATGTT ATCAGTATTA GTGCCA 156

(2) INFORMATION FOR SEQ ID NO: 4710:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4710:

GTTGATATTC CTGTACCACC TATAATCGTT TAATCGATGG GGGGGACGCA TAGGATAGGC 60

TCGTTAAGGC TGAGCTGTGA TGGGGAGAA 149

(2) INFORMATION FOR SEQ ID NO: 4711:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4711:

TTGACTTCAA TACCATGGGC CAGGTACnCT TTAAATGTTG TTGTCTCAGT TAATATTAAT 60

TGGCTTTTCT TTTGCATAAT TGACAATGGC TTCTGCCAAT GGGTGTTCAG AATCTTTTTC 120

AGCAGTAGCA AGTAGTTGGT AGCGTTTGAT TGGTCACCAG 160

(2) INFORMATION FOR SEQ ID NO: 4712:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4712:

ATAGTGAACC AGTACCGTGA GGACnAGGTG AAAAGCACCC CGGAACGACG TGAAATAGAA 60

CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC GTGCCTTTTG 120

TAGAATGAAC CGGCGAGTTA CGATTTGATG C 151

(2) INFORMATION FOR SEQ ID NO: 4713:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4713:

ACCAGTTGAT CTACCCTTGG TCAGGTTGAA GTTCAGGTAA CACTGAATGG AGGACCGAAC 60

CGACTTACGT TGGAAAAGTG AGCGGGATGA ACTGnGGGTA GCGGAGAAAT TCCAATCGAA 120

CCTGGGAGAT AGCTGGTTCT CTCCG 145

(2) INFORMATION FOR SEQ ID NO: 4714:

(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4714:

TGTnACGCAG AGATCGCGGG TTCGATTCCC GTCGAGACCG CCATTTAATT TTATAATTAA 60

TAGCGATGTA CCTATAATAA TGGAGGAATA CCCAAGTCCG GCTGAAGGGA TCGGTCTTGA 120

AAACCGACAG GCCTTAACGG GCCGCGGGGG T 151

(2) INFORMATION FOR SEQ ID NO: 4715:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4715:

TCGTATTGAA TGGCTTCGTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT 60

GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACG TGTAATTTTA CTTTGnAATA 120

CTTTAAAAAA ATAAGACACT TTGCCAACTT G 151

(2) INFORMATION FOR SEQ ID NO: 4716:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4716:

GCTGTCATCG GAAAAACAAG AAGTTAAGTG ACAAGGGTTT ACATGTTGCT TAGCTTCTTT 60

TATTATGCGT AATGATGTAA AAAGACGAAT ATTCATTTGT TTGTAAAAGT GGCATTTCTA 120

TGTCTTAAAA GTGACGAAAC TTCACnCTGT GC 152

(2) INFORMATION FOR SEQ ID NO: 4717:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4717:

GGATACTAGT AAAACCATAT TTAGTAAATA CAGATGGAnT AAATCTTTTA AGGCTTATAA 60

ACGCTCATCT GACATTGTAG AATTCATGCT TTCAAAAGAC GATATACTAC GACACTCCTA 120

CGAACTTGTC CAAGGATTAC GAAA 144

(2) INFORMATION FOR SEQ ID NO: 4718:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4718:

ATCATAAGGG GCATGATGAT TTACGTCATC CCCACCTTCC TCCGGTTTGT CACCGCAGTC 60

AACTTAGAGT GCCCAACTnA ATGATGGCAA CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA 120

CTTAACCCAA CATCTCACGA CACGA 145

(2) INFORMATION FOR SEQ ID NO: 4719:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4719:

AAATACCTTT CCACGATCTT CAGCTGGGCG CCTCTGCACT CGCAAACGCA CTTGATGCAT 60

CAACAACACC ACCAAATAGT CCCTGCAATA ACCTCACAGT ACAAACTGTA ATGGTGTCGT 120

ACACnATGCC ATTTAAAAAT AGCATACCGG CAAAGC 156

(2) INFORMATION FOR SEQ ID NO: 4720:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4720:

TTAAATCGAG TCTCTTTTAC AGGTCCATAT TTTGTTACGT ATCGACCGGT GGCTAACTAC 60

TAACTCGGAT CAAATTCGTC TCGATGACCT GG 152

(2) INFORMATION FOR SEQ ID NO: 4721:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4721:

CACTAGTTCA AGTTCAAGTG GCGACGATTG GTATTTTACA AGAATTTTAT CAACAAGGAT 60

TTAATTAGCT TAAACGCnGC AATCCCTGTG TTACTAGGGC GGATAACATT GGTACCACGG 120

TTACAGCTAT CTTAGCTAGT TTAGCC 146

(2) INFORMATION FOR SEQ ID NO: 4722:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4722:

CCACACCAAT ATTTTGCGCT AAGTAnATCG CATTAAACGT TTGTCTTCCG CCATTTGAGC 60

CACACTGCTC CAGCTCATAG CGCTATATCG CAGGGAATAA TCATTCCGCC ACCACAACCC 120

TAACATTACC CAGCCATACA GCCATACCAG GGCCAC 156

(2) INFORMATION FOR SEQ ID NO: 4723:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4723:

ACGGTCTTGC TGTCACTTAT AGATGGATCC GCGCTGCATT AGCTAGTTGG TAAGGTAACn 60

GCTTACCAAG GCAACGATGG CATGAGCCGA CCTGGAGAGG GTGGATCGGG CCACACTGGG 120

AACTGAGACA CGGTCCAGAC TCCTACGGGG AGGCAGCAGT A 161

(2) INFORMATION FOR SEQ ID NO: 4724:

(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4724:

CAGAAAGCTC ACGGGGCTTT CGTCTGTCGC GGGTAACCTG CATCTTCACA GGTACTATGA 60

TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGnCTTTCGT GCGGGTCGGA 120

ACTTACCCGA CAAGTAATTT CGCTACCTTA GGACCGTTAT AGTTA 165

(2) INFORMATION FOR SEQ ID NO: 4725:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4725:

GGACGTTATA AGTGCTGAAA CATCTAAGCA TGAAGCCCCC CTCAAGATGA nATTTCCCAA 60

CTTCGGTTAT AAGATCCCTC AAAGATGATT AGGTTAATAG GTTCGAGGTG GAAGCATGGT 120

GACATGTGGA GCTGGACGAA TACTAATCG 149

(2) INFORMATION FOR SEQ ID NO: 4726:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4726:

TTGAATTTTT GAAAAAAAAA TGCCGAAATA AAAGATGCCA AGATATCCGC CGGGTAAAAA 60

ATTAAGTTTC CGAAAAACCA GGTGTTGGTA CCCATTGCAT CTGGGGTGGC AAAAGCATTT 120

GCAGATAAAA TTGTCATCAG TGGTTACGAT GGTGGTACAG GGCTTCACCC AAACGAGTAT 180

CAGCATGCCG GTGTTCCTGG GAGATGGTTA GCAGAACACA TCAACATAAA CTAATGCTAA 240

GAnCGGTAAA GTAGACAnCG GTAGTATACT GAAAT 275

(2) INFORMATION FOR SEQ ID NO: 4727:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4727:

ATCAATGAAC AACACATACA GATGGTACTG CGACGCCTAG AGTAACAAAA TAAGTTTTGT 60

AACTCTATCC AAAGACATAC AGTCAATACA AAACATTACG TATCTTTACA ACAGTAATCA 120

TGCATTCTAT GATGCTTCTA ACTGAATnA 149

(2) INFORMATION FOR SEQ ID NO: 4728:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4728:

GCACGTTATT CCATTATCTT AATGGTTATC TTATCCTCAA CTAAATTGGA GGAATCACTA 60

TGACAATTAA TAAAGAACCG TTCTTGGCGC AGCACAATGG GCGCTCACTG GCAGACTTTT 120

GTGATGCTGA CTTAAAGTAA ACTATTAGAT ATTGnGTG 158

(2) INFORMATION FOR SEQ ID NO: 4729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4729:

TCATTGACAT CGCTGGAATA GGTGTAAATC CTGCGATTCG ATCTGGACCA TATTTTTTTA 60

TTGTATACAG TAATTGTGCT GCGATTATCT CTGTAACGTC TTTCCAATTT GAnCGCACGT 120

GCCCTCCCAT ACCTCGGG 138

(2) INFORMATION FOR SEQ ID NO: 4730:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TAAAGACTAT ACCATTCTAT CCAATAATAA TTGGATTCGG ATTTGTCTGA ATTCGTAACC 60

GAGAGGCCCC TCGTCCAAAC AGTGCTCTAn CTCCAATAAT CATCACTTGA GGCTAGCCCT 120

AAAGTATTTC GGAGAGAACC AGCTATTTCC AGTTCGATTG GAATTTCTCC GCTACCCTCA 180

GTTCATC 187

(2) INFORMATION FOR SEQ ID NO: 4731:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4731:

CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT TCGCCATTAA AGCGGTACGA 60

AGCTGGGTTC AGAACGTCGT GAGACAGTTC GGTTCCCTAT CCGTCGTGGG CGTAGGAAAT 120

TTnAGAGGAG CTGTCCT 137

(2) INFORMATION FOR SEQ ID NO: 4732:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4732:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60

TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120

TCTTCAACTA AGTCACG 137

(2) INFORMATION FOR SEQ ID NO: 4733:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4733:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60

TCTTCAACTA AGTCACG 137

(2) INFORMATION FOR SEQ ID NO: 4734:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4734:

AAAACATAAA TACAAAAATA TAGCTATTAC TATAAAAAAC AGCAGTAAGC ATATTTCCAA 60

ATTGCAAATT ATCCTACTGC TGTTCTTTTT GGGCAGTGGG nACAGCAAAT GATATTTTCG 120

ACAAAATTTA TTTCGTCGTC CCACCCCAAC TTG 153

(2) INFORMATION FOR SEQ ID NO: 4735:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4735:

TAGAAATTAC GGACCCAATT TCTCTATGTT GGGGCCCATC CCCAACTTGC ACATnATTGC 60

AAGCTGACTT TTCGTCACTT GCTTTGTTGG GGCCCCGCCA ATAAGCGTTG TAGTGCCTAG 120

TACTTTGATT GATGTCCAAG TT 142

(2) INFORMATION FOR SEQ ID NO: 4736:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4736:

ATGTTATTCA AAGTAAATTG CTTTGCCTGA TTTTGCAGAC TGATAAATCG CTTCAAGAAT 60

TTTTGTAACT ACCATTGCTT GTTCCGGTTT CACAACTGGT TCAGTATCAT TTACAACnGC 120

ATCAATCCAA GCTTTTG 137

(2) INFORMATION FOR SEQ ID NO: 4737:

(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4737:

GGTCGTTTAG TATTTGGTCG TACACCGCAA ACCAGGTGCA TCTACCCTTG GTCAGGTTGA 60

AGTTCAGGTA ACACTGAAAT GGAGGACCGA ACCGACTTAC GTTGAAAAAnT GAGCGGATGA 120

ACTGAGGGTA GCGGAGAAAT TCCA 144

(2) INFORMATION FOR SEQ ID NO: 4738:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4738:

GGGTAGCTAT GTGTGGACGG GATAAGTGCT GAAACATCTA AGCATGAACC CCCCTCAAGA 60

TGAGATTTCC CACTTCGGTT ATAAGATCCT CAAAGATGAT GAGGTTAATA GGTCGAGGTG 120

GAACATGGTG ACATGTnATC TGCTTTTCTA ATCATAC 157

(2) INFORMATION FOR SEQ ID NO: 4739:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4739:

GCTTTATGTC TAAAACGTCA AAATAAAAAG CAAACACAAA GAAAAATGGC TTGGCGAAGT 60

GAAAACGGTT GAATCTGACG AAACGAGAAA AGAACGCAAC GAGTTTAGTA GAGCTAnATG 120

AGTAAGTGAG AGCCGAAGAG AGGGA 145

(2) INFORMATION FOR SEQ ID NO: 4740:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4740:

TAGTAGCACC ACCCTTAGAC CTTCTTGATT TGACATCGTT GTTCTTCCTT CCTTCGGTCT 60

CGTTACTCAT TTAGCTCTAC TAAACTCGTT GCGTCTTTTC TCGTTTCGTC AGATCAAACG 120

TTTCACTTCG CCAAGCCATT TTTCTTGTGT TTATTTTATT TGACGTTTAG ACATAAAAAA 180

GAGACCCACG TTCAACTTGC CnGCACGTTC TACTCTGCGG AnTAGTGGCT ACCA 234

(2) INFORMATION FOR SEQ ID NO: 4741:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4741:

GCAAGTCTTT TTAAAGGTAA CACTATCATT TATGCAATAC GGCGCATTAC CAGAGTTGCA 60

TGGTCAAAAT ATATTGTTGT CATTTGAAGA TGGACGTGTA CAAAAATGCG TGTTACGTGA 120

TCATGATACT GTCAn 135

(2) INFORMATION FOR SEQ ID NO: 4742:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4742:

ACCCTGGTAC AGTTGAATTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA 60

AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGA GAnAGCTGGT 120

TCTCTCCGAA ATAGCTTTAG GGCTA 145

(2) INFORMATION FOR SEQ ID NO: 4743:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4743:

TGATTATCAT GGGTGCGGGT ATTAACCATT GGTTTAACTC AGATACGATT TATnGTGCAA 120

TCTTAAACTT AGTTATGGTA TGTGGCGTCA A 151

(2) INFORMATION FOR SEQ ID NO: 4744:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4744:

TAAAGCTAAA AACACAGCTC ATAATATCAA AAAAGGTGCA GAAGAAATGG TTGAAGCGGC 60

AGGCGATAAA ATCAnAGATG GTGCATCTTG GTTAGGCGAT AAAATCGGCG ATGTGTGGGA 120

TTATGTACAA CA 132

(2) INFORMATION FOR SEQ ID NO: 4745:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4745:

CGTGCGCTCT AACCAGCTGA GCTATAGGCC CATTAATTTG AATGAACAAA CATTCAAAAC 60

TGAATACAAT ATGTCACGTT ATTCCGCATC TTCTGAAGAA GATGTTCCGn ATATATCCTT 120

AGAAAGGAGG TG 132

(2) INFORMATION FOR SEQ ID NO: 4746:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4746:

GTGATCCGAC TCAGATAGCG ATCCGACTCA GATAGCGACT CAGATTCAGA CAGCGATTCA 60

GATTCAGACA GCGATTCAGA TTCAGATAGC GATTCAGATT CCGACAGTGA CTCAGATTCC 120

GACAnTGACT CGGATTCA 138

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4747:

CATTATTGTA AACTGAACTT TTCGTCACTT GCTGGTGnTT GGGGACCCCA CCAACTTGGC 60

ACATTATTGG TAAGCTGACT TTTCGTCACT TACTGTGTTG GGGCCCCGCC AACTTGCATT 120

GTCTGTAGAA ATTGGGAATC CAATTTCTCT ATGTTGGGGC CCACACCCCA ACTCGACATT 180

GCCTG 185

(2) INFORMATION FOR SEQ ID NO: 4748:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4748:

ACCGAATCCC TTCAGACCGG TACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGACAGT 60

ACTCGAACCT GACGTACCGA AACGGTTATG AAGACCGTTA nCTCTAACCA ACTGAGCTAA 120

AGGATCCTAA ATATAATTTT ACAACTAATA AATAGTGGAC GGTGGAGGGA TCG 173

(2) INFORMATION FOR SEQ ID NO: 4749:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4749:

ACACAAGGAT AAGGCATTGT TGGATGTGGG ATGCTTTAAC TGGGCAAGCG ATTGGTCGTC 60

CTAAAACAGG TACATATGCC GGCTATCTGA CCTAGTCGGT TTAGATATTG CAGTGTCTGT 120

AATTAAAGGG CATGCAACCA AGTAnCTGAG GAAACAACTT ATTTTCATGG TGTCAAAAAT 180

TGnTAAATAC GGTGTTTGAC AATTGCGCAC CT 212

(2) INFORMATION FOR SEQ ID NO: 4750:

(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4750:

AATCTCAGGT TTTACCAAGC AAAACCGATG AATAAAGAGT TTTAAATAAG CTTGAATTCA 60

TAAGAAATAA TCGCTAGTGT TCGAAAGACn GCAGCAAGAT TAATAACGCG TTTAAATCTT 120

TTTATAAAAG AAAACGTTTA 140

(2) INFORMATION FOR SEQ ID NO: 4751:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4751:

ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT CATCATCTTT 60

GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGTTCAT GCTAGATGCT 120

TCAGACTATC CCGTCCACAC ATGTAACCAG nATGCGTGGA CGCATGGAAC AGGGATGTCA 180

TCCG 184

(2) INFORMATION FOR SEQ ID NO: 4752:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4752:

GGGATCTTCC GCAATGGGCG AAACTGTACG GAGCAACGCC GCGTGAGTGA TGAAGGTCTT 60

CGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG CACATCTTnA 120

CGGTACCTAA TCA 133

(2) INFORMATION FOR SEQ ID NO: 4753:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4753:

GTATGCTGTG TGGCTTGTCA TGTTCGGGTT TGGTGGCGGA CCTGATTATT CCTGCGnTAT 60

ACGCTATGGC TGGAGCAGTG TGGCCAAATG GCGGAAGACA AACGTTTAAT GCGATCTACT 120

TGGCGCAAAA TATTGGTGTG GCTGTCGGTG CTGCAATGGG CG 162

(2) INFORMATION FOR SEQ ID NO: 4754:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4754:

AATTCGATTC CCTTAGTAGC GGCGACGAAA ACGGGAAnGA GCCCAAACCA ACAAGCTTGC 60

TTTGGGGGTT TGTAGGACAC TCTATACGGG GTTAACAAAG GACGACATTA GACGAATCAT 120

CTTGGGAAAG ATGA 134

(2) INFORMATION FOR SEQ ID NO: 4755:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4755:

AGAGTGCGTA ATAGCTCACT AGTCGAGTGA CACTGCGCCG AAAATGTACC GGGGCTAAAC 60

ATATTACCGC AAGCTGTGGA TTGTCCTTTG GACATGGCTA GGAGAGCGTT CTAAGGGCGT 120

TGAAGCATGn ATCGTAAGG 139

(2) INFORMATION FOR SEQ ID NO: 4756:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4756:

CGTGAAATGC GCAGAGATAT GGAGGAACAC CAGTGGCCGA AAGCCACTTT CTGGTCTGTA 120

ACTGGACGCT GGATGTGCCA AACCTGGGGG ATCAAACAGG TTA 163

(2) INFORMATION FOR SEQ ID NO: 4757:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4757:

CATGAAACTA GATAAGTAGT AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG 60

TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ATCACAnGAT 120

TAATACCGCG TTTAATCTTT TATAAAGGAC CGTAACTTCA 160

(2) INFORMATION FOR SEQ ID NO: 4758:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4758:

TACATGGGTT TATTGTTGAA GATGACGAAA TTGTAGAAAT TTAATATTCT AAAAAGGTTG 60

GGGACATAAA TCCCCCTAAA AAAACCAGCA GTAAGATAAT TTTCAATTAG AAAATATCTT 120

ACTGCTGTTC TCTATTTATA CCAnATTACT TTCGTAATTG TTAAAATTTT AAAAGGA 177

(2) INFORMATION FOR SEQ ID NO: 4759:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4759:

CGGTGTGTAC AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG 60

ATTCCAGCTT CATGTAGTCG AGTTACAGAC TACAATCCGA ACTGAGAACA ACnTTATGGG 120

ATTTGCT 127

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4760:

GGGCCCCTCG TCGGGTTACC GAATTCAGAC AAACTCCGnA ATGCCAATTA ATTTAACTTG 60

GGAGTCAGAA CATGGGTGAT AAGTCCGTGT TCGAAAGGAA ACAGCCCAGA CCACCAGCTA 120

AGTCCCAAAT ATATGTTAAT GAAAG 145

(2) INFORMATION FOR SEQ ID NO: 4761:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4761:

TAAACAAGGC GCGTTGGGCC TATTCACTGC GGCTCTTCTG GGCGTTAACC CTAAAGAGCA 60

CCCCTTCTCC CGAAGTTACG GGGTCATTTT GCCGAGTTCC TTAACGAGAT TGCTCGCTCA 120

CCTTAGAATT CCATCTGACT ACGGTCGTTG CGTACGGCAC TATTTCTTCA AGCTTCCGCA 180

TTAACACACC AAAACAGCTC CCACCACCAC TAnATCGAnC AACACTAG 228

(2) INFORMATION FOR SEQ ID NO: 4762:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4762:

TnGCCAAATC TTAGTAGTCG CTTGGTTCGG TTGTGGTGCG ACAGCTGTGA AATCATCACT 60

ACGTTGCTCA TCACTCACTG TCTCTCCGCT TCCTTGCGTT GCAACAGCTT GAATTGTATC 120

AGCAGGGTTG 130

(2) INFORMATION FOR SEQ ID NO: 4763:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4763:

CAACTCGTAG TCAGGGTCGA AAGACGGGAC TTAGTGATCC GGTGGTTCCG TCATGGGTAG 60

GGCCATCGTC TCAACGGTAT AAAAGCTACC CCGGGGATAA CAGGCTTATC TnCCCCAAGA 120

GTTCACATCG ACGGGGAGGT TTGGCACCTC G 151

(2) INFORMATION FOR SEQ ID NO: 4764:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4764:

ACCCCAACTT GCATTGnCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCCGC 60

CGGCAAGGTT GACTAGAATT GACCAAAAGC TTGTTACAAG CGCATTTTCG TTCAGTCAAC 120

TACTGCCA 128

(2) INFORMATION FOR SEQ ID NO: 4765:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4765:

AATACAGCCC CAGAGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT CGATGTGAAC 60

TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG CGGATGGCCC 120

TTTCCATGTG GnAAC 135

(2) INFORMATION FOR SEQ ID NO: 4766:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GATTCTCACC CGTCTTTCGC TACTCACACC GGCATTCTCA CTTCTAAGCG CTCCACATGT 60

CCTTACGATC ATGCTTCAAC GCCCTTAGAA CnCTCTCCTA CCATTGTCCA AAGGACAATC 120

CACAGC 126

(2) INFORMATION FOR SEQ ID NO: 4767:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4767:

TTAATAGTTT TATAAGAGAG GTGTTTGATC TTGAGCTAAC CACnTCATTC GAGTACTGTC 60

ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT GGGGTATATG CATATAAGAT 120

GATTTTTAAC 130

(2) INFORMATION FOR SEQ ID NO: 4768:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4768:

GTTAACCCTA AAGAGCACCC CTTATACCGA AGTTACGGGG TCATTTTGCC GAGTTCCTTA 60

AnGCGCGTTC GATCGCTCAC CTTAGGAATT CTCATCTTGA CTACCTGTGT CGGTTTGCGG 120

TAGGGCACCT ATTTTCCTAT CT 142

(2) INFORMATION FOR SEQ ID NO: 4769:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4769:

CCTTGGGACC GACTACAGCC CCAGGATGCG ATGAGCCGAC ATCGAGGTGC CAAACCTCCC 60

CGTCGATGTG AACTCTTGnG TGGAGATAAG CCTGTTATCC CCGGGGTGAG CTTTGTATCC 120

(2) INFORMATION FOR SEQ ID NO: 4770:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4770:

CTAAAAGTTG TATTTTAAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA 60

ACCGTTAAAC AATGCATAGT TTGCTTAACT TCCAATATTG ACTCATCATT ACAATTGACA 120

TAGAGCTATT AAGCGTnGCC ATGAG 145

(2) INFORMATION FOR SEQ ID NO: 4771:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4771:

TCGAGTGACA CTGTCGCCGA AAATGTACCG GGGCTAAACA TATTACCGAA GCTGTGGATT 60

GTGCCTTTGG AAATGGTGAG GnGAGCGTTC TAAGGGCGTT GGAAGCATGA TCGTAAGGAC 120

ATGTGGGA 128

(2) INFORMATION FOR SEQ ID NO: 4772:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4772:

GGGCAGATGT TCCTGCAGTC ATAGTGCCGT CAACTTTAAA TACTGTACGT AATTTGGCTA 60

ATGCCTCCAT CGTGGnTGTC AGGGCGTATA AATTCATCTT GGGTCAAAGA TATTTGGTGT 120

GTACTT 126

(2) INFORMATION FOR SEQ ID NO: 4773:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4773:

GTCTTTTCTC GTTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT 60

GTTTACTTTT TATTTTGACG TTTTAGGATA AAAAAAAGAn ACCTTGCGGT CTCAATGCGG 120

CTCATC 126

(2) INFORMATION FOR SEQ ID NO: 4774:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:

ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC 60

TGCATCTTnA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 120

TACG 124

(2) INFORMATION FOR SEQ ID NO: 4775:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:

ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAAGTG AGCCGGAAAC 60

ACCAACACCA CCGACACCAG AAGTGCCGAG TGAnCCAGAA ACTCCAACAC CGCCAACACC 120

AGAG 124

(2) INFORMATION FOR SEQ ID NO: 4776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CCCGCTAGTC TCCACCATTT ATTTTTTACA CGATGAACAT TGAAAACTnA ATACAATATG 60

CAACGTTAAT TCCAAAAAAC GTAACTATAA GTTACAAACA TTATTTAGTA TTTATGAGCT 120

AATCAAACAT CATAA 135

(2) INFORMATION FOR SEQ ID NO: 4777:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4777:

AGTGCAGAAG AGGAAAGTGG AATAnCCCCA ACATAGCGGT GAAATGCGCA GAGATATGGA 60

GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG GACGCTGGAT GTGCGAAACG 120

TTGGGGGTTC AAACAGGATT TAGA 144

(2) INFORMATION FOR SEQ ID NO: 4778:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4778:

AATTTTTGAT GACGGGTCCC TTCCTAGGGT GCCGTCTCAG CCACCCCAAC CGGCACATTG 60

TTGTAAGCTG ACTATATGTC nTTCATGTGT TGGGGCCCCT GTCTTCGACT GGCACTGCTC 120

CCT 123

(2) INFORMATION FOR SEQ ID NO: 4779:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4779:

GCGCATTAAC TATCGCGATA TTAATCGCTA TTCTATATCG TCACTTTAGA GGATATCCTG 60

AACAATATAG CTCAGGTATT ACGTTTTCAT CTAAATATTT ATTAAGATTT GCAATCATCC 120

(2) INFORMATION FOR SEQ ID NO: 4780:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4780:

GGTAATATGT TTAGCCCCGG TACATTTTCG GCGCAnTGTC CTCGACTAGT GAGCTATTAC 60

GCACTCTTTA AATGATGGCT GCTTCTAAGC CAACATCCTA GTTGTCTGGG CAACGTCACA 120

TCCTTTT 127

(2) INFORMATION FOR SEQ ID NO: 4781:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4781:

ACACnGGGTG AGAATTTGTC GCTATTTGTA AATTGTATCC TGGCTTAAGT TGGCCAAAGT 60

GTCTTATTTT TTTAAAGTAT TTAAAAGTAA AATTACATGT TAATACGTAG TATTAAATGG 120

CGAGACTCC 129

(2) INFORMATION FOR SEQ ID NO: 4782:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4782:

CTCATTCCCG TTGCATTTTA TCTTCTGCAA CAACAACATT TCGTCTTTAT CGTCTTCCAT 60

AGTAGTAGGA TTTTCTACTA CTTGACCATT CATAATCTGT TGCATTTCAT GTTTGnTTTG 120

GTCAGATTTA GGACCA 136

(2) INFORMATION FOR SEQ ID NO: 4783:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4783:

CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 60

AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGATT ATTGnGACGG TATTGTTGG 119

(2) INFORMATION FOR SEQ ID NO: 4784:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4784:

ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC ATACGTGTTT TAACCTGCGT 60

nATCCCATTG CATCCCATAA TTGTGAATGG ACCAAGTTTC CAGTTGAACC CCCAGACAAG 120

CGCACGG 127

(2) INFORMATION FOR SEQ ID NO: 4785:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4785:

ACACCGGCAT GCTGAATACT CGTTTTGGGT GAAGCCCCTG nACCACCATC GTAACCACTG 60

ATGACAATTT TATCTGCAAA TGCTTTTGCC ACCCCAGATG CAATGGTACC AACACCTGT 119

(2) INFORMATION FOR SEQ ID NO: 4786:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4786:

CTTTCTAAAC CCGnCACCAC TTTATCGTGG TGGGGAGACA GTGTTCAGGC GGGCCAGTTT 60

AATCATTCAT AGAGTGT 137

(2) INFORMATION FOR SEQ ID NO: 4787:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4787:

GTTTTTAACA CTGTTACCGT TTTCATCTTT TAATGTTACC GTTACGCCAG AnATACCTTT 60

TTCATCTTGG TCTTGGATAC CATTTTTATT TGTATCTTCC CAGACATAGT CACCTAAGT 119

(2) INFORMATION FOR SEQ ID NO: 4788:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4788:

CATGCTTCCA CCTCGAACCT ATTAACCTnC ATCATCTTTG AGGGATCTTA TAACCGCAGT 60

TGGGAAATCT CATCTTGTAG GGGGGCTTCA TGCTTCAGAT GCTTTGCAGC ACTTAGCCCG 120

GCCACACATA GCTACCCAGC T 141

(2) INFORMATION FOR SEQ ID NO: 4789:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4789:

CTGGGTTCAG AACGTCTAAG CAGTTCGGTC CCTATCCGTC GTGGGCGTAA GAAATTTGAG 60

AGGAGCTGTC CTTAGTACGA GAAGACCGGG ATGGACTACC TCTnGTGTAC CAATTGTCGT 120

GCCAACGCAT AGCTGGGTA 139

(2) INFORMATION FOR SEQ ID NO: 4790:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4790:

CATTATTTAG TATTTATGAG CTAATCAAAC AnCATAATTT TTATGGAGAG TTTGATCCTG 60

GCTCAGGATG AGCGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGACGAGATG 120

CTTGCTTCG 129

(2) INFORMATION FOR SEQ ID NO: 4791:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4791:

GGGTGCTCTT TAGGGTTAAC GCCCAGAAGA GCCGCAGTGC AATAGGCCCA AGCGACTGTT 60

TATCAAAAnC ACAGGTCTCT GCTAAACCGT AAGGTGATGT ATAGGGGCTG ACGGCTTCCC 120

(2) INFORMATION FOR SEQ ID NO: 4792:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4792:

CAAATTCTTT CGCTACTTGA ATGACAACAC TTTGTTTTAC GCCTGAAATG GCTTCTTGCC 60

AAGCAGGTGT ATATTTTGAT TCTGCATCGT CGTATCCTTT TGATCTAATT ATGATCAAAC 120

CGn 123

(2) INFORMATION FOR SEQ ID NO: 4793:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4793:

AGTTTTGAAT GTTTGTTCAT TCAAATTAAT GGGCCTATAG CTCAGCTGGT TAGAGCGCAC 120

nCCTGATAAC 130

(2) INFORMATION FOR SEQ ID NO: 4794:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4794:

CACAGCCACA AGTGATTAAA GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT 60

TAACTCATTT TTCAATAGAT CAGGAAGACT ACCAAGCTTA TGTnGAAGGA CATCT 115

(2) INFORMATION FOR SEQ ID NO: 4795:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4795:

nTTAAAAAAA ATTCCCAATT TTTTTTGGGG GGTTGGGAAT TTAAAAATTT GGTTTTTAAC 60

CCAAAGGCCC TTTTCCCAAA AATTTAAATT CCCTTAAAAA TTTAAAATTT GGGAATTTTT 120

TTTTnGGCCC AAAATTTTTT CCCTTTTTTT AAAGGCCCCA ATTTTTAATT TAACCCTTAA 180

AACCCCCAAA CCTTTTTTCC TTTTTTAAAA TTTTTTTAAA TGGA 224

(2) INFORMATION FOR SEQ ID NO: 4796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4796:

TCGCGTACCG CTTTAATGGG CGAACAGCAA GACCTTGGGC ACCGACTACA GCCCCAnGAT 60

GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCGTCGAT GTGAACTCTT GGGGGCAGAT 120

(2) INFORMATION FOR SEQ ID NO: 4797:

(A) LENGTH: 125 base pairs
(B) TYPE: nucl ic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4797:

AATTCGATTC CCTTAGTAGC GGCGAGCGAA ACGTGAAGAG CCCCAnACCA ACAAGCTTGG 60

CTGTTGTGGT TGTAGGACAC TCTATAACGG GAGTTACAAA GGACCGACAT TAGACGAATC 120

ATCTG 125

(2) INFORMATION FOR SEQ ID NO: 4798:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4798:

CAAAATAATG ACTCCTACGG GnCTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 60

AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACC 113

(2) INFORMATION FOR SEQ ID NO: 4799:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4799:

CCGGTGGGAG GTAACCTTTT AGGAGCTAGC CGTCGnAGGT GGGACAAATG ATTGGGGTGA 60

AGTCGTAACA AGGTAGCCGT ATCGGAAGGT GCGGCTGGAT CACCTCCTTT CTAAGG 116

(2) INFORMATION FOR SEQ ID NO: 4800:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4800:

TCAGTGCGAT GATTCGTGAA ATTGAAACGC AAGATTTCGA TATCGAnCAC CT 112

(2) INFORMATION FOR SEQ ID NO: 4801:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4801:

ATAGGATAGG CGACGTGCGA TTGGATTGCA CGTCTAAGCA nTAAGGCTGA GTATTAGGAA 60

ATCCGGTACT CGTTAAGGCT GACTGTGATG GGGAGAAACA TTGTGTCTTC 110

(2) INFORMATION FOR SEQ ID NO: 4802:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4802:

GAACCAAGTT GTTATTGAAA AnTCGTTCGT AAAGTTACGG TACGCCCACC GTGAGTGCTT 60

TTACTTCTAT ATCAGCACCT ACTGTATCTT TCATTAATTT AACGTCTTCT GCAGTCGCAC 120

CGCCACCTGC AAAACCTGTT GAATTTTACG AGTCCGCACC GCGCTTTGTA ATCATnCTTA 180

CATTCTCTGT CACAACGCCA TACCTTCGGG ACTGACTCAC AGCTCAGCGG AACACAA 237

(2) INFORMATION FOR SEQ ID NO: 4803:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4803:

CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA CCAATTGAGC TAAGCCGGGC 60

AATATGTAAG AATAAATGGT GGAGAATTGA CGGGTTCGAA CCGCCGAnCC TCTG 114

(2) INFORMATION FOR SEQ ID NO: 4804:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4804:

GGATCAAACA GGATTAGATA CCCTGGnTAG TCCACGCCGT TAAACGCATG AGTGCTAAGT 60

GTTAGGGGTT TCCGCCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCT 113

(2) INFORMATION FOR SEQ ID NO: 4805:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4805:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC GCATCAGCGT CnGTTACAGA 60

CCAGGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT CTGCGCAT 108

(2) INFORMATION FOR SEQ ID NO: 4806:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4806:

TTTCAGCACT TATCCCGTCC ACACATAGTC TACCCAGGCT ATGCCGTTGG CACGACAACT 60

GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGAnAGCTC CTCTC 115

(2) INFORMATION FOR SEQ ID NO: 4807:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4807:

CAGCCACATA ACATAACTAA GTTTAAGATT GAACGATAAA TCGTATCTGA GTTAAACCAA 60

TGGTTAATAC CCGCACCCAT GATAATCATT GAACGCCTTC AGTATCGTAG GTTTGGAATT 120

(2) INFORMATION FOR SEQ ID NO: 4808:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808:

TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGCAGCTAA ATTACCTTGC 60

ATCATTGCTA GCTTTTCTTG TATTAACTGA TAnTTACTAA TTGGTTTGCC GAATTGCT 118

(2) INFORMATION FOR SEQ ID NO: 4809:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:

TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCGA TTGGAATTTC 60

TCCnATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG 120

TACCTGACTT CAACTGACCA GGGTAGACAC 150

(2) INFORMATION FOR SEQ ID NO: 4810:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:

AAGAAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCAn 60

AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA 107

(2) INFORMATION FOR SEQ ID NO: 4811:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4811:

AGAGTGnATT AGGTTATGAA GGTGGGCAAA ATAGGGTAAC CAGTCATTCG AGGAAGACAC 60

AGAAGAAGAC AAACCTAAAT ATGAACCAAG GTGGCATATC GTAGATATCG ATTTCCA 117

(2) INFORMATION FOR SEQ ID NO: 4812:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4812:

CTTTTATCCG TTGAACGATG GCCCTTCCAT GCGGAACCAC CCGATnACTA AATCCGTCTT 60

TCGACCCTGC TCGACTTGTA AGTCTCGCAA TCAAGTCCCT TATGCCTTTA CACTCTATGA 120

ATG 123

(2) INFORMATION FOR SEQ ID NO: 4813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4813:

TAACCCGAGA GGGTCCCCTn GTCCAAACAG TGCTCTACCT CCAATATCAT CACTTGAGGC 60

TAGCCCTAAA GCTATTTCGG AGAGAACCAG CTATCTCCAG GTTCGA 106

(2) INFORMATION FOR SEQ ID NO: 4814:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4814:

CTATTGCTTT AGATGCATAT GAATCATTGA nTGACGCGAT GCCGATGATT TCTGAACACG 60

GAATCGCGAA CGTTGGCCAA CTGCCAACGA TTGGCGTGGG AATCATCCAG TG 112

(2) INFORMATION FOR SEQ ID NO: 4815:

(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4815:

ACGTGGAGAG CATGTCCGTT CAAGCAGAGG GGCGGCGGTT GAACCCGTCA TTCTGCACCA 60

TTTATTCTTA CATATTGCCG GnCTAGCTCA ATTGGTAGAG CAACTGACCT TGTAATCAGT 120

AGGTT 125

(2) INFORMATION FOR SEQ ID NO: 4816:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4816:

GTGCTGGCGC AGTTGCGATG GTTATTGCAC ATAATCCAAG CATGGCATTA AATGAAGATG 60

CTGTTGCTTA CACTGAAGAC GTTTATGnTT TCTGGCGTCC AACT 104

(2) INFORMATION FOR SEQ ID NO: 4817:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4817:

GTCGGGTAAG TTCCGGCCCG CACGAAAGGC GTAACGATTT GGGCACTGTC TCAACGnGAG 60

ACTCGGTGAA ATCATAGTAC CTGTGAAGAT GCAGGTTACC CGCGGCAGGG CGGAAAG 117

(2) INFORMATION FOR SEQ ID NO: 4818:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4818:

TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGACGCTCT TTTCTCGnTT CGTCAGATTC 120

A 121

(2) INFORMATION FOR SEQ ID NO: 4819:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4819:

TCAGTTCGGT ATTGTGAGTC TGCAACTCGA CTGACATGAA GCTGGAATCG CTAGTAATCG 60

TAGATCAGCA TGCTACGGTG AATACGTTCC CGGGTCTTGT ACACAACGCC CGTnAAGA 118

(2) INFORMATION FOR SEQ ID NO: 4820:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4820:

CAAACAGTGC TCTACCTACA ATAATCATCA CTTGAGGCTA GCCCTAAAGC TATTTCGGAG 60

AGAACCAGCT ATCTnCAGGT TCGATTGGAA TTTCTCCGCT ACCC 104

(2) INFORMATION FOR SEQ ID NO: 4821:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4821:

TCGTAGTGGT TTCCAACCAA GTTTTTATAA GTCAAACGCT CACATACGGC TTCGTTTTCA 60

TTATTTTAAA TGCTCATTTA CATAGTnAAC TCGCTTTAAA ATAATTTAAC TCATGTCGCT 120

AACGTTTTCT TTTATAAAAG TTTAACGGTT TTATCTGTGG TGTCT 165

(2) INFORMATION FOR SEQ ID NO: 4822:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4822:

GAGTTTGATC CGGGCTCAGG ATGAACGCTG GCGGCGTGCC TAATACATGG CAATCGAGCG 60

AACGGACGAG AAGCTTGCTT CnCTGAGGTA GCGGCGGACG GGTGAGTAAC ACG 113

(2) INFORMATION FOR SEQ ID NO: 4823:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4823:

CCGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCTACC ATCGACGCTA AGAACCTTTC 60

TTTGAnTTGT GACAATCGCT TGCTTCTTTC CTCTTCTTCG GCTCTC 106

(2) INFORMATION FOR SEQ ID NO: 4824:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4824:

TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC 60

CGACCCGCAC GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACTAGAGn 108

(2) INFORMATION FOR SEQ ID NO: 4825:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4825:

TCTAGTGACC GATAGTGAAC CAGTACCGTG AGGATAAGGT GAAAAGCACC CCGGAAGTAG 60

nTGTAAATAG AACCTGAAAC CGTGTGCTTA CAAGTAGTCA GAGCCCGGTA ATGGGT 116

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4826:

ATAATATTGT AAATTAATCC ATTGATGCCA CAAGTGCCGG ACCAGAAATG ATGGTATTTA 60

ATAATGTGCC ATCTTTATCT TTACGCCAAT CATAATTGGT AAAAATTCCC CCTTCTAATA 120

ATCCTTGTAT TGCGTGTCAT AnAGTCTTTG CTCCTTGCAC 160

(2) INFORMATION FOR SEQ ID NO: 4827:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4827:

CGCATTGAGA CCGCAAGCTC TTTTTTTTAT GTCTAAAACG TCAAAATAAA AAGTAAACAC 60

AAAGAAAATG GTTGGCCnAG TGAAAACGTT TGAATCTGAC GAAACGAGAA AGAGC 115

(2) INFORMATION FOR SEQ ID NO: 4828:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4828:

CCAAAATAGC CTTCATAATC CAAAAACAGG CTCCTTTGAC TATAGATTTT CGTTTCTGGT 60

TCAGAAAGCT TTTGATTAAC TTTAAAGTAT nCCCAATTAT AAT 103

(2) INFORMATION FOR SEQ ID NO: 4829:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGACCGAACT GTCTCACGAC GTTCTnAACC CATCTCGCGT ACCGCTTTAA TGGGCGAACA 60

GCCAACCCTT GGGACCGACT ACAGCCCCAT GATGCGATGA GCCGACATCG A 111

(2) INFORMATION FOR SEQ ID NO: 4830:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4830:

GTTGTTGGGG CCCCGCCGGC AAGGTTGACT AGAATTGAGA AAAGCTTGTT ACAACGCTAT 60

TTTCGTTCAG TCAACnACTG CCAATATAAC TTTGTAGAGC ATTGA 105

(2) INFORMATION FOR SEQ ID NO: 4831:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4831:

ACATTGAGTC TTCGAGTCGT TGCATTTCAC ACTGCCGnGA AAAGCCTCTA GATAGAAAAT 60

AGGTGCCCGT ACCGCAAACC GACACAGGTA GTCAAGATGA GA 102

(2) INFORMATION FOR SEQ ID NO: 4832:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4832:

TTnTAGAATG AACCGGCGAG TTACGATTTG ATGCAAGGTT AAGCAGTAAA TGTGGAGCCG 60

TAGCGATAAG GAGGTCTGAA TAGGGCGTTT AGTATTTGGT CGTAGCC 107

(2) INFORMATION FOR SEQ ID NO: 4833:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4833:

TGCAACTAAT GAAAAGTAGA GTTCCGGGGA GTTAAAACCA GTGACTGTTG ACCTTGTTGT 60

CTCCATTGGA ATGTACTACC TGATGCAAGA TAATTATCAT CACTTTGTTG ACGTGCTTnA 120

TTTTCAGCAT CAATTTGATC AATC 144

(2) INFORMATION FOR SEQ ID NO: 4834:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4834:

GGCTCAGATG nACGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGCACCAGAA 60

GCTTGCTTCT CTGGATGTTA GCGGCGGACG GGTGTAGTAA CACGTGGG 108

(2) INFORMATION FOR SEQ ID NO: 4835:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4835:

GACAATGGTA GGnGAGCGTT CTAAGGGCGT TGAAGCATGA TCGTAAGGAC ATGTGGAGCG 60

CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGCA GT 102

(2) INFORMATION FOR SEQ ID NO: 4836:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4836:

TTGCAGACTA CAATCCGGAA CTGGAGTAAC AACTTTATGG GATTTGnCTT GACCTCGCGG 60

TTTCGCTGGC CCTTTGGTAT TGTCCATTGT AGCACGTGTG TAGCCCAAA 109

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 bas pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4837:

CTCCACGTAA GCTAGCGCTC ACGTTTCAAA GGCTCCTACC TATCCTGGTA CAAGCTGTGC 60

CGGAATTTCA ATTTGCAnGC TACAGTAAAG CTCCACGGGG GTC 103

(2) INFORMATION FOR SEQ ID NO: 4838:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

TCAAACACTC nCATACTGCT TTATTTTCAT AAACAATATC ACTTTAACCA AAAAATATTT 60

GAATGTTAAA TAAACATTCA AAACTGAATA CAATATGTCA CGTTATTCCA CATCTTCTGG 120

A 121

(2) INFORMATION FOR SEQ ID NO: 4839:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4839:

AAACCATGAA TTAAGAATCC AGAAACAGGA GATGTAGTTA GACCACCGGT CGATTAGCGT 60

ACCAAAATAT GGACCTGTAA AAGGAGACTC GATTGTAGAn AAAG 104

(2) INFORMATION FOR SEQ ID NO: 4840:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CCGTGGAGTT TATGTAGCCT GATATTGAAT TCGGCACAGT TGTACAGGTA GGTAGGAGCC 60

TTGAAACGTG AGCGCTATTA GTGnAGGCGT GGTGGGTACT ACCCTAGCTG TGTTGGCTTT 120

CTAACCC 127

(2) INFORMATION FOR SEQ ID NO: 4841:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4841:

CATCCCACCC CGGGCAAGGT TGACTAGAAT TGGAAAAAAA CTTGGTTACA ACGTTATTTT 60

CATTCAGTCA ACTACTGCCA ATATAATATT GnAAACTATA GGACATTTAT TAGTGTTTCA 120

GTTCT 125

(2) INFORMATION FOR SEQ ID NO: 4842:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4842:

TGGTACGGCA TCTCACCCGT CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAnGCGCTC 60

CACATGATCC TTACGATCAT GACTTCAACG CCCTTAGAAC GCTCGTCC 108

(2) INFORMATION FOR SEQ ID NO: 4843:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4843:

TAATGAAGGT CTTCGGATCG TAAAACTCTG TTATTAAGnA GGAACATGTG TGTAAGTAGC 60

TGTGCACATC TTGACGGTAC CTAATCAGAA AGCCACGGCT AACTACGT 108

(2) INFORMATION FOR SEQ ID NO: 4844:

(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4844:

CGGTCTCAAT GCGGCTCATC GCATCCATTT TTGACCTGG GCAACGTTCT ACTCTAGCGG 60

AACCTAAGTT GGGCTACCAT CGACGnCTAA GAACCTTTCT TGACTTGTGT ACAATCG 117

(2) INFORMATION FOR SEQ ID NO: 4845:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4845:

GACTGTTTAT CAAAAACACA GGTCTCTGCT AAACCGTAAG TGATGTATAG GGGGCTGACG 60

CCTGnCCGGG TTCTGGTAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAA 108

(2) INFORMATION FOR SEQ ID NO: 4846:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4846:

CAATATTTGA AGCGATTGGC TTGTCTCATG ATGTGATTGA TCGTTATTTT ACTGGGACAC 60

AGTCTAAGTT ATCTGGTATT TCGATTGATC AAATTnTGCC TGAAAAAGAC GCACAAGT 118

(2) INFORMATION FOR SEQ ID NO: 4847:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4847:

GATCCCCGGA CGGAGTGCTT AATGCGTTAC TGACAGCACT AAGGGGCGGA AACCCCCTAA 60

(2) INFORMATION FOR SEQ ID NO: 4848:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4848:

CTGGCGATTA TGCTCTGTAA CGTGCTTTCC AATTTGGAAC GCACGTGnCC CTGCCCATAC 60

CTACGGGACT TGACTTATAT TGTTTGGCTT TGTACGTCAT TTCAACAATA GACGCCCATG 120

CCAGCAACGC GATTACC 137

(2) INFORMATION FOR SEQ ID NO: 4849:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4849:

GTTTAGGCTC ATCTTAAGAT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTACTTACCG 60

TTTTGGCAGA CGGCACTTGG TGGTACTTTA GAAGTCAAAG ACAnGGGGGG GGGGGG 116

(2) INFORMATION FOR SEQ ID NO: 4850:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4850:

TCCTTTCGTG ACGGGCTCGG TAACTTACCC GACAAGGTAA TTTCGCTACC TTAGGnACCG 60

TTATAGTTAC GGTCCGCCGT TTACTGGGGC TTCGATTCGT ATCTTCGCAG CTATATCTCA 120

CTCCT 125

(2) INFORMATION FOR SEQ ID NO: 4851:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4851:

AAGTTGTATT TTAAAAATAG TTCTTTAAAT TATATACCCA CCACATTTGG TGGGAGAACC 60

TAAAAAAAAG CACTTTCCCC AAAAATGGGA AAGTGC 96

(2) INFORMATION FOR SEQ ID NO: 4852:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4852:

ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGnAT 60

GAACCGGCGA GTTCACGATT TAGATGCAAG GTTGAAGCAG 100

(2) INFORMATION FOR SEQ ID NO: 4853:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4853:

CCGACAGCGT AGnCGATGGA TAACAGGTTG ATATTCCTGG TACCACCTAT AATCGTTTTA 60

ATCGATGGGG GACCCATAGG ATAGCGAACC TGCGATTGGA T 101

(2) INFORMATION FOR SEQ ID NO: 4854:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4854:

GGACATCTCC TAAGGCTAAA TACTCTCTAG TGACCGTAGT GAACCAGACC GTGAGGAAAG 60

GTGAAAnACC CCGGAGGGGA GTGAATAGAC CTGAAACCGT GT 102

(2) INFORMATION FOR SEQ ID NO: 4855:

(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4855:

ATAACCGCAA TTGGCGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA 60

CTTATCCCGT CCACACATAn CTACCCAGCT ATGCCGTTGG CACG 104

(2) INFORMATION FOR SEQ ID NO: 4856:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4856:

CTACTGTCTT CATTCTTTCA GTTCTTTTTT ACGGGTCTGT TTTCTAATTT GAGCACATCT 60

TCGATTCTTT ATCAAATGAC TACCAATTAA ATCTATTCCT CTnTGGTAAA TCGCTAACTC 120

CATCTCCTTA ACCCGGTA 138

(2) INFORMATION FOR SEQ ID NO: 4857:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4857:

TCAAACGnTT GTCATCTATT AAAGAAGTAG GTCTAGATAT ATCACGTACG TAATGTGTAA 60

TGGATGGCGC TATTGCTTTA GGTCATCCAT TAGGTGCTAC 100

(2) INFORMATION FOR SEQ ID NO: 4858:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4858:

CCTGTGTGTT TGATAAACAG TCGGTTGGGC CTATTCACTG CGGCTT 106

(2) INFORMATION FOR SEQ ID NO: 4859:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4859:

GTAACTCGCC GGTTCATTCT ACAAAAGGGC ACGCCAATCA CCCATTAACG GGCTCCTGAA 60

CTACTTGTTA AGCAACACGG TTTCCAGGGT TCTATTTCCA CTTCCCCTTT CCGGGGTnGC 120

TTTTTCAACC TTTTTCCCCC TCCACGGTTA CT 152

(2) INFORMATION FOR SEQ ID NO: 4860:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4860:

GCCCGTACCG CAAACCGACA CAGGTAGTCA AGATGAnGAA TTCTAAGGTG AGCGAGCGAA 60

CTCTCGTTAA GGAACTCGGC AAACTGACCC CGTCACTTCG 100

(2) INFORMATION FOR SEQ ID NO: 4861:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4861:

CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTAA AAAGTAAGCG GATGAACTAA 60

AGGTAGCnGA GAAATTCCAA TCGAACCTGG AGATAGCTGG TTCT 104

(2) INFORMATION FOR SEQ ID NO: 4862:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4862:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60

CCTCCTGCGT GCAAAGCAGG CGCTCTG 87

(2) INFORMATION FOR SEQ ID NO: 4863:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4863:

ACCGTTTGAT TTCTTATCTA ATTCAAGCTT ATTTAAAACT CTTTATTCAC TCGGTTTTGG 60

CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAnTTTTCA ATGTA 105

(2) INFORMATION FOR SEQ ID NO: 4864:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4864:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60

TGCCTTGCTG GATGATGCTA TGATATTGCA CATATCGAAT CAACAGTGGT GCATGAACCT 120

GCAnTGGCT 129

(2) INFORMATION FOR SEQ ID NO: 4865:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4865:

AAACCGCAAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC 60

TCGACTACnT GAAGCTGGAA ATCGCTATAA ATCGTAGATC 100

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucl ic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4866:

GTGATAAGAT TAGCAGAAAA TGGATGGTGT TAAGAGAGTT AATTGGTTTG GnGGTATGCT 60

TATTTTTAAT GGCATTGTGT ACGAGAGCAT TAGAGTTTGT ACTTGTGAGG TTATT 115

(2) INFORMATION FOR SEQ ID NO: 4867:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4867:

ACACCACTCC TCATTAACCT TCCAGCACCG CAGCAGGCGT CACCCCTATA CATCACCTTA 60

CGGTTTAGCA GAGACCTGTG TTTTTGATAA 90

(2) INFORMATION FOR SEQ ID NO: 4868:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4868:

CACGAACGAT TGTCTTGCGT GCGGGGATTA TCTGACACGG TACCGGTCAA ACAGTGAATC 60

GCTACTGCTC ATCAGGGATT ACAAACC 87

(2) INFORMATION FOR SEQ ID NO: 4869:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4869:

CGCTCACCTT AGAATCTATT TACACTGGTG TTGGTAGGCA CTTTTTTCAA GCTTCCGATT 120

AACACATGAA AAGCTTCCAA AGTACTAGGA CGTTCAATAC ATGTA 165

(2) INFORMATION FOR SEQ ID NO: 4870:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4870:

AATATCATTT ATAACATTAA GTAATAACTT TTTTTATCTT GTCCATTTTA TTTTTnAACC 60

AAAATTTGAT TAAAAAACTG CCTGGCAACG TTCTACTCTA GCGGAACTAA G 111

(2) INFORMATION FOR SEQ ID NO: 4871:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4871:

TAGCAGAGAC CTGTGTTTTT TGATAAACAG TCGCTTGGGC CTATTCACTG CGGCTCTTCT 60

GGGCGTTAAC CCTAAAGAGC ACCC 84

(2) INFORMATION FOR SEQ ID NO: 4872:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4872:

ACAGTAAAGC TCCACGGGTC TTTCCGTCCT GTCGCGGGTA ACTGCATCTT CACAGGTACT 60

ATGATTTCAC CGATCTCTCn ATGAACAGTG CCAAATCGTA C 101

(2) INFORMATION FOR SEQ ID NO: 4873:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4873:

GACAGGCGTA GGCGATGGAT AACAGGTTGT ATTCCTGTAC CACCTATGAT CGTTTTAATC 60

GATGGGGGGA AGCATAGGAT AGGCGAA 87

(2) INFORMATION FOR SEQ ID NO: 4874:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4874:

GGGAGAGCGC CTGCTTTGCA CGCAGGAGGT CAGCGGTTCG ATCCCGCTAG TCTCCACCAT 60

TATTTGTACA TTGAAAACTA G 81

(2) INFORMATION FOR SEQ ID NO: 4875:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4875:

TATGTTTCGA AATATCTTTA TCACTCTAAA ATGATATACA AGAAATCCAA GAAAAATAAG 60

CGAACTGAAT AAATAAAGAT T 81

(2) INFORMATION FOR SEQ ID NO: 4876:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4876:

AACGCGTTAA ATCTTTTTAT AAAAGACGTA ACTTCATGTT AACGTTGCTT ATAAAAATGG 60

TGGAACATAG ATTAAGTTAT TAAGGGC 87

(2) INFORMATION FOR SEQ ID NO: 4877:

(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4877:

ACAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG TTCACATCGA 60

CGGGGAGGTT TGnCCTCAAT GTGGCTCATC GGATCTTGGG G 101

(2) INFORMATION FOR SEQ ID NO: 4878:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4878:

ATTTATTAGG TGTACAAATG ACCACCGCAT CAACAAGTTT AAACAGCTCG CTAGGTGTCT 60

CAACTGCATG AGGTATATT 79

(2) INFORMATION FOR SEQ ID NO: 4879:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4879:

ACATCGTTTC AATGGGTCGC TAACGCTGCT AGGACATTAT AACAGACGTG TACAAAAAGA 60

AAATTGGTAT GGTAATTGTG GCA 83

(2) INFORMATION FOR SEQ ID NO: 4880:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4880:

CTTCATCCTG ATCCAGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 60

(2) INFORMATION FOR SEQ ID NO: 4881:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4881:

TTGTGCAGTT GCATCGCCAT TGATCAATAA CACGTTGAGC TGCAGTTATT TCAGTTTCTG 60

CTTCACGCTT CTTCGCATTA 80

(2) INFORMATION FOR SEQ ID NO: 4882:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4882:

TCTGATGTGA AAGCCCACGG CTCAACCGTG GAGGGTCATT GGAAACTGGA AAACTTGAGT 60

GCAGAAGAGG AAAGTGGGTT CCATGT 86

(2) INFORMATION FOR SEQ ID NO: 4883:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4883:

TGATCGCATA TCTACGCAAC ATCGGCATAA GTnTGATGAC AAACAAGCTT CCATGACAAA 60

AGTAATGGAC GAATATCGCA TTTGGGGAAA GTCCTCTAAA AATGCCTTTT GAAGGAACGT 120

CGGTTAA 127

(2) INFORMATION FOR SEQ ID NO: 4884:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4884:

AGTAGGAATC GAACCCACAC CAAAGTTTTG GAGACCTCTA TTCTACCTTG AACTATGCCC 60

CTATTAAAAA TAATAAAT 78

(2) INFORMATION FOR SEQ ID NO: 4885:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4885:

CTCACTATTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60

GTGGATTGTC CTTTGGAAAT GGGT 84

(2) INFORMATION FOR SEQ ID NO: 4886:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4886:

GGTATCTGTT CACTCTTCCG GTGGTGCAGT TGCGACCAAC AATGGGTTGG AGATTGGATT 60

TCATCCTTCT CAATTAATCG TTGCCGTACT TTTCAAnTGG TACCCCATCC AAAAGGG 117

(2) INFORMATION FOR SEQ ID NO: 4887:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4887:

CGGATCTGGG AGGAAATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCAGT 60

ACCGTGAGGA AAGGTGAAAA 80

(2) INFORMATION FOR SEQ ID NO: 4888:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4888:

AATATGCAAG CACATGGTGA ATATGACGAG GTTGCAACTT CAACGGCGAA GATGATGGAA 60

GGCCTTACGT TTGCGTG 77

(2) INFORMATION FOR SEQ ID NO: 4889:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4889:

TCTTCTGGGC GTTAACCCTA AAGAGCACCC CTTCTCCCGA GTTACGGGGT CTTTTGCCGA 60

GTTCCTTAAC GAGAGT 76

(2) INFORMATION FOR SEQ ID NO: 4890:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4890:

GTGGGGGCCC CAACATAGGA GCTGATTTTC TGTCAGCTTA CCATnATGTG GCAAGTTGGC 60

GGGGGCCCCC AAACCAAGGA GCTGGCTTTC TGTCACTTTA CCATTAATGT GGCAAGT 117

(2) INFORMATION FOR SEQ ID NO: 4891:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4891:

TTAATCCnCC TGCATATGAT GACTTTGTTG AACCGTCATT GCATACTTTC AACATGAATA 60

CGCTGAACAC CTTCACTTAC TGCATATCTT AGTTCCTCGG TCTGTCTTA 109

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:

CTCTTAACCT TGCAGCACCG GGCAGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGCAG 60

AGACCGTGTG TTTTTGAGAA ACAGGTGC 88

(2) INFORMATION FOR SEQ ID NO: 4893:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893:

TAGCGAATGA GATAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTCG GCAGTTCGAA 60

TCTGCCCCCC TCCATTTATT ATTTTnAAAA AAAGCATAGT TC 102

(2) INFORMATION FOR SEQ ID NO: 4894:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:

CGAGCGATTC CGACTCAGAC AATGACTCGG AATTCAGATA ACGAATCTGA CTCAGACAGT 60

GACTCAGATT CCGACAGT 78

(2) INFORMATION FOR SEQ ID NO: 4895:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:

TTAGTATTCG CACTCACATG TCACATGCTT CACTCGACCT ATTACCTCAC ACTTGGGGAC 120

TTATACCGAG TnGGAATCTC A 141

(2) INFORMATION FOR SEQ ID NO: 4896:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:

GTTCGGATTT AATTTGATTC ATTTGTTGCG TAATTTCAGA AGCCATTTTA TGAAAAGAGT 60

GATTTAATTC ATAAATTTCT 80

(2) INFORMATION FOR SEQ ID NO: 4897:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897:

GGTATGGCTG GCGCTTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC 60

AAACCAATTA GTA 73

(2) INFORMATION FOR SEQ ID NO: 4898:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:

GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG 60

TGCGTCTGCC A 71

(2) INFORMATION FOR SEQ ID NO: 4899:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:

AGCCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT 60

TAAGGCTGGA GCTGTnGATG GGGAGAAGAC ATGTGTGCTT ACGTAGTGCG TGGTTT 116

(2) INFORMATION FOR SEQ ID NO: 4900:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:

TTCCGGCCCC TGGCGGTnTC CTAGGAGTTC CACGGAACCC CAGGATTTTG TAGGACCCCC 60

CGGGCAGAGT CCCCTTCGAC TAAGAAAATC TCACATTCTT CAGGGACTTT TAC 113

(2) INFORMATION FOR SEQ ID NO: 4901:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:

ACTTAATGGA TTGATTAAGT AGTGGGTTCT TAACATTAGG CCTCAGCTAA TGTGGTACTT 60

AAAAATAGGG AATACATG 78

(2) INFORMATION FOR SEQ ID NO: 4902:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:

ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT 60

CAAAACTAGA TAGTAAGTAA AAGT 84

(2) INFORMATION FOR SEQ ID NO: 4903:

(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:

TTGTCGGGTA AGTTCCGACC CGCACGAAAG GCGTAACGAT TTTGGCACTG TCTCAACGAG 60

AGACTCGGTG 70

(2) INFORMATION FOR SEQ ID NO: 4904:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:

TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60

TCCTCTTCTT GGCTCTGCTT CTATTTGCCT CTAATGTGGC TTTTTGTTGT AATAAGTTAT 120

GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A 151

(2) INFORMATION FOR SEQ ID NO: 4905:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:

TGACTTGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC 60

TTATCGTGGT GGGGA 75

(2) INFORMATION FOR SEQ ID NO: 4906:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:

ACTCAGACAG TGACTCAGAT CAGATAGTGn CTCGGATTCA GCGATTATTC AG 112

(2) INFORMATION FOR SEQ ID NO: 4907:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:

GTAAAAACAC CCCAGCCAGG TCACTTTACG CCTACGCATC GCTTGTACAC GTGCTACTAA 60

AGGTTTACCA 70

(2) INFORMATION FOR SEQ ID NO: 4908:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:

AGAAGATACA AATAAAGnTA AACCCAAATT ATTCAATTTC GGTGGGACAC AATAGTGTTG 60

ACTTTGAAGA AGATACACTT TCCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC 120

C 121

(2) INFORMATION FOR SEQ ID NO: 4909:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:

GGGAACAAAG TGGACAGGTG GTGCATGGTT GTCGTCAACT CGTGTCGTGA GATGTTGGGG 60

TTAAGTCCCG 70

(2) INFORMATION FOR SEQ ID NO: 4910:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:

GGACACCCGG AGAACTGAAA CATTTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG 60

TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG 100

(2) INFORMATION FOR SEQ ID NO: 4911:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:

nTCTGTGTTC GGCATGGGAA CAGGTGTGAC CTCCTTGCTA TAGTCACCAG ACAAAATAAC 60

TTACTTATTC ATGATACACG CTTAATTAAT AAGGTGCAAT AGTTAATTTT ACACTTTGAT 120

GTAAACTTTG GCACATCAGC TTTTAGTGTG TTTCG 155

(2) INFORMATION FOR SEQ ID NO: 4912:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:

CCCGTCACAC CACGAGATTT GTAACACCCG AAAGCCGGTG GAGTGAACCT TTTAGGAGCT 60

AGCCGTCGA 69

(2) INFORMATION FOR SEQ ID NO: 4913:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:

TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTTAAAACTG CCTGGCAACG TTCTACTCTA 60

GCGGAACGT 69

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:

CAAATGCTTC TGTCAATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA 60

ATACTTCAT 69

(2) INFORMATION FOR SEQ ID NO: 4915:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:

TATTTCGGAG AGAACCAGCT ATTTCCAGGC TCGATTGGAA TTTCTCCGGT ACCCTCAGTT 60

CATCCGCTCA 70

(2) INFORMATION FOR SEQ ID NO: 4916:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:

TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTTCT ATTTCACTCC 60

CCTTCCG 67

(2) INFORMATION FOR SEQ ID NO: 4917:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:

TCCACCGTTG ACTAAGGTTC CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA 120

GGCGCACGTA GGCGATGATA CAGGTTATAT CCTnACACCT A 161

(2) INFORMATION FOR SEQ ID NO: 4918:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

GCACGTAGTT AGCCGTTGGC TTTCTGATTA GGTACCGGCA AGATGTGCAC AGTTACTTAC 60

ACATATGT 68

(2) INFORMATION FOR SEQ ID NO: 4919:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919:

GAAAGCAAAT GTCTTCGTTG CAATTCGATC AAATCAATGT CTTCAACAGA TAGATTGCTG 60

AGTGACAATA CTTCAGGG 78

(2) INFORMATION FOR SEQ ID NO: 4920:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:

AATTTCGCTA CCTTAGGGAC CGTTATAGTT ACGGCCGACG TTTACTGGGG CTTCGATTCG 60

TACTTCGC 68

(2) INFORMATION FOR SEQ ID NO: 4921:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:

AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC 60

TTTACTG 67

(2) INFORMATION FOR SEQ ID NO: 4922:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:

GGGAGCTGTA ATAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT 60

GTCATG 66

(2) INFORMATION FOR SEQ ID NO: 4923:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:

GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTTGGCT TTCTAACCCG CAACCACTTA 60

TCGTGGGTGG GAG 73

(2) INFORMATION FOR SEQ ID NO: 4924:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:

GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTTATTT TTTACACGAT GACATGAAAC 60

TGATGACATA TGCACCGTAA TTCCAAAAA 89

(2) INFORMATION FOR SEQ ID NO: 4925:

(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:

AATGGCATCG GAGTTGTCTG AATTCGGTAA CCCGAGAGGC CCCTCGTCCA AACAGGCTCT 60

ACCTCCAA 68

(2) INFORMATION FOR SEQ ID NO: 4926:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:

ACGAAAGGCG TAACGATTTG GGCACTGATC TCGACGAGAG ACTCGTGAAA ATCATAGATA 60

CCTGTGAAGA TGC 73

(2) INFORMATION FOR SEQ ID NO: 4927:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:

ATTTCTATTA ATTATTTGCA TAGAAATCAG CTTTTTTGAT ATGTATTTTA TAATGTACAG 60

CTCGTTGAG 69

(2) INFORMATION FOR SEQ ID NO: 4928:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:

AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCCC 60

(2) INFORMATION FOR SEQ ID NO: 4929:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:

GGCGGGGCCC CAACACAGAG GCTGGCGGAA AGTGCAGCTT ACAATAGTGT GCAAGTTGGG 60

GTGGGTCCCG ACACAGAGAA ATT 83

(2) INFORMATION FOR SEQ ID NO: 4930:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930:

CTTGGTAGAG CACTTGGTTT GGGACCAAGG GGTCGCAGTT CGAATCCTGT CTTCCCGATT 60

ACTCTA 66

(2) INFORMATION FOR SEQ ID NO: 4931:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:

AAGAAGCTTG TTATGCTGCA ACACCAGCAA TTCAAGTAGC TAAAGATTAT TTAGCAACTA 60

GACCG 65

(2) INFORMATION FOR SEQ ID NO: 4932:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TGCAGAAGAG GAAAGTGGAA TTCCATGTGT AGGGTGAAAT GCGCATAGAT ATGGCAGGAA 60

CACCAGTGGG CGA 73

(2) INFORMATION FOR SEQ ID NO: 4933:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:

TCGCTATCCG AGTCTGGGTC GCTATCTGAG TCTGAGTCGC TATCTGAGTC TGAAATCGCT 60

GTCTG 65

(2) INFORMATION FOR SEQ ID NO: 4934:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:

GAGCATGTGG GTTTAATTCG AAGCAACGCA GAGAACCTTG ACCAAATCTT GGACATCCnT 60

TGACAACTCT GAGAGATTAG AGCCTTGCCC CTTGCGGGGT AACAAATGTA CAGGTTGGTG 120

(2) INFORMATION FOR SEQ ID NO: 4935:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:

GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCCGAGCAG GTACGGCGAT 60

GGATAACGGT TG 72

(2) INFORMATION FOR SEQ ID NO: 4936:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:

CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT 60

CTGC 64

(2) INFORMATION FOR SEQ ID NO: 4937:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:

ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA AAATTCATGT 60

TGGT 64

(2) INFORMATION FOR SEQ ID NO: 4938:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:

CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA 60

GAT 63

(2) INFORMATION FOR SEQ ID NO: 4939:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:

TAGAAATCAG CTTTTTTGCA TATGTATTTT ATAATGTACA GCTCGTTGAG CTGCTATTTT 60

CCT 63

(2) INFORMATION FOR SEQ ID NO: 4940:

(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:

GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGGAGAAT 60

TAGCTCAG 68

(2) INFORMATION FOR SEQ ID NO: 4941:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:

CTGAAACATC TTAGTACCCG GAGAAGAGAA AGAAAATTCG ATTCCCTTAG TAGCGGCGAG 60

CG 62

(2) INFORMATION FOR SEQ ID NO: 4942:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:

TTACAACAAT GCAATTGGCG GGGCCCAACA TAGAACTGGC AATAGTTACT TTCAATAATG 60

TGCAAGTTGG GGTAGGGCCC AACACAGAA 89

(2) INFORMATION FOR SEQ ID NO: 4943:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:

AATGGACAAT ATGTCAACGT TAATTCCAAA AAACGGTAAC TATAATTTAC AAACATTATT 60

(2) INFORMATION FOR SEQ ID NO: 4944:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:

CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT 60

GACGAATACG TAATTGA 77

(2) INFORMATION FOR SEQ ID NO: 4945:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:

GAATAGGTCG ATGTATTTGG CGACCGAAAC CAGGAATCTA CCCTTGGTCA GGTTGAAGTT 60

CAGGTAACAC TGAAT 75

(2) INFORMATION FOR SEQ ID NO: 4946:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:

ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTCGAT 60

TCCCTATAGC GGCGnCGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG 120

TACAGCGCTG ACACT 135

(2) INFORMATION FOR SEQ ID NO: 4947:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

GATTTGGGCT CTTCCATTTC GCTCGCCGCT ACTAAGGGAA TCGAATTTCC TTTCTCTTCC 60

T 61

(2) INFORMATION FOR SEQ ID NO: 4948:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:

GCTTTTGAGG AATTTAATAT CAATATATAT TCTGTGTATG AAAATATTTT TCATAAAAAT 60

TGTTTGAATC 70

(2) INFORMATION FOR SEQ ID NO: 4949:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:

CTTCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC 60

CTATTC 66

(2) INFORMATION FOR SEQ ID NO: 4950:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4950:

GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GGTACGTTTT 60

TCACCGTAGG CATGCTGG 78

(2) INFORMATION FOR SEQ ID NO: 4951:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:

CCGCGATAAT AAAAAATAAT GGCGGAGGAA GAGGGATTCG AACCCCCGTG GCCCGTTAAG 60

G 61

(2) INFORMATION FOR SEQ ID NO: 4952:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:

ACTTATCTAG TTTTCAATGT ACAATGTCTT TTTAGTCAGC GCTCGCATAA GCAATATCAC 60

TGTAACCA 68

(2) INFORMATION FOR SEQ ID NO: 4953:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:

ACTGACGCTG ATGTGCGAAA GCGTGGGGAT CAAACAGGAT TAGATACCCT GGTAGTCCA 59

(2) INFORMATION FOR SEQ ID NO: 4954:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:

CGTGAGCGCT AGCTGTACGT GGAGGCGCTG GTGGGATACT ACCCTAGCTG TGTTGGCTTT 60

(2) INFORMATION FOR SEQ ID NO: 4955:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:

AAGGCGTAAC GATTTGGGCA CTGTCTCAAC GAGAGACTCG GTGAAATCAT AGTACCTGT 59

(2) INFORMATION FOR SEQ ID NO: 4956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:

AATAGGTGCC CGTACCGCAA ACCGACACAG GTAGTCAAGA TGAGAATTCT AAGGTGAGC 59

(2) INFORMATION FOR SEQ ID NO: 4957:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:

ACACGTTTAG TTCACGCGGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT 60

TTTCAATGTA CAATTTC 77

(2) INFORMATION FOR SEQ ID NO: 4958:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:

TGTCGTCAGC TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAA 59

(2) INFORMATION FOR SEQ ID NO: 4959:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:

GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 59

(2) INFORMATION FOR SEQ ID NO: 4960:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:

TATTAACTGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA 59

(2) INFORMATION FOR SEQ ID NO: 4961:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:

ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTTAGC GGGTGGTGAT TTACCAAGA 59

(2) INFORMATION FOR SEQ ID NO: 4962:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:

CGCCGAAAAT TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA 59

(2) INFORMATION FOR SEQ ID NO: 4963:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGACTGCCGG TGACAAACCG 60

(2) INFORMATION FOR SEQ ID NO: 4964:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:

TAGTTTTGGT ACGGTAACAA ATTTATTTGA AGAAACAATC TCAAATAAAG AATTGTTTG 59

(2) INFORMATION FOR SEQ ID NO: 4965:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:

AGTTCGGTCC CTATCCGTCG TGGGGCGTAG GAAATTTTAG AGGAGCTGTC CTTAGTACG 59

(2) INFORMATION FOR SEQ ID NO: 4966:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:

TACAAAGGGC AGCGAAACCG TGAGTCAAAG CAAATCCCAT AAAGTTGTTC TCAGTTCGG 59

(2) INFORMATION FOR SEQ ID NO: 4967:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:

CCATTGCAGC ACCGACAGCC ACACCATTTA TTTTTGCGCT ATGTATATCG CATTAAACGT 60

(2) INFORMATION FOR SEQ ID NO: 4968:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:

GCCTCCGTTA CTTTTAGAGG CGACGCCCAG TCAAACTGCC CGCTGACACT GTCTCCCACC 60

(2) INFORMATION FOR SEQ ID NO: 4969:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:

CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCG 59

(2) INFORMATION FOR SEQ ID NO: 4970:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:

CATCTGTCAC AGGTACTATG GATTTCACCG GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60

TTACG 65

(2) INFORMATION FOR SEQ ID NO: 4971:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:

CTAGAGTTGG CATACCAGTC CGTCGCTAAG GAACCTTTCT TGACTTGATG ACAATCGACT 60

(2) INFORMATION FOR SEQ ID NO: 4972:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:

AGACCCCGTG GAGCTTTACT GTAGCCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT 60

AGGTAGG 67

(2) INFORMATION FOR SEQ ID NO: 4973:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:

TGTGTACTTA AAAATATGAA TACATGAGTA AAACTCATGC ATAAGAAATA CTAATTTC 58

(2) INFORMATION FOR SEQ ID NO: 4974:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:

ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAAGCTAT TTCGGAGAGA ACCAGCTA 58

(2) INFORMATION FOR SEQ ID NO: 4975:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:

GACGCCACAT CCTTTTCCAC TTGGCGTGTG TTTTGGGACC TTGGCTGGTG GTCTGGGCTG 60

(2) INFORMATION FOR SEQ ID NO: 4976:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:

TCACTAAGTC CGTCTTTCGA CCCTGACTCG ACTTGTAGGT CTCGCAGTCA AGCTCCCTT 59

(2) INFORMATION FOR SEQ ID NO: 4977:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:

TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG TTTTAAAT 58

(2) INFORMATION FOR SEQ ID NO: 4978:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:

GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG 58

(2) INFORMATION FOR SEQ ID NO: 4979:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:

TCGCTATCTG AATCCGAGGT CGCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC 60

(2) INFORMATION FOR SEQ ID NO: 4980:

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:

AAGAAGGTAA TAATCCTGTA GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGAGTAC 58

(2) INFORMATION FOR SEQ ID NO: 4981:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:

GTGGTGTGTT AGGGCACTCT ATACGGGTTA CAAAGTACGA CATTAGACGG ATCATCTGGA 60

AAGATGAATC AAAGT 75

(2) INFORMATION FOR SEQ ID NO: 4982:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:

GTTTTTCATT TTCATTTATA TTTATATTAG TGTTAATCCA ATCATAGATT TATCTATA 58

(2) INFORMATION FOR SEQ ID NO: 4983:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:

TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAACTTGCA TTGTCTGTAG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 4984:

(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:

GGTGTTTTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG 60

GAAA 64

(2) INFORMATION FOR SEQ ID NO: 4985:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:

CAGCATACAA TAATGTGCAA GTTGGTCGGG GCCCCAACAT AGAGAATTTC AAAAGAAAT 59

(2) INFORMATION FOR SEQ ID NO: 4986:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986:

TGATGAAGGT CTTCGGATCG TAAAACTCTG TTATTAGGGA AGAACATATG TGTAAGT 57

(2) INFORMATION FOR SEQ ID NO: 4987:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:

AAAGAATTTG CGCAAAACGC TATCGATACT GAAGGGCGTT CAATGATTAT CATGGGT 57

(2) INFORMATION FOR SEQ ID NO: 4988:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:

TTGTCACAAG TCAAGAAAGG TCTTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA 57

(2) INFORMATION FOR SEQ ID NO: 4989:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:

TAGGACCGTT ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAG 57

(2) INFORMATION FOR SEQ ID NO: 4990:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:

AAAGTCAACG TTAATTCCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT 60

G 61

(2) INFORMATION FOR SEQ ID NO: 4991:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:

TCCACGGGGT CTTTCCATCC TGTCTCGGGT AACCTGCATC TTCACAGGTA CTATGATTTC 60

ACCGA 65

(2) INFORMATION FOR SEQ ID NO: 4992:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:

GTGCGGCTGG ATCACCTCCT TTCTAAGGAT ATATTCGGAA CATCTTCTTC AGAAGAT 57

(2) INFORMATION FOR SEQ ID NO: 4993:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:

CCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACG 57

(2) INFORMATION FOR SEQ ID NO: 4994:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:

CTGGTTTCGG GTCTACGACA AATACTAAAC GCCTATTCAG ACTCGCTTTC GCTACGG 57

(2) INFORMATION FOR SEQ ID NO: 4995:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:

CAAACTCTCG TGGTGTGACG GGCGGTGTGG TACAAGCCCC GGGAACGTAT TCACCGTAGC 60

ATGCCGGTCT ACG 73

(2) INFORMATION FOR SEQ ID NO: 4996:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:

ACTAATTTCT ATAGGAAAAG TATTCTTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG 60

TAAGC 65

(2) INFORMATION FOR SEQ ID NO: 4997:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:

ATTGGATTCC CAATTTCTAC AGACAATGCA GTTGGGGTGG GACGTCGAAA TAAATTTT 58

(2) INFORMATION FOR SEQ ID NO: 4998:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:

AACTTCAACA GGTTTTGCAG GTGGCGGTGC GACTGCAGGA AGACGTTAAA TTAATG 56

(2) INFORMATION FOR SEQ ID NO: 4999:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:

GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTTAGCA GAGACCTGTG TTTTTG 56

(2) INFORMATION FOR SEQ ID NO: 5000:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:

TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC 56

(2) INFORMATION FOR SEQ ID NO: 5001:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:

GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGC 56

(2) INFORMATION FOR SEQ ID NO: 5002:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:

CCTGTCGGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG 56

(2) INFORMATION FOR SEQ ID NO: 5003:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCA 56

(2) INFORMATION FOR SEQ ID NO: 5004:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:

(2) INFORMATION FOR SEQ ID NO: 5005:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:

GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCACTAGAA GCCGATG 57

(2) INFORMATION FOR SEQ ID NO: 5006:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:

GGAACCACTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCCAC TCCCCTG 57

(2) INFORMATION FOR SEQ ID NO: 5007:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:

CGCTACGTTT TTCCTCAACA TTTAAGAAAA TAAAGAATGC TACAATTACG ATTGCAATCA 60

AACCAAAGA 69

(2) INFORMATION FOR SEQ ID NO: 5008:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:

AAAAGCTTGT TACAAGCGCT ATTTTCGTTC AGTCAACTAC TGCCAATATA ACTTCGT 57

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:

ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTCGATTCC CTTAGTAGCG GCGAGC 56

(2) INFORMATION FOR SEQ ID NO: 5010:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:

GTTTGGACGA GGGGCCCTCT CGGGTTACGA TTCAGACAAA CTCCGATGCA ATTAATTTAC 60

TTGGG 65

(2) INFORMATION FOR SEQ ID NO: 5011:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:

TTTACTTGTA TTGGAATAAT TTCATCTTTG AACCGACCAT CACGTTGTGC GTCATA 56

(2) INFORMATION FOR SEQ ID NO: 5012:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5012:

CCTTATACAT CACCTTTACG GTTTTAGCAG AAACCTGTGT TTTTTGATAA ACAGTCGCTT 60

(2) INFORMATION FOR SEQ ID NO: 5013:

(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:

GGGCCCAACA CAGAAGCTGG CGAAAAGTCA GCATACAAAA TTGTGCAAGT TGGCGGGTCC 60

ACA 63

(2) INFORMATION FOR SEQ ID NO: 5014:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:

TAGGGTAGTA TCCCACCAGT GGCCTCCACG TAAGCTAGCG CTTCACGTTT CAAAGGCT 58

(2) INFORMATION FOR SEQ ID NO: 5015:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:

CAACTCCGAT GCAATTAATT TAACTTGGGA nCAGACATGG GTGATAAGGT CGTGTTCGAA 60

GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAA 105

(2) INFORMATION FOR SEQ ID NO: 5016:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:

CAAACGATTT ATTTATATGC TTATTTCTTT ATTTATTATT ATTACAATTA CATTTT 56

(2) INFORMATION FOR SEQ ID NO: 5017:

(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:

TCTGTAGAAA TTGGGGAATC CAATTTCTCT TGGTTTGGGT CCCATCCCCA ACTTGCACAT 60

TATTG 65

(2) INFORMATION FOR SEQ ID NO: 5018:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:

GGGGATGGGC CCCAACAAAG AGAAATTGGA TTCCCAATTT CTACAGACAA TGCAAC 56

(2) INFORMATION FOR SEQ ID NO: 5019:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTC 55

(2) INFORMATION FOR SEQ ID NO: 5020:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:

TACGGCGTTT AGTATTTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGGTT 58

(2) INFORMATION FOR SEQ ID NO: 5021:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:

TTGTGCGGGT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA 55

(2) INFORMATION FOR SEQ ID NO: 5022:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5022:

AGAGTTCACA TCGACGGGGA GGTTTGGCAC CTCGATGTCG GCTCATCGCA TCCTG 55

(2) INFORMATION FOR SEQ ID NO: 5023:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:

CCTTAGCTGG TGGTCTGGGC TGTTTCCCTT TCGAACACGG ACCTTATCAC CCATGGTC 58

(2) INFORMATION FOR SEQ ID NO: 5024:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:

TAAAGGCTAA ACTACCAATG TTTTCAATGG ATTTCCAAAA TGAATCATCT GGGAT 55

(2) INFORMATION FOR SEQ ID NO: 5025:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:

TCAAACCGGA GGGGTCATTG GAAACTGGAA AACTTGAGTG CAGAAGAGGA AAGTGGAATT 60

CCA 63

(2) INFORMATION FOR SEQ ID NO: 5026:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:

GCTTGCGTAC CTAAAGAGCA CCCCTTCTCC GAATTACGGG GTCATTTTGC CGAGTTCCTT 60

AACG 64

(2) INFORMATION FOR SEQ ID NO: 5027:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:

AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA 56

(2) INFORMATION FOR SEQ ID NO: 5028:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:

GGGCCCCTCT CGGGTTACCA ATTCAGACAA ACTCCGAATG CCAATTAATT TAACT 55

(2) INFORMATION FOR SEQ ID NO: 5029:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:

CGTAACTATA ACGGTCCTAA GGTAGCCGAA ATTCCTTGTC GGGTAAGTTC CGAC 54

(2) INFORMATION FOR SEQ ID NO: 5030:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:

ATCCCCGGGG CCCCAACACA GAGAATTTCG AAAAGAAATT CTACAGGCAA TGCAAGT 57

(2) INFORMATION FOR SEQ ID NO: 5031:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:

TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA TTTC 54

(2) INFORMATION FOR SEQ ID NO: 5032:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGA 54

(2) INFORMATION FOR SEQ ID NO: 5033:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:

(2) INFORMATION FOR SEQ ID NO: 5034:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:

TATCTGAATC TGAGTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC 54

(2) INFORMATION FOR SEQ ID NO: 5035:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:

CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGA AAAA 54

(2) INFORMATION FOR SEQ ID NO: 5036:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:

CTACCATCGA CGCTAAGAGC TTAACTTCTG TGTTCGGCAT GGGAACAGGT GTGA 54

(2) INFORMATION FOR SEQ ID NO: 5037:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:

CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG CGGAAG 56

(2) INFORMATION FOR SEQ ID NO: 5038:

(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

GACCGGGATG GACATACCTC TGGTGTACCA GTTTGTCGTG CCAACGCATA AGCT 54

(2) INFORMATION FOR SEQ ID NO: 5039:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:

TTTCACCGAG TCTCTCGTTG AGCAGTGCCC AAATCGTTAC GCCTTTCGTG CGGG 54

(2) INFORMATION FOR SEQ ID NO: 5040:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:

TTATAACACG TATGCTTGGG GAGTGTAATA AGCTTGATCA GAGATTCCnA TGGGAACCAG 60

CATGAGTTAT GTCATTTATC ATATGTGATC ATAGCATATC AAAGG 105

(2) INFORMATION FOR SEQ ID NO: 5041:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:

GGCACCTATT TTCTATCTAG AGGCTTTTCT CGGCAGTGTG GAAATCAACG ACTC 54

(2) INFORMATION FOR SEQ ID NO: 5042:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCG 54

(2) INFORMATION FOR SEQ ID NO: 5043:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:

CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA 53

(2) INFORMATION FOR SEQ ID NO: 5044:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:

ACTAGAGAGT ATTTAGACTT AGGAGTGGTC CTCCCAGATT CCGACGGATT TCACGTGCT 59

(2) INFORMATION FOR SEQ ID NO: 5045:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:

TTTCGTCGTC CCACCCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG 60

TT 62

(2) INFORMATION FOR SEQ ID NO: 5046:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:

CGTCATCCCC ACCTTCCTCC GGTTTGTCAC CGGCAGTCAA CTTAGAGTGC CCA 53

(2) INFORMATION FOR SEQ ID NO: 5047:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:

TATTTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG 53

(2) INFORMATION FOR SEQ ID NO: 5048:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:

CCTCGGCACC ATTTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA 53

(2) INFORMATION FOR SEQ ID NO: 5049:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:

AAATGGCCAA CTTAAGCCAG GATACAATTT ACAAATAGCG ACAAATTCTC AATGTGTTT 59

(2) INFORMATION FOR SEQ ID NO: 5050:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CGAAAGACAC nCACAAGATT AATAACGCGT TTGAGTCTTT TTATAAAGAC GTACTTCATG 60

TTACGTTGAC TTTAAGATGG TGGAACATAG TTAGTTTTAG GGCCACGGGG G 111

(2) INFORMATION FOR SEQ ID NO: 5051:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:

ACGTTGACAT ATTGTCATTC AGTTTTCAAT GTTCATTAAT GTTCAATCTC TTT 53

(2) INFORMATION FOR SEQ ID NO: 5052:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:

CTGAATTCGG TAACCCGAGA GGGCCCCTCG TCCAAACAGT GCTCTACCTC CAA 53

(2) INFORMATION FOR SEQ ID NO: 5053:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:

TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC CGG 53

(2) INFORMATION FOR SEQ ID NO: 5054:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:

(2) INFORMATION FOR SEQ ID NO: 5055:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055:

TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAGAGCAC TGTTTGGACG AGG 53

(2) INFORMATION FOR SEQ ID NO: 5056:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:

ACTGCTTTGA AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTTCTTTT GCATAATTGA 60

CAA 63

(2) INFORMATION FOR SEQ ID NO: 5057:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:

CTATGTTGGG GCCCCGCCAA CTTGCATTGT CTGTAGAATT CCTTTTCGAA ATTC 54

(2) INFORMATION FOR SEQ ID NO: 5058:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:

CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG 53

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:

TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG TGATGTCAA 59

(2) INFORMATION FOR SEQ ID NO: 5060:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:

AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT AAAAAACAGC AGT 53

(2) INFORMATION FOR SEQ ID NO: 5061:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:

TTAAAGAGTG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAAT GTACC 55

(2) INFORMATION FOR SEQ ID NO: 5062:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC ACATCAGCGT CA 52

(2) INFORMATION FOR SEQ ID NO: 5063:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:

TCGCCAAGCC ATTTTTCTTT GTGTTTCTTT TTATTTTGAC GTTTTAGACA TA 52

(2) INFORMATION FOR SEQ ID NO: 5064:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:

CTCAAGCTCC CTTGTGCCTT TACACTCTAT GTGTGCTTTC CGACCGTTCT GGGGGGAACT 60

TTGGAGCGCC TCCGTT 76

(2) INFORMATION FOR SEQ ID NO: 5065:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:

CCACCGCTTG TGCGGGTCCC CGTCAATTCC TTTGAGTCGC AACCTTGCGG TCGT 54

(2) INFORMATION FOR SEQ ID NO: 5066:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:

TCCCCGGGCT AAACATATTA CCGAAGCTGT GGATTGTCCT TTGGACAATG GTAGG 55

(2) INFORMATION FOR SEQ ID NO: 5067:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:

GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AA 52

(2) INFORMATION FOR SEQ ID NO: 5068:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:

CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA 60

GCGAGCGGAA ACAACAACAA CG 82

(2) INFORMATION FOR SEQ ID NO: 5069:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:

TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACTTTT TCATTCGGTC TA 52

(2) INFORMATION FOR SEQ ID NO: 5070:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:

CGACTCGAAG ACTCAATGTC TTCTCCCCAT CACAGCTCAG CCTTAACGAG TA 52

(2) INFORMATION FOR SEQ ID NO: 5071:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:

GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GA 52

(2) INFORMATION FOR SEQ ID NO: 5072:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:

CACTTCACCA CAGCCGCCAT GGCATGGGCA GTAGGAATCG AACCCACACC AAA 53

(2) INFORMATION FOR SEQ ID NO: 5073:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:

GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTTCCG CAATGGGCGA AA 52

(2) INFORMATION FOR SEQ ID NO: 5074:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:

TGTTGGCTTA GAATCAGCCA TCATTTAAAG AGTGCGTAAT AGCTCACTAG TCGC 54

(2) INFORMATION FOR SEQ ID NO: 5075:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:

AAACTTCCCT TTGG 74

(2) INFORMATION FOR SEQ ID NO: 5076:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:

TGAGCTAATC AGACATCATA ATTTTTATGG AGAGTTTGAT CCTGGCTCAA GAT 53

(2) INFORMATION FOR SEQ ID NO: 5077:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:

GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC CGCTAGAGTA GA 52

(2) INFORMATION FOR SEQ ID NO: 5078:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:

GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTTGGG CACTGTCTCA AC 52

(2) INFORMATION FOR SEQ ID NO: 5079:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:

ATTAATCCAT TGTGCCACAA GTGCCGGACC AGAAATGATG GTATTTAATA AT 52

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:

AATAGCGACG AATCACACCT TCTGCGGCAC CACGGAATAA TACACCATGT GG 52

(2) INFORMATION FOR SEQ ID NO: 5081:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:

CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA 52

(2) INFORMATION FOR SEQ ID NO: 5082:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:

CAGACAGCGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA 56

(2) INFORMATION FOR SEQ ID NO: 5083:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5083:

AGGGTATGAT CCATCCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTTCCTA 60

CG 62

(2) INFORMATION FOR SEQ ID NO: 5084:

(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:

GTGTACCAGT TGTCGTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG 52

(2) INFORMATION FOR SEQ ID NO: 5085:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:

TTGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGGCAGATTC GAATGCGAAC 60

CCGAGGAGCG GATTAACA 78

(2) INFORMATION FOR SEQ ID NO: 5086:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:

ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATACCCTG GT 52

(2) INFORMATION FOR SEQ ID NO: 5087:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:

AAGTTGTTCT CAGTTCGGAT TGTAGTCTGC AACTCGACTA CATGAAGCTG G 51

(2) INFORMATION FOR SEQ ID NO: 5088:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:

AATACTTTAA AAAAATAAGA CACTTTGGCC AACTTAAGCC AGGATACAAT T 51

(2) INFORMATION FOR SEQ ID NO: 5089:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:

AGAACGTAAA TTTAATCCTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G 51

(2) INFORMATION FOR SEQ ID NO: 5090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:

CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCGGTC C 51

(2) INFORMATION FOR SEQ ID NO: 5091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:

CATGGGTGAT AAGGTCCGTG TTCGAAAGGG AAACAGCCCA GACCACCAGC T 51

(2) INFORMATION FOR SEQ ID NO: 5092:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:

TTGTGCGGAT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA 55

(2) INFORMATION FOR SEQ ID NO: 5093:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:

CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG A 51

(2) INFORMATION FOR SEQ ID NO: 5094:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:

ACGAATACTA ATCGATCGAA GACTTAATCA AAATAAATGT TTTGCGACAA A 51

(2) INFORMATION FOR SEQ ID NO: 5095:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:

AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT 60

ATTGTGCCAC CGATTGA 77

(2) INFORMATION FOR SEQ ID NO: 5096:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

TTCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CG 52

(2) INFORMATION FOR SEQ ID NO: 5097:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:

GGGTCTGTTT TCTAATTTGA GCACAATCTT CGTTCTCAAT AGAATGATTT A 51

(2) INFORMATION FOR SEQ ID NO: 5098:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:

CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCCAAC T 51

(2) INFORMATION FOR SEQ ID NO: 5099:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099:

CTGTGGATTG TCCTTTGGCA TGAGATAGGA GAGCGTTCTA AGGGCGTTGA A 51

(2) INFORMATION FOR SEQ ID NO: 5100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:

GGTTCAGAAC GTCGTGAGAC AGTTCGGTCC CTATCCGTCG TGGGCGTAGG A 51

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:

TGACTGATAC GATCAATGCG CTTGTAACAA GCTTTTTTCA ATTCTAGTCA GGGGCCCCAA 60

CACA 64

(2) INFORMATION FOR SEQ ID NO: 5102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:

TATTTGCATT TATATTGACG TTTTAAACAT AAAAAAAGAA ACCTTGCGGT CTCAATGG 58

(2) INFORMATION FOR SEQ ID NO: 5103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:

ATTACCATTT TGGTATACCA CATCGTTATT CAACACATTA TCTTTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 5104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

GGACACTGCT CCCTCAGGAG TCTCGCCATT AATACTACGT ATTAACATGT AAT 53

(2) INFORMATION FOR SEQ ID NO: 5105:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:

ATTTCTTCTT TTTCTACAAT CGAGTCTCCT TTTACAGGTC CATATTTTGT 50

(2) INFORMATION FOR SEQ ID NO: 5106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:

TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGGCGGTAAC ACGGGTTCGA 50

(2) INFORMATION FOR SEQ ID NO: 5107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:

TTTTTAGCAG TAATTGCCAC ATCTGTGTGA CGATAATGAT ATGCGACAGT 50

(2) INFORMATION FOR SEQ ID NO: 5108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:

CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGACATAA 50

(2) INFORMATION FOR SEQ ID NO: 5109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:

AGCCGATGAA GGACGTTACT AACGACGATA TGCTTTGGGG AGCTGTAAGT 50

(2) INFORMATION FOR SEQ ID NO: 5110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:

ATCCATAACG TTTGGTATCT GTAGCAATAA CTAATACTTT TTCATTCGGT CTA 53

(2) INFORMATION FOR SEQ ID NO: 5111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:

CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCCGCCTGA GGAGTACGAC CTC 53

(2) INFORMATION FOR SEQ ID NO: 5112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:

GGAGTCAAAG TCCGTTGCCT TACCGCTTGG CTATAGCCCA ATATATAGAT 50

(2) INFORMATION FOR SEQ ID NO: 5113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

AGAnTTTCTT TTCGAAATTC TTTATGTTGG GGCCCCGCCA ACTTGCATTG 50

(2) INFORMATION FOR SEQ ID NO: 5114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:

GCTGTGATGG GGAGAAGACA TTGTGTCTTC GAGTCGTTGA TTTCACACTG 50

(2) INFORMATION FOR SEQ ID NO: 5115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:

CTTGATTAAC TCATTATCAA GTTATGCACG TGTAAATGAA TTCGGCTTTA TCGAA 55

(2) INFORMATION FOR SEQ ID NO: 5116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:

GTACTTAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA 50

(2) INFORMATION FOR SEQ ID NO: 5117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:

CAGAATCAGA TAGCGACTCA GAATCAGATA GTGAGTCAGA TTCAGCAGTn 50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:

CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA 50

(2) INFORMATION FOR SEQ ID NO: 5119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:

AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACTTTTAC TTACTATCTA 60

(2) INFORMATION FOR SEQ ID NO: 5120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:

CCGAAGTTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG 50

(2) INFORMATION FOR SEQ ID NO: 5121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:

ATAATCCTGT AGTCGAAAAT GTTGTCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG 60

T 61

(2) INFORMATION FOR SEQ ID NO: 5122:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:

TAGCGACTCA GATTCAGACA GCGATTCAGA CAGCGACTCA GACTCAGATA 50

(2) INFORMATION FOR SEQ ID NO: 5123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:

TATTTGTAAA TTGTATCCTG GCTTAAGTTG GCCATTTTTC ATATGGTCTT 50

(2) INFORMATION FOR SEQ ID NO: 5124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:

CACGAGCTGA CGACAACCAT GCACCACCTG TCACTTTGTC CCCCGAGAAG GTCTCTATCT 60

(2) INFORMATION FOR SEQ ID NO: 5125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:

AGAACACATT GCAGTCTTCG AGTCGTTGAT TTCACACTGC CGTAGTAAAA GCCTCTAGAT 60

AGAA 64

(2) INFORMATION FOR SEQ ID NO: 5126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:

GGACGACATT AGACGAATCA TCTGGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT 57

(2) INFORMATION FOR SEQ ID NO: 5127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:

GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAGTTG 50

(2) INFORMATION FOR SEQ ID NO: 5128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5128:

GCCGATTTTA GCAGTTGTTG CTTCGTTCAA TTTTATGGGG CCATTTATGG 50

(2) INFORMATION FOR SEQ ID NO: 5129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:

TCCACACATA GCTACCCAGT CTATGCCGTT TGCACTACAA CTGGTACACC A 51

(2) INFORMATION FOR SEQ ID NO: 5130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:

CTCAGTTGGT TGAGCATCTG ACTTTTAATC AAAGGGTCAA GGGTCGAATC CTCTTTT 57

(2) INFORMATION FOR SEQ ID NO: 5131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:

TGATATTCAC TTCAATGTTA TCAATATTAG TGCCATCTAT GACATCTGCC A 51

(2) INFORMATION FOR SEQ ID NO: 5132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:

TCCTGTAGTC GAACGTGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG A 51

(2) INFORMATION FOR SEQ ID NO: 5133:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:

ACTCAGACAT TGGATTCAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC 59

(2) INFORMATION FOR SEQ ID NO: 5134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:

(2) INFORMATION FOR SEQ ID NO: 5135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:

CAATACnAAG GGCAGCGAAA CCGTGATTCA AGCAAATCCC ATAAAGTTGG 50

(2) INFORMATION FOR SEQ ID NO: 5136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:

GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGCCCA AC 52

(2) INFORMATION FOR SEQ ID NO: 5137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:

TTGTAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGAnT 50

(2) INFORMATION FOR SEQ ID NO: 5138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:

CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT AnAGCTCCAC 50

(2) INFORMATION FOR SEQ ID NO: 5139:

(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:

GGTTCGAATC CTGTCTTCCC GATATACTGT AATTATTATG GGGGCTTTGC TC 52

(2) INFORMATION FOR SEQ ID NO: 5140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:

GCTACTGAAC CTATAAAATG TATGATGGCG GTCTCGAGGG AATCGAACCC AGATCT 56

(2) INFORMATION FOR SEQ ID NO: 5141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:

AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA 52

(2) INFORMATION FOR SEQ ID NO: 5142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:

CACGCTTTCG ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT 56

(2) INFORMATION FOR SEQ ID NO: 5143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5143:

CTCCTAAAAC AATTTACATC CAAACCTTCA TCACTCACGC GGCGTTGCTC CGTCAGCTTT 60

CGCCATTGCG AAGAT 75

(2) INFORMATION FOR SEQ ID NO: 5144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:

GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT 55

(2) INFORMATION FOR SEQ ID NO: 5145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:

GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG 53

(2) INFORMATION FOR SEQ ID NO: 5146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:

AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T 51

(2) INFORMATION FOR SEQ ID NO: 5147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:

CTCTTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA 50

(2) INFORMATION FOR SEQ ID NO: 5148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:

GAACTAATTC TCCAAAATAA TGACTCCTAC AGGAACTCGA ACCCGTATAA CCGCCGTAAA 60

(2) INFORMATION FOR SEQ ID NO: 5149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:

AAAGCACACC CGGAAAACTG AAACATCTTA AGTACCCGGA GnAAGAGAAA 50

(2) INFORMATION FOR SEQ ID NO: 5150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:

GTAAGTTCGC ACTACCATCG ACGCTAAGGG AGCTTAACTT CTGTGGTTCG GCATGG 56

(2) INFORMATION FOR SEQ ID NO: 5151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:

(2) INFORMATION FOR SEQ ID NO: 5152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:

CTATTCTCTG TGTCGGGCTC ACCCCAACTT GCACACTATT GTAAGCTGAC TTTCCTCCA 59

(2) INFORMATION FOR SEQ ID NO: 5153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:

TAACCACATC ATTCGGATAC TGTTCATGGA AGTAATTTCT CTATTCTTCG GACCAGGAAA 60

ATACA 65

(2) INFORMATION FOR SEQ ID NO: 5154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:

CCATATGTGT CAGTCACTGT GCACATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC 60

TCCGTGCCAG CCGCCGCGGT ACTACGTGGT G 91

(2) INFORMATION FOR SEQ ID NO: 5155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:

(2) INFORMATION FOR SEQ ID NO: 5156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:

GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCT CGTGACCGAT AGTGAACC 58

(2) INFORMATION FOR SEQ ID NO: 5157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:

TTGTAACTCC GGTATAGGAG TGTCCTACAA CCCCAACAAG CAAGCTTGTT G 51

(2) INFORMATION FOR SEQ ID NO: 5158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:

TAGTnACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC 50

(2) INFORMATION FOR SEQ ID NO: 5159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159:

TTCGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTTCTC TTCCTCCGGG T 51

(2) INFORMATION FOR SEQ ID NO: 5160:

(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:

AACTGGAGAA ACAACTTTAT GGGGTTTGCT TGAACCTCGC GGTTTCGCTG CCCTTTGTAT 60

T 61

(2) INFORMATION FOR SEQ ID NO: 5161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:

AGACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T 51

(2) INFORMATION FOR SEQ ID NO: 5162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:

CCGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT 55

(2) INFORMATION FOR SEQ ID NO: 5163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:

CTTGATCTGT ATTTAAAATG ATATTTTCTA TCTTTTCTTT ATTATTAACG TCTATGACGT 60

CGTAGTATAA GATTCCGTGT A 81

(2) INFORMATION FOR SEQ ID NO: 5164:

(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:

GTTCGAATCC CGTCTTCTGC TCCATTATTT TGCCGGGGTG GCGGCAACTC TCACACGCAC 60

AG 62

(2) INFORMATION FOR SEQ ID NO: 5165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:

CAGGGGTCTT TCGTCCTGTG TGGGTAACTG CATCTTCACA GGTACTATGA TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 5166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:

AAGCTGAGGC CGACAGCGTA GGCGATGGAT GACAGGTTGA TATTGCCGGT ACCACCCGAT 60

AA 62

(2) INFORMATION FOR SEQ ID NO: 5167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:

CTTGCGTCTC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA CG 52

(2) INFORMATION FOR SEQ ID NO: 5168:

(A) LENGTH: 56 base pairs
(B) TYPE: nucl ic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:

TCGTCCGCTA TCTCCACCAT TATTTGTACA TTGAAACTAG ATAAGTAGTA AATATA 56

(2) INFORMATION FOR SEQ ID NO: 5169:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:

CTTGGACGTC GGTGGGTAGT CGAAACTTAC GTTCCGCTAG AGTAGAACGT TGCCA 55

(2) INFORMATION FOR SEQ ID NO: 5170:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:

CTACTGCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCA TA 52

(2) INFORMATION FOR SEQ ID NO: 5171:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:

GGGCTTnGGA CATTAAGTTC TnAGGCAATG TAAAAAAGCT GATTTCTATT 50

(2) INFORMATION FOR SEQ ID NO: 5172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5172:

AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCATTG CCATTCGAAG 60

(2) INFORMATION FOR SEQ ID NO: 5173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:

GTTTTATTTT TTTAAAGTAT GTAAAAGTAA AATTACATGn TAATACGTAn 50

(2) INFORMATION FOR SEQ ID NO: 5174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

CAACTCTCGT TAAGGAACTC GGCAAAATAC CCCGTAACTT CGGAGTAGGT CTCTTTA 57

(2) INFORMATION FOR SEQ ID NO: 5175:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:

GGAAACTGGA ATAAATAAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA 60

(2) INFORMATION FOR SEQ ID NO: 5176:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GTAACGGACG CGCTCAAAGG TTCCCTCACA ATGGTTGGAA ATCATTCATA 50

(2) INFORMATION FOR SEQ ID NO: 5177:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:

AGTTACGTTC TTTTATAAAG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG 50

(2) INFORMATION FOR SEQ ID NO: 5178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:

GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATTCCGT CGGCAATCTG GGG 53

(2) INFORMATION FOR SEQ ID NO: 5179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:

CGGTAACTTC ATACCTTTTA ACATATTTTG CATTTGATTG CGTTTACCTT TTTTACCTTT 60

ACCGCCACCA GTGAACTGTT TCA 83

(2) INFORMATION FOR SEQ ID NO: 5180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:

TTTAAA 66

(2) INFORMATION FOR SEQ ID NO: 5181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:

GTTCGGTAAC TCGAGCGGGT CTCATAACCC GTAGGTCGGG TGGTTCAAAT CCGTCCTCCC 60

GCAATAT 67

(2) INFORMATION FOR SEQ ID NO: 5182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:

TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCAGTAG CGAAGGCAAC TTTCT 55

(2) INFORMATION FOR SEQ ID NO: 5183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:

GAATTCCATG TGTAGCGGTG AAATGCGCAG AGATATGnAC GAACACCAAT 50

(2) INFORMATION FOR SEQ ID NO: 5184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:

CC 62

(2) INFORMATION FOR SEQ ID NO: 5185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:

GAGACCTTGT CGGTCCATAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGT 55

(2) INFORMATION FOR SEQ ID NO: 5186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:

CCATCATTAA GTTGGGCACT CTAAGTTGAC TGCCGGnGnC ACCnAAGAAG 50

(2) INFORMATION FOR SEQ ID NO: 5187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187:

TTAATACGTT GCAATCCAAT CGCACGCTTC GCCTATCCTA CTGCCnTCCC 50

(2) INFORMATION FOR SEQ ID NO: 5188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:

AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCTnAGTC GCTAnnCCAG 50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:

ATAGATGCCC TTACCGCAAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT 54

(2) INFORMATION FOR SEQ ID NO: 5190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:

CTTTAATGGG CGAACAGnAC CCTTGGACCG ACTACAGCCC AGATCGATGA 50

(2) INFORMATION FOR SEQ ID NO: 5191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:

ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCCGGCCT 60

(2) INFORMATION FOR SEQ ID NO:5192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5192:

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu
1 5 10 15

20 25 30

Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Val Ala Asp Thr Met Lys
35 40 45

Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu
50 55 60

Asn Lys Ile Leu Ala Asp Lys Tyr Lys Asn Lys Val Asn Asp Lys Lys
65 70 75 80

Ile Asp Glu Gln Ile Glu Lys Met Gln Lys Gln Tyr Gly Gly Lys Asp
85 90 95

Lys Phe Glu Lys Ala Leu Gln Gln Gln Gly Leu Thr Ala Asp Lys Tyr
100 105 110

Lys Glu Asn Leu Arg Thr Ala Ala Tyr His Lys Glu Leu Leu Ser Asp
115 120 125

Lys Ile Lys Ile Ser Asp Ser Glu Ile Lys Glu Asp Ser Lys Lys Ala
130 135 140

Ser His Ile Leu Ile Lys Val Lys Ser Lys Lys Ser Asp Xaa Glu Gly
145 150 155 160

Leu Asp Asp Lys Glu Ala Lys Gln Lys Ala Glu Glu Ile Gln Lys Glu
165 170 175

Val Ser Lys Asp Pro Ser Lys Phe Gly Glu Ile Ala Lys Lys Glu Ser
180 185 190

Met Asp Thr Gly Ser Ala Lys Lys Asp Gly Glu Leu Gly Tyr Val Leu
195 200 205

Lys Gly Gln Thr Asp Lys Asp Phe Glu Lys Ala Leu Phe Lys Leu Lys
210 215 220

Asp Gly Glu Val Ser Glu Val Val Lys Ser Ser Phe Gly Tyr His Ile
225 230 235 240

Ile Lys Ala Asp Lys Pro Thr Asp Phe Asn Ser Glu Lys Gln Ser Leu
245 250 255

Lys Glu Lys Leu Val Asp Gln Lys Val Gln Lys Asn Pro Lys Leu Leu
260 265 270

Thr Asp Ala Tyr Lys Asp Leu Leu Lys Glu Tyr Asp Val Asp Phe Lys
275 280 285

Asp Arg Asp Ile Lys Ser Val Val Glu Asp Lys Ile Leu Asn Pro Glu
290 295 300

Lys Leu Lys Gln Gly Gly Ala Gln Gly Gly Gln Ser Gly Met Ser Gln
305 310 315 320

(2) INFORMATION FOR SEQ ID NO:5193:

(A) LENGTH: 330 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

```
Met Asn Lys Val Ile Lys Met Leu Val Val Thr Leu Ala Phe Leu Leu
1               5                  10                  15

Val Leu Ala Gly Cys Ser Gly Asn Ser Asn Lys Gln Ser Ser Asp Asn
            20                  25                  30

Lys Asp Lys Glu Thr Thr Ser Ile Lys His Ala Met Gly Thr Thr Glu
        35                  40                  45

Ile Lys Gly Lys Pro Lys Arg Val Val Thr Leu Tyr Gln Gly Ala Thr
    50                  55                  60

Asp Val Ala Val Ser Leu Gly Val Lys Pro Val Gly Ala Val Glu Ser
65                  70                  75                  80

Trp Thr Gln Lys Pro Lys Phe Glu Tyr Ile Lys Asn Asp Leu Lys Asp
                85                  90                  95

Thr Lys Ile Val Gly Gln Glu Pro Ala Pro Asn Leu Glu Glu Ile Ser
            100                 105                 110

Lys Leu Lys Pro Asp Leu Ile Val Ala Ser Lys Val Arg Asn Glu Lys
        115                 120                 125

Val Tyr Asp Gln Leu Ser Lys Ile Ala Pro Thr Val Ser Thr Asp Thr
    130                 135                 140

Val Phe Lys Phe Lys Asp Thr Thr Lys Leu Met Gly Lys Ala Leu Gly
145                 150                 155                 160

Lys Glu Lys Glu Ala Glu Asp Leu Leu Lys Lys Tyr Asp Asp Lys Val
                165                 170                 175

Ala Ala Phe Gln Lys Asp Ala Lys Ala Lys Tyr Lys Asp Ala Trp Pro
            180                 185                 190

Leu Lys Ala Ser Val Val Asn Phe Arg Ala Asp His Thr Arg Ile Tyr
        195                 200                 205

Ala Gly Gly Tyr Ala Gly Glu Ile Leu Asn Asp Leu Gly Phe Lys Arg
    210                 215                 220

Asn Lys Asp Leu Gln Lys Gln Val Asp Asn Gly Lys Asp Ile Ile Gln
225                 230                 235                 240

Leu Thr Ser Lys Glu Ser Ile Pro Leu Met Asn Ala Asp His Ile Phe
                245                 250                 255
```

Val Val Lys Ser Asp Pro Asn Ala Lys Asp Ala Ala Leu Val Lys Lys
260 265 270

Thr Glu Ser Glu Trp Thr Ser Ser Lys Glu Trp Lys Asn Leu Asp Ala
275 280 285

Val Lys Asn Asn Gln Val Ser Asp Asp Leu Asp Glu Ile Thr Trp Asn
290 295 300

Leu Ala Gly Gly Tyr Lys Ser Ser Leu Lys Leu Ile Asp Asp Leu Tyr
305 310 315 320

Glu Lys Leu Asn Ile Glu Lys Gln Ser Lys
325 330

(2) INFORMATION FOR SEQ ID NO:5194:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

Met Thr Arg Lys Phe Arg Thr Leu Ile Leu Ile Leu Ile Ala Thr Ile
1 5 10 15

Ala Leu Ser Gly Cys Ala Asn Asp Asp Gly Ile Tyr Ser Asp Lys Gly
20 25 30

Gln Val Phe Arg Lys Ile Leu Ser Ser Asp Leu Thr Ser Leu Asp Thr
35 40 45

Ser Leu Ile Thr Asp Glu Ile Ser Ser Glu Val Thr Ala Gln Thr Phe
50 55 60

Glu Gly Leu Tyr Thr Leu Gly Lys Gly Asp Lys Pro Val Leu Gly Val
65 70 75 80

Ala Lys Ala Phe Pro Glu Lys Ser Lys Asp Gly Lys Thr Leu Lys Val
85 90 95

Lys Leu Arg Ser Asp Ala Lys Trp Ser Asn Gly Asp Lys Val Thr Ala
100 105 110

Gln Asp Phe Val Tyr Ala Trp Arg Lys Thr Val Asp Pro Lys Thr Gly
115 120 125

Ser Glu Phe Ala Tyr Ile Met Gly Asp Ile Lys Asn Ala Ser Asp Ile
130 135 140

Ser Thr Gly Lys Lys Pro Val Glu Gln Leu Gly Ile Lys Ala Leu Asn
145 150 155 160

Asp Glu Thr Leu Gln Ile Glu Leu Glu Lys Pr Val Pro Tyr Ile Asn
165 170 175

Gln Leu Leu Ala Leu Asn Thr Phe Ala Pro Gln Asn Glu Lys Val Ala
180 185 190

Lys Lys Tyr Gly Lys Asn Tyr Gly Thr Ala Ala Asp Arg Ala Val Tyr
195 200 205

Asn Gly Pro Phe Lys Val Asp Asp Trp Lys Gln Glu Asp Lys Thr Leu
210 215 220

Leu Ser Lys Asn Gln Tyr Tyr Trp Asp Lys Lys Asn Val Lys Leu Asp
225 230 235 240

Lys Val Asn Tyr Lys Val Ile Lys Asp Leu Gln Ala Gly Ala Ser Leu
245 250 255

Tyr Asp Thr Glu Ser Val Asp Asp Ala Phe Ile Thr Ala Asp Gln Val
260 265 270

Asn Lys Tyr Lys Asp Asn Lys Gly Leu Asn Phe Val Leu Thr Thr Gly
275 280 285

Thr Phe Phe Val Lys Met Asn Glu Lys Gln Tyr Pro Asp Phe Lys Asn
290 295 300

Lys Asn Leu Arg Leu Xaa Ser His Lys Gln
305 310

(2) INFORMATION FOR SEQ ID NO:5195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5195:

Met Lys Arg Leu Ile Gly Leu Val Ile Val Ala Leu Val Leu Leu Ala
1 5 10 15

Ala Cys Gly Gly Asn Asn Asp Lys Lys Val Thr Ile Gly Val Ala Ser
20 25 30

Asn Asp Thr Lys Ala Trp Glu Lys Val Lys Glu Leu Ala Lys Lys Asp
35 40 45

Asp Ile Asp Val Glu Ile Lys His Phe Ser Asp Tyr Asn Leu Pro Asn
50 55 60

Lys Ala Leu Asn Asp Gly Asp Ile Asp Met Asn Ala Phe Gln His Phe
65 70 75 80

```
Ala Phe Leu Asp Gln Tyr Lys Lys Ala His Lys Gly Thr Lys Ile S r
                  85                  90                  95

Ala Leu Ser Thr Thr Val Leu Ala Pro Leu Gly Ile Tyr Ser Asp Lys
              100                 105                 110

Ile Lys Asp Val Lys Lys Val Lys Asp Gly Ala Lys Val Val Ile Pro
          115                 120                 125

Asn Asp Val Ser Asn Gln Ala Arg Ala Leu Lys Leu Leu Glu Ala Ala
      130                 135                 140

Gly Leu Ile Lys Leu Lys Lys Asp Phe Gly Leu Ala Gly Thr Val Lys
145                 150                 155                 160

Asp Ile Thr Ser Asn Pro Lys His Leu Lys Ile Thr Ala Val Asp Ala
                  165                 170                 175

Gln Gln Thr Ala Arg Ala Leu Ser Asp Val Asp Ile Ala Val Ile Asn
              180                 185                 190

Asn Gly Val Ala Thr Lys Ala Gly Lys Asp Pro Lys Asn Asp Pro Ile
          195                 200                 205

Phe Leu Glu Lys Ser Asn Ser Asp Ala Val Lys Pro Tyr Ile Asn Ile
      210                 215                 220

Val Ala Val Asn Asp Lys Asp Leu Asp Asn Lys Thr Tyr Ala Lys Ile
225                 230                 235                 240

Val Glu Leu Tyr His Ser Lys Glu Ala Gln Lys Ala Leu Gln Glu Asp
                  245                 250                 255

Val Lys Asp Gly Glu Lys Pro Val Asn Leu Ser Lys Asp Glu Ile Lys
              260                 265                 270

Ala Ile Glu Thr Ser Leu Ala Lys
          275                 280
```

(2) INFORMATION FOR SEQ ID NO:5196:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196:

```
Met Lys Lys Leu Phe Gly Leu Ile Leu Val Leu Thr Phe Ala Val Val
1               5                  10                  15

Leu Ala Ala Cys Gly Asn Gly Asn Lys Ser Gly Ser Asp Asp Lys Lys
            20                  25                  30
```

Ile Thr Val Ser Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys
35 40 45

Ala Lys Pro Leu Leu Glu Lys Lys Gly Tyr Glu Leu Asp Ile Lys Thr
50 55 60

Ile Asn Asp Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile
65 70 75 80

Asp Ala Asn Tyr Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Lys Lys
85 90 95

Asp Lys Gly Tyr Lys Ile Val Ser Ala Gly Asp Val His Leu Glu Pro
100 105 110

Met Ala Val Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Glu Leu Pro Lys
115 120 125

Gly Ala Thr Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe
130 135 140

Leu Lys Phe Phe Val Asp Ala Gly Leu Ile Lys Ile Lys Lys Gly Val
145 150 155 160

Lys Ile Glu Asp Ala Lys Phe Ser Asp Ile Thr Glu Asn Lys Lys Asp
165 170 175

Ile Lys Phe Asn Asn Lys Gln Ser Ala Glu Phe Leu Pro Lys Ile Tyr
180 185 190

Gln Asn Glu Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Phe Ala Ile
195 200 205

Glu Gln Lys Leu Asn Pro Lys Lys Asp Ser Ile Ala Val Glu Ser Ala
210 215 220

Lys Asp Asn Pro Tyr Ala Asn Leu Ile Ala Val Lys Glu Gly His Gln
225 230 235 240

Asp Asp Lys Lys Ile Lys Ala Leu Ile Glu Val Leu Gln Ser Lys Asp
245 250 255

Ile Gln Asp Phe Ile Asn Glu Lys Tyr Asn Gly Ala Val Ile Pro Ala
260 265 270

Lys

(2) INFORMATION FOR SEQ ID NO:5197:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

```
Met Lys Lys Ile Lys Tyr Ile Leu Val Val Phe Val Leu Ser Leu Thr
1               5                  10                  15

Val Leu Ser Gly Cys Ser Leu Pro Gly Leu Gly Ser Lys Ser Thr Lys
            20                  25                  30

Asn Asp Val Lys Ile Thr Ala Leu Ser Thr Ser Glu Ser Gln Ile Ile
        35                  40                  45

Ser His Met Leu Arg Leu Leu Ile Glu His Asp Thr His Gly Lys Ile
    50                  55                  60

Lys Pro Thr Leu Val Asn Asn Leu Gly Ser Ser Thr Ile Gln His Asn
65                  70                  75                  80

Ala Leu Ile Asn Gly Asp Ala Asn Ile Ser Gly Val Arg Tyr Asn Gly
                85                  90                  95

Thr Asp Leu Thr Gly Ala Leu Lys Glu Ala Pro Ile Lys Asn Pro Lys
            100                 105                 110

Lys Ala Met Ile Ala Thr Gln Gln Gly Phe Lys Lys Lys Phe Asp Gln
        115                 120                 125

Thr Phe Phe Asp Ser Tyr Gly Phe Ala Asn Thr Tyr Ala Phe Met Val
    130                 135                 140

Thr Lys Glu Thr Ala Lys Lys Tyr His Leu Glu Thr Val Ser Asp Leu
145                 150                 155                 160

Ala Lys His Ser Lys Asp Leu Arg Leu Gly Met Asp Ser Ser Trp Met
                165                 170                 175

Asn Arg Lys Gly Asp Gly Tyr Glu Gly Phe Lys Lys Glu Tyr Gly Phe
            180                 185                 190

Asp Phe Gly Thr Val Arg Pro Met Gln Ile Gly Leu Val Tyr Asp Ala
        195                 200                 205

Leu Asn Ser Glu Lys Leu Asp Val Ala Leu Gly Tyr Ser Thr Asp Gly
    210                 215                 220

Arg Ile Ala Ala Tyr Asp Leu Lys Val Leu Lys Asp Asp Lys Gln Phe
225                 230                 235                 240

Phe Pro Pro Tyr Ala Ala Ser Ala Val Ala Thr Asn Glu Leu Leu Arg
                245                 250                 255

Gln His Pro Glu Leu Lys Thr Thr Ile Asn Lys Leu Thr Gly Lys Ile
            260                 265                 270

Ser Thr Ser Glu Met Gln Arg Leu Asn Tyr Glu Ala Asp Gly Lys Gly
        275                 280                 285

Lys Glu Pro Ala Val Val Ala Glu Glu Phe Leu Lys Lys His His Tyr
    290                 295                 300
```

Phe Asp Lys Gln Lys Gly Gly His Lys
305 310

(2) INFORMATION FOR SEQ ID NO:5198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 284 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
1 5 10 15

Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
20 25 30

Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr
35 40 45

Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
50 55 60

Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
65 70 75 80

Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
85 90 95

Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
100 105 110

Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
115 120 125

Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
130 135 140

Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
145 150 155 160

Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
165 170 175

Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile
180 185 190

Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
195 200 205

Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys
210 215 220

```
Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
225                 230                 235                 240

Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
                245                 250                 255

Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
            260                 265                 270

Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
        275                 280
```

(2) INFORMATION FOR SEQ ID NO:5199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 284 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

```
Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
1               5                   10                  15

Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
            20                  25                  30

Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr
        35                  40                  45

Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
    50                  55                  60

Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
65                  70                  75                  80

Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
                85                  90                  95

Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
            100                 105                 110

Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
        115                 120                 125

Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
    130                 135                 140

Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
145                 150                 155                 160

Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
                165                 170                 175
```

Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Ile
180 185 190

Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
195 200 205

Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys
210 215 220

Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
225 230 235 240

Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
245 250 255

Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
260 265 270

Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
275 280

(2) INFORMATION FOR SEQ ID NO:5200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5200:

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu
1 5 10 15

Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn
20 25 30

Asp Thr Asn Lys Lys Thr Gln Gln Thr Asp Asn Thr Thr Gln Ser Asn
35 40 45

Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn
50 55 60

Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys
65 70 75 80

Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu
85 90 95

Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn
100 105 110

Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys
115 120 125

Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn
130 135 140

Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile
145 150 155 160

Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro
165 170 175

Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu
180 185 190

Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys
195 200 205

(2) INFORMATION FOR SEQ ID NO:5201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

Met Leu Lys Gly Cys Gly Gly Cys Leu Ile Ser Phe Ile Leu Leu Ile
1 5 10 15

Ile Leu Leu Ser Ala Cys Ser Met Met Phe Ser Asn Asn Asp Asn Ser
20 25 30

Thr Asn Asn Gln Ser Ser Lys Thr Gln Leu Thr Gln Lys Asp Glu Asn
35 40 45

Lys Asn Glu Asp Lys Pro Glu Glu Lys Ser Glu Thr Ala Thr Asp Glu
50 55 60

Asp Leu Gln Ser Thr Glu Glu Val Pro Ala Asn Glu Asn Thr Glu Asn
65 70 75 80

Asn Gln His Glu Ile Asp Glu Ile Thr Thr Lys Asp Gln Ser Asp Asp
85 90 95

Asp Ile Asn Thr Pro Asn Val Ala Glu Asp Lys Ser Gln Asp Asp Leu
100 105 110

Lys Asp Asp Leu Lys Glu Lys Gln Gln Ser Ser Asn His His Gln Ser
115 120 125

Thr Gln Pro Lys Thr Ser Pro Ser Thr Glu Thr Asn Thr Gln Gln Ser
130 135 140

Phe Ala Asn Cys Lys Gln Leu Arg Gln Val Tyr Pro Asn Gly Val Thr

Ala Asp His Pro Ala Tyr Arg Pro His Leu Asp Arg Asp Lys Asp Lys
165 170 175

Arg Ala Cys Glu Pro Asp Lys Tyr
180

(2) INFORMATION FOR SEQ ID NO:5202:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile
1 5 10 15

Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr
20 25 30

Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys
35 40 45

Asp Ile Phe Xaa Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu
50 55 60

Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu
65 70 75 80

Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser
85 90 95

Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser
100 105 110

Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu
115 120 125

Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu Met Met Asn
130 135 140

Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile
145 150 155 160

Glu Lys Leu Ser Tyr Gln Pro Gln Asn Lys Ile Asn Val Val Asp Val
165 170 175

Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile
180 185 190

Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys

(2) INFORMATION FOR SEQ ID NO:5203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 283 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5203:

```
Met Lys Ser Lys Ile Tyr Ile Leu Leu Leu Xaa Leu Ile Phe Leu Ser
1               5                  10                  15

Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr
            20                  25                  30

Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu
        35                  40                  45

Xaa Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr
    50                  55                  60

Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly
65                  70                  75                  80

Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu
                85                  90                  95

Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp
            100                 105                 110

Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr
        115                 120                 125

Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly
    130                 135                 140

Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser
145                 150                 155                 160

Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr
                165                 170                 175

Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala
            180                 185                 190

Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly
        195                 200                 205

Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys
    210                 215                 220
```

225 230 235 240

Leu Asn Val Asp Gly Ile Ala Leu Val Lys Asn Ala His Pro His Pro
245 250 255

Lys Arg Lys Lys Leu Val Gln Tyr Leu Thr Ser Arg Ser Val Gln Gln
260 265 270

Arg Leu Val Ala Glu Phe Asp Ala Lys Ser Ile
275 280

(2) INFORMATION FOR SEQ ID NO:5204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5204:

Met Lys Lys Phe Ile Gly Ser Val Leu Ala Thr Thr Leu Ile Leu Gly
1 5 10 15

Gly Cys Ser Thr Met Glu Asn Glu Ser Lys Lys Asp Thr Lys Thr Glu
20 25 30

Thr Lys Ser Val Pro Glu Glu Met Glu Ala Ser Lys Tyr Val Gly Gln
35 40 45

Gly Phe Gln Pro Pro Ala Glu Lys Asn Ala Ile Glu Phe Ala Lys Lys
50 55 60

His Arg Lys Glu Phe Glu Lys Val Gly Glu Gln Phe Phe Lys Asp Asn
65 70 75 80

Phe Gly Leu Lys Val Lys Ala Thr Asn Val Val Gly Lys Asp Asp Gly
85 90 95

Val Glu Val Tyr Val His Cys Glu Asp His Gly Ile Val Phe Asn Ala
100 105 110

Ser Leu Pro Leu Tyr Lys Asp Ala Ile His Gln Lys Gly Ser Met Arg
115 120 125

Ser Asn Asp Asn Gly Asp Asp Met Ser Met Met Val Gly Thr Val Leu
130 135 140

Ser Gly Phe Glu Tyr Arg Ala Gln Lys Glu Lys Tyr Asp Asn Leu Tyr
145 150 155 160

Lys Phe Phe Lys Glu Asn Glu Lys Lys Tyr Gln Tyr Thr Gly Phe Thr
165 170 175

```
                180                 185                 190

Phe Tyr Ile Thr Tyr Ser Ser Arg Ser Leu Lys Glu Tyr Arg Lys Tyr
        195                 200                 205

Tyr Glu Pro Leu Ile Arg Lys Asn Asp Lys Glu Phe Lys Glu Gly Met
    210                 215                 220

Glu Arg Ala Arg Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Ala Val
225                 230                 235                 240

Ala Thr Leu Phe Ser Thr Lys Lys Asn Phe Thr Lys Asp Asn Thr Val
                245                 250                 255

Asp Asp Val Ile Glu Leu Ser Asp Lys Leu Tyr Asn Leu Lys Asn Lys
            260                 265                 270

Pro Asp Lys Ser Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn
        275                 280                 285

Thr Lys Lys Ala Phe Tyr Asp Asp Asn Arg Pro Ile Glu Tyr Gly Val
    290                 295                 300

His Ser Lys Asp Glu
305
```

(2) INFORMATION FOR SEQ ID NO:5205:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

```
Met Lys Lys Leu Val Ser Ile Val Gly Ala Thr Leu Leu Leu Ala Gly
1               5                   10                  15

Cys Gly Ser Gln Asn Leu Ala Pro Leu Glu Glu Lys Thr Thr Asp Leu
            20                  25                  30

Arg Glu Asp Asn His Gln Leu Lys Leu Asp Ile Gln Glu Leu Asn Gln
        35                  40                  45

Gln Ile Ser Asp Ser Lys Ser Lys Ile Lys Gly Leu Glu Lys Asp Lys
    50                  55                  60

Glu Asn Ser Lys Lys Thr Ala Ser Asn Asn Thr Lys Ile Lys Leu Met
65                  70                  75                  80

Asn Val Thr Ser Thr Tyr Tyr Asp Lys Val Ala Lys Ala Leu Lys Ser
                85                  90                  95
```

100 105 110

Val Gln Ser Lys Leu Asn Gln Ile Ser Asn Asp Ile Gln Ser Ala His
115 120 125

Thr Ser Tyr Lys Asp Ala Ile Asp Gly Leu Ser Leu Ser Asp Asp Asp
130 135 140

Lys Lys Thr Ser Lys Asn Ile Asp Lys Leu Asn Ser Asp Leu Asn His
145 150 155 160

Ala Phe Asp Asp Ile Lys Asn Gly Tyr Gln Asn Lys Asp Lys Lys Gln
165 170 175

Leu Thr Lys Gly Gln Gln Ala Leu Ser Lys Leu Asn Leu Asn Ala Lys
180 185 190

Ser

(2) INFORMATION FOR SEQ ID NO:5206:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

Met Lys Arg Leu Leu Phe Val Met Ile Ala Phe Val Phe Ile Leu Ala
1 5 10 15

Ala Cys Gly Asn Asn Ser Ser Lys Asp Lys Glu Ala Ser Lys Asp Ser
20 25 30

Lys Thr Ile Asn Val Gly Thr Glu Gly Thr Tyr Ala Pro Phe Ser Phe
35 40 45

His Asp Lys Asp Gly Lys Leu Thr Gly Tyr Asp Ile Asp Val Ile Lys
50 55 60

Ala Val Ala Lys Glu Glu Gly Leu Lys Leu Lys Phe Asn Glu Thr Ser
65 70 75 80

Trp Asp Ser Met Phe Ala Gly Leu Asp Ala Gly Arg Phe Asp Val Ile
85 90 95

Ala Asn Gln Val Gly Ile Asn Pro Asp Arg Glu Lys Lys Tyr Lys Phe
100 105 110

Ser Lys Pro Tyr Thr Phe Ser Ser Ala Val Leu Val Ile Arg Glu Asn
115 120 125

```
    130                 135                 140

Gln Thr Phe Thr Ser Asn Tyr Gly Lys Leu Ala Lys Asp Lys Gly Ala
145                 150                 155                 160

Asp Ile Thr Lys Val Asp Gly Phe Asn Gln Ser Met Asp Leu Leu Leu
                165                 170                 175

Ser Lys Arg Val Asp Gly Thr Phe Asn Asp Ser Leu Ser Tyr Leu Asp
            180                 185                 190

Tyr Lys Lys Gln Lys Pro Asn Ala Lys Ile Lys Ala Ile Lys Gly Asn
        195                 200                 205

Ala Glu Gln Ser Arg Ser Ala Phe Ala Phe Ser Lys Lys Ala Asp Asp
    210                 215                 220

Glu Thr Val Gln Lys Phe Asn Asp Gly Leu Lys Lys Ile Glu Glu Asn
225                 230                 235                 240

Gly Glu Leu Ala Lys Ile Gly Lys Lys Trp Phe Gly Gln Asp Val Ser
                245                 250                 255

Lys Ser Lys
```

(2) INFORMATION FOR SEQ ID NO:5207:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5207:

```
Met Gly Val His Ser Met Lys Leu Lys Arg Leu Phe Ala Val Val Ile
1               5                   10                  15

Ala Met Leu Leu Val Leu Ala Gly Cys Ser Asn Ser Asn Asp Asn Asn
            20                  25                  30

Glu Ser Lys Lys Asp Asp Ala Asp Asn Gly Lys Lys Gln Glu Ile Gln
        35                  40                  45

Val Ala Ala Ala Ala Ser Leu Thr Asp Val Thr Lys Lys Leu Ala Ser
    50                  55                  60

Glu Phe Lys Lys Glu His Lys Asn Ala Asp Ile Lys Phe Asn Tyr Gly
65                  70                  75                  80

Gly Ser Gly Ala Leu Arg Lys Gln Ile Glu Ser Gly Ala Pro Val Asp
                85                  90                  95
```

100 105 110

Asn Lys Ala His Asp Thr Tyr Lys Tyr Ala Lys Asn Ser Leu Val Leu
115 120 125

Ile Gly Asp Lys Asp Ser Asn Tyr Thr Ser Val Lys Asp Leu Lys Asp
130 135 140

Asn Asp Lys Leu Ala Leu Gly Glu Val Lys Thr Val Pro Ala Gly Lys
145 150 155 160

Tyr Ala Lys Gln Tyr Leu Asp Asn Asn Asn Leu Phe Lys Glu Val Glu
165 170 175

Ser Xaa Ile Val Tyr Ala Lys Asp Val Lys Gln Val Leu Asn Tyr Val
180 185 190

Xaa Lys Gly Asn Ala Lys Gln Gly Phe Val Tyr
195 200

(2) INFORMATION FOR SEQ ID NO:5208:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5208:

Met Lys Lys Trp Gln Phe Val Gly Thr Thr Ala Leu Gly Ala Thr Leu
1 5 10 15

Leu Leu Gly Ala Cys Gly Gly Gly Asn Gly Gly Ser Gly Asn Ser Asp
20 25 30

Leu Lys Gly Glu Ala Lys Gly Asp Gly Ser Ser Thr Val Ala Pro Ile
35 40 45

Val Glu Lys Leu Asn Glu Lys Trp Ala Gln Asp His Ser Asp Ala Lys
50 55 60

Ile Ser Ala Gly Gln Ala Gly Thr Gly Ala Gly Phe Gln Lys Phe Ile
65 70 75 80

Ala Gly Asp Ile Asp Phe Ala Asp Ala Ser Arg Pro Ile Lys Asp Glu
85 90 95

Glu Lys Gln Lys Leu Gln Asp Lys Asn Ile Lys Tyr Lys Glu Phe Lys
100 105 110

Ile Ala Gln Asp Gly Val Thr Val Ala Val Asn Lys Glu Asn Asp Phe
115 120 125

```
     130                 135                 140

Ala Lys Thr Trp Lys Asp Val Asn Ser Lys Trp Pro Asp Lys Lys Ile
145                 150                 155                 160

Asn Ala Val Ser Pro Asn Ser Ser His Gly Thr Tyr Asp Phe Phe Glu
                165                 170                 175

Asn Glu Val Met Asn Lys Glu Asp Ile Lys Ala Glu Lys Asn Ala Asp
            180                 185                 190

Thr Asn Ala Ile Val Ser Ser Val Thr Lys Asn Lys Glu Gly Ile Gly
        195                 200                 205

Tyr Phe Gly Tyr Asn Phe Tyr Val Gln Asn Lys Asp Lys Leu Lys Glu
    210                 215                 220

Val Lys Ile Lys Asp Glu Asn Gly Lys Ala Thr Glu Pro Thr Lys Lys
225                 230                 235                 240

Thr Ile Gln Asp Asn Ser Tyr Ala Leu Ser Arg Pro Leu Phe Ile Tyr
                245                 250                 255

Val Asn Glu Lys Ala Leu Lys Asp Asn Lys Val Met Ser Glu Phe Ile
            260                 265                 270

Lys Phe Val Leu Glu Asp Lys Gly Lys Ala Ala Glu Glu Ala Gly Tyr
        275                 280                 285

Val Ala Ala Pro Glu Lys Thr Tyr Lys Ser Gln Leu Asp Asp Leu Lys
    290                 295                 300

Ala Phe Ile Asp Lys Asn Gln Lys Ser Asp Asp Lys Lys Ser Asp Asp
305                 310                 315                 320

Lys Lys Ser Glu Asp Lys Lys
                325
```

(2) INFORMATION FOR SEQ ID NO:5209:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5209:

```
Met Lys Arg Leu Ser Ile Ile Val Ile Ile Gly Ile Phe Ile Ile Thr
1               5                   10                  15

Gly Cys Asp Trp Gln Arg Thr Ser Lys Glu Arg Ser Lys Asn Ala Gln
            20                  25                  30
```

```
                35                  40                  45

Asn Leu Met Met Thr Lys Lys Leu Leu Ser Gln Tyr Asn His Pro Lys
    50                  55                  60

Tyr Lys Leu Glu Leu Val Lys Phe Asn Asn Trp Pro Asp Leu Met Asp
65                  70                  75                  80

Ala Leu Asn Ser Gly Arg Ile Asp Gly Ala Ser Thr Leu Ile Glu Leu
                85                  90                  95

Ala Met Lys Ser Lys Gln Lys Gly Ser Asn Ile Lys Ala Val Ala Leu
            100                 105                 110

Gly His His Glu Gly Asn Val Ile Met Gly Gln Lys Gly Met His Leu
        115                 120                 125

Asn Glu Phe Asn Asn Asn Gly Asp Asp Tyr His Phe Gly Ile Pro His
    130                 135                 140

Arg Tyr Ser Thr His Tyr Leu Leu Leu Glu Glu Leu Arg Lys Gln Leu
145                 150                 155                 160

Lys Ile Lys Pro Gly His Phe Ser Tyr His Glu Met Ser Pro Ala Glu
                165                 170                 175

Met Pro Ala Ala Leu Ser Glu His Arg Ile Thr Gly Tyr Ser Val Ala
            180                 185                 190

Glu Pro Phe Gly Ala Leu Gly Glu Lys Leu Gly Lys Gly Lys Thr Leu
        195                 200                 205

Lys His Gly Asp Asp Val Ile Pro Asp Ala Tyr Cys Cys Val Leu Val
    210                 215                 220

Leu Arg Gly Glu Leu Leu Asp Gln His Lys Asp Val Ala Gln Ala Phe
225                 230                 235                 240

Val Gln Asp Tyr Lys Lys Ser Gly Phe Lys Met Asn Asp Arg Lys Gln
                245                 250                 255

Ser Val Asp Ile Met Thr His His Phe Lys Gln Ser Arg Asp Val Leu
            260                 265                 270

Thr Gln Ser Ala Ala Trp Thr Ser Tyr Gly Asp Leu Thr Ile Lys Pro
        275                 280                 285

Ser Gly Tyr Gln Glu Ile Thr Thr Leu Val Lys Gln His His Leu Phe
    290                 295                 300

Asn Pro Pro Ala Tyr Asp Asp Phe Val Glu Pro Ser Leu Tyr Lys Glu
305                 310                 315                 320

Ala Ser Arg Ser
```

(2) INFORMATION FOR SEQ ID NO:5210:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5210:

```
Met Lys Lys Thr Leu Gly Cys Leu Leu Leu Ile Met Leu Leu Val Val
1               5                  10                  15

Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Lys Ser
            20                  25                  30

Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys
        35                  40                  45

Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly
    50                  55                  60

Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu
65                  70                  75                  80

Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys
                85                  90                  95

Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp
            100                 105                 110

Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys
        115                 120                 125

Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln
    130                 135                 140

Val Asp Tyr Trp
145
```

(2) INFORMATION FOR SEQ ID NO:5211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5211:

```
Trp Pro Cys Ala Thr Xaa Gln Glx Glu Trp Trp Ser Arg His Xaa Trp
1               5                  10                  15
```

20 25 30

His

(2) INFORMATION FOR SEQ ID NO:5212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 490 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5212:

```
Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys
1               5                  10                  15

Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn
            20                  25                  30

Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
        35                  40                  45

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
    50                  55                  60

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
65                  70                  75                  80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
                85                  90                  95

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
            100                 105                 110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
        115                 120                 125

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
    130                 135                 140

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
145                 150                 155                 160

Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro
                165                 170                 175

Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile
            180                 185                 190

Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn
        195                 200                 205
```

```
     210                 215                 220

Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg Leu
225                 230                 235                 240

Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp Gln
                245                 250                 255

Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile Gly
            260                 265                 270

Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala Asp
        275                 280                 285

Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys Ala
    290                 295                 300

Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile Arg
305                 310                 315                 320

Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser Val
                325                 330                 335

Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu Asp
            340                 345                 350

Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala Tyr
        355                 360                 365

Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser Ala
    370                 375                 380

Ser Ser Asn Thr Val Lys Pro Val Ala Ser Ala Trp Lys Arg Asn Lys
385                 390                 395                 400

Tyr Gly Thr Tyr Tyr Met Glu Glu Ser Ala Arg Phe Thr Asn Gly Asn
                405                 410                 415

Gln Pro Ile Thr Val Arg Lys Val Gly Pro Phe Leu Ser Cys Pro Val
            420                 425                 430

Gly Tyr Gln Phe Gln Pro Gly Gly Tyr Cys Asp Tyr Thr Glu Val Met
        435                 440                 445

Leu Gln Asp Gly His Val Trp Val Gly Tyr Thr Trp Glu Gly Gln Arg
    450                 455                 460

Tyr Tyr Leu Pro Ile Arg Thr Trp Asn Gly Ser Ala Pro Pro Asn Gln
465                 470                 475                 480

Ile Leu Gly Asp Leu Trp Gly Glu Ile Ser
                485                 490
```

(2) INFORMATION FOR SEQ ID NO:5213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5213:

```
Gly Asp Lys Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu
1               5                  10                  15

Ser Val Ala Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala
            20                  25                  30

Phe Ala Lys Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile
        35                  40                  45

Pro Ala Ser Gln Lys Ala Asn Leu Gly Asn Gln Asn Ile Met Ala Val
    50                  55                  60

Ala Trp Tyr Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly
65                  70                  75                  80

Tyr Asn Ser Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys
                85                  90                  95

Gly Lys His Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu
            100                 105                 110

Asp Asn Ser Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe
        115                 120                 125

Pro Glu Gly Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val
    130                 135                 140

Tyr Gly Ala Lys Glu Phe Leu Lys Tyr Ala Asp Lys Lys Gly Val Asp
145                 150                 155                 160

Ile Tyr Tyr Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr
                165                 170                 175

Gln Lys Asn Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His
            180                 185                 190

Ile Leu Leu Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln
        195                 200                 205

Met Val Gln Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu
    210                 215                 220

Leu Asp Phe Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala
225                 230                 235                 240

Leu Ile Glu Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe
                245                 250                 255

Pro Asn Pro Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn
            260                 265                 270
```

275 280 285

Lys Gln Phe Asp Pro Lys Thr Gly Glu Val Lys
290 295

(2) INFORMATION FOR SEQ ID NO:5214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5214:

Leu Asn Lys Cys Lys Ile Ile Ile Trp Arg Ile Ile Asn Met Lys Asn
1 5 10 15

Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile Gly Ile Thr
20 25 30

Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro
35 40 45

Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn
50 55 60

Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro
65 70 75 80

Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp
85 90 95

Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala
100 105 110

Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln
115 120 125

Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg
130 135 140

Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys
145 150 155 160

Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu
165 170 175

Val Lys

(2) INFORMATION FOR SEQ ID NO:5215:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5215:

```
Lys Glu Arg Val Leu Met Lys Lys Leu Leu Thr Ala Ser Ile Ile Ala
1               5                  10                  15

Cys Ser Val Val Met Gly Val Gly Leu Val Asn Thr Ser Ala Glu Ala
            20                  25                  30

Ala Ser Gly Asn Ser Ile Asp Thr Val Lys Gln Leu Ile Lys Gly Asp
        35                  40                  45

Gln Ser Leu Glu Asn Val Lys Ile Gly Glu Ser Ile Lys Asp Val Leu
    50                  55                  60

Thr Lys Tyr Lys Asn Pro Met Tyr Ser Tyr Asn Glu Asp Gly Thr Glu
65                  70                  75                  80

His Tyr Tyr Glu Phe His Thr Lys Lys Gly Met Leu Leu Val Thr Thr
                85                  90                  95

Asp Gly Lys Lys Asn Asn Gly Lys Val Thr His Ile Ser Met Met Tyr
            100                 105                 110

Asn Asp Ala Asn Gly Pro Thr Tyr Gln Ala Val Lys Asn Tyr Val Gly
        115                 120                 125

Lys Ala Val Thr His Thr Glu Tyr Ser Lys Val Ala Gly Asn Phe Gly
    130                 135                 140

Tyr Ile Glu Lys Gly Lys Thr Thr Tyr Gln Phe Ala Ser Ala Pro Lys
145                 150                 155                 160

Asp Lys Asn Ile Lys Leu Tyr Arg Ile Asp Leu Glu Lys
                165                 170
```

(2) INFORMATION FOR SEQ ID NO:5216:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

```
1               5                   10                  15

Asn Glu Asp Gly Ser Lys Lys Lys Met Ser Thr Thr Ala Lys Val Val
            20                  25                  30

Ser Ile Ala Thr Val Leu Leu Leu Leu Gly Gly Leu Val Phe Ala Ile
        35                  40                  45

Phe Ala Tyr Val Asp His Ser Asn Lys Ala Lys Glu Arg Met Leu Asn
    50                  55                  60

Glu Gln Lys Gln Glu Gln Lys Glu Lys Arg Gln Lys Glu Asn Ala Glu
65                  70                  75                  80

Lys Glu Arg Lys Lys Lys Gln Gln Glu Glu Lys Glu Gln Asn Glu Leu
                85                  90                  95

Asp Ser Gln Ala Asn Gln Tyr Gln Gln Leu Pro Gln Gln Asn Gln Tyr
            100                 105                 110

Gln Tyr Val Pro Pro Gln Gln Gln Ala Pro Thr Lys Gln Arg Pro Ala
        115                 120                 125

Lys Glu Glu Asn Asp Asp Lys Ala Ser Lys Asp Glu Ser Lys Asp Lys
    130                 135                 140

Asp Asp Lys Ala Ser Gln Asp Lys Ser Asp Asp Asn Gln Lys Lys Thr
145                 150                 155                 160

Asp Asp Asn Lys Gln Pro Ala
                165
```

(2) INFORMATION FOR SEQ ID NO:5217:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5217:

```
Met Lys Arg Asn Phe Pro Lys Leu Ile Ala Leu Ser Leu Ile Phe Ser
1               5                   10                  15

Leu Ser Val Thr Pro Ile Ala Asn Ala Glu Ser Asn Ser Asn Ile Lys
            20                  25                  30

Ala Lys Asp Lys Lys His Val Gln Val Asn Val Glu Asp Lys Ser Val
        35                  40                  45

Pro Thr Asp Val Arg Asn Leu Ala Gln Lys Asp Tyr Leu Ser Tyr Val
    50                  55                  60
```

65 70 75 80

Gly Glu Pro Phe Lys Ile Tyr Lys Phe Asn Lys Lys Ser Asp Gly Asn
85 90 95

Tyr Tyr Phe Pro Val Leu Asn Thr Glu Gly Asn Ile Asp Tyr Ile Val
100 105 110

Thr Ile Ser
115

(2) INFORMATION FOR SEQ ID NO:5218:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5218:

Asn Phe Lys Met Gln Glu Val Lys Tyr Met Thr Glu Ile Thr Phe Lys
1 5 10 15

Gly Gly Pro Ile His Leu Lys Gly Gln Gln Ile Asn Glu Gly Asp Phe
20 25 30

Ala Pro Asp Phe Thr Val Leu Asp Asn Asp Leu Asn Gln Val Thr Leu
35 40 45

Ala Asp Tyr Ala Gly Lys Lys Lys Leu Ile Ser Val Val Pro Ser Ile
50 55 60

Asp Thr Gly Val Cys Asp Gln Gln Thr Arg Lys Phe Asn Ser Asp Ala
65 70 75 80

Ser Lys Glu Glu Gly Ile Val Leu Thr Ile Ser Ala Asp Leu Pro Phe
85 90 95

Ala Gln Lys Arg Trp Cys Ala Ser Ala Gly Leu Asp Asn Val Ile Thr
100 105 110

Leu Ser Asp His Arg Asp Leu Ser Phe Gly Glu Asn Tyr Gly Val Val
115 120 125

Met Glu Glu Leu Arg Leu Leu Ala Arg Ala Val Phe Val Leu Asp Ala
130 135 140

Asp Asn Lys Val Val Tyr Lys Glu Ile Val Ser Glu Gly Thr Asp Phe
145 150 155 160

Pro Asp Phe Asp Ala Ala Leu Ala Ala Tyr Lys Asn Ile
165 170

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5219:

```
Ile Glu Ser Arg Phe Ile Met Ala Lys Ile Asn Phe Asp Ala Ala Thr
1               5                  10                  15

Lys Gly Asn Pro Gly Ile Ser Thr Cys Ala Ile Val Ile Lys Glu Asp
            20                  25                  30

Glu Gln His Tyr Thr Tyr Thr His Glu Leu Gly Glu Met Asp Asn His
        35                  40                  45

Thr Ala Glu Trp Ala Ala Cys Ile Tyr Ala Leu Glu His Ala Arg Glu
    50                  55                  60

Leu Asn Val Gln Asn Ala Leu Leu Tyr Thr Asp Ser Lys Leu Ile Ala
65                  70                  75                  80

Asp Ser Ile Glu Ala Gly Tyr Val Lys Asn Ala Asn Phe Lys Pro Tyr
                85                  90                  95

Phe Asp Gln Ile Glu Ile Phe Glu Lys Asp Phe Asp Leu Leu Phe Val
            100                 105                 110

Lys Trp Ile Pro Arg Glu Gln Asn Lys Glu Ala Asn Gln His Ala Gln
        115                 120                 125

Gln Ala Leu Tyr Lys Leu Ile Lys Lys Asn Lys
    130                 135
```

(2) INFORMATION FOR SEQ ID NO:5220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5220:

```
Met Pro Gly Thr Val Leu Asp Pro Gln Met Ile Lys Asn Glu Asp Val
1               5                  10                  15
```

```
                20                  25                  30

Gly Val Asn Thr Ser Met Asp Trp Asp Arg Lys Tyr Pro Tyr Gly Asp
        35                  40                  45

Thr Leu Arg Gly Ile Phe Gly Asp Val Ser Thr Pro Ala Glu Gly Ile
    50                  55                  60

Pro Lys Glu Leu Thr Glu His Tyr Leu Ser Lys Gly Tyr Ser Arg Asn
65                  70                  75                  80

Asp Arg Val Gly Lys Ser Tyr Leu Glu Tyr Gln Tyr Glu Asp Val Leu
                85                  90                  95

Arg Gly Lys Lys Lys Glu Met Lys Tyr Thr Thr Asp Lys Ser Gly Lys
            100                 105                 110

Val Thr Ser Ser Glu Val Leu Xaa Pro Gly Ala Arg Gly Gln Asp Leu
        115                 120                 125

Lys Leu Thr Ile Asp Ile Asp Leu Gln Lys Glu Val Glu Ala Leu Leu
    130                 135                 140

Asp Lys Gln Ile Lys Lys Leu Ala Val Lys Val Pro Lys Ile Trp Ile
145                 150                 155                 160

Met Gln
```

(2) INFORMATION FOR SEQ ID NO:5221:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221:

```
Ile Met Ala Tyr Asp Gly Leu Phe Thr Lys Lys Met Val Glu Ser Leu
1               5                   10                  15

Gln Phe Leu Thr Thr Gly Arg Val His Lys Ile Asn Gln Pro Asp Asn
            20                  25                  30

Asp Thr Ile Leu Met Val Val Arg Gln Asn Arg Gln Asn His Gln Leu
        35                  40                  45

Leu Leu Ser Ile His Pro Asn Phe Ser Arg Leu Gln Leu Thr Thr Lys
    50                  55                  60

Lys Tyr Asp Asn Pro Phe Asn Pro Pro Met Phe Ala Arg Val Phe Arg
65                  70                  75                  80
```

```
                    85                  90                  95

Asp Arg Arg Ile Glu Ile Asp Ile Lys Ser Lys Asp Glu Ile Gly Asp
            100                 105                 110

Thr Ile Tyr Arg Thr Val Ile Leu Glu Ile Met Gly Lys His Ser Asn
        115                 120                 125

Leu Ile Leu Val Asp Glu Asn Arg Lys Ile Ile Glu Gly Phe Lys His
    130                 135                 140

Leu Thr Pro Asn Thr Asn His Tyr Arg Thr Val Met Pro Gly Phe Asn
145                 150                 155                 160

Tyr Glu Ala Pro Pro Thr Gln His Lys Ile Asn Pro Tyr Asp Ile Thr
                165                 170                 175

Gly Ala Glu Val Leu Lys Tyr Ile Asp Phe Asn Ala Gly Asn Ile Ala
            180                 185                 190

Lys Gln Leu Leu Asn Gln Phe Glu Gly Phe Ser Pro Leu Ile Thr Asn
        195                 200                 205

Glu Ile Val Ser Arg Arg Gln Phe Met Thr Ser Ser Thr Leu Pro Glu
    210                 215                 220

Ala Phe Asp Glu Val Met Ala Glu Thr Lys Leu Pro Pro Thr Pro Ile
225                 230                 235                 240

Phe His Lys Asn His Glu Thr Gly Lys Glu Asp Phe Tyr Phe Ile Lys
                245                 250                 255

Leu Asn Gln Phe Asn Asp Asp Thr Val Thr Tyr Asp Ser Leu Asn Asp
            260                 265                 270

Leu Leu Asp Arg Phe Tyr Asp Ala Arg Gly Glu Arg Glu Arg Val Lys
        275                 280                 285

Gln Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys
    290                 295                 300

Tyr Gln Asn Lys Leu Ala Ser
305                 310
```

(2) INFORMATION FOR SEQ ID NO:5222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

```
1               5                  10                  15
Glu Gln Leu Tyr Gly Glu Leu Ile Thr Ala Asn Ile Tyr Arg Ile Lys
            20                  25                  30
Gln Gly Asp Lys Glu Val Thr Ala Leu Asn Tyr Tyr Thr Asn Glu Glu
        35                  40                  45
Val Val Ile Pro Leu Asn Pro Thr Lys Ser Pro Ser Ala Asn Ala Gln
    50                  55                  60
Tyr Tyr Tyr Lys Gln Tyr Xaa Arg Met Lys Thr Arg Xaa Arg Glu Leu
65                  70                  75                  80
Gln His Gln Ile Gln Leu Thr Lys Asp Asn Ile Asp Tyr Phe Ser Thr
                85                  90                  95
Ile Glu Gln Gln Leu His His Ile Ser Val His Asp Ile Asp Glu Ile
            100                 105                 110
Arg Asp Glu Leu Ala Glu Gln Gly Phe Met Lys Gln Arg Lys Asn Gln
        115                 120                 125
Thr Lys Lys Lys Lys Ala Gln Ile Gln Leu Gln His Tyr Val Ser Thr
    130                 135                 140
Asp Gly Asp Asp Ile Tyr Val Gly Lys Asn Asn Lys Gln Asn Asp Tyr
145                 150                 155                 160
Leu Thr Asn Lys Lys Ala Lys Lys Thr His Thr Trp Leu His Thr Lys
                165                 170                 175
Asp Ile Pro Gly Ser His Val Val Ile Phe Asn Asp Ala Pro Ser Asp
            180                 185                 190
Thr Thr Ile Lys Glu Ala Ala Met Leu Ala Gly Tyr Phe Ser Lys Ala
        195                 200                 205
Gly Asn Ser Gly Gln Ile Pro Val Asp Tyr Thr Leu Ile Lys Asn Val
    210                 215                 220
His Lys Pro Ser Gly Ala Lys Pro Gly Phe Val Thr Tyr Asp Asn Gln
225                 230                 235                 240
Lys Thr Leu Tyr Ala
                245
```

(2) INFORMATION FOR SEQ ID NO:5223:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5223:

```
Tyr Ile Thr Asn Pro Gln Asn Pro Lys Ile Lys Ile Thr Gly Ile Ser
1               5                  10                  15

Leu Ser Ser Gly Val Gly Asn Phe Phe Ile Ile Thr Asn Gly Lys Arg
            20                  25                  30

Ile Ile Val Ala Lys Ile Lys Arg Asn Ala Asp Asn Asp Ser Ala Leu
        35                  40                  45

Lys Ser Phe Asn Ala Ile Phe Ile Ile Gly Asn Ala Asp Pro His Asn
    50                  55                  60

Met Ile Val Asn Lys Tyr Asp Arg Lys Val Val Ser Arg Ser Leu Phe
65                  70                  75                  80

Ile Asn Ile Ile Thr Pro Leu Ile Met Cys Phe Tyr Ile Lys Lys Tyr
                85                  90                  95

Asp Leu Lys
```

(2) INFORMATION FOR SEQ ID NO:5224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5224:

```
Glu Asn Val Leu Ala Lys Glu Tyr Ala Val Lys Tyr Asn Ala Val Glu
1               5                  10                  15

Ala Ile Gln His Arg Gly Glu Thr Val Thr Glu Gly Ser Ser Ser Asn
            20                  25                  30

Ala Tyr Ala Ile Lys Asp Gly Val Ile Tyr Thr His Pro Ile Asn Asn
        35                  40                  45

Tyr Ile Leu Asn Gly Ile Thr Arg Ile Val Ile Lys Lys Ile Ala Glu
    50                  55                  60

Asp Tyr Asn Ile Pro Phe Lys Glu Glu Thr Phe Thr Val Asp Phe Leu
65                  70                  75                  80

Lys Asn Ala Asp Glu Val Ile Val Ser Ser Thr Ser Ala Glu Val Thr
                85                  90                  95

Pro Val Ile Lys Leu Asp Gly Glu Pro Val Asn Asp Gly Lys Val Gly
            100                 105                 110
```

115 120 125

His Ser Ile
130

(2) INFORMATION FOR SEQ ID NO:5225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 540 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5225:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
1 5 10 15

Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
20 25 30

Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
35 40 45

Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
50 55 60

Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
65 70 75 80

Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
85 90 95

Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
100 105 110

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
115 120 125

Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
130 135 140

Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
145 150 155 160

Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
165 170 175

Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
180 185 190

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
195 200 205

```
    210                 215                 220

Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly
225                 230                 235                 240

Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn
                245                 250                 255

Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val
            260                 265                 270

Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys
        275                 280                 285

Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr
    290                 295                 300

Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp
305                 310                 315                 320

Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly
                325                 330                 335

Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu
            340                 345                 350

Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr
        355                 360                 365

Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly
    370                 375                 380

Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro
385                 390                 395                 400

Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn
                405                 410                 415

Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu
            420                 425                 430

Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr
        435                 440                 445

Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr
    450                 455                 460

Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly
465                 470                 475                 480

Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp
                485                 490                 495

Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr
            500                 505                 510

Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser
        515                 520                 525
```

530 535 540

(2) INFORMATION FOR SEQ ID NO:5226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226:

Tyr Lys Glu Leu Ser His Gly Arg Leu Ile Gly Gly Thr Lys Met His
1 5 10 15

Lys Lys Tyr Phe Ile Gly Thr Ser Ile Leu Ile Ala Val Phe Val Val
20 25 30

Ile Phe Asp Gln Val Thr Lys Tyr Ile Ile Ala Thr Thr Met Lys Ile
35 40 45

Gly Asp Ser Phe Glu Val Ile Pro His Phe Leu Asn Ile Thr Ser His
50 55 60

Arg Asn Asn Gly Ala Ala Trp Gly Ile Leu Ser Gly Lys Met Thr Phe
65 70 75 80

Phe Phe Ile Ile Thr Ile Ile Ile Leu Ile Ala Leu Val Tyr Phe Phe
85 90 95

Ile Lys Asp Ala Gln Tyr Asn Leu Phe Met Gln Val Ala Ile Ser Leu
100 105 110

Leu Phe Ala Gly Ala Leu Gly Asn Phe Ile Asp Arg Ile Leu Thr Gly
115 120 125

Glu Val Val Asp Phe Ile Asp Thr Asn Ile Phe Gly Tyr Asp Phe Pro
130 135 140

Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile
145 150 155 160

Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val
165 170 175

Lys

(2) INFORMATION FOR SEQ ID NO:5227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5227:

Ala Gly Lys Ser Ser Leu Ile Lys Ser Leu Ile Gly Glu Phe Asn Ala
1 5 10 15

Thr Gly Thr Lys Leu Leu Tyr Asn Lys Pro Ile Gln Gln Gln Leu Gln
20 25 30

His Ile Thr Tyr Ile Pro Gln Lys Ala His Ile Asp Leu Asp Phe Pro
35 40 45

Ile Ser Val Glu Gln Val Ile Leu Ser Gly Cys Tyr Lys Glu Ile Gly
50 55 60

Trp Phe Arg Arg Pro Asn Lys Ser Ala Arg Asp Lys Leu Lys Gln Leu
65 70 75 80

Leu Ser Asp Leu Glu Leu Glu Ser Leu Arg His Arg Gln Ile Ser Glu
85 90 95

Leu Ser Gly Gly Gln Leu Gln Arg Val Leu Val Ala Arg Ala Leu Met
100 105 110

Ser Xaa Ser Glu Val Tyr Phe Leu Asp Glu Pro Phe Val Gly Ile Asp
115 120 125

Phe Ser Ser Glu Lys Leu Ile Met Thr Lys Ile Glu Asn Leu Lys Gln
130 135 140

Gln Gly Lys Leu Ile Leu Ile Ile His His Asp Leu Ser Lys Ala Lys
145 150 155 160

Gln Tyr Phe Asp Arg Ile Ile Leu Leu Asn Gln Thr Leu Arg Tyr Phe
165 170 175

Gly Asp Ser Glu Glu Ala Met Ser Val Thr Arg Leu Asn Glu Thr Phe
180 185 190

Met Ser Ser Thr Asp Cys Ser Asp Pro Ser Gln Arg Ser Asn Ile Thr
195 200 205

Cys

(2) INFORMATION FOR SEQ ID NO:5228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5228:

```
Thr Phe Arg Ile Ile Phe Leu Leu Ser Ile Arg Lys Arg Ser Asn Arg
1               5                  10                  15

Thr His Val Ser Ile His Trp Ser Thr Val Asn Lys Glu Glu Ile Cys
            20                  25                  30

Leu Arg Val Lys Asp Asn Leu Gln Gln Ile Ser Thr Gln Ile Asn Asp
        35                  40                  45

Lys Ser Glu Lys Asn Asn Phe Ser Thr Lys Pro Asn Val Ile Ala Val
    50                  55                  60

Thr Lys Tyr Val Thr Ile Glu Arg Ala Lys Glu Ala Tyr Glu Ala Gly
65                  70                  75                  80

Ile Arg His Phe Gly Glu Asn Arg Leu Glu Gly Phe Phe Gln Lys Lys
                85                  90                  95

Glu Ala Leu Pro Ser Asp Ala Val Ile His Phe Ile Gly Ser Leu Gln
            100                 105                 110

Ser Arg Lys Val Lys Asp Val Ile Asn Asp Val Asp Tyr Phe His Ala
        115                 120                 125

Leu Asp Arg Leu Ser Leu Ala Lys Glu Ile Asn Lys Arg Ala Glu His
    130                 135                 140

Lys Ile Lys Cys Phe Leu Gln Val Asn Val Ser Gly Glu Ala Ser Lys
145                 150                 155                 160

His Gly Ile Ala Leu Glu Asp Val Asp Gln Phe Ile Asp Asp Leu Lys
                165                 170                 175

Lys Tyr Asp Lys Ile Glu Ile Val Gly Leu Met Thr Met Ala Pro Leu
            180                 185                 190

Thr Asp Asp Glu Ala Tyr Ile Arg Ser Leu Phe Lys Gln Leu Arg Leu
        195                 200                 205

Lys Lys Glu Glu Ile Gln Arg Leu Asn Leu Glu Tyr Ala Pro Cys Asp
    210                 215                 220

Glu Leu Ser Met Gly Met Ser Asn Asp Tyr Leu Ile Ala Val Glu Glu
225                 230                 235                 240

Gly Ala Thr Phe Val Arg Ile Gly Thr Lys Leu Val Gly Glu Glu Glu
                245                 250                 255
```

(2) INFORMATION FOR SEQ ID NO:5229:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5229:

```
Lys His Lys Leu Thr Ile Ile Thr Gly Gly Phe Phe Thr Met Lys Lys
1               5                  10                  15

Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val Thr Gly Tyr
            20                  25                  30

Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val Asn Val Asp
        35                  40                  45

Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp Gln Leu Asn
    50                  55                  60

Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe Val Lys Asp
65                  70                  75                  80

Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp Ser Trp Ser
                85                  90                  95

Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn Val Ala Gly
            100                 105                 110

Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val Gln Ser Val
        115                 120                 125

Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala Val Ser Ala
    130                 135                 140

Pro Thr Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser Ser Val Arg
145                 150                 155                 160

Leu Ser Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser Ala Ala Gln
                165                 170                 175

Ile Met Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp Ala Ala Ile
            180                 185                 190

Ile Ala Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn Pro Ser Gly
        195                 200                 205

Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Pro Thr Asn Thr
    210                 215                 220

Val Asp Gln Gln Ile Asn Ala Ala Val Lys Ala Tyr Lys Ala Gln Gly
225                 230                 235                 240

Leu Gly Ala Trp Gly Phe
                245
```

(2) INFORMATION FOR SEQ ID NO:5230:

(A) LENGTH: 519 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5230:

```
Lys Glu Pro His Lys Met Lys Lys Ile Tyr Lys Ser Leu Thr Val Ser
1               5                  10                  15

Ala Ile Val Ala Thr Val Ser Leu Ser Ala Leu Pro Gln Ser Leu Ala
            20                  25                  30

Ile Thr His Glu Ser Gln Pro Thr Lys Gln Gln Arg Thr Val Leu Phe
        35                  40                  45

Asp Arg Ser His Gly Gln Thr Ala Gly Ala Ala Asp Trp Val Ser Asp
    50                  55                  60

Gly Ala Phe Ser Asp Tyr Ala Asp Ser Ile Gln Lys Gln Gly Tyr Asp
65                  70                  75                  80

Val Lys Ala Ile Asp Gly His Ser Asn Ile Thr Glu Ala Ser Leu Lys
                85                  90                  95

Ser Ser Lys Ile Phe Val Ile Pro Glu Ala Asn Ile Pro Phe Lys Glu
            100                 105                 110

Ser Glu Gln Ala Ala Ile Val Lys Tyr Val Lys Gln Gly Gly Asn Val
        115                 120                 125

Val Phe Ile Ser Asp His Tyr Asn Ala Asp Arg Asn Leu Asn Arg Ile
    130                 135                 140

Asp Ser Ser Glu Ala Met Asn Gly Tyr Arg Arg Gly Ala Tyr Glu Asp
145                 150                 155                 160

Met Ser Lys Gly Met Asn Ala Glu Glu Lys Ser Ser Thr Ala Met Gln
                165                 170                 175

Gly Val Lys Ser Ser Asp Trp Leu Ser Thr Asn Phe Gly Val Arg Phe
            180                 185                 190

Arg Tyr Asn Ala Leu Gly Asp Leu Asn Thr Ser Asn Ile Val Ser Ser
        195                 200                 205

Lys Glu Ser Phe Gly Ile Thr Glu Gly Val Lys Ser Val Ser Met His
    210                 215                 220

Ala Gly Ser Thr Leu Ala Ile Thr Asn Pro Glu Lys Ala Lys Gly Ile
225                 230                 235                 240

Val Tyr Thr Pro Glu Gln Leu Pro Ala Lys Ser Lys Trp Ser His Ala
                245                 250                 255
```

```
Val Asp Gln Gly Ile Tyr Asn Gly Gly Gly Lys Ala Glu Gly Pro Tyr
            260                 265                 270

Val Ala Ile Ser Lys Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp
        275                 280                 285

Ser Ser Leu Val Glu Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn
    290                 295                 300

Gly Glu Lys Lys Lys Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly
305                 310                 315                 320

Lys Leu Leu Asn Asn Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly
                325                 330                 335

Lys Ser Leu Lys Ala Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu
            340                 345                 350

Leu Asp Phe Glu Arg Pro Glu Arg Ser Thr Glu Pro Glu Lys Glu Pro
        355                 360                 365

Trp Ser Gln Pro Pro Ser Gly Tyr Lys Trp Tyr Asp Pro Thr Thr Phe
    370                 375                 380

Lys Ala Gly Ser Tyr Gly Ser Glu Lys Gly Ala Asp Pro Gln Pro Asn
385                 390                 395                 400

Thr Pro Asp Asp His Thr Pro Pro Asn Gln Asn Glu Lys Val Thr Phe
                405                 410                 415

Asp Ile Pro Gln Asn Val Ser Val Asn Glu Pro Phe Glu Met Thr Ile
            420                 425                 430

His Leu Lys Gly Phe Glu Ala Asn Gln Thr Leu Glu Asn Leu Arg Val
        435                 440                 445

Gly Ile Tyr Lys Glu Gly Gly Arg Gln Ile Gly Gln Phe Ser Ser Lys
    450                 455                 460

Asp Asn Asp Tyr Asn Pro Pro Gly Tyr Ser Thr Leu Pro Thr Val Lys
465                 470                 475                 480

Ala Asp Glu Asn Gly Asn Val Thr Ile Lys Val Asn Ala Lys Val Leu
                485                 490                 495

Glu Ser Met Glu Gly Ser Lys Ile Arg Leu Lys Leu Gly Asp Lys Thr
            500                 505                 510

Leu Ile Thr Thr Asp Phe Lys
        515
```

(2) INFORMATION FOR SEQ ID NO:5231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5231:

```
Arg Asp Glu Arg Ile Lys Thr Met Thr Asn Ser Ser Lys Ser Phe Thr
1               5                  10                  15

Lys Phe Met Ala Ala Ser Ala Val Phe Thr Met Gly Phe Leu Ser Val
            20                  25                  30

Pro Thr Ala Gly Ala Glu Gln Thr Asn Gln Ile Ala Asn Lys Pro Gln
        35                  40                  45

Ala Ile Gln Trp His Thr Asn Leu Thr Asn Glu Arg Phe Thr Thr Ile
    50                  55                  60

Ala His Arg Gly Ala Ser Gly Tyr Ala Pro Glu His Thr Phe Gln Ala
65                  70                  75                  80

Tyr Asp Lys Ser His Asn Glu Leu Lys Ala Ser Tyr Ile Glu Ile Asp
                85                  90                  95

Leu Gln Arg Thr Lys Asp Gly His Leu Val Ala Met His Asp Glu Thr
            100                 105                 110

Val Asn Arg Thr Thr Asn Gly His Gly Lys Val Glu Asp Tyr Thr Leu
        115                 120                 125

Asp Glu Leu Lys Gln Leu Asp Ala Gly Ser Trp Phe Asn Lys Lys Tyr
    130                 135                 140

Pro Lys Tyr Ala Arg Ala Ser Tyr Lys Asn Ala Lys Val Pro Thr Leu
145                 150                 155                 160

Asp Glu Ile Leu Glu Arg Tyr Gly Pro Asn Ala Asn Tyr Tyr Ile Glu
                165                 170                 175

Thr Lys Ser Pro Asp Val Tyr Pro Gly Met Glu Glu Gln Leu Leu Ala
            180                 185                 190

Ser Leu Lys Lys His His Leu Leu Asn Asn Asn Lys Leu Lys Asn Gly
        195                 200                 205

His Val Met Ile Gln Ser Phe Ser Asp Glu Ser Leu Lys Lys Ile His
    210                 215                 220

Arg Gln Asn Lys His Val Pro Leu Val Lys Leu Val Asp Lys Gly Glu
225                 230                 235                 240

Leu Gln Gln Phe Asn Asp Gln Arg Leu Lys Glu Ile Arg Ser Tyr Ala
                245                 250                 255

Ile Gly Leu Gly Pro Asp Tyr Thr Asp Leu Thr Glu Gln Asn Thr His
            260                 265                 270

His Leu Lys Asp Leu Gly Phe Ile Val His Pro Tyr Thr Val Asn Glu
        275                 280                 285
```

Lys Ala Asp Met Leu Arg Leu Asn Lys Tyr Gly Val Asp Gly Val Phe
290 295 300

Thr Asn Phe Ala Asp Lys Tyr Lys Glu Val Ile Lys
305 310 315

(2) INFORMATION FOR SEQ ID NO:5232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 433 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5232:

Arg Phe Met Lys Asn Leu Ile Ser Ile Ile Ile Leu Cys Leu Thr
1 5 10 15

Leu Ser Ile Met Thr Pro Tyr Ala Gln Ala Thr Asn Ser Asp Val Thr
20 25 30

Pro Val Gln Ala Ala Asn Gln Tyr Gly Tyr Ala Gly Leu Ser Ala Ala
35 40 45

Tyr Glu Pro Thr Ser Ala Val Asn Val Ser Gln Thr Gly Gln Leu Leu
50 55 60

Tyr Gln Tyr Asn Ile Asp Thr Lys Trp Asn Pro Ala Ser Met Thr Lys
65 70 75 80

Leu Met Thr Met Tyr Leu Thr Leu Glu Ala Val Asn Lys Gly Gln Leu
85 90 95

Ser Leu Asp Asp Thr Val Thr Met Thr Asn Lys Glu Tyr Ile Met Ser
100 105 110

Thr Leu Pro Glu Leu Ser Asn Thr Lys Leu Tyr Pro Gly Gln Val Trp
115 120 125

Thr Ile Ala Asp Leu Leu Gln Ile Thr Val Ser Asn Ser Ser Asn Ala
130 135 140

Ala Ala Leu Ile Leu Ala Lys Lys Val Ser Lys Asn Thr Ser Asp Phe
145 150 155 160

Val Asp Leu Met Asn Asn Lys Ala Lys Ala Ile Gly Met Lys Asn Thr
165 170 175

His Phe Val Asn Pro Thr Gly Ala Glu Asn Ser Arg Leu Arg Thr Phe
180 185 190

Ala Pro Thr Lys Tyr Lys Asp Gln Glu Arg Thr Val Thr Thr Ala Arg
195 200 205

Asp Tyr Ala Ile Leu Asp Leu His Val Ile Lys Glu Thr Pro Lys Ile
210 215 220

Leu Asp Phe Thr Lys Gln Leu Ala Pro Thr Thr His Ala Val Thr Tyr
225 230 235 240

Tyr Thr Phe Asn Phe Ser Leu Glu Gly Ala Lys Met Ser Leu Pro Gly
245 250 255

Thr Asp Gly Leu Lys Thr Gly Ser Ser Asp Thr Ala Asn Tyr Asn His
260 265 270

Thr Ile Thr Thr Lys Arg Gly Lys Phe Arg Ile Asn Gln Val Ile Met
275 280 285

Gly Ala Gly Asp Tyr Lys Asn Leu Gly Gly Glu Lys Gln Arg Asn Met
290 295 300

Met Gly Asn Ala Leu Met Glu Arg Ser Phe Asp Gln Tyr Lys Tyr Val
305 310 315 320

Lys Ile Leu Ser Lys Gly Glu Gln Arg Ile Asn Gly Lys Lys Tyr Tyr
325 330 335

Val Glu Asn Asp Leu Tyr Asp Val Leu Pro Ser Asp Phe Ser Lys Lys
340 345 350

Asp Tyr Lys Leu Val Val Glu Asp Gly Lys Val His Ala Asp Tyr Pro
355 360 365

Arg Glu Phe Ile Asn Lys Asp Tyr Gly Pro Pro Thr Val Glu Val His
370 375 380

Gln Pro Ile Ile Gln Lys Ala Asn Thr Val Ala Lys Ser Met Trp Glu
385 390 395 400

Glu His Pro Leu Phe Thr Ile Ile Gly Gly Thr Cys Leu Val Ala Gly
405 410 415

Leu Ala Leu Ile Val His Met Ile Ile Asn Arg Leu Phe Arg Lys Arg
420 425 430

Lys

(2) INFORMATION FOR SEQ ID NO:5233:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

```
Leu Thr Lys Glu Arg Glu Tyr Met Lys Leu Lys Ser Phe Ile Thr Val
1               5                  10                  15

Thr Leu Ala Leu Gly Met Ile Ala Thr Thr Gly Ala Thr Val Ala Gly
            20                  25                  30

Asn Glu Val Ser Ala Ala Glu Lys Asp Lys Leu Pro Ala Thr Gln Lys
        35                  40                  45

Ala Lys Glu Met Gln Asn Val Pro Tyr Thr Ile Ala Val Asp Gly Ile
    50                  55                  60

Met Ala Phe Asn Gln Ser Tyr Leu Asn Leu Pro Lys Asp Ser Gln Leu
65                  70                  75                  80

Ser Tyr Leu Asp Leu Gly Asn Lys Val Lys Ala Leu Leu Tyr Asp Glu
                85                  90                  95

Arg Gly Val Thr Pro Glu Lys Ile Arg Asn Ala Lys Ser Ala Val Tyr
            100                 105                 110

Thr Ile Thr Trp Lys Asp Gly Ser Lys Lys Glu Val Asp Leu Lys Lys
        115                 120                 125

Asp Ser Tyr Thr Ala Asn Leu Phe Asp Ser Asn Ser Ile Lys Gln Ile
    130                 135                 140

Asp Ile Asn Val Lys Thr Lys
145                 150
```

(2) INFORMATION FOR SEQ ID NO:5234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 497 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5234:

```
Asn His Cys Asn Arg Ile Glu Arg Lys Met Ala Met Ser Asn Asn Phe
1               5                  10                  15

Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile Asp Thr Asn Ser His
            20                  25                  30

Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln Ser Glu Leu Glu His
        35                  40                  45

Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe Pro Pro Arg Asn Ala
    50                  55                  60

Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr Asn His Asn Lys Gln
65                  70                  75                  80
```

```
Val His Asn Glu Ser Gln Thr Ser Glu Asp Asn Val Gln Asn Glu Ala
                85                  90                  95

Gly Thr Ile Asp Asp Arg Gln Val Glu Ser Ser His Ser Thr Glu Ser
            100                 105                 110

Gln Glu Pro Ser His Gln Asp Ser Thr Pro Gln His Glu Glu Glu Tyr
        115                 120                 125

Tyr Asn Lys Asn Ala Phe Ala Met Asp Lys Ser His Pro Glu Pro Ile
    130                 135                 140

Glu Asp Asn Asp Lys His Asp Thr Ile Lys Asn Ala Glu Asn Asn Thr
145                 150                 155                 160

Glu His Ser Thr Val Ser Asp Lys Ser Glu Ala Glu Gln Ser Gln Gln
                165                 170                 175

Pro Lys Pro Tyr Phe Thr Thr Gly Ala Asn Gln Ser Glu Thr Ser Lys
            180                 185                 190

Asn Glu His Asp Asn Asp Ser Val Lys Gln Asp Gln Asp Glu Pro Lys
        195                 200                 205

Glu His His Asn Gly Lys Lys Ala Ala Ala Ile Gly Ala Gly Thr Ala
    210                 215                 220

Gly Val Ala Gly Ala Ala Gly Ala Met Ala Ala Ser Lys Ala Lys Lys
225                 230                 235                 240

His Ser Asn Asp Ala Gln Asn Lys Ser Asn Ser Gly Lys Ala Asn Asn
                245                 250                 255

Ser Thr Glu Asp Lys Ala Ser Gln Asp Lys Ser Lys Asp His His Asn
            260                 265                 270

Gly Lys Lys Gly Ala Ala Ile Gly Ala Gly Thr Ala Gly Leu Ala Gly
        275                 280                 285

Gly Ala Ala Ser Lys Ser Ala Ser Ala Ala Ser Lys Pro His Ala Ser
    290                 295                 300

Asn Asn Ala Ser Gln Asn His Asp Glu His Asp Asn His Asp Arg Asp
305                 310                 315                 320

Lys Glu Arg Lys Lys Gly Gly Met Ala Lys Val Leu Leu Pro Leu Ile
                325                 330                 335

Ala Ala Val Leu Ile Ile Gly Ala Leu Ala Ile Phe Gly Gly Met Ala
            340                 345                 350

Leu Asn Asn His Asn Asn Gly Thr Lys Glu Asn Lys Ile Ala Asn Thr
        355                 360                 365

Asn Lys Asn Asn Ala Asp Glu Ser Lys Asp Lys Asp Thr Ser Lys Asp
    370                 375                 380

Ala Ser Lys Asp Lys Ser Lys Ser Thr Asp Ser Asp Lys Ser Lys Glu
385                 390                 395                 400
```

Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn
405 410 415

Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln Gln
420 425 430

Ala Asn Gln Asn Gln Gln Gln Gln Gln Gln Arg Gln Gly Gly Gly Gln
435 440 445

Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln
450 455 460

Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu Lys Ile Arg Arg Ala
465 470 475 480

Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile
485 490 495

Pro

(2) INFORMATION FOR SEQ ID NO:5235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 886 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5235:

Leu Leu Ser Ile Lys Tyr Asn Leu Ile Gly Val Val Asn Asn Met Asn
1 5 10 15

Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys Ser Thr
20 25 30

Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile Thr Ser
35 40 45

Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp Lys Ile
50 55 60

Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro Lys Asp
65 70 75 80

Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala Lys Asn
85 90 95

Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp Pro Ala
100 105 110

Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val Asn Phe
115 120 125

```
Gln Leu Leu Asp Lys Asn Asn Glu Thr Gln Tyr Tyr His Phe Phe Ser
    130                 135                 140

Il  Lys Asp Pro Ala Asp Val Tyr Tyr Thr Lys Lys Lys Ala Glu Val
145                 150                 155                 160

Glu Leu Asp Ile Asn Thr Ala Ser Thr Trp Lys Lys Phe Glu Val Tyr
                165                 170                 175

Glu Asn Asn Gln Lys Leu Pro Val Arg Leu Val Ser Tyr Ser Pro Val
            180                 185                 190

Pro Glu Asp His Ala Tyr Ile Arg Phe Pro Val Ser Asp Gly Thr Gln
        195                 200                 205

Glu Leu Lys Ile Val Ser Ser Thr Gln Ile Asp Asp Gly Glu Glu Thr
    210                 215                 220

Asn Tyr Asp Tyr Thr Lys Leu Val Phe Ala Lys Pro Ile Tyr Asn Asp
225                 230                 235                 240

Pro Ser Leu Val Lys Ser Asp Thr Asn Asp Ala Val Val Thr Asn Asp
                245                 250                 255

Gln Ser Ser Ser Val Ala Ser Asn Gln Thr Asn Thr Asn Thr Ser Asn
            260                 265                 270

Gln Asn Ile Ser Thr Ile Asn Asn Ala Asn Asn Gln Pro Gln Ala Thr
        275                 280                 285

Thr Asn Met Ser Gln Pro Ala Gln Pro Lys Ser Ser Thr Asn Ala Asp
    290                 295                 300

Gln Ala Ser Ser Gln Pro Ala His Glu Thr Asn Ser Asn Gly Asn Thr
305                 310                 315                 320

Asn Asp Lys Thr Asn Glu Ser Ser Asn Gln Ser Asp Val Asn Gln Gln
                325                 330                 335

Tyr Pro Pro Ala Asp Glu Ser Leu Gln Asp Ala Ile Lys Asn Pro Ala
            340                 345                 350

Ile Ile Asp Lys Glu His Thr Ala Asp Asn Trp Arg Pro Ile Asp Phe
        355                 360                 365

Gln Met Lys Asn Asp Lys Gly Glu Arg Gln Phe Tyr His Tyr Ala Ser
    370                 375                 380

Thr Val Glu Pro Ala Thr Val Ile Phe Thr Lys Thr Gly Pro Ile Ile
385                 390                 395                 400

Glu Leu Gly Leu Lys Thr Ala Ser Thr Trp Lys Lys Phe Glu Val Tyr
                405                 410                 415

Glu Gly Asp Lys Lys Leu Pro Val Glu Leu Val Ser Tyr Asp Ser Asp
            420                 425                 430

Lys Asp Tyr Ala Tyr Ile Arg Phe Pro Val Ser Asn Gly Thr Arg Glu
        435                 440                 445
```

```
Val Lys Ile Val Ser Ser Ile Glu Tyr Gly Glu Asn Ile His Glu Asp
    450                 455                 460

Tyr Asp Tyr Thr Leu Met Val Phe Ala Gln Pro Ile Thr Asn Asn Pro
465                 470                 475                 480

Asp Asp Tyr Val Asp Glu Glu Thr Tyr Asn Leu Gln Lys Leu Leu Ala
                485                 490                 495

Pro Tyr His Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Glu
            500                 505                 510

Lys Leu Gln Glu Lys Leu Pro Glu Lys Tyr Lys Ala Glu Tyr Lys Lys
        515                 520                 525

Lys Leu Asp Gln Thr Arg Val Glu Leu Ala Asp Gln Val Lys Ser Ala
    530                 535                 540

Val Thr Glu Phe Glu Asn Val Thr Pro Thr Asn Asp Gln Leu Thr Asp
545                 550                 555                 560

Leu Gln Glu Ala His Phe Val Val Phe Glu Ser Glu Glu Asn Ser Glu
                565                 570                 575

Ser Val Met Asp Gly Phe Val Glu His Pro Phe Tyr Thr Ala Thr Leu
            580                 585                 590

Asn Gly Gln Lys Tyr Val Val Met Lys Thr Lys Asp Asp Ser Tyr Trp
        595                 600                 605

Lys Asp Leu Ile Val Glu Gly Lys Arg Val Thr Thr Val Ser Lys Asp
    610                 615                 620

Pro Lys Asn Asn Ser Arg Thr Leu Ile Phe Pro Tyr Ile Pro Asp Lys
625                 630                 635                 640

Ala Val Tyr Asn Ala Ile Val Lys Val Val Val Ala Asn Ile Gly Tyr
                645                 650                 655

Glu Gly Gln Tyr His Val Arg Ile Ile Asn Gln Asp Ile Asn Thr Lys
            660                 665                 670

Asp Asp Asp Thr Ser Gln Asn Asn Thr Ser Glu Pro Leu Asn Val Gln
        675                 680                 685

Thr Gly Gln Glu Gly Lys Val Ala Asp Thr Asp Val Ala Glu Asn Ser
    690                 695                 700

Ser Thr Ala Thr Asn Pro Lys Asp Ala Ser Asp Lys Ala Asp Val Ile
705                 710                 715                 720

Glu Pro Glu Ser Asp Val Val Lys Asp Ala Asp Asn Asn Ile Asp Lys
                725                 730                 735

Asp Val Gln His Asp Val Asp His Leu Ser Asp Met Ser Asp Asn Asn
            740                 745                 750

His Phe Asp Lys Tyr Asp Leu Lys Glu Met Asp Thr Gln Ile Ala Lys
        755                 760                 765
```

```
Asp Thr Asp Arg Asn Val Asp Lys Asp Ala Asp Asn Ser Val Gly Met
    770                 775                 780

Ser Ser Asn Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys Asp Lys
785                 790                 795                 800

Val Ile Gln Leu Asn His Ile Ala Asp Lys Asn Asn His Thr Gly Lys
                805                 810                 815

Ala Ala Lys Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr Asp Lys
            820                 825                 830

Val Thr Asp Lys Lys Thr Thr Glu His Leu Pro Ser Asp Ile His Lys
        835                 840                 845

Thr Val Asp Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr Pro Ser
    850                 855                 860

Lys Glu Asn Lys Leu Ser Gln Ser Lys Met Leu Thr Lys Asn Trp Arg
865                 870                 875                 880

Asn Asn Xaa Gln Ala Asn
                885
```

(2) INFORMATION FOR SEQ ID NO:5236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5236:

```
Asn Met Asn Lys Asn Val Met Val Lys Gly Leu Thr Ala Leu Thr Ile
1               5                   10                  15

Leu Thr Ser Leu Gly Phe Ala Glu Asn Ile Ser Asn Gln Xaa His Ser
            20                  25                  30

Ile Ala Lys Ala Glu Lys Asn Val Lys Glu Ile Thr Asp Ala Thr Lys
        35                  40                  45

Glu Pro Tyr Asn Ser Val Val Ala Phe Val Gly Gly Thr Gly Val Val
    50                  55                  60

Val Gly Lys Asn Thr Ile Val Thr Asn Lys His Ile Ala Lys Ser Asn
65                  70                  75                  80

Asp Ile Phe Lys Asn Arg Val Ser Ala His His Ser Ser Lys Gly Lys
                85                  90                  95

Gly Gly Gly Asn Tyr Asp Val Lys Asp Ile Val Glu Tyr Pro Gly Lys
            100                 105                 110
```

```
Glu Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu
        115                 120                 125

Asn Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys
    130                 135                 140

Val Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys Gly Ala Gln Thr
145                 150                 155                 160

Lys Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly
                165                 170                 175

Thr Phe Met Glu Phe Asp Ala Tyr Ala Gln Pro Gly Asn Ser Gly Ser
            180                 185                 190

Pro Val Leu Asn Ser Lys His Xaa Leu Ile Gly Ile Leu Tyr Ala Gly
        195                 200                 205

Ser Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro
    210                 215                 220

Gln Leu Xaa Xaa Phe Ile Pro Asn Asn Ile Glu Lys
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:5237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5237:

```
Tyr Arg Leu Glu His Thr Ile Met Lys Met Arg Thr Ile Ala Lys Thr
1               5                   10                  15

Ser Leu Ala Leu Gly Leu Leu Thr Thr Gly Ala Ile Thr Val Thr Thr
            20                  25                  30

Gln Ser Val Lys Ala Glu Lys Ile Gln Ser Thr Lys Val Asp Lys Val
        35                  40                  45

Pro Thr Leu Lys Ala Glu Arg Leu Ala Met Ile Asn Ile Thr Ala Gly
    50                  55                  60

Ala Asn Ser Ala Thr Thr Gln Ala Ala Asn Thr Arg Gln Glu Arg Thr
65                  70                  75                  80

Pro Lys Leu Glu Lys Ala Pro Asn Thr Asn Glu Glu Lys Thr Ser Ala
                85                  90                  95

Ser Lys Ile Glu Lys Ile Ser Gln Pro Lys Gln Glu Glu Gln Lys Thr
            100                 105                 110
```

```
Leu Asn Ile Ser Ala Thr Pro Ala Pro Lys Gln Glu Gln Ser Gln Thr
        115                 120                 125

Thr Thr Glu Ser Thr Thr Pro Lys Thr Lys Val Thr Thr Pro Pro Ser
    130                 135                 140

Thr Asn Thr Pro Gln Pro Met Gln Ser Thr Lys Ser Asp Thr Pro Gln
145                 150                 155                 160

Ser Pro Thr Ile Lys Gln Ala Gln Thr Asp Met Thr Pro Lys Tyr Glu
                165                 170                 175

Asp Leu Arg Ala Tyr Tyr Thr Lys Pro Ser Phe Glu Phe Glu Lys Gln
            180                 185                 190

Phe Gly Phe Met Leu Lys Pro Trp Thr Thr Val Arg Phe Met Asn Val
        195                 200                 205

Ile Pro Asn Arg Phe Ile Tyr Lys Ile Ala Leu Val Gly Lys Asp Glu
    210                 215                 220

Lys Lys Tyr Lys Asp Gly Pro Tyr Asp Asn Ile Asp Val Phe Ile Val
225                 230                 235                 240

Leu Glu Asp Asn Lys Tyr Gln Leu Lys Lys Tyr Ser Val Gly Gly Ile
                245                 250                 255

Thr Lys Thr Asn Ser Lys Lys Val Asn His Lys Val Glu Leu Ser Ile
            260                 265                 270

Thr Lys Lys Asp Asn Gln Gly Met Ile Ser Arg Asp Val Ser Glu Tyr
        275                 280                 285

Met Ile Thr Lys Glu Glu Ile Ser Leu Lys Glu Leu Asp Phe Lys Leu
    290                 295                 300

Arg Lys Gln Leu Ile Glu Lys His Asn Leu Tyr Gly Asn Met Gly Ser
305                 310                 315                 320

Gly Thr Ile Val Ile Lys Met Lys Asn Gly Gly Lys Tyr Thr Phe Glu
                325                 330                 335

Leu His Lys Lys Leu Gln Glu His Arg Met Ala Asp Val Ile Asp Gly
            340                 345                 350

Thr Asn Ile Asp Asn Ile Glu Val Asn Ile Lys
        355                 360
```

(2) INFORMATION FOR SEQ ID NO:5238:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5238:

```
Phe Met Lys Phe Lys Ser Leu Ile Thr Thr Thr Leu Ala Leu Gly Val
1               5                  10                  15

Leu Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala
            20                  25                  30

Ala Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser
        35                  40                  45

Lys Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn
    50                  55                  60

Ile Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys
65                  70                  75                  80

Asp Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile
                85                  90                  95

Ser Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr
            100                 105                 110

Phe Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr
        115                 120                 125

Thr Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn
    130                 135                 140

Val Asp Thr Lys Lys Gln
145                 150
```

(2) INFORMATION FOR SEQ ID NO:5239:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5239:

```
Glu Lys Arg Phe Met Gln Met Ala Arg Lys Val Val Val Val Asp Asp
1               5                  10                  15

Glu Lys Pro Ile Ala Asp Ile Leu Glu Phe Asn Leu Lys Lys Glu Gly
            20                  25                  30

Tyr Asp Val Tyr Cys Ala Tyr Asp Gly Asn Asp Ala Val Asp Leu Ile
        35                  40                  45

Tyr Glu Glu Glu Pro Asp Ile Val Leu Leu Asp Ile Met Leu Pro Gly
    50                  55                  60
```

```
Arg Asp Gly Met Glu Val Cys Arg Glu Val Arg Lys Lys Tyr Glu M t
65                  70                  75                  80

Pro Ile Ile Met Leu Thr Ala Lys Asp Ser Glu Ile Asp Lys Val Leu
                85                  90                  95

Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser Thr
            100                 105                 110

Arg Glu Leu Ile Ala Arg Val Lys Ala Asn Leu Arg Arg His Tyr Ser
        115                 120                 125

Gln Pro Ala Gln Asp Thr Gly Asn Val Thr Asn Glu Ile Thr Ile Lys
    130                 135                 140

Asp Ile Val Ile Tyr Pro Asp Ala Tyr Ser Ile Lys Lys Arg Gly Glu
145                 150                 155                 160

Asp Ile Glu Leu Thr His Arg Glu Phe Glu Leu Phe His Tyr Leu Ser
                165                 170                 175

Lys His Met Gly Gln Val Met Thr Arg Glu His Leu Leu Gln Thr Val
            180                 185                 190

Trp Gly Tyr Asp Tyr Phe Gly Asp Val Arg Thr Val Asp Val Thr Ile
        195                 200                 205

Arg Arg Leu Arg Glu Lys Ile Glu Asp Asp Pro Ser His Pro Glu Tyr
    210                 215                 220

Ile Val Thr Arg Arg Gly Val Gly Tyr Phe Leu Gln Gln His Glu
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:5240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5240:

```
Xaa Leu Ser Thr Val Ile Gly Ala Xaa Leu Phe Phe Lys Ser Ser Val
1               5                   10                  15

Ser Leu Val Phe Lys Met Val Lys Lys Phe Arg Xaa Gly Val Ile Ser
            20                  25                  30

Val Asn Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys
        35                  40                  45

Asn Ala Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val
    50                  55                  60
```

Ser Val Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu
65 70 75 80

Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys
85 90 95

Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe
100 105 110

Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu
115 120 125

Phe Asp Val Lys Ala
130

(2) INFORMATION FOR SEQ ID NO:5241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 508 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:

Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val
1 5 10 15

Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly
20 25 30

Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro
35 40 45

Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp
50 55 60

Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser
65 70 75 80

Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp
85 90 95

Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn
100 105 110

Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala
115 120 125

Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly
130 135 140

Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu
145 150 155 160

```
Pro Ile Gly Val Val Gly Ala Val Val Ala Trp Asn Ph  Pro Met Leu
                165                 170                 175

Leu Ala Ala Trp Lys Ile Ala Pro Ala Il  Ala Ala Gly Asn Thr Ile
            180                 185                 190

Val Ile Gln Pro Ser Ser Ser Thr Pro Leu Ser Leu Leu Glu Val Ala
        195                 200                 205

Lys Ile Phe Gln Glu Val Leu Pro Lys Gly Val Val Asn Ile Leu Thr
    210                 215                 220

Gly Lys Gly Ser Glu Ser Gly Asn Ala Ile Phe Asn His Asp Gly Val
225                 230                 235                 240

Asp Lys Leu Ser Phe Thr Gly Ser Thr Asp Val Gly Tyr Gln Val Ala
                245                 250                 255

Glu Ala Ala Ala Lys His Leu Val Pro Ala Thr Leu Glu Leu Gly Gly
            260                 265                 270

Lys Ser Ala Asn Ile Ile Leu Asp Asp Ala Asn Leu Asp Leu Ala Val
        275                 280                 285

Glu Gly Ile Gln Leu Gly Ile Leu Phe Asn Gln Gly Glu Val Cys Ser
    290                 295                 300

Ala Gly Ser Arg Leu Leu Val His Glu Lys Ile Tyr Asp Gln Leu Val
305                 310                 315                 320

Pro Arg Leu Gln Glu Ala Phe Ser Asn Ile Lys Val Gly Asn Pro Gln
                325                 330                 335

Asp Glu Ala Thr Gln Met Gly Ser Gln Thr Gly Lys Asp Gln Leu Asp
            340                 345                 350

Lys Ile Gln Ser Tyr Ile Asp Ala Ala Lys Glu Ser Asp Ala Gln Ile
        355                 360                 365

Leu Ala Gly Gly His Arg Leu Thr Glu Asn Gly Leu Asp Lys Gly Phe
    370                 375                 380

Phe Phe Glu Pro Thr Leu Ile Ala Val Pro Asp Asn His His Lys Leu
385                 390                 395                 400

Ala Gln Glu Glu Ile Phe Gly Pro Val Leu Thr Val Ile Lys Val Lys
                405                 410                 415

Asp Asp Gln Glu Ala Ile Asp Ile Ala Asn Asp Ser Glu Tyr Gly Leu
            420                 425                 430

Ala Gly Gly Val Phe Ser Gln Asn Ile Thr Arg Ala Leu Asn Ile Ala
        435                 440                 445

Lys Ala Val Arg Thr Gly Arg Ile Trp Ile Asn Thr Tyr Asn Gln Val
    450                 455                 460

Pro Glu Gly Ala Pro Phe Gly Gly Tyr Lys Lys Ser Gly Ile Gly Arg
465                 470                 475                 480
```

Glu Thr Tyr Lys Gly Ala Leu Ser Asn Tyr Gln Gln Val Lys Asn Ile
485 490 495

Tyr Ile Asp Thr Ser Asn Ala Leu Lys Gly Leu Tyr
500 505

(2) INFORMATION FOR SEQ ID NO:5242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 540 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5242:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
1 5 10 15

Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
20 25 30

Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
35 40 45

Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
50 55 60

Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
65 70 75 80

Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
85 90 95

Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
100 105 110

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
115 120 125

Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
130 135 140

Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
145 150 155 160

Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
165 170 175

Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
180 185 190

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
195 200 205

```
Pro Ala Ile Ser Thr Asp Glu Asn Arg Gln Asp Pro Thr Val Thr Val
    210                 215                 220

Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly
225                 230                 235                 240

Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn
                245                 250                 255

Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val
            260                 265                 270

Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys
        275                 280                 285

Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr
    290                 295                 300

Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp
305                 310                 315                 320

Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly
                325                 330                 335

Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu
            340                 345                 350

Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr
        355                 360                 365

Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly
    370                 375                 380

Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro
385                 390                 395                 400

Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn
                405                 410                 415

Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu
            420                 425                 430

Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr
        435                 440                 445

Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr
    450                 455                 460

Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly
465                 470                 475                 480

Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp
                485                 490                 495

Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr
            500                 505                 510

Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser
        515                 520                 525
```

Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His
530 535 540

(2) INFORMATION FOR SEQ ID NO:5243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5243:

Ile Thr Leu Lys Thr Val Ser Gln Leu Ile Asp Met Lys Gln Lys Gln
1 5 10 15

Thr Lys Ile Ser Met Val Thr Ala Tyr Asp Phe Pro Ser Ala Lys Gln
20 25 30

Val Glu Ala Ala Gly Ile Asp Met Ile Leu Val Gly Asp Ser Leu Gly
35 40 45

Met Thr Val Leu Gly Tyr Glu Ser Thr Val Gln Val Thr Leu Ala Asp
50 55 60

Met Ile His His Gly Arg Ala Val Arg Arg Gly Ala Pro Asn Thr Phe
65 70 75 80

Val Val Val Asp Met Pro Ile Gly Ala Val Gly Ile Ser Met Thr Gln
85 90 95

Asp Leu Asn His Ala Leu Lys Leu Tyr Gln Glu Thr Asn Ala Asn Ala
100 105 110

Ile Lys Ala Glu Gly Ala His Ile Thr Pro Phe Ile Glu Lys Ala Thr
115 120 125

Ala Ile Gly Ile Pro Val Val Ala His Leu Gly Leu Thr Pro Gln Ser
130 135 140

Val Gly Val Met Gly Tyr Lys Leu Gln Gly Ala Thr Lys Glu Ala Ala
145 150 155 160

Glu Gln Leu Ile Leu Asp Ala Lys Asn Val Glu Gln Ala Gly Ala Val
165 170 175

Ala Leu Val Leu Glu Ala Ile Pro Asn Asp Leu Ala Glu Glu Ile Ser
180 185 190

Lys His Leu Thr Ile Pro Val Ile Gly Ile Gly Ala Gly Lys Gly Thr
195 200 205

Asp Gly Gln Val Leu Val Tyr His Asp Met Leu Asn Tyr Gly Val Glu
210 215 220

His Lys Ala Lys Phe Val Lys Gln Phe Ala Asp Phe S r Val Gly Val
225 230 235 240

Asp Gly Leu Lys Gln Tyr Asp Gln Glu Val Lys Ser Gly Ala Ph Pro
245 250 255

Ser Glu Glu Tyr Thr Tyr Lys Lys Lys Ile Met Asn Glu Val Asn Asn
260 265 270

Asn Asp

(2) INFORMATION FOR SEQ ID NO:5244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 430 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5244:

Ser Asp Asp Trp Pro Lys Ser Ile Thr Ser Leu Ser Ile Arg Gly Val
1 5 10 15

Arg Met Lys His Gln Glu Thr Thr Ser Gln Gln Tyr Asn Phe Ser Ile
20 25 30

Ile Lys His Gly Asp Ile Ser Thr Pro Gln Gly Phe Thr Ala Gly Gly
35 40 45

Met His Ile Gly Leu Arg Ala Asn Lys Lys Asp Phe Gly Trp Ile Tyr
50 55 60

Ser Ser Ser Leu Ala Ser Ala Ala Ala Val Tyr Thr Leu Asn Gln Phe
65 70 75 80

Lys Ala Ala Pro Leu Ile Val Thr Glu Asp Thr Leu Gln Lys Ser Lys
85 90 95

Gly Lys Leu Gln Ala Leu Val Val Asn Ser Ala Asn Ala Asn Ser Cys
100 105 110

Thr Gly Gln Gln Gly Ile Asp Asp Ala Arg Gln Thr Gln Thr Trp Val
115 120 125

Ala Gln Gln Leu Gln Ile Pro Ser Glu His Val Ala Val Ala Ser Thr
130 135 140

Gly Val Ile Gly Glu Tyr Leu Pro Met Asp Lys Ile Lys Thr Gly Thr
145 150 155 160

Glu His Ile Lys Asp Ala Asn Phe Ala Thr Pro Gly Ala Phe Asn Glu
165 170 175

```
Ala Ile Leu Thr Thr Asp Thr Cys Thr Lys His Ile Ala Val Ser Leu
            180                 185                 190

Lys Ile Asp Gly Lys Thr Val Thr Ile Gly Gly Ser Thr Lys Gly Ser
        195                 200                 205

Gly Met Ile His Pro Asn Met Ala Thr Met Leu Ala Phe Ile Thr Thr
    210                 215                 220

Asp Ala Ser Ile Glu Ser Asn Thr Leu His Gln Leu Leu Lys Ser Ser
225                 230                 235                 240

Thr Asp His Thr Phe Asn Met Ile Thr Val Asp Gly Asp Thr Ser Thr
                245                 250                 255

Asn Asp Met Val Leu Val Met Ala Asn His Gln Val Glu His Gln Ile
            260                 265                 270

Leu Ser Gln Asp His Pro Gln Trp Glu Thr Phe Val Asp Ala Phe Asn
        275                 280                 285

Phe Val Cys Thr Phe Leu Ala Lys Ala Ile Ala Arg Asp Gly Glu Gly
    290                 295                 300

Ala Thr Lys Leu Ile Ser Val Asn Val Ser Gly Ala Lys Ser Ile Ser
305                 310                 315                 320

Asp Ala Arg Lys Ile Gly Lys Thr Ile Val Ser Ser Asn Leu Val Lys
                325                 330                 335

Ser Ala Ile Phe Gly Glu Asp Ala Asn Phe Gly Arg Ile Ile Thr Ala
            340                 345                 350

Ile Gly Tyr Ser Gly Cys Glu Ile Asp Pro Asn Cys Thr Tyr Val Gln
        355                 360                 365

Leu Asn Gln Ile Pro Val Val Asp Lys Gly Met Ala Val Leu Phe Asp
    370                 375                 380

Glu Gln Ala Met Ser Asn Thr Leu Thr His Glu Asn Val Thr Ile Asp
385                 390                 395                 400

Val Gln Leu Gly Leu Gly Asn Ala Ala Ala Thr Ala Tyr Gly Cys Asp
                405                 410                 415

Leu Ser Tyr Asp Tyr Val Arg Ile Asn Ala Ser Tyr Arg Thr
            420                 425                 430
```

(2) INFORMATION FOR SEQ ID NO:5245:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 469 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5245:

```
Asn Pro Ala Leu Thr Val Phe Ala Phe Ile Met Ile Ile Ser Ile Leu
1               5                  10                  15

Leu Ala Tyr Val Phe Lys Trp Leu Gly Leu Val Asp Asp Val Leu Leu
            20                  25                  30

Met Val Ile Ile Ile Ser Thr Ile Ser Leu Gly Val Val Val Pro Thr
        35                  40                  45

Leu Lys Glu Met Asn Ile Met Arg Thr Thr Ile Gly Gln Phe Ile Leu
    50                  55                  60

Leu Val Ala Val Leu Ala Asp Leu Val Thr Met Ile Leu Leu Thr Val
65                  70                  75                  80

Tyr Gly Ala Ile Asn Gly Gln Gly Gly Ser Thr Ile Trp Leu Ile Gly
                85                  90                  95

Ile Leu Val Val Phe Thr Ala Ile Ser Tyr Ile Leu Gly Val Gln Phe
            100                 105                 110

Lys Arg Met Ser Phe Leu Gln Lys Leu Met Asp Gly Thr Thr Gln Ile
        115                 120                 125

Gly Ile Arg Ala Val Phe Ala Leu Ile Ile Leu Leu Val Ala Leu Ala
    130                 135                 140

Glu Gly Val Gly Ala Glu Asn Ile Leu Gly Ala Phe Leu Ala Gly Val
145                 150                 155                 160

Val Val Ser Leu Leu Asn Pro Asp Glu Glu Met Val Glu Lys Leu Asp
                165                 170                 175

Ser Phe Gly Tyr Gly Phe Phe Ile Pro Ile Phe Phe Ile Met Xaa Gly
            180                 185                 190

Val Asp Leu Asn Ile Pro Ser Leu Ile Lys Glu Pro Lys Leu Leu Ile
        195                 200                 205

Ile Ile Pro Ile Leu Ile Val Ala Phe Ile Ile Ser Lys Leu Ile Pro
    210                 215                 220

Val Met Phe Ile Arg Arg Trp Phe Asp Met Lys Thr Thr Ile Ala Ser
225                 230                 235                 240

Ala Phe Leu Leu Thr Ser Thr Leu Ser Leu Val Ile Ala Ala Ala Lys
                245                 250                 255

Ile Ser Glu Arg Leu Asn Ala Ile Ser Ala Glu Thr Ser Gly Ile Leu
            260                 265                 270

Ile Leu Ser Ala Val Ile Thr Cys Val Phe Val Pro Ile Ile Phe Lys
        275                 280                 285

Lys Leu Phe Pro Val Pro Asp Glu Phe Asn Arg Lys Ile Glu Val Ser
    290                 295                 300
```

```
Leu Ile Gly Lys Asn Gln Leu Thr Ile Pro Ile Ala Gln Asn Leu Thr
305                 310                 315                 320

Ser Gln Leu Tyr Asp Val Thr Leu Tyr Tyr Arg Lys Asp Leu Ser Asp
                325                 330                 335

Arg Arg Gln Leu Ser Asp Asp Ile Thr Met Ile Glu Ile Ala Asp Tyr
            340                 345                 350

Glu Gln Asp Val Leu Glu Arg Leu Gly Leu Phe Asp Arg Asp Ile Val
        355                 360                 365

Val Cys Ala Thr Asn Asp Asp Asp Ile Asn Arg Lys Val Ala Lys Leu
    370                 375                 380

Ala Lys Ala His Gln Val Glu Arg Val Ile Cys Arg Leu Glu Ser Thr
385                 390                 395                 400

Thr Asp Asp Thr Glu Leu Val Asp Ser Gly Ile Glu Ile Phe Ser Ser
                405                 410                 415

Tyr Leu Ser Asn Lys Ile Leu Leu Lys Gly Leu Ile Glu Thr Pro Asn
            420                 425                 430

Met Leu Asn Leu Leu Ser Asn Val Glu Thr Ser Leu Tyr Glu Ile Gln
        435                 440                 445

Met Leu Asn Tyr Lys Tyr Glu Asn Ile Gln Leu Arg Asn Phe Pro Phe
    450                 455                 460

Gly Gly Asp Ile Ile
465
```

(2) INFORMATION FOR SEQ ID NO:5246:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5246:

```
Ala Ile Ile Val Ile Leu Leu Phe Leu Arg Asn Ile Arg Thr Thr Ala
1               5                   10                  15

Ile Ser Ile Ile Ser Ile Pro Leu Ser Leu Leu Met Ala Leu Ile Ala
            20                  25                  30

Leu Lys Leu Ser Asp Val Ser Leu Asn Ile Leu Thr Leu Gly Ala Leu
        35                  40                  45

Thr Val Ala Ile Gly Arg Val Ile Asp Asp Ser Ile Val Val Val Glu
    50                  55                  60
```

Asn Ile Tyr Arg Arg Leu Thr Asp Ser Glu Glu Gln Leu Lys Gly Glu
65 70 75 80

Asn Leu Ile Ile Ser Ala Thr Thr Glu Val Phe Lys Pro Ile Met Ser
85 90 95

Ser Thr Leu Val Thr Ile Ile Val Phe Leu Pro Leu Val Phe Val Ser
100 105 110

Gly Ser Val Gly Glu Met Phe Arg Pro Phe Ala Leu Ala Ile Ala Phe
115 120 125

Ser Leu Leu Ala Ser Leu Leu Val Ser Ile Thr Leu Val Pro Ala Leu
130 135 140

Ala Ala Thr Leu Phe Lys Lys Gly Val Lys Arg Arg Asn Lys Gln His
145 150 155 160

Gln Glu Gly Leu Gly Val Val Ser Thr Thr Tyr Lys Lys Val Leu His
165 170 175

Trp Ser Leu Asn His Lys Trp Ile Val Ile Ile Leu Ser Thr Leu Ile
180 185 190

Leu Val Ala Thr Ile Val Phe Gly Gly Pro Arg Leu Gly Thr Ser Phe
195 200 205

Ile Ser Ala Gly Asp Asp Lys Phe Leu Ala Ile Thr Tyr Thr Pro Lys
210 215 220

Pro Gly Glu Thr Glu Gln Ala Val Leu Asn His Ala Lys Asp Val Glu
225 230 235 240

Lys Tyr Leu Lys Gln Lys Lys His Val Lys Thr Ile Gln Tyr Ser Val
245 250 255

Gly Gly Ser Ser Pro Val Asp Pro Thr Gly Ser Thr Asn Ser Met Ala
260 265 270

Ile Met Val Glu Tyr Asp Asn Asp Thr Pro Asn Phe Asp Val Glu Ala
275 280 285

Asp Lys Val Ile Lys His Ala Asp Gly Phe Lys His Pro Gly Glu Trp
290 295 300

Lys Asn Gln Asp Leu Gly Thr Gly Ala Gly Asn Lys Ser Val Glu Val
305 310 315 320

Thr Val Lys Gly Pro Ser Met Asp Ala Ile Lys Ser Thr Val Lys Asp
325 330 335

Ile Glu Gln Lys Met Lys Gln Val Lys Gly Leu Ala Asn Val Lys Ser
340 345 350

Asp Leu Ser Gln Thr Tyr Asp Gln Tyr Glu Ile Lys Val Asp Gln Asn
355 360 365

Lys Ala Ala Glu Asn Gly Ile Ser Ala Ser Gln Leu Ala Met His Leu
370 375 380

```
Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly
385                 390                 395                 400

Lys Thr Val Asp Val Lys Val Lys Gln Asn Lys Gln Thr Ala
                405                 410
```

(2) INFORMATION FOR SEQ ID NO:5247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 555 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5247:

```
Gly Lys Pro Phe Ile Ile Gly Leu Gly Asp Ile Ile Val Lys Lys Leu
1               5                   10                  15

Thr Thr Ile Leu Phe Gln Tyr Lys Ile Phe Pro Val Leu Met Phe Leu
            20                  25                  30

Val Ser Thr Gly Leu Gly Ile Ile Val Ile Thr Gln Asn Ile Leu Ile
        35                  40                  45

Ala Asp Phe Leu Ala Lys Ile Ile Arg His Gln Phe Gln Gly Leu Trp
    50                  55                  60

Ile Val Leu Phe Ile Leu Leu Gly Val Leu Leu Leu Arg Ala Thr Val
65                  70                  75                  80

Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val Lys
                85                  90                  95

His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro Ile
            100                 105                 110

Gly Glu Gln Met Thr Ile Leu Thr Glu Asn Ile Asp Gly Leu Ala Pro
        115                 120                 125

Phe Tyr Lys Ser Tyr Leu Pro Gln Val Phe Lys Ser Met Met Val Pro
    130                 135                 140

Leu Ile Ile Ile Ile Ala Met Phe Phe Ile His Phe Asn Thr Ala Leu
145                 150                 155                 160

Ile Met Leu Ile Thr Ala Pro Phe Ile Pro Leu Phe Tyr Ile Ile Phe
                165                 170                 175

Gly Leu Lys Thr Arg Asp Glu Ser Lys Asp Gln Met Thr Tyr Leu Asn
            180                 185                 190

Gln Phe Ser Gln Arg Phe Leu Asn Ile Ala Lys Gly Leu Val Thr Leu
        195                 200                 205
```

```
Lys Leu Phe Asn Arg Thr Glu Gln Thr Glu Lys His Ile Tyr Asp Asp
    210                 215                 220

Ser Thr Gln Phe Arg Thr Leu Thr Met Arg Il  Leu Arg Ser Ala Phe
225                 230                 235                 240

Leu Ser Gly Leu Met Leu Glu Phe Ile Ser Met Leu Gly Ile Gly Leu
                245                 250                 255

Val Ala Leu Glu Ala Thr Leu Ser Leu Val Val Phe His Asn Ile Asp
            260                 265                 270

Phe Lys Thr Ala Ala Ile Ala Ile Ile Leu Ala Pro Glu Phe Tyr Asn
        275                 280                 285

Ala Ile Lys Asp Leu Gly Gln Ala Phe His Thr Gly Lys Gln Ser Glu
    290                 295                 300

Gly Ala Ser Asp Val Val Phe Glu Phe Leu Glu Gln Pro Asn Tyr Asn
305                 310                 315                 320

Asn Glu Phe Leu Leu Lys Tyr Glu Glu Asn Gln Lys Pro Phe Ile Gln
                325                 330                 335

Leu Thr Asp Ile Ser Phe Arg Tyr Asp Asp Ser Asp Arg Leu Val Leu
            340                 345                 350

Asn Asp Leu Asn Leu Glu Ile Phe Lys Gly Asp Gln Ile Ala Leu Val
        355                 360                 365

Gly Pro Ser Gly Ala Gly Lys Ser Thr Leu Thr His Leu Ile Ala Gly
    370                 375                 380

Val Tyr Gln Pro Thr Ile Gly Thr Ile Ser Thr Asn Gln Arg Asp Leu
385                 390                 395                 400

Asn Ile Gly Ile Leu Ser Gln Gln Pro Tyr Ile Phe Ser Ala Ser Ile
                405                 410                 415

Lys Glu Asn Ile Thr Met Phe Lys Asp Ile Glu Asn Asn Thr Ile Glu
            420                 425                 430

Glu Val Leu Asp Glu Val Gly Leu Leu Asp Lys Val Gln Ser Phe Thr
        435                 440                 445

Lys Gly Ile Asn Thr Ile Ile Gly Glu Gly Gly Glu Met Leu Ser Gly
    450                 455                 460

Gly Gln Met Arg Arg Ile Glu Leu Cys Arg Leu Leu Val Met Lys Pro
465                 470                 475                 480

Asp Leu Val Ile Phe Asp Glu Pro Ala Thr Gly Leu Asp Ile Gln Thr
                485                 490                 495

Glu His Met Ile Gln Asn Val Leu Phe Gln His Phe Lys Asp Thr Thr
            500                 505                 510

Met Ile Val Ile Ala His Arg Asp Asn Thr Ile Arg His Leu Gln Arg
        515                 520                 525
```

Arg Leu Tyr Ile Glu Asn Gly Arg Leu Ile Ala Asp Asp Arg Asn Ile
530 535 540

Ser Val Asn Ile Thr Glu Asn Gly Asp Asp Leu
545 550 555

(2) INFORMATION FOR SEQ ID NO:5248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5248:

Val Trp Lys Leu Lys Met Arg Trp Ile Lys Arg Lys Lys Lys Asn Phe
1 5 10 15

Leu Asn Ser Lys Phe Asn Phe Asn Asn Gly Lys Ile Ala Thr Tyr Leu
20 25 30

Tyr Lys Glu Arg Thr Ala Met Trp Asn Lys Asn Arg Leu Thr Gln Met
35 40 45

Leu Ser Ile Glu Tyr Pro Ile Ile Gln Ala Gly Met Ala Gly Ser Thr
50 55 60

Thr Pro Lys Leu Val Ala Ser Val Ser Asn Ser Gly Gly Leu Gly Thr
65 70 75 80

Ile Gly Ala Gly Tyr Phe Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp
85 90 95

Tyr Val Arg Gln Leu Thr Ser Asn Ser Phe Gly Val Asn Val Phe Val
100 105 110

Pro Ser Gln Gln Ser Tyr Thr Ser Ser Gln Ile Glu Asn Met Asn Ala
115 120 125

Trp Leu Lys Pro Tyr Arg Arg Ala Leu His Leu Glu Glu Pro Val Val
130 135 140

Lys Ile Thr Glu Glu Gln Gln Phe Lys Cys His Ile Asp Thr Ile Ile
145 150 155 160

Lys Lys Gln Val Pro Val Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu
165 170 175

Gln Ile Ile Ser Arg Leu Lys Ala Ala Asn Val Lys Leu Ile Gly Thr
180 185 190

Ala Thr Ser Val Asp Glu Ala Ile Ala Asn Glu Lys Ala Gly Met Asp
195 200 205

```
Ala Ile Val Ala Gln Gly Ser Glu Ala Gly Gly His Arg Gly Ser Phe
    210                 215                 220

Leu Lys Pro Lys Asn Gln Leu Pro Met Val Gly Thr Ile Ser Leu Val
225                 230                 235                 240

Pro Gln Ile Val Asp Val Val Ser Ile Pro Val Ile Ala Ala Gly Gly
                245                 250                 255

Ile Met Asp Gly Arg Gly Val Leu Ala Ser Ile Val Leu Gly Ala Glu
            260                 265                 270

Gly Val Gln Met Gly Thr Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala
        275                 280                 285

Ser Glu Leu Leu Arg Asp Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr
    290                 295                 300

Val Ile Thr Lys Ala Phe Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn
305                 310                 315                 320

Arg Phe Ile Glu Glu Met Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr
                325                 330                 335

Pro Ile Gln Asn Glu Leu Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn
            340                 345                 350

Ile Gly Asp Lys Glu Leu Ile His Met Trp Ser Gly Gln Ser Pro Arg
        355                 360                 365

Leu Ala Thr Thr His Pro Ala Asn Thr Ile Met Ser Asn Ile Ile Asn
    370                 375                 380

Gln Ile Asn Gln Ile Met Gln Tyr Lys
385                 390
```

(2) INFORMATION FOR SEQ ID NO:5249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 936 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5249:

```
Asn Asp Phe Leu Lys Arg Gly Asn Lys Met Asn Met Lys Lys Lys Glu
1               5                   10                  15

Lys His Ala Ile Arg Lys Lys Ser Ile Gly Val Ala Ser Val Leu Val
            20                  25                  30

Gly Thr Leu Ile Gly Phe Gly Leu Leu Ser Ser Lys Glu Ala Asp Ala
        35                  40                  45
```

```
Ser Glu Asn Ser Val Thr Gln Ser Asp Ser Ala Ser Asn Glu Ser Lys
    50                  55                  60

Ser Asn Asp Ser Ser Ser Val Ser Ala Ala Pro Lys Thr Asp Asp Thr
65                  70                  75                  80

Asn Val Ser Asp Thr Lys Thr Ser Ser Asn Thr Asn Asn Gly Glu Thr
                85                  90                  95

Ser Val Ala Gln Asn Pro Ala Gln Gln Glu Thr Thr Gln Ser Ser Ser
            100                 105                 110

Thr Asn Ala Thr Thr Glu Glu Thr Pro Val Thr Gly Glu Ala Thr Thr
        115                 120                 125

Thr Thr Thr Asn Gln Ala Asn Thr Pro Ala Thr Thr Gln Ser Ser Asn
    130                 135                 140

Thr Asn Ala Glu Glu Leu Val Asn Gln Thr Ser Asn Glu Thr Thr Ser
145                 150                 155                 160

Asn Asp Thr Asn Thr Val Ser Ser Val Asn Ser Pro Gln Asn Ser Thr
                165                 170                 175

Asn Ala Glu Asn Val Ser Thr Thr Gln Asp Thr Ser Thr Glu Ala Thr
            180                 185                 190

Pro Ser Asn Asn Glu Ser Ala Pro Gln Ser Thr Asp Ala Ser Asn Lys
        195                 200                 205

Asp Val Val Asn Gln Ala Val Asn Thr Ser Ala Pro Arg Met Arg Ala
    210                 215                 220

Phe Ser Leu Ala Ala Val Ala Ala Asp Ala Pro Val Ala Gly Thr Asp
225                 230                 235                 240

Ile Thr Asn Gln Leu Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr
                245                 250                 255

Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe
            260                 265                 270

Ser Val Pro Asn Ser Ala Val Lys Gly Asp Thr Phe Lys Ile Thr Val
        275                 280                 285

Pro Lys Glu Leu Asn Leu Asn Gly Val Thr Ser Thr Ala Lys Val Pro
    290                 295                 300

Pro Ile Met Ala Gly Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser
305                 310                 315                 320

Asp Gly Asn Val Ile Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp
                325                 330                 335

Asp Val Lys Ala Thr Leu Thr Met Pro Ala Tyr Ile Asp Pro Glu Asn
            340                 345                 350

Val Lys Lys Thr Gly Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr
        355                 360                 365
```

```
Thr Ala Asn Lys Thr Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys Phe
370                 375                 380

Tyr Asn Leu Ser Ile Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr Asn
385                 390                 395                 400

Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val
                405                 410                 415

Ile Ala Pro Val Leu Thr Gly Asn Leu Lys Pro Asn Thr Asp Ser Asn
            420                 425                 430

Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp
        435                 440                 445

Asn Ala Ala Asp Leu Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe
    450                 455                 460

Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln
465                 470                 475                 480

Tyr Lys Val Glu Phe Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr
                485                 490                 495

Ile Val Val Val Asn Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu
            500                 505                 510

Ala Leu Arg Ser Thr Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg
        515                 520                 525

Ser Met Ser Trp Asp Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser
    530                 535                 540

Gly Asp Gly Ile Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro
545                 550                 555                 560

Gly Glu Ile Glu Pro Ile Pro Glu Asp Ser Asp Ser Asp Pro Gly Ser
                565                 570                 575

Asp Ser Gly Ser Asp Ser Asn Ser Asp Ser Gly Ser Asp Ser Gly Ser
            580                 585                 590

Asp Ser Thr Ser Asp Ser Gly Ser Asp Ser Ala Ser Asp Ser Asp Ser
        595                 600                 605

Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser
    610                 615                 620

Asp Ser Ala Ser Asp Ser Asp Ser Asp Asn Asp Ser Asp Ser Asp Ser
625                 630                 635                 640

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
                645                 650                 655

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
            660                 665                 670

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
        675                 680                 685
```

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
690 695 700

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
705 710 715 720

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
725 730 735

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
740 745 750

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
755 760 765

Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp Ser
770 775 780

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
785 790 795 800

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
805 810 815

Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
820 825 830

Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Gly Ser
835 840 845

Asp Ser Asp Ser Ser Ser Asp Ser Asp Ser Glu Ser Asp Ser Asn Ser
850 855 860

Asp Ser Glu Ser Val Ser Asn Asn Asn Val Val Pro Pro Asn Ser Pro
865 870 875 880

Lys Asn Gly Thr Asn Ala Ser Asn Lys Asn Glu Ala Lys Asp Ser Lys
885 890 895

Glu Pro Leu Pro Asp Thr Gly Ser Glu Asp Glu Ala Asn Thr Ser Leu
900 905 910

Ile Trp Gly Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg
915 920 925

Lys Lys Glu Asn Lys Asp Lys Lys
930 935

(2) INFORMATION FOR SEQ ID NO:5250:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5250:

```
Val Ser Lys Leu Lys Lys Glu Ile Leu Glu Trp Ile Ile Ser Ile Ala
1               5                  10                  15

Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro
            20                  25                  30

Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu
        35                  40                  45

Arg Val Ala Val Asn Ile Val Gly Tyr Lys Thr Gly Gly Leu Glu Lys
    50                  55                  60

Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys
65                  70                  75                  80

Arg Val Ile Gly Val Pro Gly Asp Lys Val Glu Tyr Lys Asn Asp Thr
                85                  90                  95

Leu Tyr Val Asn Gly Lys Lys Gln Asp Glu Pro Tyr Leu Asn Tyr Asn
            100                 105                 110

Leu Lys His Lys Gln Gly Asp Tyr Ile Thr Gly Thr Phe Gln Val Lys
        115                 120                 125

Asp Leu Pro Asn Ala Asn Pro Lys Ser Asn Val Ile Pro Lys Gly Lys
    130                 135                 140

Tyr Leu Val Leu Gly Asp Asn Arg Glu Val Ser Lys Asp Ser Arg Ala
145                 150                 155                 160

Phe Gly Leu Ile Asp Glu Asp Gln Ile Val Gly Lys Val Ser Phe Gln
                165                 170                 175

Val Leu Ala His Phe Ser Glu Phe Gln Thr Ser Ile Ser Xaa Leu Lys
            180                 185                 190

Ile Leu
```

(2) INFORMATION FOR SEQ ID NO:5251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 559 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5251:

```
Leu Lys Ala Xaa Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp
1               5                  10                  15
```

```
Val Thr Asp Asn Met Ser Leu Asp Phe Asp Thr Asn Gly Gly Tyr Ser
                20                  25                  30

Leu Asn Phe Asn Asn Leu Asp Gln S r Lys Asn Tyr Val Ile Lys Tyr
        35                  40                  45

Glu Gly Tyr Tyr Asp Ser Asn Ala Ser Asn Leu Glu Phe Gln Thr His
    50                  55                  60

Leu Phe Gly Tyr Tyr Asn Tyr Tyr Tyr Thr Ser Asn Leu Thr Trp Lys
65                  70                  75                  80

Asn Gly Val Ala Phe Tyr Ser Asn Asn Ala Gln Gly Asp Gly Lys Asp
                85                  90                  95

Lys Leu Lys Glu Pro Ile Ile Glu His Ser Thr Pro Ile Glu Leu Glu
            100                 105                 110

Phe Lys Ser Glu Pro Pro Val Glu Lys His Glu Leu Thr Gly Thr Ile
        115                 120                 125

Glu Glu Ser Asn Asp Ser Lys Pro Ile Asp Phe Glu Tyr His Thr Ala
    130                 135                 140

Val Glu Gly Ala Glu Gly His Ala Glu Gly Thr Ile Glu Thr Glu Glu
145                 150                 155                 160

Asp Ser Ile His Val Asp Phe Glu Glu Ser Thr His Glu Asn Ser Lys
                165                 170                 175

His His Ala Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro Gly Gly
            180                 185                 190

Gly Gln Val Thr Thr Glu Ser Asn Leu Val Glu Phe Asp Glu Asp Ser
        195                 200                 205

Thr Lys Gly Ile Val Thr Gly Ala Val Ser Asp His Thr Thr Ile Glu
    210                 215                 220

Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn Leu Ile Glu Leu Val Asp
225                 230                 235                 240

Glu Leu Pro Glu Glu His Gly Gln Ala Gln Gly Pro Ile Glu Glu Ile
                245                 250                 255

Thr Glu Asn Asn His His Ile Ser His Ser Gly Leu Gly Thr Glu Asn
            260                 265                 270

Gly His Gly Asn Tyr Gly Val Ile Glu Glu Ile Glu Glu Asn Ser His
        275                 280                 285

Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu Gly Gly Gln Asn Ser Gly
    290                 295                 300

Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro Lys Tyr Glu
305                 310                 315                 320

Gln Gly Gly Asn Ile Val Asp Ile Asp Phe Asp Ser Val Pro Gln Ile
                325                 330                 335
```

```
His Gly Gln Asn Asn Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Lys
            340                 345                 350

Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe
        355                 360                 365

Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu Ile Ile
    370                 375                 380

Glu Glu Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His
385                 390                 395                 400

Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Gln Val Ser Gly His
                405                 410                 415

Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile Val
            420                 425                 430

Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro
        435                 440                 445

Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro
    450                 455                 460

Pro Thr Pro Glu Val Pro Thr Glu Pro Gly Lys Pro Ile Pro Pro Ala
465                 470                 475                 480

Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu Gln Gly Lys Val
                485                 490                 495

Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys Ala Val Val Pro
            500                 505                 510

Thr Lys Lys Ala Gln Ser Lys Lys Ser Glu Leu Pro Glu Thr Gly Gly
        515                 520                 525

Glu Glu Ser Thr Asn Asn Gly Met Leu Phe Gly Gly Leu Phe Ser Ile
    530                 535                 540

Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn His Lys Ala
545                 550                 555
```

(2) INFORMATION FOR SEQ ID NO:5252:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5252:

```
Thr Lys Asn Glu Lys Ile Asn Asp Val Thr Ala Val Ala Glu Lys Glu
1               5                   10                  15
```

```
Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr Asn Lys Val
            20                  25                  30

Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln Asp Thr Asn
        35                  40                  45

Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp
    50                  55                  60

Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu
65                  70                  75                  80

Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg Lys Val Pro
                85                  90                  95

Glu Ile Lys Ser Thr Asp Gly Gln Val Met Ala Thr Gly Glu Ile Ile
            100                 105                 110

Gly Glu Arg Lys Val Arg Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys
        115                 120                 125

Lys Asp Leu Thr Ala Glu Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr
    130                 135                 140

Thr Val Thr Gln Lys Gly Asn Gln Asn Val Glu Val Lys Leu Gly Glu
145                 150                 155                 160

Thr Thr Val Ser Lys Ile Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg
                165                 170                 175

Asp Asn Trp Gly Val Thr Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys
            180                 185                 190

Val Asp Gly Lys Phe Ser His Phe Ala Tyr Met Lys Pro Asn Asn Gln
        195                 200                 205

Ser Leu Ser Ser Val Thr Val Thr Gly Gln Val Thr Lys Gly Asn Lys
    210                 215                 220

Pro Gly Val Asn Asn Pro Thr Val Lys Val Tyr Lys His Ile Gly Ser
225                 230                 235                 240

Asp Asp Leu Ala Glu Ser Xaa Xaa Cys Lys Ala
                245                 250
```

(2) INFORMATION FOR SEQ ID NO:5253:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:

```
Ile Leu His Leu Arg Glu Asn Ile Ile Val Lys Ser Asn Leu Arg Tyr
1               5                  10                  15

Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
            20                  25                  30

Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu
        35                  40                  45

Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser
    50                  55                  60

Lys Ala Ser Glu Thr Gln Thr Thr Thr Asn Asn Val Asn Thr Ile Asp
65                  70                  75                  80

Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser
                85                  90                  95

Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys
            100                 105                 110

Val Glu Thr Ser Arg Val Asp Leu Pro Ser Glu Lys Val Ala Asp Lys
        115                 120                 125

Glu Thr Thr Gly Thr Gln Val Asp Ile Ala Gln Pro Ser Asn Val Ser
    130                 135                 140

Glu Ile Lys Pro Arg Met Lys Arg Ser Met Thr Leu Gln Gln Leu Gln
145                 150                 155                 160

Arg Lys Lys
```

(2) INFORMATION FOR SEQ ID NO:5254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1027 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5254:

```
Ile Leu His Leu Lys Gly Asp Ile Ile Val Lys Asn Asn Leu Arg Tyr
1               5                  10                  15

Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
            20                  25                  30

Met Ile Val Val Gly Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu
        35                  40                  45

Gln Lys Thr Thr Thr Val Glu Glu Asn Gly Asn Ser Ala Thr Asp Asn
    50                  55                  60
```

```
Lys Thr Ser Glu Thr Gln Thr Thr Ala Thr Asn Val Asn His Ile Glu
65                  70                  75                  80

Glu Thr Gln Ser Tyr Asn Ala Thr Val Thr Glu Gln Pro Ser Asn Ala
                85                  90                  95

Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Ala Val Gln Ala Pro Gln
            100                 105                 110

Thr Ala Gln Pro Ala Asn Ile Glu Thr Val Lys Glu Glu Val Val Lys
        115                 120                 125

Glu Glu Ala Lys Pro Gln Val Lys Glu Thr Thr Gln Ser Gln Asp Asn
    130                 135                 140

Ser Gly Asp Gln Arg Gln Val Asp Leu Thr Pro Lys Lys Ala Thr Gln
145                 150                 155                 160

Asn Gln Val Ala Glu Thr Gln Val Glu Val Ala Gln Pro Arg Thr Ala
                165                 170                 175

Ser Glu Ser Lys Pro Arg Val Thr Arg Ser Ala Asp Val Ala Glu Ala
            180                 185                 190

Lys Glu Ala Ser Asn Ala Lys Val Glu Thr Gly Thr Asp Val Thr Ser
        195                 200                 205

Lys Val Thr Val Glu Ile Gly Ser Ile Glu Gly His Asn Asn Thr Asn
    210                 215                 220

Lys Val Glu Pro His Ala Gly Gln Arg Ala Val Leu Lys Tyr Lys Leu
225                 230                 235                 240

Lys Phe Glu Asn Gly Leu His Gln Gly Asp Tyr Phe Asp Phe Thr Leu
                245                 250                 255

Ser Asn Asn Val Asn Thr His Gly Val Ser Thr Ala Arg Lys Val Pro
            260                 265                 270

Glu Ile Lys Asn Gly Ser Val Val Met Ala Thr Gly Glu Val Leu Glu
        275                 280                 285

Gly Gly Lys Ile Arg Tyr Thr Phe Thr Asn Asp Ile Glu Asp Lys Val
    290                 295                 300

Asp Val Thr Ala Glu Leu Glu Ile Asn Leu Phe Ile Asp Pro Lys Thr
305                 310                 315                 320

Val Gln Thr Asn Gly Asn Gln Thr Ile Thr Ser Thr Leu Asn Glu Glu
                325                 330                 335

Gln Thr Ser Lys Glu Leu Asp Val Lys Tyr Lys Asp Gly Ile Gly Asn
            340                 345                 350

Tyr Tyr Ala Asn Leu Asn Gly Ser Ile Glu Thr Phe Asn Lys Ala Asn
        355                 360                 365

Asn Arg Phe Ser His Val Ala Phe Ile Lys Pro Asn Asn Gly Lys Thr
    370                 375                 380
```

Thr Ser Val Thr Val Thr Gly Thr Leu Met Lys Gly Ser Asn Gln Asn
385 390 395 400

Gly Asn Gln Pro Lys Val Arg Ile Phe Glu Tyr Leu Gly Asn Asn Glu
405 410 415

Asp Ile Ala Lys Ser Val Tyr Ala Asn Thr Thr Asp Thr Ser Lys Phe
420 425 430

Lys Glu Val Thr Ser Asn Met Ser Gly Asn Leu Asn Leu Gln Asn Asn
435 440 445

Gly Ser Tyr Ser Leu Asn Ile Glu Asn Leu Asp Lys Thr Tyr Val Val
450 455 460

His Tyr Asp Gly Glu Tyr Leu Asn Gly Thr Asp Glu Val Asp Phe Arg
465 470 475 480

Thr Gln Met Val Gly His Pro Glu Gln Leu Tyr Lys Tyr Tyr Tyr Asp
485 490 495

Arg Gly Tyr Thr Leu Thr Trp Asp Asn Gly Leu Val Leu Tyr Ser Asn
500 505 510

Lys Ala Asn Gly Asn Glu Lys Asn Gly Pro Ile Ile Gln Asn Asn Lys
515 520 525

Phe Glu Tyr Lys Glu Asp Thr Ile Lys Glu Thr Leu Thr Gly Gln Tyr
530 535 540

Asp Lys Asn Leu Val Thr Thr Val Glu Glu Glu Tyr Asp Ser Ser Thr
545 550 555 560

Leu Asp Ile Asp Tyr His Thr Ala Ile Asp Gly Gly Gly Gly Tyr Val
565 570 575

Asp Gly Tyr Ile Glu Thr Ile Glu Glu Thr Asp Ser Ser Ala Ile Asp
580 585 590

Ile Asp Tyr His Thr Ala Val Asp Ser Glu Ala Gly His Val Gly Gly
595 600 605

Tyr Thr Glu Ser Ser Glu Glu Ser Asn Pro Ile Asp Phe Glu Glu Ser
610 615 620

Thr His Glu Asn Ser Lys His His Ala Asp Val Val Glu Tyr Glu Glu
625 630 635 640

Asp Thr Asn Pro Gly Gly Gly Gln Val Thr Thr Glu Ser Asn Leu Val
645 650 655

Glu Phe Asp Glu Glu Ser Thr Lys Gly Ile Val Thr Gly Ala Val Ser
660 665 670

Asp His Thr Thr Val Glu Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn
675 680 685

Leu Ile Glu Leu Val Asp Glu Leu Pro Glu Glu His Gly Gln Ala Gln
690 695 700

```
Gly Pro Val Glu Glu Ile Thr Lys Asn Asn His His Ile Ser His Ser
705                 710                 715                 720

Gly Leu Gly Thr Glu Asn Gly His Gly Asn Tyr Asp Val Ile Glu Glu
                725                 730                 735

Ile Glu Glu Asn Ser His Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu
            740                 745                 750

Gly Gly Gln Asn Ser Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu
        755                 760                 765

Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Val Asp Ile Asp Phe
    770                 775                 780

Asp Ser Val Pro Gln Ile His Gly Gln Asn Lys Gly Asn Gln Ser Phe
785                 790                 795                 800

Glu Glu Asp Thr Glu Lys Asp Lys Pro Lys Tyr Glu His Gly Gly Asn
                805                 810                 815

Ile Ile Asp Ile Asp Phe Asp Ser Val Pro His Ile His Gly Phe Asn
            820                 825                 830

Lys His Thr Glu Ile Ile Glu Glu Asp Thr Asn Lys Asp Lys Pro Ser
        835                 840                 845

Tyr Gln Phe Gly Gly His Asn Ser Val Asp Phe Glu Glu Asp Thr Leu
    850                 855                 860

Pro Lys Val Ser Gly Gln Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp
865                 870                 875                 880

Thr Thr Pro Pro Ile Val Pro Pro Thr Pro Pro Thr Pro Glu Val Pro
                885                 890                 895

Ser Glu Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu
            900                 905                 910

Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu
        915                 920                 925

Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ala Glu Pro Gly Lys Pro
    930                 935                 940

Val Pro Pro Ala Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu
945                 950                 955                 960

Gln Gly Lys Val Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys
                965                 970                 975

Ala Val Ala Pro Thr Lys Lys Pro Gln Ser Lys Lys Ser Glu Leu Pro
            980                 985                 990

Glu Thr Gly Gly Glu Glu Ser Thr Asn Lys Gly Met Leu Phe Gly Gly
        995                 1000                1005

Leu Phe Ser Ile Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn
    1010                1015                1020
```

His Lys Ala
1025

(2) INFORMATION FOR SEQ ID NO:5255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:

Gly Glu Lys Cys Met Phe Leu Ala Trp Asn Glu Ile Arg Arg Asn Lys
1 5 10 15

Leu Lys Phe Gly Leu Ile Ile Gly Val Leu Thr Met Ile Ser Tyr Leu
20 25 30

Leu Phe Leu Leu Ser Gly Leu Ala Asn Gly Leu Ile Asn Met Asn Lys
35 40 45

Glu Gly Ile Asp Lys Trp Gln Ala Asp Ala Ile Val Leu Asn Lys Asp
50 55 60

Ala Asn Gln Thr Val Gln Gln Ser Val Phe Asn Lys Lys Asp Ile Glu
65 70 75 80

Asn Lys Tyr Lys Lys Gln Ala Thr Leu Lys Gln Thr Gly Glu Ile Val
85 90 95

Ser Asn Gly His Gln Lys Asp Asn Val Leu Val Phe Gly Val Glu Lys
100 105 110

Ser Ser Phe Leu Val Pro Ser Leu Ile Glu Gly His Lys Ala Thr Lys
115 120 125

Asp Asn Glu Val Leu Ala Asp Glu Thr Leu Lys Asn Lys Gly Leu Lys
130 135 140

Leu Gly Asp Thr Leu Ser Leu Ser Xaa Xaa Arg
145 150 155

Claims

1. Computer readable medium having recorded thereon a nucleotide sequence of the Staphylococcus aureus genome as depicted in SEQ ID NOS:1-5,191, a representative fragment thereof or a nucleotide sequence at least 95 % identical to a nucleotide sequence depicted in SEQ ID NOS:1-5,191.

2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a degenerate variant thereof.

3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.

5. A computer-based system for identifying fragments of the *Staphylococcus aureus* genome of commercial importance comprising the following elements:

(a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS: 1-5,191;
(b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
(c) retrieval means for obtaining said homologous sequence(s) of step (b).

6. A method for identifying commercially important nucleic acid fragments of the *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS: 1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.

7. A method for identifying an expression modulating fragment of *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.

8. A protein-encoding nucleic acid fragment of the Staphylococcus aureus genome,
wherein said fragment comprises the nucleotide sequence of any one of the fragments of SEQ ID NOS: 1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence, or a degenerate variant of any of the aforementioned sequences.

9. The nucleic acid fragment of claim 8 which is DNA.

10. The nucleic acid fragment of claim 8 which is RNA.

11. A vector comprising a fragment of claim 8.

12. A fragment of the Staphylococcus aureus genome, wherein said fragment modulates the expression of an operably liked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.

13. A vector comprising a fragment of claim 12.

14. A organism which has been altered to contain any one of the fragments of the Staphylococcus aureus genome of claim 8.

15. A method for producing a polypeptide in a host cell comprising the steps of:

(a) incubating an organism of claim 14 under conditions where said fragment is expressed to produce said protein, and
(b) isolating said protein.

16. An organism which has been altered to contain any one of the fragments of the Staphylococcus aureus genome

of claim 12.

17. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecul a nucleic acid molecule consisting of the nucleotide sequenc from about 30 to 300 bases 5' to any ne of the fragments of the Staphylococcus aur us genome depicted in Seq ID Nos:1-5,191 and Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.

18. A nucleic acid molecule being a homolog of any of the fragments of the Staphylococcus aureus genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:

(a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS: 1-5,191 and Tables 2 and 3, including fragments thereof;
(b) identifying members of said library which contain sequences that hybridize to said target sequence;
(c) isolating the nucleic acid molecules from said members identified in step (b).

19. A DNA molecule being a homolog of any one of the fragments of the Staphylococcus aureus genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:

(a) isolating mRNA, DNA, or cDNA produced from an organism;
(b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Staphylococcus aureus* genome to prime said amplification;
(c) isolating said amplified sequences produced in step (b).

20. A polypeptide encoded by a fragment of claim 8.

21. An antibody which selectively binds to any one of the polypeptides of claim 20.

22. A kit for analyzing samples for the presence of polynucleotides derived from Staphylococcus aureus, comprising at least one polynucleotide containing a nucleotide sequence of any one of the fragments SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical thereto or a degenerate variant of any of the aforementioned sequences, that will hybridize to a staphylococcus aureus polynucleotide under stringent hybridization conditions, and a suitable container.

23. A Staphylococcus aureus polypeptide comprising an amino acid sequence identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:5,192 to 5,255 or comprising an amino acid sequence having at least 95% identity to such a sequence.

24. A Staphylococcus aureus polypeptide antigen comprising at least one epitope derived from a Staphylococcus aureus polypeptide selected from the group consisting of SEQ ID NOS:5,192 to 5,255.

25. A polypeptide comprising at least one epitope encoded by a Staphylococcus aureus amino acid sequence selected from the group consisting of the epitopic sequences listed in Table 4.

26. The polypeptide of claim 24 or 26, wherein said polypeptide is fixed to a solid phase.

27. A diagnostic kit for detecting Staphylococcus aureus infection comprising

(a) an isolated polypeptide antigen of claim 24, and
(b) means for detecting the binding of an antibody contained in a biological fluid to said antigen.

28. A vaccine composition comprising a polypeptide of claim 24 present in a pharmaceutically acceptable carrier.

29. A method of vaccinating an individual against Staphylococcus aureus infection comprising, administering to an individual the vaccine composition of claim 28.

Figure 1

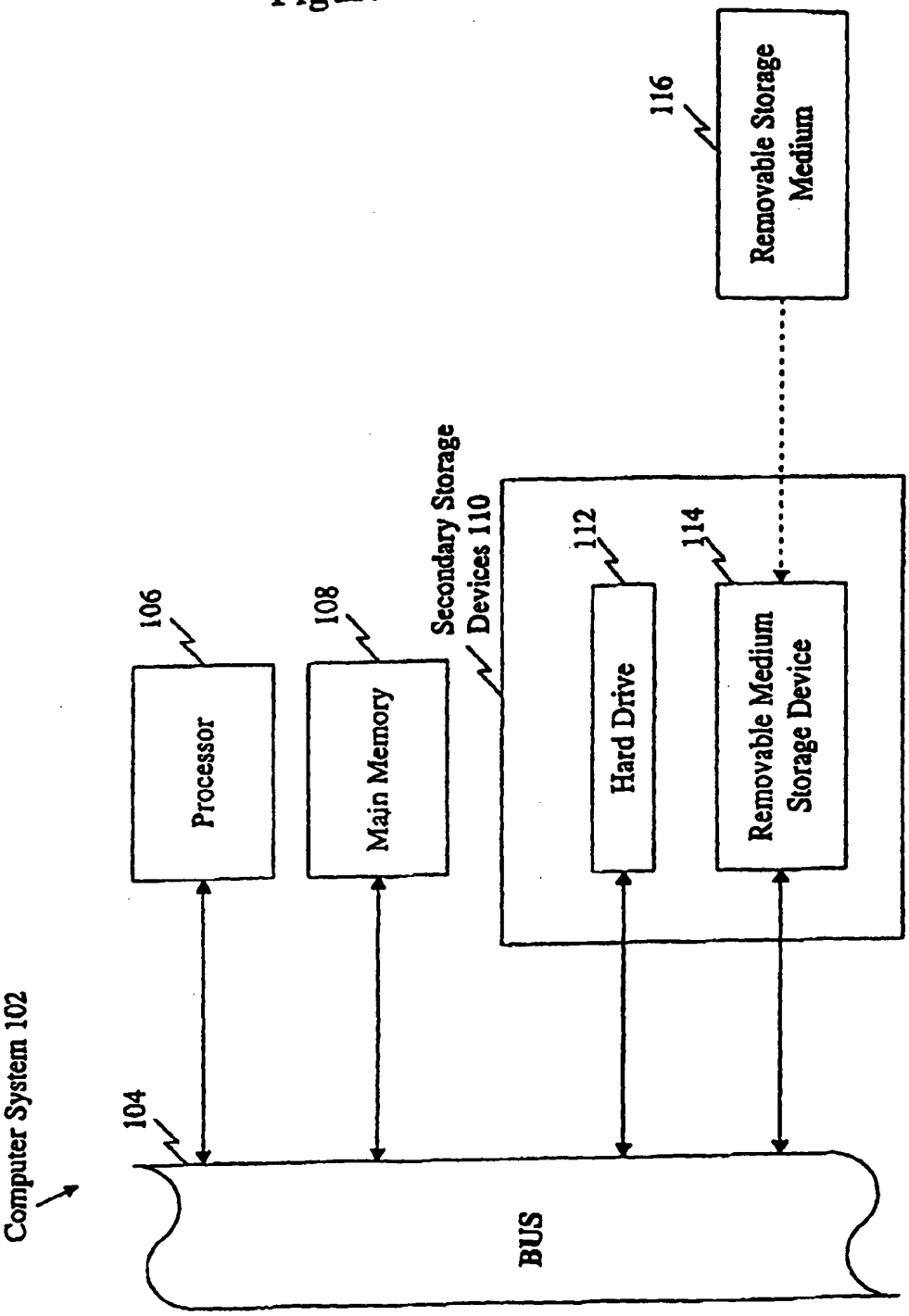
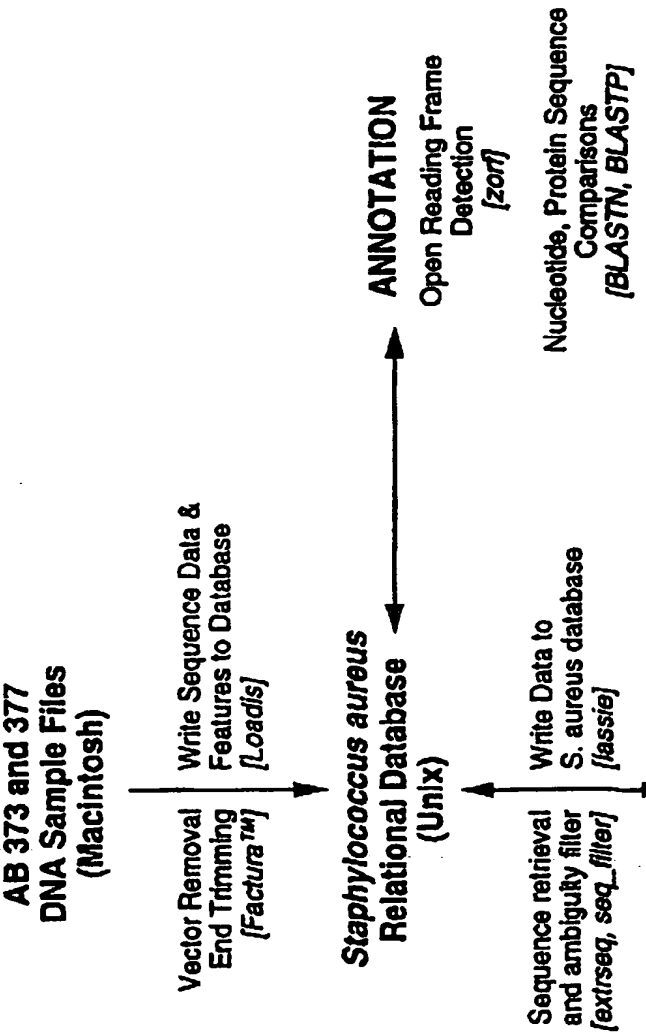

116
Removable Storage Medium
Secondary Storage Devices 110
112
Hard Drive
114
Removable Medium Storage Device
106
Processor
108
Main Memory
Computer System 102
104
BUS

Figure 2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End Trimming
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Features to Database
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Detection
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